BLAST ® » blastp suite » RID-S5699NNH014

BLAST Results

Job title: P_LRG1_DLLLPQPDLR

RID S5699NNH014 (Expires on 08-04 11:31 am)

Query ID	lcl|Query_278477	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	10	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Leucine-rich alpha-2-glycoprotein 1 [Homo sapiens]	35.4	35.4	100%	0.17	100%	AAH34389.1
leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]	35.4	35.4	100%	0.17	100%	NP_443204.1
leucine-rich alpha-2-glycoprotein 1 [synthetic construct]	35.4	35.4	100%	0.17	100%	ADQ31727.1
unnamed protein product [Homo sapiens]	35.4	35.4	100%	0.17	100%	BAG64800.1
leucine-rich alpha-2-glycoprotein isoform X2 [Papio anubis]	31.6	31.6	100%	4.0	90%	XP_009191475.2
Leucine-rich alpha-2-glycoprotein [Macaca mulatta]	31.6	31.6	100%	4.0	90%	EHH29497.1
glycosyltransferase family 2 protein [Paracoccus sediminis]	31.2	31.2	100%	5.6	90%	WP_089389101.1
DNA polymerase III, beta subunit [Aquisalimonas asiatica]	29.5	29.5	90%	23	89%	SEP00564.1
unnamed protein product [Tetraodon nigroviridis]	29.5	29.5	90%	23	89%	CAG13939.1
protein of unknown function DUF1212 [Penicillium griseofulvum]	29.1	29.1	80%	32	100%	KXG53419.1
hypothetical protein [Microbacterium sp. Leaf151]	29.1	29.1	80%	32	100%	WP_055957168.1
hypothetical protein A2051_13765 [Desulfovibrionales bacterium GWA2_65_9]	29.1	29.1	90%	32	89%	OGR34546.1
hypothetical protein [Desulfovibrio mexicanus]	29.1	29.1	90%	32	89%	WP_089274376.1
ROK family transcriptional regulator [Variovorax sp. HW608]	29.1	29.1	80%	32	100%	WP_088956439.1
protein NOV-like protein [Camelus ferus]	29.1	29.1	80%	32	100%	EPY79685.1
Protein NOV like protein [Myotis brandtii]	29.1	29.1	80%	32	100%	EPQ19998.1
Protein NOV like protein [Pteropus alecto]	29.1	29.1	80%	32	100%	ELK08583.1
hypothetical protein PANDA_019777 [Ailuropoda melanoleuca]	29.1	29.1	80%	32	100%	EFB22686.1
protein NOV homolog precursor [Bos taurus]	29.1	29.1	80%	32	100%	NP_001095852.1
Protein NOV-like protein [Bos mutus]	29.1	29.1	80%	32	100%	ELR55310.1
polyprenyl synthetase family protein [Thalassobaculum salexigens]	29.1	29.1	80%	32	100%	WP_028792582.1
aldo/keto reductase [Haloterrigena salina]	29.1	29.1	80%	32	100%	WP_049914531.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
aldo/keto reductase [Haloterrigena turkmenica]	29.1	29.1	80%	32	100%	WP_012943215.1
aldo/keto reductase [Natronococcus amylolyticus]	29.1	29.1	80%	32	100%	WP_005559589.1
Protein NOV like protein [Myotis davidii]	29.1	29.1	80%	32	100%	ELK26193.1
aldo/keto reductase [Haloterrigena salina JCM 13891]	29.1	29.1	80%	32	100%	ELZ17323.1
transferase [Xanthomonas gardneri]	29.1	29.1	90%	32	89%	WP_074057735.1
transferase [Xanthomonas sp. Leaf148]	29.1	29.1	90%	32	89%	WP_055844703.1
transferase [Xanthomonas sp. Leaf131]	29.1	29.1	90%	32	89%	WP_055820636.1
transferase [Xanthomonas pisi]	29.1	29.1	90%	32	89%	WP_046964631.1
transferase [Xanthomonas gardneri]	29.1	29.1	90%	32	89%	WP_043908566.1
transferase [Xanthomonas vesicatoria]	29.1	29.1	90%	32	89%	WP_039420827.1
transferase [Xanthomonas hortorum]	29.1	29.1	90%	32	89%	WP_023903611.1
hypothetical protein [Xanthomonas vesicatoria]	29.1	29.1	90%	32	89%	WP_005996689.1
hypothetical protein [Allokutzneria albata]	29.1	29.1	90%	32	89%	WP_030432363.1
hypothetical protein XGA_1972 [Xanthomonas gardneri ATCC 19865]	29.1	29.1	90%	32	89%	EGD19366.1
NOV [Cervus elaphus hippelaphus]	29.1	29.1	80%	33	100%	OWK04260.1
tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE [Perlucidibaca piscinae]	29.1	29.1	90%	33	89%	WP_051144618.1
conserved hypothetical protein [Leishmania infantum JPCM5]	28.6	28.6	80%	45	100%	CAM70779.1
hypothetical protein, conserved [Leishmania donovani]	28.6	28.6	80%	45	100%	CBZ36765.1
conserved hypothetical protein [Leishmania major strain Friedlin]	28.6	28.6	80%	45	100%	CAJ08491.1
ribonuclease E [Kushneria aurantia]	28.6	28.6	80%	45	100%	WP_019951630.1
hypothetical protein VITISV_035270 [Vitis vinifera]	28.6	28.6	80%	45	100%	CAN78697.1
adenylosuccinate synthase [candidate division Kazan bacterium RIFCSPHIGHO2_01_FULL_49_10]	28.6	28.6	100%	45	80%	OGB75287.1
hypothetical protein [Arthrobacter sp. Leaf141]	28.6	28.6	100%	46	80%	WP_056598102.1
hypothetical protein [Arthrobacter sp. ZBG10]	28.6	28.6	100%	46	80%	WP_050684507.1
FAD5-like desaturase [Klebsormidium nitens]	28.6	28.6	90%	46	89%	GAQ93176.1
hypothetical protein EAG_10490 [Camponotus floridanus]	28.6	28.6	100%	46	80%	EFN67953.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Tyrosine recombinase XerD [Thermoanaerobacterales bacterium 50_218]	28.6	28.6	100%	46	80%	KUK32512.1
heme ABC exporter ATP-binding protein CcmA [Halothermothrix orenii]	28.6	28.6	80%	46	100%	WP_083762893.1
hypothetical protein ACU18_05425 [Arthrobacter sp. ZBG10]	28.6	28.6	100%	46	80%	KNH19646.1
heme exporter protein CcmA [Halothermothrix orenii H 168]	28.6	28.6	80%	46	100%	ACL69137.1
peptide ABC transporter permease [Agrobacterium vitis]	28.2	28.2	100%	64	82%	WP_071585029.1
peptide ABC transporter permease [Agrobacterium vitis]	28.2	28.2	100%	64	82%	WP_071205451.1
ABC transporter ATP-binding protein [Pseudomonas massiliensis]	28.2	28.2	100%	64	82%	WP_040263219.1
exosortase A [Sulfuricella sp. T08]	28.2	28.2	90%	64	89%	WP_059417975.1
tripartite tricarboxylate transporter substrate binding protein [Comamonas testosteroni]	28.2	28.2	100%	65	80%	WP_087081624.1
putative exported protein [Comamonas testosteroni]	28.2	28.2	100%	65	80%	GAW74681.1
hypothetical protein [Idiomarina sediminum]	28.2	28.2	90%	65	89%	WP_026861401.1
hypothetical protein A0O28_0061840 [Trichoderma guizhouense]	27.8	27.8	90%	91	89%	OPB46063.1
hypothetical protein SELMODRAFT_50132 [Selaginella moellendorffii]	27.8	27.8	90%	91	89%	EFJ20143.1
hypothetical protein SELMODRAFT_40134 [Selaginella moellendorffii]	27.8	27.8	90%	91	89%	EFJ14268.1
hypothetical protein VOLCADRAFT_98525 [Volvox carteri f. nagariensis]	27.8	27.8	90%	91	89%	EFJ41472.1
radical SAM protein [Frankia sp. CcI156]	27.8	27.8	90%	91	90%	WP_083718654.1
radical SAM protein [Frankia sp. CgIM4]	27.8	27.8	90%	91	90%	WP_083282385.1
radical SAM protein [Frankia sp. BR]	27.8	27.8	90%	91	90%	WP_083970037.1
MULTISPECIES: Fe-S oxidoreductase [Frankia]	27.8	27.8	90%	91	90%	WP_023841622.1
MULTISPECIES: radical SAM protein [Frankia]	27.8	27.8	90%	91	90%	WP_011436239.1
Radical SAM superfamily enzyme YgiQ, UPF0313 family [Micromonospora inyonensis]	27.8	27.8	90%	91	90%	SCL19795.1
B12-binding domain-containing radical SAM protein [Frankia sp. EAN1pec]	27.8	27.8	90%	91	90%	WP_020460198.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein PAMH19_5480 [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	CEI20477.1
hypothetical protein P38_3120 [Pseudomonas aeruginosa MH38]	27.8	27.8	100%	91	90%	CDH71369.1
hypothetical protein PAMH27_3150 [Pseudomonas aeruginosa MH27]	27.8	27.8	100%	91	90%	CDH77543.1
hypothetical protein GPECTOR_4g925 [Gonium pectorale]	27.8	27.8	90%	91	89%	KXZ54853.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_088170936.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_086239525.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_086340123.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_086257547.1
hypothetical protein BKN49_08415 [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	ORE47038.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_083567954.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_079200703.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_079200266.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_074202698.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_073666564.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_073658673.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_073657560.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_073655164.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_073654679.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_073648613.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_073646864.1
hypothetical protein AM469_002157 [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	OKO35205.1
MULTISPECIES: hypothetical protein [Pseudomonas]	27.8	27.8	100%	91	90%	WP_070609364.1
MULTISPECIES: hypothetical protein [Pseudomonas]	27.8	27.8	100%	91	90%	WP_070654121.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_070345083.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_070342308.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_070342031.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_070340501.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_070336254.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_070335531.1
hypothetical protein [Pseudomonas aeruginosa]	27.8	27.8	100%	91	90%	WP_070334440.1

Alignments

Leucine-rich alpha-2-glycoprotein 1 [Homo sapiens]
Sequence ID: **AAH34389.1** Length: 347 Number of Matches: 1

See 6 more title(s)
Range 1: 230 to 239

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DLLLPQPDLR  10
           DLLLPQPDLR
Sbjct  230  DLLLPQPDLR  239
```

leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]
Sequence ID: **NP_443204.1** Length: 347 Number of Matches: 1

See 3 more title(s)
Range 1: 230 to 239

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DLLLPQPDLR  10
           DLLLPQPDLR
Sbjct  230  DLLLPQPDLR  239
```

leucine-rich alpha-2-glycoprotein 1, partial [synthetic construct]

Sequence ID: **ADQ31727.1** Length: 347 Number of Matches: 1
Range 1: 230 to 239

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DLLLPQPDLR  10
            DLLLPQPDLR
Sbjct  230  DLLLPQPDLR  239
```

unnamed protein product [Homo sapiens]

Sequence ID: **BAG64800.1** Length: 330 Number of Matches: 1
Range 1: 213 to 222

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DLLLPQPDLR  10
            DLLLPQPDLR
Sbjct  213  DLLLPQPDLR  222
```

leucine-rich alpha-2-glycoprotein isoform X2 [Papio anubis]

Sequence ID: **XP_009191475.2** Length: 373 Number of Matches: 1
Range 1: 256 to 265

Score	Expect	Method	Identities	Positives	Gaps	Frame
31.6 bits(67)	4.0()		9/10(90%)	9/10(90%)	0/10(0%)	

Features:

```
Query  1    DLLLPQPDLR  10
            DLL PQPDLR
Sbjct  256  DLLVPQPDLR  265
```

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BLAST Results

Job title: P_LRG1_VAAGAFQGLR

RID S569HUB7014 (Expires on 08-04 11:32 am)

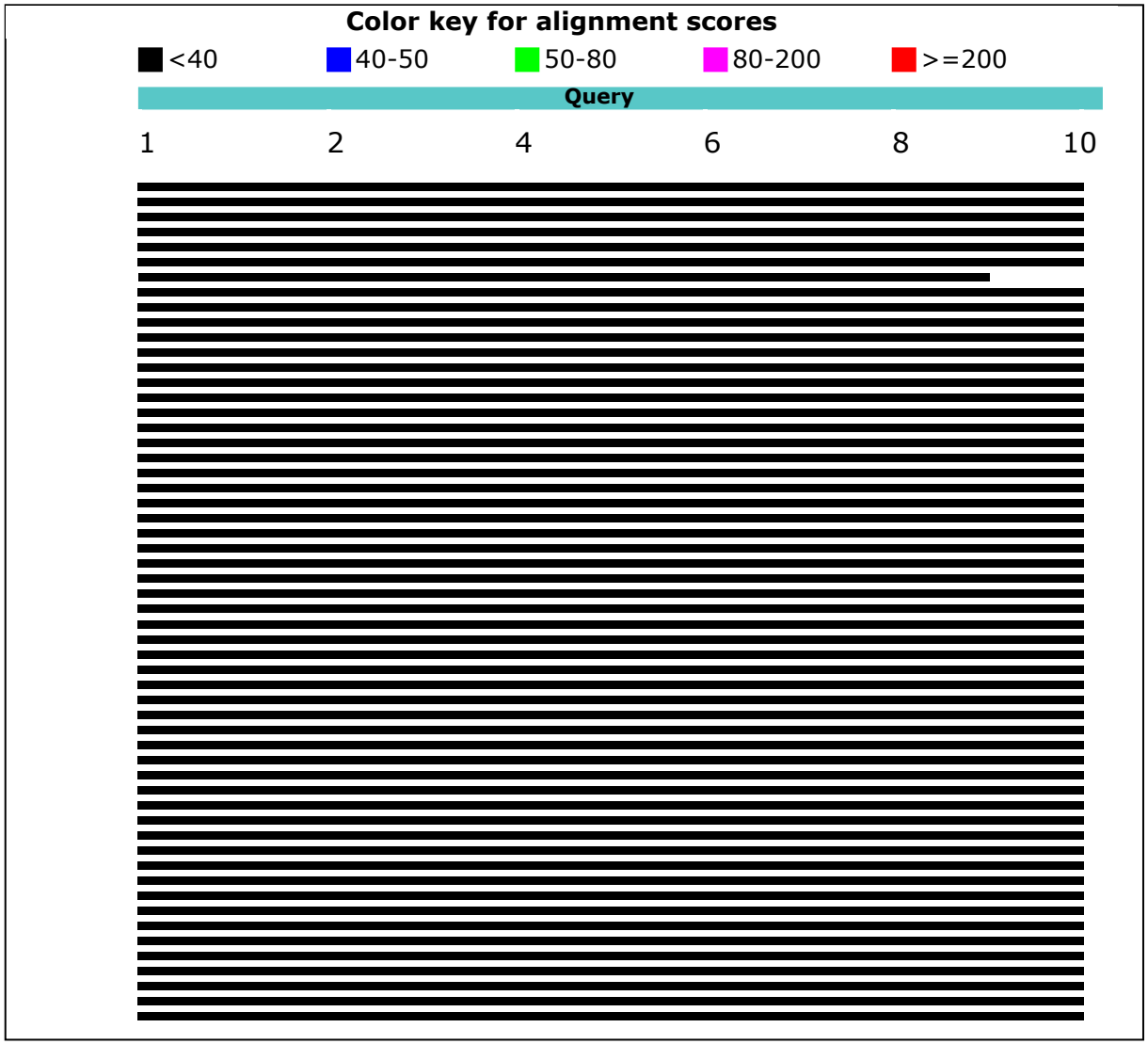
Query ID lcl|Query_282014
Description None
Molecule type amino acid
Query Length 10

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 105 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
leucine-rich alpha-2-glycoprotein isoform X2 [Papio anubis]	32.5	32.5	100%	2.0	100%	XP_009191475.2
Leucine-rich alpha-2-glycoprotein 1 [Homo sapiens]	32.5	32.5	100%	2.0	100%	AAH34389.1
leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]	32.5	32.5	100%	2.0	100%	NP_443204.1
Leucine-rich alpha-2-glycoprotein [Macaca mulatta]	32.5	32.5	100%	2.0	100%	EHH29497.1
leucine-rich alpha-2-glycoprotein 1 [synthetic construct]	32.5	32.5	100%	2.0	100%	ADQ31727.1
unnamed protein product [Homo sapiens]	32.5	32.5	100%	2.0	100%	BAG64800.1
Leucine-rich alpha-2-glycoprotein [Pteropus alecto]	29.1	29.1	90%	32	100%	ELK19414.1
hypothetical protein [Thauera sp. 28]	28.6	28.6	100%	45	90%	WP_002928448.1
hypothetical protein A6R68_23109 [Neotoma lepida]	28.2	28.2	100%	65	90%	OBS82891.1
Leucine-rich alpha-2-glycoprotein [Heterocephalus glaber]	28.2	28.2	100%	65	90%	EHB14608.1
TIGR02099 family protein [Burkholderia stabilis]	26.9	26.9	100%	183	90%	BAX59838.1
TIGR02099 family protein [Burkholderia cepacia]	26.9	26.9	100%	183	90%	WP_069272446.1
DUF3971 domain-containing protein [Burkholderia sp. AU16741]	26.9	26.9	100%	183	90%	WP_089466727.1
MULTISPECIES: DUF3971 domain-containing protein [Burkholderia]	26.9	26.9	100%	183	90%	WP_072436274.1
MULTISPECIES: hypothetical protein [Burkholderia]	26.9	26.9	100%	183	90%	WP_069616696.1
TIGR02099 family protein [Burkholderia metallica]	26.9	26.9	100%	183	90%	WP_069255832.1
hypothetical protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_069229333.1
TIGR02099 family protein [Burkholderia diffusa]	26.9	26.9	100%	183	90%	WP_069225158.1
TIGR02099 family protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_063548173.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060339354.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060346698.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060273707.1
DUF3971 domain-containing protein [Burkholderia diffusa]	26.9	26.9	100%	183	90%	WP_060321146.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060297833.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060176280.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060135969.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060127470.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060261463.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060109353.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_060021452.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059797855.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059952225.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059870095.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059977577.1
DUF3971 domain-containing protein [Burkholderia cepacia]	26.9	26.9	100%	183	90%	WP_059904050.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059943889.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059808349.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059848560.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059768419.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
DUF3971 domain-containing protein [Burkholderia cepacia]	26.9	26.9	100%	183	90%	WP_059664342.1
DUF3971 domain-containing protein [Burkholderia cepacia]	26.9	26.9	100%	183	90%	WP_059731168.1
DUF3971 domain-containing protein [Burkholderia diffusa]	26.9	26.9	100%	183	90%	WP_059511025.1
DUF3971 domain-containing protein [Burkholderia cepacia]	26.9	26.9	100%	183	90%	WP_059528973.1
DUF3971 domain-containing protein [Burkholderia sp. MSMB0856]	26.9	26.9	100%	183	90%	WP_059820474.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059506959.1
DUF3971 domain-containing protein [Burkholderia diffusa]	26.9	26.9	100%	183	90%	WP_059538304.1
DUF3971 domain-containing protein [Burkholderia sp. FL-7-2-10-S1-D7]	26.9	26.9	100%	183	90%	WP_059681260.1
DUF3971 domain-containing protein [Burkholderia sp. LA-2-3-30-S1-D2]	26.9	26.9	100%	183	90%	WP_059608293.1
DUF3971 domain-containing protein [Burkholderia diffusa]	26.9	26.9	100%	183	90%	WP_059595898.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059546828.1
DUF3971 domain-containing protein [Burkholderia diffusa]	26.9	26.9	100%	183	90%	WP_059465447.1
MULTISPECIES: DUF3971 domain-containing protein [Burkholderia cepacia complex]	26.9	26.9	100%	183	90%	WP_059535401.1
DUF3971 domain-containing protein [Burkholderia territorii]	26.9	26.9	100%	183	90%	WP_059451320.1
DUF3971 domain-containing protein [Burkholderia sp. RF4-BP95]	26.9	26.9	100%	183	90%	WP_059689048.1
DUF3971 domain-containing protein [Burkholderia sp. RF2-non_BP3]	26.9	26.9	100%	183	90%	WP_059700677.1
DUF3971 domain-containing protein [Burkholderia pyrrocinia]	26.9	26.9	100%	183	90%	WP_034182787.1
L-lactate permease [Actinomadura flavalba]	26.9	26.9	100%	184	80%	WP_018656717.1
leucine-rich repeat and transmembrane domain-containing protein 1 [Alligator mississippiensis]	26.9	26.9	90%	184	89%	KYO29788.1
polyketide synthase 12 [Micromonospora eburnea]	26.5	48.4	100%	259	67%	SCL59855.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Phormidium sp. HE10JO]	26.5	26.5	100%	259	80%	WP_087707966.1
hypothetical protein XELAEV_18008960mg [Xenopus laevis]	26.5	26.5	100%	260	80%	OCT96745.1
Slit2-a protein [Xenopus laevis]	26.5	26.5	100%	260	80%	AAI70476.1
slit guidance ligand 2 S homeolog precursor [Xenopus laevis]	26.5	26.5	100%	260	80%	NP_001081137.1
hypothetical protein XELAEV_18005166mg [Xenopus laevis]	26.5	26.5	100%	260	80%	OCT99388.1
phage tail tape measure protein [Pseudomonas syringae]	26.5	26.5	90%	260	89%	WP_025389027.1
ATPase AAA [Thermodesulfobacterium thermophilum]	26.5	26.5	90%	261	89%	WP_022854997.1
ATPase AAA-2 domain protein [Thermodesulfobacterium commune]	26.5	26.5	90%	261	89%	KUK38665.1
ATPase [Thermodesulfobacterium commune]	26.5	26.5	90%	261	89%	WP_038060013.1
ATPase [Thermodesulfobacterium hveragerdense]	26.5	26.5	90%	261	89%	WP_028841821.1
hypothetical protein GUITHDRAFT_81857 [Guillardia theta CCMP2712]	26.5	92.5	90%	261	89%	EKX33000.1
hypothetical protein XENTR_v900005371mg, partial [Xenopus tropicalis]	26.5	26.5	100%	262	80%	OCA48024.1
ATPase AAA-2 domain protein [Thermodesulfobacterium sp. 37_54]	26.5	26.5	90%	262	89%	KUJ98276.1
predicted protein [Ostreococcus lucimarinus CCE9901]	26.5	26.5	90%	263	89%	ABO98460.1
MULTISPECIES: type 1 fimbrial protein [Enterobacteriaceae]	26.5	26.5	90%	264	89%	WP_032689875.1
hypothetical protein [Sulfitobacter sp. HI0054]	26.5	26.5	90%	264	89%	WP_082852033.1
cyclic beta 1-2 glucan synthetase [Omnitrophica bacterium GWA2_50_21]	26.1	26.1	80%	368	100%	OGW68609.1
hypothetical protein BGP01_05910 [Paludibacter sp. 47-17]	26.1	26.1	100%	369	80%	OJX88866.1
hypothetical protein [Photobacterium galatheae]	26.1	26.1	90%	369	89%	WP_036749788.1
hypothetical protein CAEBREN_13830 [Caenorhabditis brenneri]	26.1	26.1	80%	369	100%	EGT57967.1
GGDEF-domain containing protein [Deinococcus apachensis]	26.1	26.1	80%	369	100%	WP_019585993.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
glucosamine-6-phosphate deaminase [Solitalea canadensis]	26.1	26.1	90%	370	89%	WP_014682273.1
hypothetical protein OCBIM_22020010mg [Octopus bimaculoides]	26.1	26.1	80%	370	100%	KOF85629.1
hypothetical protein [Halocynthiibacter namhaensis]	26.1	26.1	90%	370	89%	WP_039019101.1
methyl-accepting chemotaxis protein [Pseudomonas stutzeri]	26.1	26.1	80%	370	100%	WP_003285421.1
hypothetical protein [Bacillus massiliogorillae]	26.1	26.1	90%	370	89%	WP_042347184.1
D-inositol-3-phosphate glycosyltransferase [actinobacterium LLX17]	26.1	26.1	100%	371	80%	WP_081692479.1
hypothetical protein [Mycoplasma columbinum]	26.1	26.1	80%	371	100%	WP_006608379.1
poly-gamma-glutamate synthase PgsB/CapB [Idiomarina maritima]	26.1	26.1	100%	371	80%	SFR44665.1
MULTISPECIES: hypothetical protein [Bacillus]	26.1	26.1	80%	371	100%	WP_035420618.1
hypothetical protein JSE7799_01685 [Jannaschia seosinensis]	26.1	26.1	90%	373	89%	CUH38966.1
hypothetical protein BWK79_06370 [Beggiatoa sp. IS2]	26.1	26.1	80%	373	100%	OQW94335.1
hypothetical protein [Jannaschia seosinensis]	26.1	26.1	90%	374	89%	WP_055663217.1
hypothetical protein [Yonghaparkia sp. Soil809]	26.1	26.1	90%	374	89%	WP_055857331.1
hypothetical protein [Yonghaparkia sp. Root332]	26.1	26.1	90%	374	89%	WP_055896814.1
hypothetical protein [Mesorhizobium sp. F7]	26.1	26.1	90%	374	89%	WP_052225080.1
hypothetical protein Celaphus_00006747 [Cervus elaphus hippelaphus]	26.1	26.1	90%	377	89%	OWK10955.1
hypothetical protein SINV_15320 [Solenopsis invicta]	25.7	25.7	90%	523	89%	EFZ15099.1
conserved unknown protein [Ectocarpus siliculosus]	25.7	25.7	90%	524	89%	CBJ30169.1
phage tail tape measure protein [Pseudomonas amygdali pv. lachrymans str. M301315]	25.7	25.7	90%	524	89%	EGH85963.1
Leucine-rich repeat-containing protein 15 [Lonchura striata domestica]	25.7	46.7	90%	524	89%	OWK62222.1

Alignments

leucine-rich alpha-2-glycoprotein isoform X2 [Papio anubis]

Sequence ID: **XP_009191475.2** Length: 373 Number of Matches: 1

Range 1: 277 to 286

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.5 bits(69)	2.0()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    VAAGAFQGLR  10
           VAAGAFQGLR
Sbjct  277  VAAGAFQGLR  286
```

Leucine-rich alpha-2-glycoprotein 1 [Homo sapiens]

Sequence ID: **AAH34389.1** Length: 347 Number of Matches: 1

See 6 more title(s)

Range 1: 251 to 260

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.5 bits(69)	2.0()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    VAAGAFQGLR  10
           VAAGAFQGLR
Sbjct  251  VAAGAFQGLR  260
```

leucine-rich alpha-2-glycoprotein precursor [Homo sapiens]

Sequence ID: **NP_443204.1** Length: 347 Number of Matches: 1

See 3 more title(s)

Range 1: 251 to 260

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.5 bits(69)	2.0()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    VAAGAFQGLR  10
           VAAGAFQGLR
Sbjct  251  VAAGAFQGLR  260
```

Leucine-rich alpha-2-glycoprotein [Macaca mulatta]

Sequence ID: **EHH29497.1** Length: 347 Number of Matches: 1

See 1 more title(s)

Range 1: 251 to 260

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.5 bits(69)	2.0()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    VAAGAFQGLR  10
           VAAGAFQGLR
Sbjct  251  VAAGAFQGLR  260
```

leucine-rich alpha-2-glycoprotein 1, partial [synthetic construct]

Sequence ID: **ADQ31727.1** Length: 347 Number of Matches: 1

Range 1: 251 to 260

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.5 bits(69)	2.0()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    VAAGAFQGLR  10
           VAAGAFQGLR
Sbjct  251  VAAGAFQGLR  260
```

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BLAST ® » blastp suite » RID-S56A5UP1014

BLAST Results

Job title: P_LUM_FNALQYLR

RID S56A5UP1014 (Expires on 08-04 11:32 am)

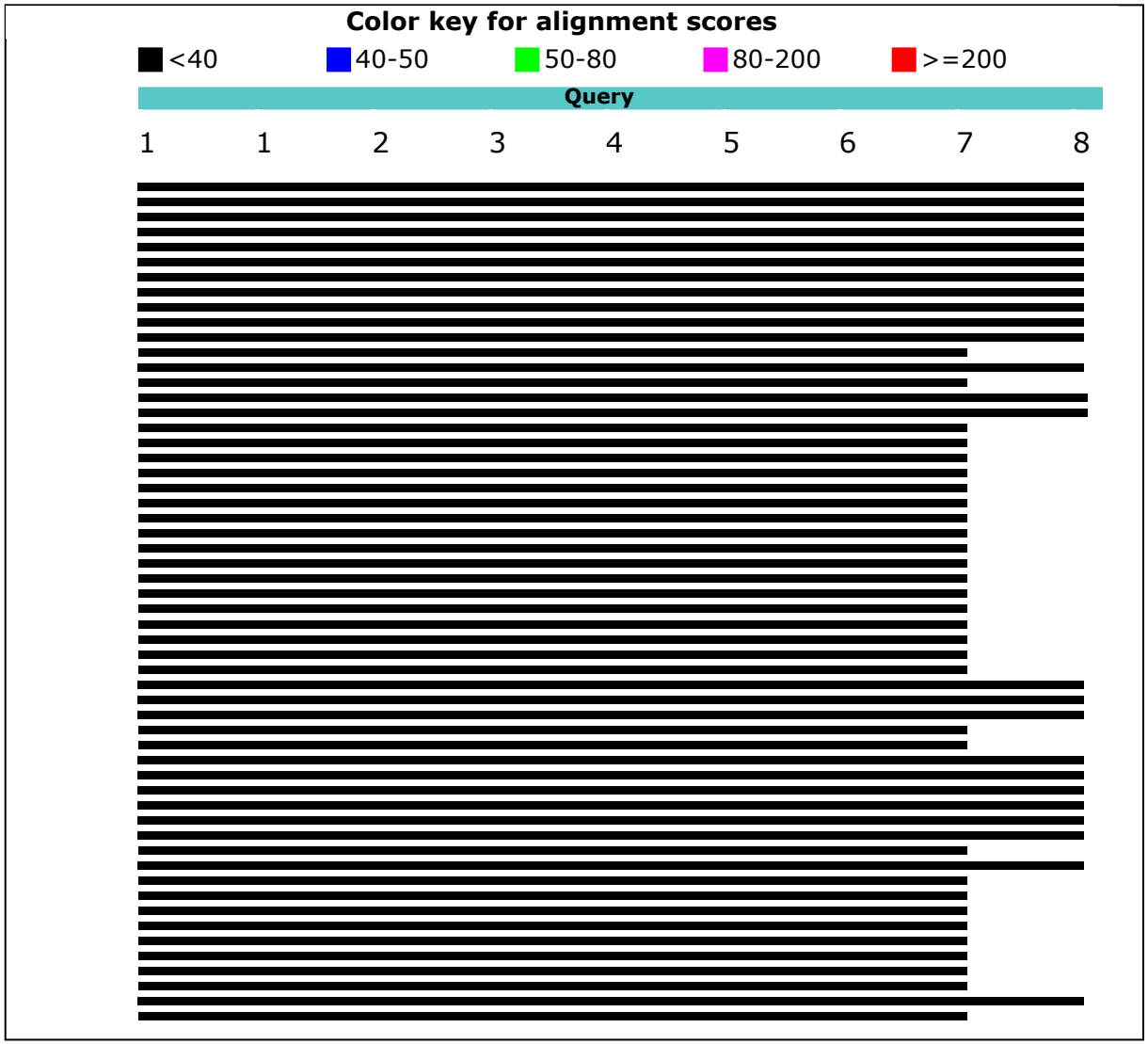
Query ID lcl|Query_197330
Description None
Molecule type amino acid
Query Length 8

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 103 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Lumican [Heterocephalus glaber]	29.9	29.9	100%	10	100%	EHB12256.1
Lumican [Fukomys damarensis]	29.9	29.9	100%	10	100%	KFO29374.1
hypothetical protein CERSUDRAFT_100757 [Gelatoporia subvermispora B]	29.9	29.9	100%	10	100%	EMD31032.1
Homo sapiens lumican [synthetic construct]	29.9	29.9	100%	10	100%	AAP36678.1
lumican precursor [Homo sapiens]	29.9	29.9	100%	10	100%	NP_002336.1
lumican [Homo sapiens]	29.9	29.9	100%	10	100%	AAA85268.1
lumican precursor [Pongo abelii]	29.9	29.9	100%	10	100%	NP_001124646.1
lumican precursor [Macaca mulatta]	29.9	29.9	100%	10	100%	NP_001253256.1
lumican variant [Homo sapiens]	29.9	29.9	100%	10	100%	BAD96897.1
hypothetical protein AMS18_06570 [Gemmatimonas sp. SG8_17]	29.9	29.9	100%	10	100%	KPJ92815.1
hypothetical protein TU85_24895 [Pseudomonas helleri]	27.4	27.4	100%	88	88%	KMN16613.1
kl-2 1-beta dynein heavy chain [Drosophila grimshawi]	26.5	26.5	87%	167	100%	ACC62144.2
hypothetical protein A1O7_07372 [Cladophialophora yegresii CBS 114405]	26.5	26.5	100%	167	88%	EXJ57028.1
E3 ubiquitin-protein ligase HUWE1-like [Tropilaelaps mercedesae]	26.5	26.5	87%	167	100%	OQR79954.1
hypothetical protein [Tateyamaria sp. ANG-S1]	26.5	47.1	100%	167	100%	WP_082029651.1
hypothetical protein RA29_20630 [Tateyamaria sp. ANG-S1]	26.5	47.1	100%	168	100%	KIC45449.1
hypothetical protein SISSUDRAFT_1058496 [Sistotremastrum suecicum HHB10207 ss-3]	26.5	26.5	87%	168	100%	KZT42404.1
hypothetical protein SISNIDRAFT_484879 [Sistotremastrum niveocremeum HHB9708]	26.5	26.5	87%	168	100%	KZS93912.1
tetratricopeptide repeat domain protein [Microscilla marina]	26.5	26.5	87%	168	100%	WP_002696972.1
hypothetical protein [Geminicoccus roseus]	26.5	26.5	87%	168	100%	WP_084506409.1
hypothetical protein [Rickettsia helvetica]	26.5	26.5	87%	168	100%	WP_010422316.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein PPL_12272 [Polysphondylium pallidum PN500]	26.5	26.5	87%	168	100%	EFA77664.1
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-4 [Toxocara canis]	26.5	26.5	87%	168	100%	KHN85628.1
1-phosphatidylinositol- -bisphosphate phosphodiesterase delta-3-a [Ascaris suum]	26.5	26.5	87%	168	100%	ERG79677.1
Uncharacterized conserved protein, contains ParB-like and HNH nuclease domains [Mucilaginibacter gossypiicola]	26.5	26.5	87%	168	100%	SEO65125.1
probable alpha-glucosidase (maltase) [Fusarium mangiferae]	26.5	26.5	87%	169	100%	CVL00474.1
Uncharacterized protein LW93_5101 [Fusarium fujikuroi]	26.5	26.5	87%	169	100%	KLO87935.1
probable alpha-glucosidase (maltase) [Fusarium proliferatum ET1]	26.5	26.5	87%	169	100%	CZR40714.1
probable alpha-glucosidase (maltase) [Fusarium proliferatum]	26.5	26.5	87%	169	100%	CVL13811.1
putative alpha-glucosidase (maltase) [Fusarium fujikuroi]	26.5	26.5	87%	169	100%	KLO99167.1
probable alpha-glucosidase (maltase) [Fusarium fujikuroi IMI 58289]	26.5	26.5	87%	169	100%	CCT70913.1
hypothetical protein QG37_07161 [[Candida] auris]	26.5	26.5	87%	169	100%	KND96426.1
hypothetical protein TRIADDRAFT_58706 [Trichoplax adhaerens]	26.5	45.0	87%	169	100%	EDV22786.1
hypothetical protein [Alistipes finegoldii]	26.5	26.5	100%	169	88%	WP_055201571.1
hypothetical protein [Alistipes finegoldii]	26.5	26.5	100%	169	88%	WP_055211783.1
uncharacterized protein BN590_00843 [Alistipes sp. CAG:29]	26.5	26.5	100%	169	88%	CDD26299.1
putative Folliculin [Daphnia magna]	26.5	26.5	87%	169	100%	KZS03185.1
Loquacious [Daphnia magna]	26.5	26.5	87%	170	100%	KZS09510.1
LUM [Cervus elaphus hippelaphus]	26.5	26.5	100%	170	88%	OWK16893.1
Lumican [Bos mutus]	26.5	26.5	100%	170	88%	ELR45834.1
lumican precursor [Bos taurus]	26.5	26.5	100%	170	88%	NP_776359.1
lumican [Equus caballus]	26.5	26.5	100%	170	88%	ABC69292.1
lumican precursor [Equus caballus]	26.5	26.5	100%	170	88%	NP_001075249.1
lumican precursor [Oryctolagus cuniculus]	26.5	26.5	100%	170	88%	NP_001182609.1
permease [Papillibacter cinnamivorans]	26.5	26.5	87%	170	100%	WP_084234816.1
lumican [Camelus ferus]	26.5	26.5	100%	170	88%	EPY84072.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ribonucleotide-diphosphate reductase subunit beta [Lactobacillus hominis]	26.5	26.5	87%	170	100%	WP_008471590.1
hypothetical protein BGP03_05320 [Pseudonocardia sp. 73-21]	26.5	26.5	87%	170	100%	OJY38390.1
ribonucleotide-diphosphate reductase subunit beta [Lactobacillus kefiranofaciens]	26.5	26.5	87%	170	100%	WP_054640632.1
ribonucleotide-diphosphate reductase subunit beta [Lactobacillus kefiranofaciens]	26.5	26.5	87%	170	100%	WP_013854775.1
EamA family transporter [Methylibium sp. CF059]	26.5	26.5	87%	170	100%	WP_082000656.1
EamA family transporter [Janthinobacterium sp. S3-2]	26.5	26.5	87%	170	100%	WP_065309524.1
hypothetical protein AYK19_20675, partial [Theionarchaea archaeon DG-70-1]	26.5	26.5	87%	171	100%	KYK28700.1
amylopullulanase [Paenibacillus macquariensis]	26.5	26.5	87%	171	100%	WP_068594907.1
RecName: Full=Lumican; AltName: Full=Keratan sulfate proteoglycan lumican; Short=KSPG lumican	26.5	26.5	100%	172	88%	O46379.1
MarR family transcriptional regulator [Caloranaerobacter azorensis]	26.5	26.5	87%	173	100%	WP_073195483.1
MarR family transcriptional regulator [Caloranaerobacter ferrireducens]	26.5	26.5	87%	173	100%	WP_069649178.1
MarR family transcriptional regulator [Caloranaerobacter sp. TR13]	26.5	26.5	87%	173	100%	WP_054869859.1
MarR family transcriptional regulator [Caloranaerobacter azorensis]	26.5	26.5	87%	173	100%	WP_035162743.1
hypothetical protein [Vibrio tasmaniensis]	26.5	26.5	87%	176	100%	WP_017097586.1
hypothetical protein A2415_01150 [candidate division WWE3 bacterium RIFOXYC1_FULL_39_7]	26.5	26.5	87%	178	100%	OGC68600.1
hypothetical protein PSTG_09220 [Puccinia striiformis f. sp. tritici PST-78]	26.1	26.1	87%	237	100%	KNE97528.1
helicase-exonuclease AddAB subunit AddB [Lysinibacillus odysseyi]	26.1	26.1	87%	238	100%	WP_036155700.1
hypothetical protein AUI01_12165 [Ktedonobacter sp. 13_2_20CM_2_56_8]	26.1	26.1	87%	238	100%	OLB53225.1
hypothetical protein AUH05_06915 [Ktedonobacter sp. 13_2_20CM_53_11]	26.1	26.1	87%	238	100%	OLB42501.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein AUG82_03200 [Ktedonobacter sp. 13_1_20CM_4_53_11]	26.1	26.1	87%	238	100%	OLE06481.1
keratocan [Amazona aestiva]	26.1	26.1	100%	239	88%	KQK74050.1
peptide ABC transporter substrate-binding protein [Paenalcaligenes hominis]	26.1	26.1	87%	239	100%	WP_077734774.1
hypothetical protein [Acinetobacter bohemicus]	26.1	26.1	87%	239	100%	WP_081410413.1
hypothetical protein BAUCODRAFT_26389 [Baudoinia panamericana UAMH 10762]	26.1	26.1	87%	239	100%	EMC94213.1
hypothetical protein [Lactobacillus casei]	26.1	26.1	87%	239	100%	WP_063557666.1
hypothetical protein [Lactobacillus paracasei]	26.1	26.1	87%	239	100%	WP_016380563.1
hypothetical protein [Lactobacillus paracasei]	26.1	26.1	87%	239	100%	WP_016388543.1
MULTISPECIES: hypothetical protein [Lactobacillus casei group]	26.1	26.1	87%	239	100%	WP_016386095.1
MULTISPECIES: hypothetical protein [Lactobacillus casei group]	26.1	26.1	87%	239	100%	WP_003604095.1
hypothetical protein [Lactobacillus casei]	26.1	26.1	87%	239	100%	WP_003597446.1
Ser/Thr kinase [Leptolyngbya sp. ISBN3-Nov-94-8]	26.1	26.1	100%	239	88%	AMH40427.1
hypothetical protein LCAUW4_0149 [Lactobacillus casei UW4]	26.1	26.1	87%	239	100%	EKQ24649.1
MULTISPECIES: hypothetical protein [Hydrogenophaga]	26.1	26.1	87%	239	100%	WP_081922004.1
His Kinase A phosphoacceptor domain-containing protein 1 [Hydrogenophaga intermedia]	26.1	26.1	87%	239	100%	CDN89501.1
Hypothetical protein, putative [Bodo saltans]	26.1	26.1	87%	240	100%	CUG89908.1
FAD-binding oxidoreductase [Sulfolobus acidocaldarius]	26.1	26.1	100%	240	88%	WP_011278692.1
FAD-linked oxidase [Sulfolobus acidocaldarius SUSAZ]	26.1	26.1	100%	240	88%	AHC52037.1
cytochrome P450 family protein [Rhizoctonia solani AG-3 Rhs1AP]	26.1	26.1	100%	240	88%	EUC54997.1
sigma-70 family RNA polymerase sigma factor [Chryseobacterium sp. FH2]	26.1	26.1	87%	240	100%	WP_048509006.1
RNA polymerase sigma factor [Chryseobacterium contaminans]	26.1	26.1	87%	240	100%	WP_066694620.1
sigma-70 family RNA polymerase sigma factor [Chryseobacterium sp. 6021061333]	26.1	26.1	87%	240	100%	WP_080780065.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
sigma-70 family RNA polymerase sigma factor [Chryseobacterium kwangjuense]	26.1	26.1	87%	240	100%	WP_062648882.1
RNA polymerase sigma factor [Chryseobacterium sp. JAH]	26.1	26.1	87%	240	100%	WP_082671894.1
RNA polymerase sigma factor [Chryseobacterium sp. YR005]	26.1	26.1	87%	240	100%	WP_082002067.1
sigma-70 family RNA polymerase sigma factor [Chryseobacterium arthrosphaerae]	26.1	26.1	87%	240	100%	WP_065398742.1
hypothetical protein XELAEV_18017464mg [Xenopus laevis]	26.1	26.1	100%	240	88%	OCT88835.1
lumican precursor [Xenopus tropicalis]	26.1	26.1	100%	240	88%	NP_001011006.1
lumican L homeolog precursor [Xenopus laevis]	26.1	26.1	100%	240	88%	NP_001079803.1
hypothetical protein EHI_143590 [Entamoeba histolytica HM-1:IMSS]	26.1	26.1	87%	240	100%	EAL46972.1
hypothetical protein ENU1_068020 [Entamoeba nuttalli P19]	26.1	26.1	87%	240	100%	EKE41098.1
hypothetical protein, conserved [Entamoeba dispar SAW760]	26.1	26.1	87%	240	100%	EDR22973.1
Lumican [Lonchura striata domestica]	26.1	26.1	100%	241	88%	OWK63029.1
hypothetical protein ASPACDRAFT_45931 [Aspergillus aculeatus ATCC 16872]	26.1	26.1	87%	241	100%	OJJ97077.1
Lumican [Charadrius vociferus]	26.1	26.1	100%	241	88%	KGL91329.1

Alignments

Lumican [Heterocephalus glaber]

Sequence ID: **EHB12256.1** Length: 534 Number of Matches: 1
Range 1: 424 to 431

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	10()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FNALQYLR  8
            FNALQYLR
Sbjct  424  FNALQYLR  431
```

Lumican [Fukomys damarensis]

Sequence ID: **KFO29374.1** Length: 427 Number of Matches: 1
Range 1: 317 to 324

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	10()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FNALQYLR  8
            FNALQYLR
Sbjct  317  FNALQYLR  324
```

hypothetical protein CERSUDRAFT_100757 [Gelatoporia subvermispora B]

Sequence ID: **EMD31032.1** Length: 414 Number of Matches: 1
Range 1: 212 to 219

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	10()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FNALQYLR  8
            FNALQYLR
Sbjct  212  FNALQYLR  219
```

Homo sapiens lumican, partial [synthetic construct]

Sequence ID: **AAP36678.1** Length: 339 Number of Matches: 1

See 2 more title(s)

Range 1: 228 to 235

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	10()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FNALQYLR  8
            FNALQYLR
Sbjct  228  FNALQYLR  235
```

lumican precursor [Homo sapiens]

Sequence ID: **NP_002336.1** Length: 338 Number of Matches: 1

See 16 more title(s)

Range 1: 228 to 235

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	10()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FNALQYLR  8
            FNALQYLR
Sbjct  228  FNALQYLR  235
```

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BLAST ® » blastp suite » RID-S56AG1KC014

BLAST Results

Job title: P_LUM_NNQIDHIDEK

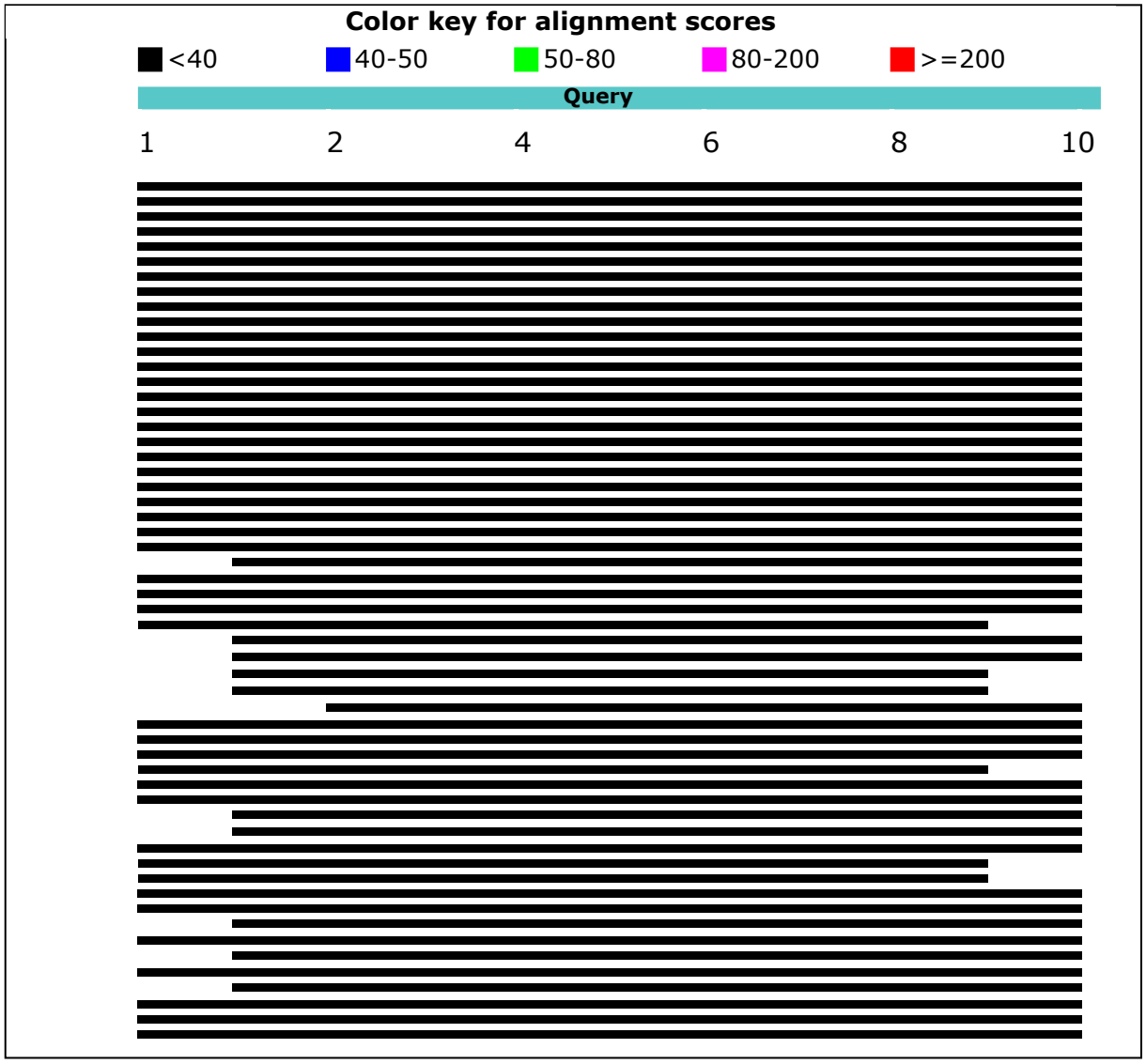
RID S56AG1KC014 (Expires on 08-04 11:32 am)

Query ID	lcl|Query_204173	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	10	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 118 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
decorin-like protein [Cricetulus griseus]	37.1	37.1	100%	0.043	100%	ERE89590.1
Lumican [Fukomys damarensis]	37.1	37.1	100%	0.043	100%	KFO29374.1
Lumican [Cricetulus griseus]	37.1	37.1	100%	0.043	100%	EGW02695.1
lumican [Equus caballus]	37.1	37.1	100%	0.043	100%	ABC69292.1
Lumican [Tupaia chinensis]	37.1	37.1	100%	0.043	100%	ELW61489.1
lumican precursor [Equus caballus]	37.1	37.1	100%	0.043	100%	NP_001075249.1
Homo sapiens lumican [synthetic construct]	37.1	37.1	100%	0.043	100%	AAP36678.1
Lumican [Pteropus alecto]	37.1	37.1	100%	0.043	100%	ELK02558.1
lumican precursor [Homo sapiens]	37.1	37.1	100%	0.043	100%	NP_002336.1
hypothetical protein A6R68_10594 [Neotoma lepida]	37.1	37.1	100%	0.043	100%	OBS58281.1
lumican [Homo sapiens]	37.1	37.1	100%	0.043	100%	AAA85268.1
lumican precursor [Pongo abelii]	37.1	37.1	100%	0.043	100%	NP_001124646.1
lumican [Mus sp.]	37.1	37.1	100%	0.043	100%	AAB35361.1
unnamed protein product [Mus musculus]	37.1	37.1	100%	0.043	100%	BAB29264.1
lumican precursor [Mus musculus]	37.1	37.1	100%	0.043	100%	NP_032550.2
lumican precursor [Rattus norvegicus]	37.1	37.1	100%	0.043	100%	NP_112312.1
lumican precursor [Macaca mulatta]	37.1	37.1	100%	0.043	100%	NP_001253256.1
lumican variant [Homo sapiens]	37.1	37.1	100%	0.043	100%	BAD96897.1
lumican [Papio anubis]	37.1	37.1	100%	0.045	100%	ABG77273.1
hypothetical protein DAPPUDRAFT_254420 [Daphnia pulex]	34.6	34.6	100%	0.34	90%	EFX72507.1
LUM [Cervus elaphus hippelaphus]	34.6	34.6	100%	0.35	90%	OWK16893.1
Lumican [Bos mutus]	34.6	34.6	100%	0.35	90%	ELR45834.1
lumican precursor [Bos taurus]	34.6	34.6	100%	0.35	90%	NP_776359.1
lumican precursor [Sus scrofa]	34.6	34.6	100%	0.35	90%	NP_001230268.1
lumican [Camelus ferus]	34.6	34.6	100%	0.35	90%	EPY84072.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Decorin [Myotis davidii]	33.7	33.7	90%	0.69	100%	ELK33569.1
Leucine-rich repeat-containing protein 9 [Schistosoma haematobium]	33.3	33.3	100%	0.98	90%	KGB38538.1
Lumican [Heterocephalus glaber]	32.5	53.4	100%	2.0	90%	EHB12256.1
lumican precursor [Oryctolagus cuniculus]	32.5	32.5	100%	2.0	90%	NP_001182609.1
Leucine-rich repeat and immunoglobulin domain-containing NOGO receptor-interacting protein 2 [Daphnia magna]	31.6	31.6	90%	3.9	89%	KZS15434.1
hybrid sensor histidine kinase/response regulator [Flavobacterium sp. ACAM 123]	31.2	31.2	90%	5.6	89%	WP_016991160.1
Lumican [Myotis brandtii]	31.2	31.2	90%	5.6	89%	EPQ12944.1
beta-N-acetylhexosaminidase [Streptococcus oralis]	30.8	30.8	80%	7.9	100%	WP_038804726.1
beta-N-acetylhexosaminidase [Streptococcus oralis]	30.8	30.8	80%	7.9	100%	WP_000251378.1
pyridoxamine 5'-phosphate oxidase family protein [Herbidospora sakaeratensis]	30.3	30.3	80%	11	100%	WP_083977652.1
ABC transporter permease [Parabacteroides sp. An277]	29.9	29.9	100%	16	75%	WP_087331820.1
sensor histidine kinase [Clostridium saccharoperbutylacetonicum]	29.5	29.5	100%	23	80%	WP_077362899.1
sensor histidine kinase [Clostridium saccharoperbutylacetonicum]	29.5	29.5	100%	23	80%	WP_015392880.1
hypothetical protein A4S09_13510 [Proteobacteria bacterium SG_bin7]	29.5	29.5	90%	23	89%	OQW48810.1
ATP-dependent helicase [Vibrio algivorus]	29.5	29.5	100%	23	69%	WP_089123056.1
transcriptional regulator [Flavobacteriaceae bacterium TMED206]	29.5	29.5	100%	23	80%	OUW63900.1
thymidine kinase [Romboutsia timonensis]	29.5	29.5	90%	23	90%	WP_071118959.1
transcriptional regulator [Prevotella sp. CAG:891]	29.5	29.5	90%	23	89%	CDE86762.1
serine/threonine protein kinase [Rhodopirellula sallentina]	29.1	29.1	100%	32	82%	WP_008682800.1
hypothetical protein A2868_00010 [Candidatus Levybacteria bacterium RIFCSPHIGHO2_01_FULL_40_15b]	29.1	29.1	90%	32	89%	OGH19172.1
hypothetical protein RFI_38255 [Reticulomyxa filosa]	29.1	29.1	90%	32	89%	ETN99226.1
AAA family ATPase, putative [Plasmodium reichenowi]	28.6	28.6	100%	45	80%	KYN99140.1
AAA family ATPase, putative [Plasmodium reichenowi]	28.6	28.6	100%	45	80%	CDO63811.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
conserved hypothetical protein [Plasmodium berghei]	28.6	28.6	90%	45	78%	CAH94599.1
TonB-dependent siderophore receptor [Pseudomonas jinjuensis]	28.6	28.6	100%	45	80%	WP_084312829.1
hypothetical protein OCBIM_22032135mg [Octopus bimaculoides]	28.6	28.6	90%	45	78%	KOF77416.1
hypothetical protein HYPBUDRAFT_9817 [Hyphopichia burtonii NRRL Y-1933]	28.6	28.6	100%	45	80%	ODV68314.1
hypothetical protein AYK19_14470 [Theionarchaea archaeon DG-70-1]	28.6	28.6	90%	46	78%	KYK33014.1
tRNA pseudouridine(55) synthase TruB [Staphylococcus agnetis]	28.6	28.6	100%	46	90%	WP_085622313.1
tRNA pseudouridine(55) synthase TruB [Staphylococcus agnetis]	28.6	28.6	100%	46	90%	WP_060550918.1
tRNA pseudouridine(55) synthase TruB [Staphylococcus agnetis]	28.6	28.6	100%	46	90%	WP_037564643.1
hypothetical protein [Mesorhizobium amorphae]	28.6	28.6	100%	46	70%	WP_006200801.1
AAA family ATPase, putative [Plasmodium falciparum 3D7]	28.2	28.2	100%	64	80%	CAD51328.1
hypothetical protein PFHG_02316 [Plasmodium falciparum HB3]	28.2	28.2	100%	64	80%	KOB60529.1
cell division protein [Plasmodium falciparum IGH-CR14]	28.2	28.2	100%	64	80%	KNG76003.1
hypothetical protein PFNF54_02040 [Plasmodium falciparum NF54]	28.2	28.2	100%	64	80%	EWC89075.1
hypothetical protein PFNF135_02083 [Plasmodium falciparum NF135/5.C10]	28.2	28.2	100%	64	80%	ETW43546.1
hypothetical protein PFMC_01929 [Plasmodium falciparum CAMP/Malaysia]	28.2	28.2	100%	64	80%	ETW62237.1
hypothetical protein PFFCH_01281 [Plasmodium falciparum FCH/4]	28.2	28.2	100%	64	80%	ETW31261.1
hypothetical protein PFBG_01989 [Plasmodium falciparum 7G8]	28.2	28.2	100%	64	80%	EUR73375.1
hypothetical protein PFAG_01916 [Plasmodium falciparum Santa Lucia]	28.2	28.2	100%	64	80%	EUT87592.1
hypothetical protein PFMALIP_01983 [Plasmodium falciparum MaliPS096_E11]	28.2	28.2	100%	64	80%	ETW49979.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein PFUGPA_05646 [Plasmodium falciparum Palo Alto/Uganda]	28.2	28.2	100%	64	80%	ETW52640.1
hypothetical protein DICPUDRAFT_96993 [Dictyostelium purpureum]	28.2	28.2	80%	64	88%	EGC38164.1
hypothetical protein PFFVO_01959 [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	28.2	28.2	100%	64	80%	ETW19103.1
hypothetical protein [Pseudomonas sp. TTU2014-080ASC]	28.2	28.2	90%	64	78%	WP_058066333.1
hypothetical protein PFTANZ_02050 [Plasmodium falciparum Tanzania (2000708)]	28.2	28.2	100%	64	80%	ETW37247.1
hypothetical protein PFAG_01981 [Plasmodium falciparum Santa Lucia]	28.2	71.5	100%	64	88%	EUT87155.1
conserved Plasmodium protein, unknown function [Plasmodium falciparum 3D7]	28.2	71.5	100%	64	88%	CAD51281.1
hypothetical protein C923_02133 [Plasmodium falciparum UGT5.1]	28.2	71.5	100%	64	88%	EWC77207.1
hypothetical protein PFUGPA_05573 [Plasmodium falciparum Palo Alto/Uganda]	28.2	71.5	100%	64	88%	ETW52567.1
hypothetical protein PFMALIP_02039 [Plasmodium falciparum MaliPS096_E11]	28.2	71.5	100%	64	88%	ETW49849.1
hypothetical protein PFNF135_02148 [Plasmodium falciparum NF135/5.C10]	28.2	71.5	100%	64	88%	ETW43233.1
hypothetical protein PFTANZ_02101 [Plasmodium falciparum Tanzania (2000708)]	28.2	71.5	100%	64	88%	ETW37169.1
hypothetical protein PFFVO_02023 [Plasmodium falciparum Vietnam Oak-Knoll (FVO)]	28.2	71.5	100%	64	88%	ETW19004.1
hypothetical protein PFDG_01175 [Plasmodium falciparum Dd2]	28.2	47.1	90%	64	88%	KOB85860.1
hypothetical protein PFFCH_01337 [Plasmodium falciparum FCH/4]	28.2	28.2	80%	64	88%	ETW31227.1
hypothetical protein A2992_05630 [Elusimicrobia bacterium RIFCSPLOWO2_01_FULL_59_12]	28.2	28.2	80%	64	88%	OGR89230.1
Uncharacterized protein APZ42_024071 [Daphnia magna]	28.2	28.2	90%	64	78%	KZS11294.1
NAD(P)/FAD-dependent oxidoreductase [Mycobacterium moriokaense]	28.2	28.2	80%	64	88%	WP_083149228.1
hypothetical protein [Streptobacillus notomytis]	28.2	28.2	80%	65	88%	WP_073507593.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Streptobacillus ratti]	28.2	28.2	80%	65	88%	WP_072593650.1
hypothetical protein [Streptobacillus notomytis]	28.2	28.2	80%	65	88%	WP_066899778.1
ArnB2: UDP-4-amino-4-deoxy-L-arabinose-oxoglutarate aminotransferase [Candidatus Peregrinibacteria bacterium GW2011_GWC2_39_14]	28.2	28.2	80%	65	88%	KKR07391.1
16S rRNA (cytosine(1402)-N(4))-methyltransferase [Virgibacillus halodenitrificans]	28.2	28.2	80%	65	88%	WP_077358286.1
LysR family transcriptional regulator [Desulfopila aestuarii]	28.2	28.2	80%	65	88%	WP_084554003.1
DNA-binding transcriptional regulator, LysR family [Desulfopila aestuarii DSM 18488]	28.2	28.2	80%	65	88%	SHO49491.1
hypothetical protein [Nitrospirae bacterium HCH-1]	28.2	28.2	100%	65	80%	WP_085053864.1
hypothetical protein MgSA37_01431 [Mucilaginibacter gotjawali]	28.2	28.2	90%	66	78%	BAU53264.1
hypothetical protein ZOSMA_38G00010 [Zostera marina]	28.2	28.2	80%	66	88%	KMZ63895.1
Leucine-rich repeat-containing protein let-4 [Trichinella patagoniensis]	27.8	27.8	90%	91	78%	KRY20036.1
Leucine-rich repeat-containing protein let-4 [Trichinella sp. T9]	27.8	27.8	90%	91	78%	KRX59510.1
Leucine-rich repeat-containing protein let-4 [Trichinella nativa]	27.8	27.8	90%	91	78%	KRZ61995.1
Leucine-rich repeat-containing protein let-4 [Trichinella sp. T6]	27.8	27.8	90%	91	78%	KRX77944.1
hypothetical protein BBBOND_0303890 [Babesia bigemina]	27.8	27.8	80%	91	88%	CDR96485.1

Alignments

decorin-like protein [Cricetulus griseus]

Sequence ID: **ERE89590.1** Length: 772 Number of Matches: 1
Range 1: 509 to 518

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.1 bits(80)	0.043()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    NNQIDHIDEK  10
           NNQIDHIDEK
Sbjct  509  NNQIDHIDEK  518
```

Lumican [Fukomys damarensis]

Sequence ID: **KFO29374.1** Length: 427 Number of Matches: 1
Range 1: 164 to 173

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.1 bits(80)	0.043()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    NNQIDHIDEK  10
           NNQIDHIDEK
Sbjct  164  NNQIDHIDEK  173
```

Lumican [Cricetulus griseus]

Sequence ID: **EGW02695.1** Length: 399 Number of Matches: 1
Range 1: 136 to 145

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.1 bits(80)	0.043()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    NNQIDHIDEK  10
           NNQIDHIDEK
Sbjct  136  NNQIDHIDEK  145
```

lumican [Equus caballus]

Sequence ID: **ABC69292.1** Length: 341 Number of Matches: 1
Range 1: 78 to 87

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.1 bits(80)	0.043()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   NNQIDHIDEK  10
           NNQIDHIDEK
Sbjct  78  NNQIDHIDEK  87
```

Lumican [Tupaia chinensis]

Sequence ID: **ELW61489.1** Length: 341 Number of Matches: 1
Range 1: 78 to 87

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.1 bits(80)	0.043()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   NNQIDHIDEK  10
           NNQIDHIDEK
Sbjct  78  NNQIDHIDEK  87
```

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BLAST Results

Job title: NCBI BlastP_MST1_CEIAGWGETK

RID S54JBMA9014 (Expires on 08-04 11:02 am)

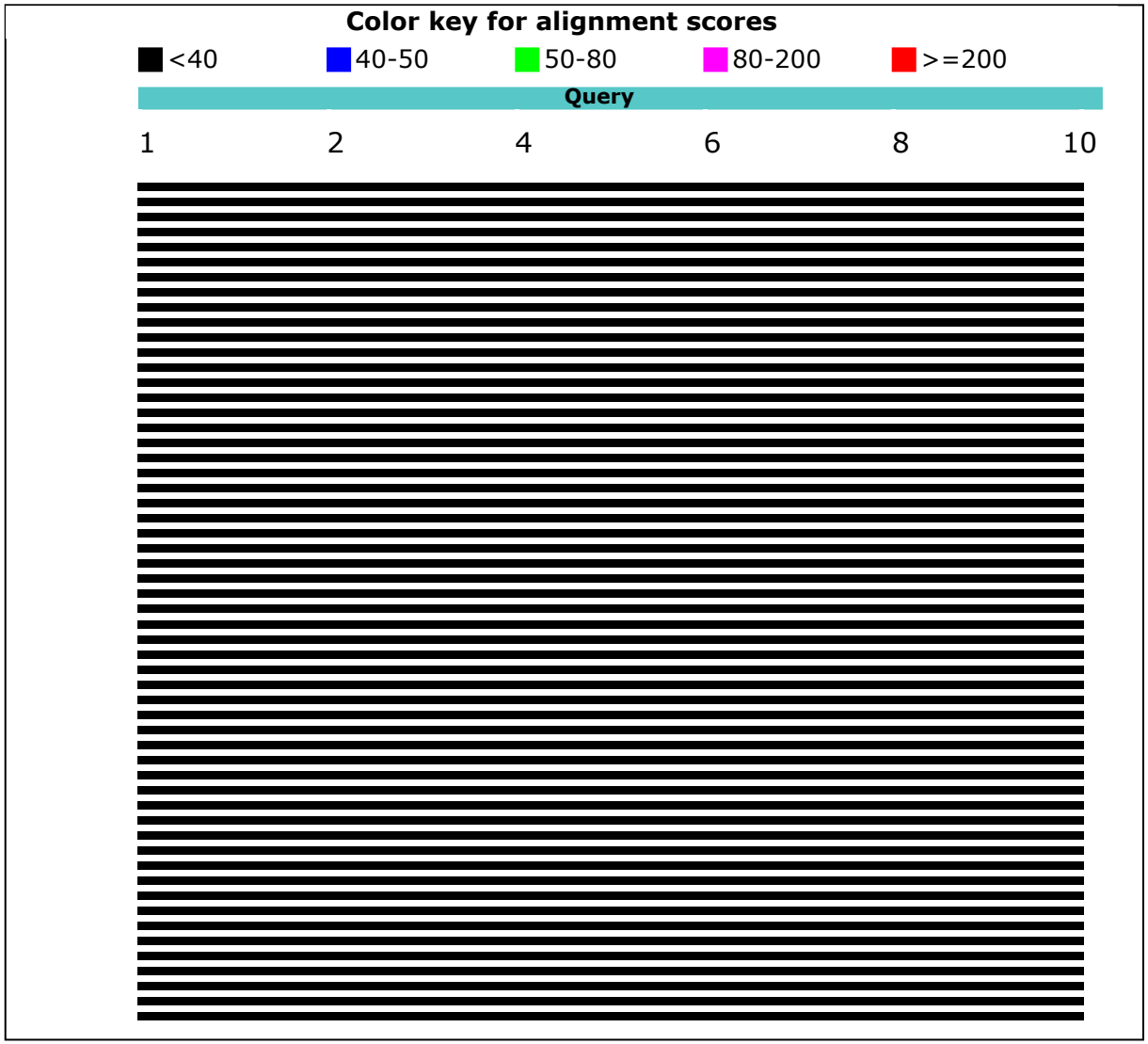
Query ID lcl|Query_218630
Description None
Molecule type amino acid
Query Length 10

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723549.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723550.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cercocebus atys]	36.7	36.7	100%	0.070	100%	XP_011889117.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cercocebus atys]	36.7	36.7	100%	0.070	100%	XP_011889118.1
PREDICTED: hepatocyte growth factor-like protein [Vicugna pacos]	36.7	36.7	100%	0.070	100%	XP_015107961.1
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723551.1
hepatocyte growth factor-like protein isoform X1 [Sus scrofa]	36.7	36.7	100%	0.070	100%	XP_020924432.1
PREDICTED: hepatocyte growth factor-like protein isoform X4 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723552.1
hepatocyte growth factor-like protein isoform X2 [Sus scrofa]	36.7	36.7	100%	0.070	100%	XP_020924433.1
PREDICTED: hepatocyte growth factor-like protein isoform X5 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723553.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bos taurus]	36.7	36.7	100%	0.070	100%	XP_005222860.1
PREDICTED: hepatocyte growth factor-like protein [Scleropages formosus]	36.7	36.7	100%	0.070	100%	XP_018593212.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Ovis aries musimon]	36.7	36.7	100%	0.070	100%	XP_011977476.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Pan troglodytes]	36.7	36.7	100%	0.070	100%	XP_016796597.1
PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein [Panthera tigris altaica]	36.7	36.7	100%	0.070	100%	XP_015395854.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chlorocebus sabaeus]	36.7	36.7	100%	0.070	100%	XP_007982444.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Homo sapiens]	36.7	36.7	100%	0.070	100%	XP_011532034.1
hepatocyte growth factor-like protein isoform X3 [Sus scrofa]	36.7	36.7	100%	0.070	100%	XP_020924434.1
hepatocyte growth factor-like protein isoform X2 [Castor canadensis]	36.7	36.7	100%	0.070	100%	XP_020029081.1
PREDICTED: hepatocyte growth factor-like protein [Camelus dromedarius]	36.7	36.7	100%	0.070	100%	XP_010976658.1
hepatocyte growth factor-like protein isoform X4 [Sus scrofa]	36.7	36.7	100%	0.070	100%	XP_020924435.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Ictalurus punctatus]	36.7	36.7	100%	0.070	100%	XP_017335875.1
PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein isoform X1 [Ovis aries]	36.7	36.7	100%	0.070	100%	XP_011955446.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Ictalurus punctatus]	36.7	36.7	100%	0.070	100%	XP_017335876.1
macrophage stimulating 1-like protein [Camelus ferus]	36.7	36.7	100%	0.070	100%	EQB77066.1
PREDICTED: hepatocyte growth factor-like protein isoform X6 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723554.1
LOW QUALITY PROTEIN: hepatocyte growth factor-like protein [Aotus nancymaae]	36.7	36.7	100%	0.070	100%	XP_012323165.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chlorocebus sabaeus]	36.7	36.7	100%	0.070	100%	XP_007982445.1
hepatocyte growth factor-like protein isoform X5 [Sus scrofa]	36.7	36.7	100%	0.070	100%	XP_013837152.2
PREDICTED: hepatocyte growth factor-like protein [Hippocampus comes]	36.7	36.7	100%	0.070	100%	XP_019712724.1
MST1 [Cervus elaphus hippelaphus]	36.7	36.7	100%	0.070	100%	OWK02388.1
LOW QUALITY PROTEIN: hepatocyte growth factor-like protein [Ictidomys tridecemlineatus]	36.7	36.7	100%	0.070	100%	XP_021583147.1
hepatocyte growth factor-like protein isoform X6 [Sus scrofa]	36.7	36.7	100%	0.070	100%	XP_003132263.2
PREDICTED: hepatocyte growth factor-like protein [Bos indicus]	36.7	36.7	100%	0.070	100%	XP_019839829.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Tursiops truncatus]	36.7	36.7	100%	0.070	100%	XP_004314855.2
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Rhinolophus sinicus]	36.7	36.7	100%	0.070	100%	XP_019579399.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Hipposideros armiger]	36.7	36.7	100%	0.070	100%	XP_019487191.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Panthera pardus]	36.7	36.7	100%	0.070	100%	XP_019272379.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Gorilla gorilla gorilla]	36.7	36.7	100%	0.070	100%	XP_004034204.2
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Capra hircus]	36.7	36.7	100%	0.070	100%	XP_017922147.1
PREDICTED: hepatocyte growth factor-like protein isoform X8 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723557.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cebus capucinus imitator]	36.7	36.7	100%	0.070	100%	XP_017359560.1
PREDICTED: hepatocyte growth factor-like protein [Macaca mulatta]	36.7	36.7	100%	0.070	100%	XP_001107946.2
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Ovis aries musimon]	36.7	36.7	100%	0.070	100%	XP_011977477.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Macaca nemestrina]	36.7	36.7	100%	0.070	100%	XP_011737656.1
PREDICTED: hepatocyte growth factor-like protein [Colobus angolensis palliatus]	36.7	36.7	100%	0.070	100%	XP_011794462.1
PREDICTED: hepatocyte growth factor-like protein [Mandrillus leucophaeus]	36.7	36.7	100%	0.070	100%	XP_011836282.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bison bison bison]	36.7	36.7	100%	0.070	100%	XP_010850155.1
PREDICTED: hepatocyte growth factor-like protein [Rhinopithecus roxellana]	36.7	36.7	100%	0.070	100%	XP_010367959.1
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chlorocebus sabaeus]	36.7	36.7	100%	0.070	100%	XP_007982448.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Callithrix jacchus]	36.7	36.7	100%	0.070	100%	XP_002758398.1
PREDICTED: hepatocyte growth factor-like protein [Lipotes vexillifer]	36.7	36.7	100%	0.070	100%	XP_007446274.1
PREDICTED: hepatocyte growth factor-like protein [Physeter catodon]	36.7	36.7	100%	0.070	100%	XP_007129906.1
PREDICTED: hepatocyte growth factor-like protein [Pantholops hodgsonii]	36.7	36.7	100%	0.070	100%	XP_005969335.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bos taurus]	36.7	36.7	100%	0.070	100%	XP_005222861.1
PREDICTED: hepatocyte growth factor-like protein [Ochotona princeps]	36.7	36.7	100%	0.070	100%	XP_004581815.1
PREDICTED: hepatocyte growth factor-like protein [Orcinus orca]	36.7	36.7	100%	0.070	100%	XP_004284002.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Felis catus]	36.7	36.7	100%	0.070	100%	XP_003982280.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Saimiri boliviensis boliviensis]	36.7	36.7	100%	0.070	100%	XP_003936704.1
hepatocyte growth factor-like protein isoform X1 [Papio anubis]	36.7	36.7	100%	0.070	100%	XP_003894463.1
PREDICTED: hepatocyte growth factor-like protein [Canis lupus familiaris]	36.7	36.7	100%	0.070	100%	XP_541884.3
PREDICTED: hepatocyte growth factor-like protein [Nomascus leucogenys]	36.7	36.7	100%	0.070	100%	XP_003257123.1
hepatocyte growth factor-like protein precursor [Homo sapiens]	36.7	36.7	100%	0.070	100%	NP_066278.3
hepatocyte growth factor-like protein isoform X1 [Castor canadensis]	36.7	36.7	100%	0.070	100%	XP_020029080.1
PREDICTED: hepatocyte growth factor-like protein isoform X9 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723558.1
PREDICTED: hepatocyte growth factor-like protein [Dasypus novemcinctus]	36.7	36.7	100%	0.070	100%	XP_012378140.1
PREDICTED: hepatocyte growth factor-like protein [Balaenoptera acutorostrata scammoni]	36.7	36.7	100%	0.070	100%	XP_007168789.1
PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein [Loxodonta africana]	36.7	36.7	100%	0.070	100%	XP_003409924.1
PREDICTED: hepatocyte growth factor-like protein [Pongo abelii]	36.7	36.7	100%	0.070	100%	XP_002813790.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Pan troglodytes]	36.7	36.7	100%	0.070	100%	XP_016796598.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Ceratotherium simum simum]	36.7	36.7	100%	0.070	100%	XP_004419765.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bison bison bison]	36.7	36.7	100%	0.070	100%	XP_010850156.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein [Marmota marmota marmota]	36.7	36.7	100%	0.070	100%	XP_015342673.1
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Ictalurus punctatus]	36.7	36.7	100%	0.070	100%	XP_017335879.1
hepatocyte growth factor-like protein isoform X1 [Odocoileus virginianus texanus]	36.7	36.7	100%	0.070	100%	XP_020771723.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Homo sapiens]	36.7	36.7	100%	0.070	100%	XP_016861949.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Pygocentrus nattereri]	36.7	36.7	100%	0.070	100%	XP_017563902.1
RecName: Full=Putative macrophage stimulating 1-like protein; AltName: Full=Brain rescue factor 1; Short=BRF-1; AltName: Full=Hepatocyte growth factor-like protein homolog; Flags: Precursor	36.7	36.7	100%	0.070	100%	Q2TV78.2
Hepatocyte growth factor-like protein [Bos mutus]	36.7	36.7	100%	0.070	100%	ELR58967.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Pygocentrus nattereri]	36.7	36.7	100%	0.070	100%	XP_017563903.1
PREDICTED: hepatocyte growth factor-like protein [Camelus bactrianus]	36.7	36.7	100%	0.070	100%	XP_010967473.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Esox lucius]	36.7	36.7	100%	0.070	100%	XP_010894385.1
PREDICTED: hepatocyte growth factor-like protein isoform X4 [Chlorocebus sabaeus]	36.7	36.7	100%	0.070	100%	XP_007982449.1
PREDICTED: hepatocyte growth factor-like protein [Clupea harengus]	36.7	36.7	100%	0.070	100%	XP_012678038.1
hepatocyte growth factor-like protein [Monopterus albus]	36.7	36.7	100%	0.070	100%	XP_020453726.1
PREDICTED: hepatocyte growth factor-like protein isoform X10 [Rhinopithecus bieti]	36.7	36.7	100%	0.070	100%	XP_017723559.1
PREDICTED: putative macrophage stimulating 1-like protein [Cynoglossus semilaevis]	36.7	36.7	100%	0.070	100%	XP_008317808.1
PREDICTED: hepatocyte growth factor-like protein [Bubalus bubalis]	36.7	36.7	100%	0.070	100%	XP_006053335.1
PREDICTED: hepatocyte growth factor-like protein [Bos mutus]	36.7	36.7	100%	0.070	100%	XP_005892185.1
TPA: hepatocyte growth factor-like protein [Bos taurus]	36.7	36.7	100%	0.070	100%	DAA16921.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hepatocyte growth factor-like protein precursor [Bos taurus]	36.7	36.7	100%	0.070	100%	NP_001069145.1
hepatocyte growth factor-like protein [Neomonachus schauinslandi]	36.7	36.7	100%	0.070	100%	XP_021542563.1
hepatocyte growth factor-like protein [Oncorhynchus mykiss]	36.7	36.7	100%	0.070	100%	XP_021465005.1
hepatocyte growth factor-like protein isoform X2 [Odocoileus virginianus texanus]	36.7	36.7	100%	0.070	100%	XP_020771724.1
LOW QUALITY PROTEIN: hepatocyte growth factor-like protein [Oncorhynchus kisutch]	36.7	36.7	100%	0.070	100%	XP_020338571.1
PREDICTED: hepatocyte growth factor-like protein [Elephantulus edwardii]	36.7	36.7	100%	0.070	100%	XP_006892963.1
PREDICTED: hepatocyte growth factor-like protein [Ailuropoda melanoleuca]	36.7	36.7	100%	0.070	100%	XP_011224940.1
hepatocyte growth factor-like protein [Carlito syrichta]	36.7	36.7	100%	0.070	100%	XP_008061363.1
PREDICTED: hepatocyte growth factor-like protein [Orycteropus afer afer]	36.7	36.7	100%	0.070	100%	XP_007953538.1
hepatocyte growth factor-like protein precursor [Macaca fascicularis]	36.7	36.7	100%	0.070	100%	NP_001306460.1

Alignments

PREDICTED: hepatocyte growth factor-like protein isoform X1 [Rhinopithecus bieti]

Sequence ID: **XP_017723549.1** Length: 799 Number of Matches: 1
Range 1: 690 to 699

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.7 bits(79)	0.070()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    CEIAGWGETK  10
           CEIAGWGETK
Sbjct  690  CEIAGWGETK  699
```

PREDICTED: hepatocyte growth factor-like protein isoform X2 [Rhinopithecus bieti]

Sequence ID: **XP_017723550.1** Length: 773 Number of Matches: 1
Range 1: 664 to 673

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.7 bits(79)	0.070()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    CEIAGWGETK  10
            CEIAGWGETK
Sbjct  664  CEIAGWGETK  673
```

PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cercocebus atys]

Sequence ID: **XP_011889117.1** Length: 773 Number of Matches: 1
Range 1: 664 to 673

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.7 bits(79)	0.070()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    CEIAGWGETK  10
            CEIAGWGETK
Sbjct  664  CEIAGWGETK  673
```

PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cercocebus atys]

Sequence ID: **XP_011889118.1** Length: 772 Number of Matches: 1
Range 1: 663 to 672

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.7 bits(79)	0.070()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    CEIAGWGETK  10
            CEIAGWGETK
Sbjct  663  CEIAGWGETK  672
```

PREDICTED: hepatocyte growth factor-like protein [Vicugna pacos]

Sequence ID: **XP_015107961.1** Length: 771 Number of Matches: 1
Range 1: 662 to 671

Score	Expect	Method	Identities	Positives	Gaps	Frame

36.7 bits(79)	0.070()	10/10(100%)	10/10(100%)	0/10(0%)

Features:

```
Query  1    CEIAGWGETK  10
            CEIAGWGETK
Sbjct  662  CEIAGWGETK  671
```

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Job title: NCBI BlastP_MST1_MVCGPSGSQLVLLK

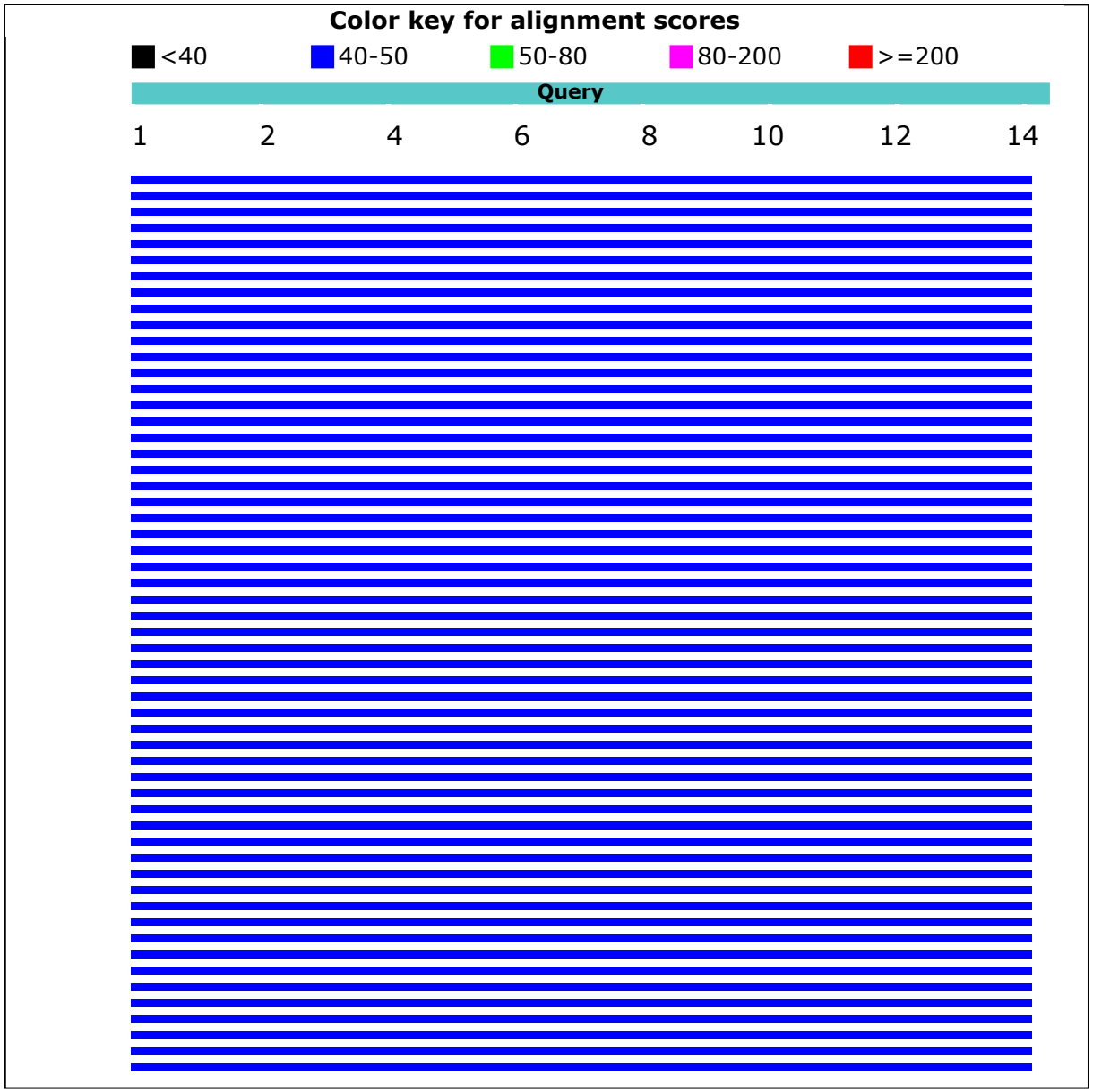
RID S54JPRJB015 (Expires on 08-04 11:02 am)

Query ID	lcl|Query_311129	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12
14

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723549.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723550.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cercocebus atys]	46.9	46.9	100%	4e-05	100%	XP_011889117.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cercocebus atys]	46.9	46.9	100%	4e-05	100%	XP_011889118.1
PREDICTED: hepatocyte growth factor-like protein [Vicugna pacos]	46.9	46.9	100%	4e-05	100%	XP_015107961.1
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723551.1
PREDICTED: hepatocyte growth factor-like protein isoform X4 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723552.1
PREDICTED: hepatocyte growth factor-like protein isoform X5 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723553.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bos taurus]	46.9	46.9	100%	4e-05	100%	XP_005222860.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Ovis aries musimon]	46.9	46.9	100%	4e-05	100%	XP_011977476.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Pan troglodytes]	46.9	46.9	100%	4e-05	100%	XP_016796597.1
PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein [Panthera tigris altaica]	46.9	46.9	100%	4e-05	100%	XP_015395854.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chlorocebus sabaeus]	46.9	46.9	100%	4e-05	100%	XP_007982444.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Homo sapiens]	46.9	46.9	100%	4e-05	100%	XP_011532034.1
PREDICTED: hepatocyte growth factor-like protein [Camelus dromedarius]	46.9	46.9	100%	4e-05	100%	XP_010976658.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Hepatocyte growth factor-like protein [Tupaia chinensis]	46.9	46.9	100%	4e-05	100%	ELV09642.1
PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein isoform X1 [Ovis aries]	46.9	46.9	100%	4e-05	100%	XP_011955446.1
macrophage stimulating 1-like protein [Camelus ferus]	46.9	46.9	100%	4e-05	100%	EQB77066.1
PREDICTED: hepatocyte growth factor-like protein isoform X7 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723555.1
PREDICTED: hepatocyte growth factor-like protein isoform X6 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723554.1
LOW QUALITY PROTEIN: hepatocyte growth factor-like protein [Aotus nancymaae]	46.9	46.9	100%	4e-05	100%	XP_012323165.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chlorocebus sabaeus]	46.9	46.9	100%	4e-05	100%	XP_007982445.1
MST1 [Cervus elaphus hippelaphus]	46.9	46.9	100%	4e-05	100%	OWK02388.1
LOW QUALITY PROTEIN: hepatocyte growth factor-like protein [Ictidomys tridecemlineatus]	46.9	46.9	100%	4e-05	100%	XP_021583147.1
PREDICTED: hepatocyte growth factor-like protein [Bos indicus]	46.9	46.9	100%	4e-05	100%	XP_019839829.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Tursiops truncatus]	46.9	46.9	100%	4e-05	100%	XP_004314855.2
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Panthera pardus]	46.9	46.9	100%	4e-05	100%	XP_019272379.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Gorilla gorilla gorilla]	46.9	46.9	100%	4e-05	100%	XP_004034204.2
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Capra hircus]	46.9	46.9	100%	4e-05	100%	XP_017922147.1
PREDICTED: hepatocyte growth factor-like protein isoform X8 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723557.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cebus capucinus imitator]	46.9	46.9	100%	4e-05	100%	XP_017359560.1
PREDICTED: hepatocyte growth factor-like protein [Macaca mulatta]	46.9	46.9	100%	4e-05	100%	XP_001107946.2
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Equus asinus]	46.9	46.9	100%	4e-05	100%	XP_014695916.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Propithecus coquereli]	46.9	46.9	100%	4e-05	100%	XP_012516185.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Ovis aries musimon]	46.9	46.9	100%	4e-05	100%	XP_011977477.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Macaca nemestrina]	46.9	46.9	100%	4e-05	100%	XP_011737656.1
PREDICTED: hepatocyte growth factor-like protein [Colobus angolensis palliatus]	46.9	46.9	100%	4e-05	100%	XP_011794462.1
PREDICTED: hepatocyte growth factor-like protein [Mandrillus leucophaeus]	46.9	46.9	100%	4e-05	100%	XP_011836282.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bison bison bison]	46.9	46.9	100%	4e-05	100%	XP_010850155.1
PREDICTED: hepatocyte growth factor-like protein [Rhinopithecus roxellana]	46.9	46.9	100%	4e-05	100%	XP_010367959.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Oryctolagus cuniculus]	46.9	46.9	100%	4e-05	100%	XP_008258874.1
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chlorocebus sabaeus]	46.9	46.9	100%	4e-05	100%	XP_007982448.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Callithrix jacchus]	46.9	46.9	100%	4e-05	100%	XP_002758398.1
PREDICTED: hepatocyte growth factor-like protein [Lipotes vexillifer]	46.9	46.9	100%	4e-05	100%	XP_007446274.1
PREDICTED: hepatocyte growth factor-like protein [Physeter catodon]	46.9	46.9	100%	4e-05	100%	XP_007129906.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Equus caballus]	46.9	46.9	100%	4e-05	100%	XP_005600716.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bos taurus]	46.9	46.9	100%	4e-05	100%	XP_005222861.1
PREDICTED: hepatocyte growth factor-like protein [Condylura cristata]	46.9	46.9	100%	4e-05	100%	XP_004676215.1
PREDICTED: hepatocyte growth factor-like protein [Orcinus orca]	46.9	46.9	100%	4e-05	100%	XP_004284002.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Felis catus]	46.9	46.9	100%	4e-05	100%	XP_003982280.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Saimiri boliviensis boliviensis]	46.9	46.9	100%	4e-05	100%	XP_003936704.1
hepatocyte growth factor-like protein isoform X1 [Papio anubis]	46.9	46.9	100%	4e-05	100%	XP_003894463.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein [Canis lupus familiaris]	46.9	46.9	100%	4e-05	100%	XP_541884.3
PREDICTED: hepatocyte growth factor-like protein [Nomascus leucogenys]	46.9	46.9	100%	4e-05	100%	XP_003257123.1
hepatocyte growth factor-like protein precursor [Homo sapiens]	46.9	46.9	100%	4e-05	100%	NP_066278.3
PREDICTED: hepatocyte growth factor-like protein isoform X9 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723558.1
PREDICTED: hepatocyte growth factor-like protein [Dasypus novemcinctus]	46.9	46.9	100%	4e-05	100%	XP_012378140.1
PREDICTED: hepatocyte growth factor-like protein [Balaenoptera acutorostrata scammoni]	46.9	46.9	100%	4e-05	100%	XP_007168789.1
PREDICTED: hepatocyte growth factor-like protein [Pongo abelii]	46.9	46.9	100%	4e-05	100%	XP_002813790.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Pan troglodytes]	46.9	46.9	100%	4e-05	100%	XP_016796598.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bison bison bison]	46.9	46.9	100%	4e-05	100%	XP_010850156.1
PREDICTED: hepatocyte growth factor-like protein [Marmota marmota marmota]	46.9	46.9	100%	4e-05	100%	XP_015342673.1
hepatocyte growth factor-like protein isoform X1 [Odocoileus virginianus texanus]	46.9	46.9	100%	4e-05	100%	XP_020771723.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Homo sapiens]	46.9	46.9	100%	4e-05	100%	XP_016861949.1
Hepatocyte growth factor-like protein [Bos mutus]	46.9	46.9	100%	4e-05	100%	ELR58967.1
PREDICTED: hepatocyte growth factor-like protein [Camelus bactrianus]	46.9	46.9	100%	4e-05	100%	XP_010967473.1
PREDICTED: hepatocyte growth factor-like protein isoform X4 [Chlorocebus sabaeus]	46.9	46.9	100%	4e-05	100%	XP_007982449.1
PREDICTED: hepatocyte growth factor-like protein isoform X10 [Rhinopithecus bieti]	46.9	46.9	100%	4e-05	100%	XP_017723559.1
PREDICTED: hepatocyte growth factor-like protein [Bubalus bubalis]	46.9	46.9	100%	4e-05	100%	XP_006053335.1
PREDICTED: hepatocyte growth factor-like protein [Bos mutus]	46.9	46.9	100%	4e-05	100%	XP_005892185.1
TPA: hepatocyte growth factor-like protein [Bos taurus]	46.9	46.9	100%	4e-05	100%	DAA16921.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hepatocyte growth factor-like protein precursor [Bos taurus]	46.9	46.9	100%	4e-05	100%	NP_001069145.1
hepatocyte growth factor-like protein [Neomonachus schauinslandi]	46.9	46.9	100%	4e-05	100%	XP_021542563.1
hepatocyte growth factor-like protein isoform X2 [Odocoileus virginianus texanus]	46.9	46.9	100%	4e-05	100%	XP_020771724.1
macrophage-stimulating protein [Homo sapiens]	46.9	46.9	100%	4e-05	100%	AAA59872.1
PREDICTED: hepatocyte growth factor-like protein [Leptonychotes weddellii]	46.9	46.9	100%	4e-05	100%	XP_006744596.1
hepatocyte growth factor-like protein [Homo sapiens]	46.9	46.9	100%	4e-05	100%	AAA50165.1
MST1 [synthetic construct]	46.9	46.9	100%	4e-05	100%	AKI71421.1
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Cercocebus atys]	46.9	46.9	100%	4e-05	100%	XP_011889119.1
PREDICTED: hepatocyte growth factor-like protein [Ailuropoda melanoleuca]	46.9	46.9	100%	4e-05	100%	XP_011224940.1
PREDICTED: hepatocyte growth factor-like protein [Galeopterus variegatus]	46.9	46.9	100%	4e-05	100%	XP_008569781.1
RecName: Full=Hepatocyte growth factor-like protein; AltName: Full=Macrophage stimulatory protein; AltName: Full=Macrophage-stimulating protein; Short=MSP; Contains: RecName: Full=Hepatocyte growth factor-like protein alpha chain; Contains: RecName: Full=Hepatocyte growth factor-like protein beta chain; Flags: Precursor	46.9	46.9	100%	4e-05	100%	P26927.2
PREDICTED: hepatocyte growth factor-like protein [Tupaia chinensis]	46.9	46.9	100%	4e-05	100%	XP_006171012.1
PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mustela putorius furo]	46.9	46.9	100%	4e-05	100%	XP_004760697.1
PREDICTED: hepatocyte growth factor-like protein [Odobenus rosmarus divergens]	46.9	46.9	100%	4e-05	100%	XP_004399304.1
hypothetical protein EGM_20500 [Macaca fascicularis]	46.9	46.9	100%	4e-05	100%	EHH62249.1
hypothetical protein EGK_11631 [Macaca mulatta]	46.9	46.9	100%	4e-05	100%	EHH16360.1
hepatocyte growth factor-like protein precursor [Macaca fascicularis]	46.9	46.9	100%	4e-05	100%	NP_001306460.1
macrophage stimulating 1 (hepatocyte growth factor-like) variant [Homo sapiens]	46.9	46.9	100%	4e-05	100%	BAD96613.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mustela putorius furo]	46.9	46.9	100%	4e-05	100%	XP_012915929.1
PREDICTED: hepatocyte growth factor-like protein [Otolemur garnettii]	46.9	46.9	100%	4e-05	100%	XP_003800642.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Gorilla gorilla gorilla]	46.9	46.9	100%	4e-05	100%	XP_018878989.1
PREDICTED: hepatocyte growth factor-like protein isoform X3 [Homo sapiens]	46.9	46.9	100%	4e-05	100%	XP_016861950.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cebus capucinus imitator]	46.9	46.9	100%	4e-05	100%	XP_017359640.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Callithrix jacchus]	46.9	46.9	100%	4e-05	100%	XP_008979888.1
PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo sapiens]	46.9	46.9	100%	4e-05	100%	XP_016861951.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Felis catus]	46.9	46.9	100%	4e-05	100%	XP_019677196.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Panthera pardus]	46.9	46.9	100%	4e-05	100%	XP_019272380.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equus asinus]	46.9	46.9	100%	4e-05	100%	XP_014695917.1
PREDICTED: hepatocyte growth factor-like protein isoform X2 [Macaca nemestrina]	46.9	46.9	100%	4e-05	100%	XP_011737657.1

Alignments

PREDICTED: hepatocyte growth factor-like protein isoform X1 [Rhinopithecus bieti]

Sequence ID: **XP_017723549.1** Length: 799 Number of Matches: 1
Range 1: 648 to 661

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	4e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MVCGPSGSQLVLLK  14
            MVCGPSGSQLVLLK
Sbjct  648  MVCGPSGSQLVLLK  661
```

PREDICTED: hepatocyte growth factor-like protein isoform X2 [Rhinopithecus bieti]

Sequence ID: **XP_017723550.1** Length: 773 Number of Matches: 1
Range 1: 622 to 635

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	4e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MVCGPSGSQLVLLK  14
            MVCGPSGSQLVLLK
Sbjct  622  MVCGPSGSQLVLLK  635
```

PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cercocebus atys]

Sequence ID: **XP_011889117.1** Length: 773 Number of Matches: 1
Range 1: 622 to 635

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	4e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MVCGPSGSQLVLLK  14
            MVCGPSGSQLVLLK
Sbjct  622  MVCGPSGSQLVLLK  635
```

PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cercocebus atys]

Sequence ID: **XP_011889118.1** Length: 772 Number of Matches: 1
Range 1: 621 to 634

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	4e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MVCGPSGSQLVLLK  14
            MVCGPSGSQLVLLK
Sbjct  621  MVCGPSGSQLVLLK  634
```

PREDICTED: hepatocyte growth factor-like protein [Vicugna pacos]

Sequence ID: **XP_015107961.1** Length: 771 Number of Matches: 1
Range 1: 620 to 633

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	4e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MVCGPSGSQLVLLK  14
           MVCGPSGSQLVLLK
Sbjct  620  MVCGPSGSQLVLLK  633
```

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BLAST Results

Job title: P_NAGLU_GDTVDLAK

RID S56AYS2D015 (Expires on 08-04 11:32 am)

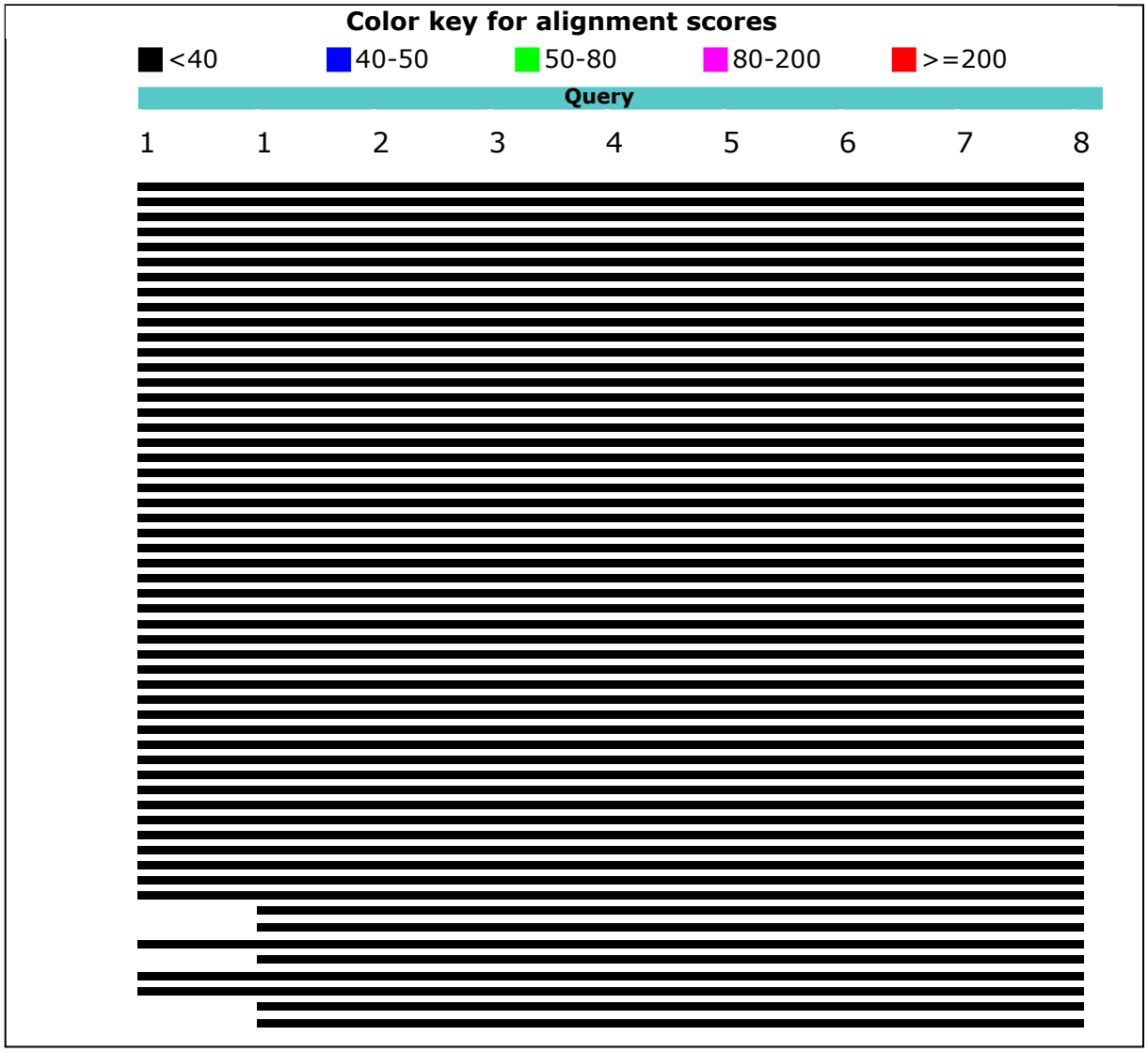
Query ID lcl|Query_214334
Description None
Molecule type amino acid
Query Length 8

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
uncharacterized protein Dvir_GJ22612 [Drosophila virilis]	26.9	26.9	100%	118	100%	EDW68296.2
v-type proton ATPase subunit a isoform 1 [Camelus ferus]	26.9	26.9	100%	118	100%	EPY88172.1
alpha-N-acetylglucosaminidase [Homo sapiens]	26.9	26.9	100%	119	100%	AAC50512.1
alpha-N-acetylglucosaminidase precursor [Homo sapiens]	26.9	26.9	100%	119	100%	NP_000254.2
Alpha-N-acetylglucosaminidase [Pteropus alecto]	26.9	26.9	100%	119	100%	ELK01481.1
hypothetical protein [Xanthomonas campestris]	26.9	26.9	100%	119	100%	WP_047698466.1
hypothetical protein [Xanthomonas vasicola]	26.9	26.9	100%	119	100%	WP_010370246.1
hypothetical protein [Xanthomonas vasicola]	26.9	26.9	100%	119	100%	WP_039441986.1
hypothetical protein [Xanthomonas campestris]	26.9	26.9	100%	119	100%	WP_010381212.1
hypothetical protein [Xanthomonas phaseoli]	26.9	26.9	100%	119	100%	WP_017167402.1
Chain A, Crystal Structure Of The Human N-acetyl-alpha-glucosaminidase	26.9	26.9	100%	119	100%	4XWH_A
Alpha-N-acetylglucosaminidase [Macaca mulatta]	26.9	26.9	100%	119	100%	EHH24987.1
NAGLU [Cervus elaphus hippelaphus]	26.9	26.9	100%	119	100%	OWK14559.1
hypothetical protein OC00_09065 [Xanthomonas vasicola]	26.9	26.9	100%	119	100%	KGT84308.1
Alpha-N-acetylglucosaminidase [Macaca fascicularis]	26.9	26.9	100%	119	100%	EHH58149.1
alpha-N-acetylglucosaminidase [Homo sapiens]	26.9	26.9	100%	119	100%	AAB36605.1
hypothetical protein PANDA_011160 [Ailuropoda melanoleuca]	26.9	26.9	100%	119	100%	EFB20123.1
bifunctional amino acid aminotransferase/2-hydroxyacid dehydrogenase [Lactobacillus sp. HMSC072E07]	26.9	26.9	100%	120	100%	WP_070552045.1
MULTISPECIES: lactate dehydrogenase [Lactobacillus]	26.9	26.9	100%	120	100%	WP_049171576.1
MULTISPECIES: lactate dehydrogenase [Lactobacillus]	26.9	26.9	100%	120	100%	WP_047678494.1
lactate dehydrogenase [Lactobacillus rhamnosus]	26.9	26.9	100%	120	100%	WP_033571651.1
MULTISPECIES: metal-dependent hydrolase [Aureimonas]	26.9	26.9	100%	121	100%	WP_056691635.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
L-ascorbate metabolism protein UlaG, beta-lactamase superfamily [Psychrobacillus psychrodurans]	26.9	26.9	100%	121	100%	SFN01412.1
L-ascorbate metabolism protein UlaG, beta-lactamase superfamily [Psychrobacillus psychrotolerans]	26.9	26.9	100%	121	100%	SFQ46060.1
L-ascorbate metabolism protein UlaG, beta-lactamase superfamily [Paenisporosarcina quisquiliarum]	26.9	26.9	100%	121	100%	SEM56028.1
L-ascorbate metabolism protein UlaG, beta-lactamase superfamily [Psychrobacillus sp. OK028]	26.9	26.9	100%	121	100%	SDM74433.1
metal-dependent hydrolase [Bacillus humi]	26.9	26.9	100%	121	100%	WP_057999435.1
metal-dependent hydrolase [Bacillus massilioanorexius]	26.9	26.9	100%	121	100%	WP_019242903.1
metal-dependent hydrolase [Bacillus sp. Marseille-P2384]	26.9	26.9	100%	121	100%	WP_075982557.1
metal-dependent hydrolase [Bacillus soli]	26.9	26.9	100%	121	100%	WP_066063512.1
lactate dehydrogenase [Lactobacillus rhamnosus]	26.9	26.9	100%	122	100%	KMO63943.1
uncharacterized protein Dana_GF16328 [Drosophila ananassae]	24.8	24.8	100%	682	88%	EDV43813.1
hypothetical protein [Xanthomonas alfalfae]	24.8	24.8	100%	682	88%	WP_071118240.1
hypothetical protein [Xanthomonas euvesicatoria]	24.8	24.8	100%	682	88%	WP_031420962.1
hypothetical protein [Xanthomonas cannabis]	24.8	24.8	100%	682	88%	WP_039404436.1
replication endonuclease [Pseudoalteromonas piscicida]	24.8	24.8	100%	683	88%	WP_088532302.1
MULTISPECIES: MCE family protein [Nocardioides]	24.8	24.8	100%	685	88%	WP_056892544.1
LLM class flavin-dependent oxidoreductase [Candidatus Phaeomarinobacter ectocarpi]	24.8	24.8	100%	687	88%	WP_043948716.1
hypothetical protein [Xanthomonas euvesicatoria]	24.8	24.8	100%	688	88%	WP_049756414.1
hypothetical protein [Xanthomonas euvesicatoria]	24.8	24.8	100%	689	88%	WP_011346323.1
hypothetical protein XEUV259_06090 [Xanthomonas euvesicatoria]	24.8	24.8	100%	689	88%	KLB47154.1
hypothetical protein XEUV683_20575 [Xanthomonas euvesicatoria]	24.8	24.8	100%	689	88%	KLA49863.1
metal-dependent hydrolase [Planomicrobium glaciei]	24.8	24.8	100%	692	88%	WP_074510633.1
metal-dependent hydrolase [Planomicrobium glaciei]	24.8	24.8	100%	692	88%	WP_053165445.1
metal-dependent hydrolase [Planomicrobium glaciei]	24.8	24.8	100%	692	88%	WP_036804800.1
metal-dependent hydrolase [Bacillus sp. 1NLA3E]	24.8	24.8	100%	692	88%	WP_015595238.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Yersinia frederiksenii]	24.8	24.8	100%	697	88%	WP_050152003.1
Uncharacterised protein [Yersinia frederiksenii]	24.8	24.8	100%	698	88%	CNL35574.1
hypothetical protein B456_004G190500 [Gossypium raimondii]	24.4	24.4	87%	964	100%	KJB25421.1
hypothetical protein B456_004G190500 [Gossypium raimondii]	24.4	24.4	87%	964	100%	KJB25422.1
hypothetical protein A5875_003419 [Enterococcus sp. 3H8_DIV0648]	24.4	24.4	100%	964	88%	OTO14262.1
Putative vacuolar sorting-associated protein 13B [Gossypium arboreum]	24.4	24.4	87%	964	100%	KHG21599.1
cell surface protein [Citrobacter freundii]	24.4	24.4	100%	965	88%	WP_071692511.1
cell surface protein [Citrobacter sp. BIDMC108]	24.4	24.4	100%	965	88%	WP_048227397.1
clathrin heavy chain [Rhizopus microsporus]	24.4	24.4	87%	965	100%	ORE16025.1
clathrin heavy chain [Rhizopus microsporus var. microsporus]	24.4	24.4	87%	965	100%	ORE08339.1
Putative Clathrin heavy chain [Rhizopus microsporus]	24.4	24.4	87%	965	100%	CEI86035.1
Putative Clathrin heavy chain [Rhizopus microsporus]	24.4	24.4	87%	965	100%	CEG67963.1
Putative Clathrin heavy chain [Rhizopus microsporus]	24.4	24.4	87%	965	100%	CEI86036.1
Putative Clathrin heavy chain [Rhizopus microsporus]	24.4	24.4	87%	965	100%	CEG67964.1
Alpha-L-fucosidase [Paraliobacillus sp. PM-2]	24.4	24.4	100%	965	88%	CQR48094.1
VWA domain-containing protein [Clostridium butyricum]	24.4	24.4	87%	966	100%	WP_058141804.1
VWA domain-containing protein [Clostridium butyricum]	24.4	24.4	87%	966	100%	WP_035778057.1
VWA domain-containing protein [Clostridium butyricum]	24.4	24.4	87%	966	100%	WP_043664567.1
VWA domain-containing protein [Clostridium butyricum]	24.4	24.4	87%	966	100%	WP_003414692.1
von Willebrand factor type A domain protein [Clostridium butyricum DKU-01]	24.4	24.4	87%	966	100%	EMU53876.1
Domain of unknown function DUF2435 [Xanthophyllomyces dendrorhous]	24.4	24.4	100%	967	88%	CDZ96162.1
Putative Clathrin heavy chain [Rhizopus microsporus]	24.4	24.4	87%	967	100%	CEI91260.1
ATPase [Sulfitobacter sp. EE-36]	24.4	24.4	87%	967	100%	WP_005849076.1
ATPase [Sulfitobacter pontiacus]	24.4	24.4	87%	967	100%	WP_074636843.1
ATPase [Sulfitobacter pontiacus]	24.4	24.4	87%	967	100%	WP_064216640.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ATPase [Sulfitobacter sp. CB2047]	24.4	24.4	87%	967	100%	WP_037942075.1
ATPase [Sulfitobacter pontiacus]	24.4	24.4	87%	967	100%	WP_037966621.1
hypothetical protein TRIVIDRAFT_223604 [Trichoderma virens Gv29-8]	24.4	24.4	87%	967	100%	EHK20913.1
hypothetical protein [Kutzneria sp. 744]	24.4	24.4	87%	967	100%	WP_052395856.1
DNA topoisomerase I [Rhodobacterales bacterium 52_120_T64]	24.4	24.4	87%	968	100%	OUS08898.1
predicted protein [Thalassiosira pseudonana CCMP1335]	24.4	24.4	100%	968	88%	EED87456.1
hypothetical protein A3F33_02640 [Candidatus Woykebacteria bacterium RIFCSPHIGHO2_12_FULL_43_10]	24.4	24.4	100%	968	88%	OGY30078.1
histidine kinase [Pseudomonas mendocina]	24.4	24.4	87%	968	100%	WP_041977405.1
sensor histidine kinase [Pseudomonas mendocina]	24.4	24.4	87%	968	100%	WP_013714377.1
alginate lyase [Bacillus sp. J13]	24.4	24.4	87%	968	100%	WP_028407274.1
heparinase II/III family protein [Paenibacillus lactis]	24.4	24.4	87%	968	100%	WP_007130102.1
hypothetical protein A2V97_02985 [Candidatus Woesebacteria bacterium RBG_16_42_24]	24.4	24.4	100%	968	88%	OGM15721.1
hypothetical protein [[Clostridium] hungatei]	24.4	24.4	100%	968	88%	WP_080063930.1
alginate lyase [Paenibacillus sp. LC231]	24.4	24.4	87%	968	100%	WP_071218561.1
Heparinase II/III-like protein [Paenibacillus sp. cl141a]	24.4	24.4	87%	968	100%	SEK46947.1
heparinase II/III family protein [Paenibacillus sp. Y412MC10]	24.4	24.4	87%	968	100%	WP_015735895.1
alginate lyase [Paenibacillus sp. FSL H8-457]	24.4	24.4	87%	968	100%	WP_036660886.1
heparinase II/III-like protein [Paenibacillus sp. HGF5]	24.4	24.4	87%	968	100%	WP_009590951.1
family 65 glycosyl hydrolase [Trichococcus palustris]	24.4	24.4	100%	969	88%	WP_087033680.1
hypothetical protein A2985_01095 [Candidatus Woesebacteria bacterium RIFCSPLOWO2_01_FULL_43_11]	24.4	24.4	100%	969	88%	OGM68394.1
maltose phosphorylase [Lactobacillus oryzae]	24.4	24.4	100%	969	88%	WP_034526033.1
tyrosine protein kinase [Noviherbaspirillum denitrificans]	24.4	24.4	87%	969	100%	WP_088710302.1
Alpha-N-acetylglucosaminidase [Cricetulus griseus]	24.4	24.4	100%	969	88%	EGW08045.1
Naglu [Mus musculus]	24.4	24.4	100%	969	88%	AAB88084.1
alpha-N-acetylglucosaminidase precursor [Mus musculus]	24.4	24.4	100%	969	88%	NP_038820.2
rCG33377, isoform CRA_b [Rattus norvegicus]	24.4	24.4	100%	969	88%	EDM06079.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Xanthomonas fragariae]	24.4	24.4	100%	969	88%	WP_088061343.1
hypothetical protein [Rhodococcus sp. 29MFTsu3.1]	24.4	24.4	87%	969	100%	WP_019664606.1
Alpha-N-acetylglucosaminidase [Tupaia chinensis]	24.4	24.4	100%	969	88%	ELW54978.1

Alignments

uncharacterized protein Dvir_GJ22612 [Drosophila virilis]
Sequence ID: **EDW68296.2** Length: 1381 Number of Matches: 1
Range 1: 907 to 914

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.9 bits(56)	118()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    GDTVDLAK  8
            GDTVDLAK
Sbjct  907  GDTVDLAK  914
```

v-type proton ATPase subunit a isoform 1 [Camelus ferus]
Sequence ID: **EPY88172.1** Length: 1327 Number of Matches: 1
Range 1: 1305 to 1312

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.9 bits(56)	118()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1     GDTVDLAK  8
             GDTVDLAK
Sbjct  1305  GDTVDLAK  1312
```

alpha-N-acetylglucosaminidase [Homo sapiens]
Sequence ID: **AAC50512.1** Length: 743 Number of Matches: 1

See 5 more title(s)
Range 1: 721 to 728

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.9 bits(56)	119()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    GDTVDLAK  8
            GDTVDLAK
Sbjct  721  GDTVDLAK  728
```

alpha-N-acetylglucosaminidase precursor [Homo sapiens]

Sequence ID: **NP_000254.2** Length: 743 Number of Matches: 1

See 2 more title(s)

Range 1: 721 to 728

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.9 bits(56)	119()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    GDTVDLAK  8
            GDTVDLAK
Sbjct  721  GDTVDLAK  728
```

Alpha-N-acetylglucosaminidase [Pteropus alecto]

Sequence ID: **ELK01481.1** Length: 740 Number of Matches: 1

Range 1: 718 to 725

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.9 bits(56)	119()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    GDTVDLAK  8
            GDTVDLAK
Sbjct  718  GDTVDLAK  725
```

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BLAST ® » blastp suite » RID-S56BP4JU014

BLAST Results

Job title: P_NAGLU_YGVSHPDAGAAWR

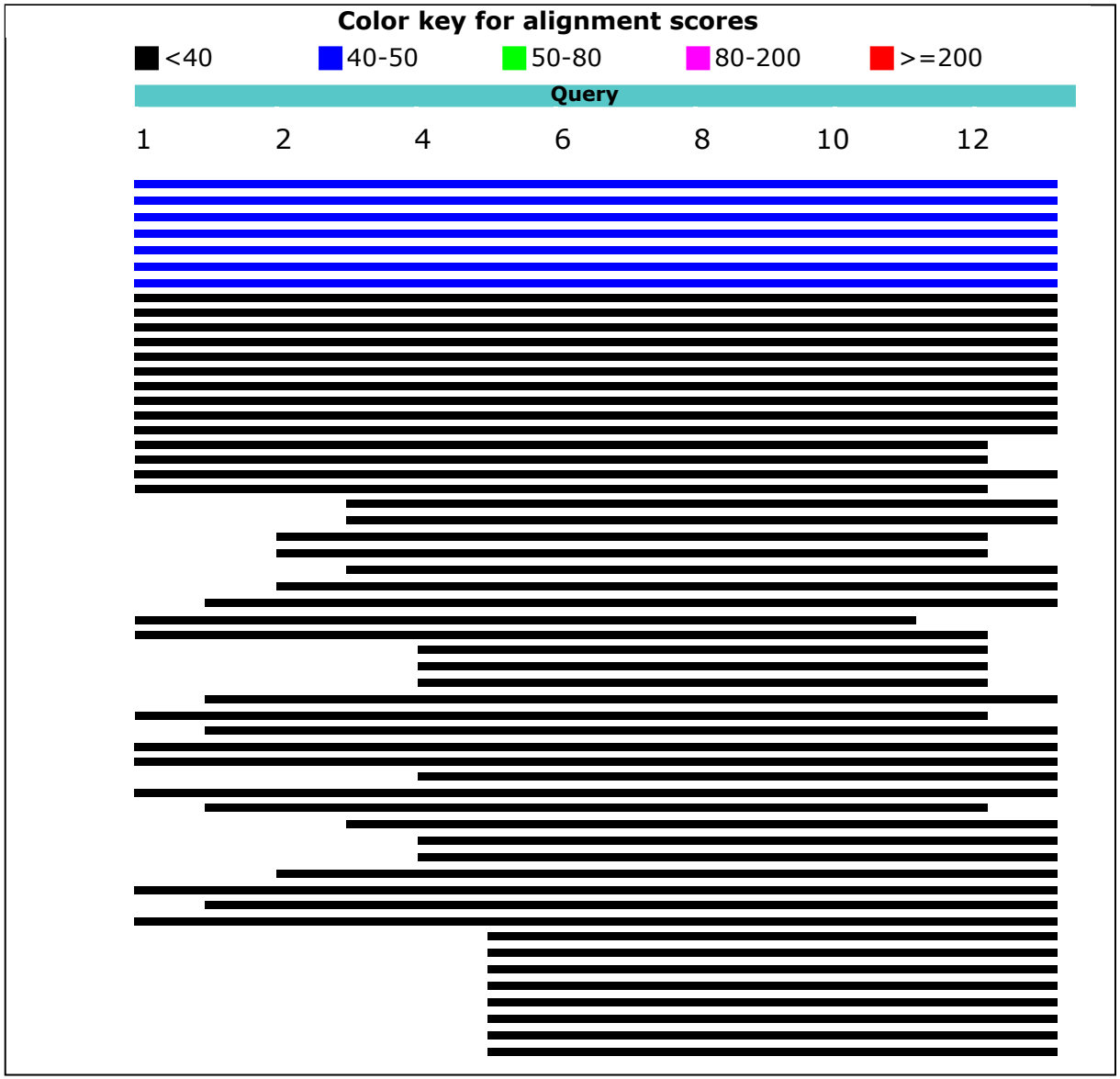
RID S56BP4JU014 (Expires on 08-04 11:33 am)

Query ID	lcl|Query_229163	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	13	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
alpha-N-acetylglucosaminidase [Homo sapiens]	45.2	45.2	100%	1e-04	100%	AAC50512.1
alpha-N-acetylglucosaminidase precursor [Homo sapiens]	45.2	45.2	100%	1e-04	100%	NP_000254.2
Chain A, Crystal Structure Of The Human N-acetyl-alpha-glucosaminidase	45.2	45.2	100%	1e-04	100%	4XWH_A
Alpha-N-acetylglucosaminidase [Macaca mulatta]	45.2	45.2	100%	1e-04	100%	EHH24987.1
Alpha-N-acetylglucosaminidase [Macaca fascicularis]	45.2	45.2	100%	1e-04	100%	EHH58149.1
alpha-N-acetylglucosaminidase [Homo sapiens]	45.2	45.2	100%	1e-04	100%	AAB36605.1
huntingtin interacting protein-1-related [Homo sapiens]	45.2	45.2	100%	1e-04	100%	BAD92767.1
alpha-N-acetylglucosaminidase-like protein [Cricetulus griseus]	37.5	37.5	100%	0.055	85%	ERE68426.1
Alpha-N-acetylglucosaminidase [Cricetulus griseus]	37.5	37.5	100%	0.055	85%	EGW08045.1
rCG33377, isoform CRA_b [Rattus norvegicus]	37.1	37.1	100%	0.078	85%	EDM06079.1
rCG33377, isoform CRA_d [Rattus norvegicus]	37.1	37.1	100%	0.078	85%	EDM06081.1
v-type proton ATPase subunit a isoform 1 [Camelus ferus]	35.0	35.0	100%	0.44	85%	EPY88172.1
Alpha-N-acetylglucosaminidase [Pteropus alecto]	35.0	35.0	100%	0.44	85%	ELK01481.1
NAGLU [Cervus elaphus hippelaphus]	35.0	35.0	100%	0.44	85%	OWK14559.1
alpha-N-acetylglucosaminidase precursor [Bos taurus]	35.0	35.0	100%	0.44	85%	NP_001095696.1
Alpha-N-acetylglucosaminidase [Bos mutus]	35.0	35.0	100%	0.44	85%	ELR53922.1
V-type proton ATPase 116 kDa subunit a isoform 1 [Fukomys damarensis]	34.6	69.1	100%	0.62	77%	KFO28536.1
Naglu [Mus musculus]	33.7	33.7	92%	1.3	83%	AAB88084.1
alpha-N-acetylglucosaminidase precursor [Mus musculus]	33.7	33.7	92%	1.3	83%	NP_038820.2
hypothetical protein A6R68_04510 [Neotoma lepida]	33.7	33.7	100%	1.3	77%	OBS66921.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB), isoform CRA_a [Mus musculus]	33.7	33.7	92%	1.3	83%	EDL03875.1
mycothiol conjugate amidase Mca [Streptomyces iranensis]	32.9	32.9	76%	2.5	90%	CDR06348.1
mycothiol conjugate amidase Mca [Streptomyces iranensis]	32.9	32.9	76%	2.5	90%	WP_044581362.1
hypothetical protein DCS_04146 [Drechmeria coniospora]	32.0	32.0	76%	5.0	90%	KYK57139.1
hypothetical protein RJ55_04636 [Drechmeria coniospora]	32.0	32.0	76%	5.1	90%	ODA79045.1
MULTISPECIES: hypothetical protein [Burkholderia]	30.8	30.8	76%	14	90%	WP_072437106.1
hypothetical protein [Oryza sativa Japonica Group]	30.3	30.3	84%	20	82%	BAD20074.1
TIGR02099 family protein [Mitsuaria sp. PDC51]	29.9	29.9	92%	29	83%	SFR95353.1
precorrin-3B synthase [Actinoplanes missouriensis]	29.9	29.9	84%	29	91%	WP_014446741.1
HDOD domain-containing protein [Oxalobacteraceae bacterium IMCC9480]	29.9	29.9	92%	29	67%	WP_009665288.1
hypothetical protein [Nocardia fusca]	29.5	29.5	61%	41	100%	WP_063130187.1
hypothetical protein [Streptomyces glauciniger]	29.5	29.5	61%	41	100%	WP_089224632.1
hypothetical protein [Streptomyces sp. BoleA5]	29.5	29.5	61%	41	100%	WP_018561664.1
DUF3488 domain-containing protein [Alcanivorax pacificus]	29.5	29.5	92%	41	69%	WP_082027669.1
uncharacterized protein LOC110654375 [Hevea brasiliensis]	29.5	29.5	92%	41	75%	XP_021666029.1
transglutaminase [Alcanivorax pacificus W11-5]	29.5	29.5	92%	41	69%	AJD48074.1
Alpha-N-acetylglucosaminidase [Heterocephalus glaber]	29.5	29.5	100%	41	69%	EHB02808.1
hypothetical protein PANDA_011160 [Ailuropoda melanoleuca]	29.5	29.5	100%	41	69%	EFB20123.1
pyridine nucleotide-disulfide oxidoreductase [Nocardia xishanensis]	29.5	29.5	69%	41	89%	WP_084501512.1
ABC transporter [Chromatiales bacterium (ex Bugula neritina AB1)]	29.5	29.5	100%	41	71%	OED36417.1
MFS transporter [Comamonas testosteroni]	29.5	29.5	84%	41	82%	WP_050874200.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein AN7585.2 [Aspergillus nidulans FGSC A4]	29.5	29.5	76%	41	80%	EAA62165.1
hypothetical protein [Streptomyces sp. NRRL S-1868]	29.5	29.5	69%	41	89%	WP_030885982.1
hypothetical protein [Streptomyces sp. NRRL F-5053]	29.5	29.5	69%	41	89%	WP_030893963.1
hypothetical protein N825_22915 [Skermanella stibiiresistens SB22]	29.5	29.5	84%	41	79%	EWY36967.1
MULTISPECIES: DUF1684 domain-containing protein [Rhizobium]	29.5	29.5	100%	41	71%	WP_037198131.1
conserved hypothetical protein [Ixodes scapularis]	29.5	29.5	92%	41	75%	EEC18925.1
hypothetical protein GA0061101_10935 [Rhizobium lusitanum]	29.5	29.5	100%	41	71%	SCB36227.1
hypothetical protein A2045_14290 [Rhodocyclales bacterium GWA2_65_20]	29.1	29.1	61%	58	100%	OHC69019.1
glycoside hydrolase family 2 [Olsenella sp. An188]	29.1	29.1	61%	58	100%	WP_087352438.1
NAD(P)/FAD-dependent oxidoreductase [Mycobacterium chubuense]	29.1	29.1	61%	58	100%	WP_014817572.1
Thermostable carboxypeptidase 1 [Prochlorococcus marinus str. MIT 1312]	29.1	29.1	61%	58	100%	KZR62692.1
histidinol-phosphate transaminase [Actinoalloteichus cyanogriseus]	29.1	29.1	61%	58	100%	WP_030105895.1
histidinol-phosphate transaminase [Actinoalloteichus cyanogriseus]	29.1	29.1	61%	58	100%	WP_026420048.1
hypothetical protein [Desulfovibrio africanus]	29.1	29.1	61%	58	100%	WP_005988324.1
DUF1684 domain-containing protein [Rhizobium leguminosarum]	29.1	29.1	61%	58	100%	WP_018069817.1
alkyl hydroperoxide reductase [Candidatus Tenderia electrophaga]	29.1	29.1	84%	58	82%	ALP54665.1
hypothetical protein [Actinoplanes sp. SE50/110]	29.1	29.1	69%	59	89%	WP_014689786.1
hypothetical protein [Actinoplanes sp. SE50/110]	29.1	29.1	69%	59	89%	WP_052311571.1
hypothetical protein AMSG_03051 [Thecamonas trahens ATCC 50062]	28.6	28.6	92%	82	75%	KNC46615.1
Alpha-N-acetylglucosaminidase [Tupaia chinensis]	28.6	28.6	100%	82	77%	ELW54978.1
hypothetical protein [Allokutzneria sp. NRRL B-24872]	28.6	28.6	92%	82	63%	WP_086829725.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ABC transporter ATP-binding protein [Pseudomonas aeruginosa]	28.6	28.6	69%	82	89%	WP_058355387.1
nucleoside ABC transporter ATP-binding protein [Massilia namucuonensis]	28.6	28.6	69%	82	89%	SFV14039.1
cysteinyl-tRNA synthetase [Ectothiorhodospira mobilis]	28.6	28.6	69%	82	90%	SFM42623.1
unnamed protein product [Podospora anserina S mat+]	28.6	28.6	100%	82	58%	CAP65853.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_060362697.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_060351097.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_060292059.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_060271155.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_060149161.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_059885047.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_060016668.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_060027526.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_059922370.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_059960846.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_059987522.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_059909698.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_059565337.1
hypothetical protein [Burkholderia stagnalis]	28.6	28.6	69%	82	89%	WP_059802405.1
TIGR02679 family protein [Streptomyces ahygroscopicus]	28.6	28.6	69%	82	90%	WP_053163249.1
hypothetical protein SLA_5794 [Streptomyces laurentii]	28.6	28.6	69%	82	90%	BAU86663.1
TIGR02679 family protein [Streptomyces sp. TN58]	28.6	28.6	69%	82	90%	APU44678.1
hypothetical protein PL81_06315 [Streptomyces sp. RSD-27]	28.6	28.6	69%	82	90%	KIF06657.1
lipase [Nocardia terpenica]	28.6	28.6	61%	82	100%	WP_067576604.1
membrane protein [Nocardia veterana]	28.6	28.6	84%	82	82%	WP_040718035.1
conserved hypothetical protein [Thiocapsa sp. KS1]	28.6	28.6	76%	82	80%	CRI65091.1
MarR family transcriptional regulator [Streptacidiphilus jeojiense]	28.6	28.6	76%	83	90%	WP_084713533.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
protein of unknown function DUF397 [Catenulispora acidiphila DSM 44928]	28.6	28.6	69%	83	90%	ACU77293.1
chromosome segregation protein SMC [Desulfocarbo indianensis]	28.2	28.2	92%	116	77%	WP_049676779.1
hypothetical protein [Olsenella sp. An188]	28.2	28.2	84%	116	82%	WP_087353867.1
glycoside hydrolase [Arthrobacter sp. ZBG10]	28.2	28.2	92%	116	75%	WP_050685486.1
MULTISPECIES: glycoside hydrolase [Frigoribacterium]	28.2	28.2	92%	116	75%	WP_055975900.1
beta-galactosidase [Catenuloplanes japonicus]	28.2	28.2	92%	116	75%	WP_033344982.1
hypothetical protein [Desulfovibrio putealis]	28.2	28.2	92%	116	59%	WP_027190666.1
endo-beta-N-acetylglucosaminidase [Streptomyces sp. WM6378]	28.2	28.2	76%	116	80%	WP_078966398.1
glycosyltransferase family 1 protein [Microbacterium sp. Root322]	28.2	28.2	100%	116	48%	WP_055873043.1
acetoacetate--CoA ligase [Desulfovirgula thermocuniculi]	28.2	28.2	69%	116	89%	WP_035108217.1
endo-beta-N-acetylglucosaminidase [Streptomyces sp. WM6378]	28.2	28.2	76%	116	80%	KOU45187.1
ABC transporter ATP-binding protein [Thiobacillus sp. 65-29]	28.2	28.2	92%	116	67%	OJZ18557.1

Alignments

alpha-N-acetylglucosaminidase [Homo sapiens]
Sequence ID: **AAC50512.1** Length: 743 Number of Matches: 1

See 5 more title(s)
Range 1: 483 to 495

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    YGVSHPDAGAAWR  13
            YGVSHPDAGAAWR
Sbjct  483  YGVSHPDAGAAWR  495
```

alpha-N-acetylglucosaminidase precursor [Homo sapiens]
Sequence ID: **NP_000254.2** Length: 743 Number of Matches: 1

See 2 more title(s)
Range 1: 483 to 495

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    YGVSHPDAGAAWR  13
            YGVSHPDAGAAWR
Sbjct  483  YGVSHPDAGAAWR  495
```

Chain A, Crystal Structure Of The Human N-acetyl-alpha-glucosaminidase
Sequence ID: **4XWH_A** Length: 720 Number of Matches: 1
Range 1: 460 to 472

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    YGVSHPDAGAAWR  13
            YGVSHPDAGAAWR
Sbjct  460  YGVSHPDAGAAWR  472
```

Alpha-N-acetylglucosaminidase, partial [Macaca mulatta]
Sequence ID: **EHH24987.1** Length: 711 Number of Matches: 1
Range 1: 451 to 463

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    YGVSHPDAGAAWR  13
            YGVSHPDAGAAWR
Sbjct  451  YGVSHPDAGAAWR  463
```

Alpha-N-acetylglucosaminidase, partial [Macaca fascicularis]

Sequence ID: **EHH58149.1** Length: 650 Number of Matches: 1
Range 1: 390 to 402

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    YGVSHPDAGAAWR  13
            YGVSHPDAGAAWR
Sbjct  390  YGVSHPDAGAAWR  402
```

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BLAST Results

Job title: P_ORM2_SDVMYTDWK

RID S56C84GH015 (Expires on 08-04 11:33 am)

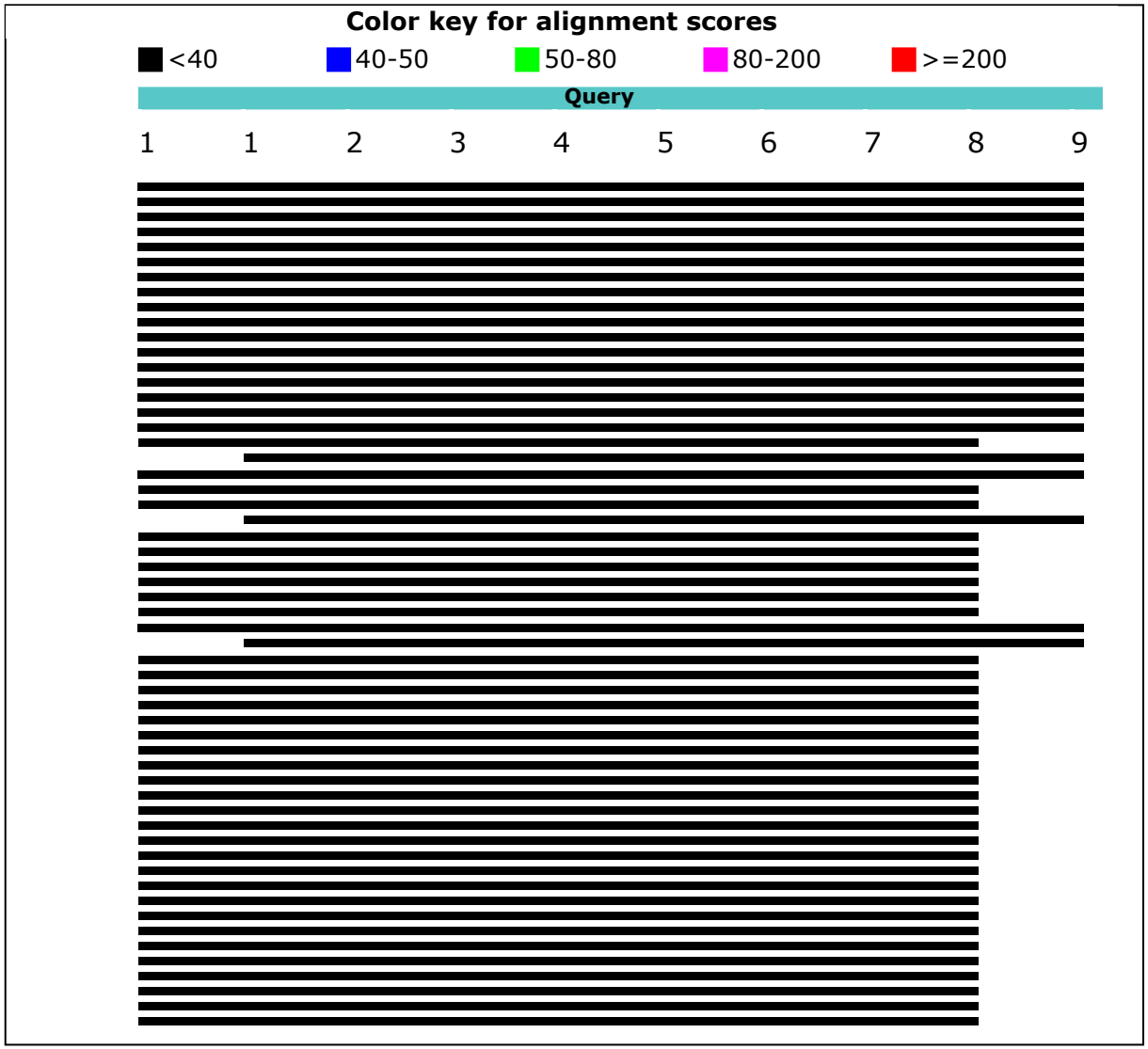
Query ID lcl|Query_326204
Description None
Molecule type amino acid
Query Length 9

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1 1 2 3 4 5 6 7 8 9

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	35.8	35.8	100%	0.10	100%	NP_000599.1
ORM2 [Homo sapiens]	35.8	35.8	100%	0.10	100%	CAG33211.1
alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	35.8	35.8	100%	0.10	100%	CAA29873.2
ORM2 [synthetic construct]	35.8	35.8	100%	0.10	100%	AIC54853.1
Orosomucoid 1 [Homo sapiens]	35.8	35.8	100%	0.10	100%	AAI43315.1
unnamed protein product [Homo sapiens]	35.8	35.8	100%	0.10	100%	BAG35159.1
Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid Glycoprotein	35.8	35.8	100%	0.10	100%	3APU_A
hepatocarcinogenesis-specific protein/alpha-1 acid glycoprotein homolog {clone HC49} [woodchucks, hepatitis B virus-infected hepatocellular carcinoma cells, Peptide Partial, 155 aa]	31.2	31.2	100%	4.7	78%	AAA82489.1
orosomucoid 1 [synthetic construct]	30.8	30.8	100%	6.5	89%	AAV38575.1
orosomucoid 1 [synthetic construct]	30.8	30.8	100%	6.5	89%	AAV38574.1
alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	30.8	30.8	100%	6.5	89%	NP_000598.2
alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	30.8	30.8	100%	6.5	89%	CAA29229.1
RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Orosomucoid-1; Short=OMD 1; Flags: Precursor	30.8	30.8	100%	6.5	89%	P02763.1
ORM1 [synthetic construct]	30.8	30.8	100%	6.5	89%	AIC54852.1
Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein	30.8	30.8	100%	6.6	89%	3KQ0_A
Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein	30.8	30.8	100%	6.6	89%	3BX6_A
protein,alpha1 acid glyco	30.8	30.8	100%	6.6	89%	720005A
hypothetical protein [Epulopiscium sp. 'N.t. morphotype B']	29.9	29.9	88%	13	88%	WP_029487673.1
DUF421 domain-containing protein [Bacillus aquimaris]	29.9	29.9	88%	13	88%	WP_064093363.1
DUF421 domain-containing protein [Bacillus solimangrovi]	29.9	29.9	100%	13	78%	WP_069718324.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein ACD_49C00066G0021 [uncultured bacterium (gcode 4)]	29.9	29.9	88%	13	88%	EKD66097.1
conserved hypothetical protein [Trypanosoma congolense IL3000]	29.1	29.1	88%	26	88%	CCC92979.1
glycoside hydrolase family 1 protein [Entomoplasma somnilux]	29.1	29.1	88%	26	88%	WP_024863440.1
beta-glucosidase [Microtetraspora glauca]	28.6	28.6	88%	37	88%	WP_061257378.1
hypothetical protein BK004_01125 [bacterium CG10_46_32]	28.6	28.6	88%	37	88%	OJI07448.1
putative two-component sensor protein [Zunongwangia profunda SM-A87]	28.6	28.6	88%	37	88%	ADF52802.1
hypothetical protein [Zunongwangia profunda]	28.6	28.6	88%	37	88%	WP_041578876.1
sodium:proton antiporter [Vibrio cincinnatiensis]	28.6	28.6	88%	37	88%	WP_078925831.1
sulfatase [Xanthomonadaceae bacterium SCN 69-320]	28.2	28.2	88%	52	88%	ODU33653.1
hypothetical protein PHAVU_009G196000g [Phaseolus vulgaris]	28.2	28.2	100%	52	78%	ESW10285.1
AAEL006443-PA [Aedes aegypti]	27.8	27.8	88%	73	75%	EAT41965.1
beta-glucosidase [Bacillus pseudalcaliphilus]	27.8	27.8	88%	73	88%	WP_047989939.1
sodium:proton antiporter [endosymbiont of Ridgeia piscesae]	27.8	27.8	88%	74	75%	WP_057956666.1
MULTISPECIES: sodium:proton antiporter [sulfur-oxidizing symbionts]	27.8	27.8	88%	74	75%	WP_005959988.1
sodium:proton antiporter [Vibrio alginolyticus]	27.8	27.8	88%	74	75%	WP_053308990.1
MULTISPECIES: sodium:proton antiporter [Vibrio harveyi group]	27.8	27.8	88%	74	75%	WP_054822504.1
MULTISPECIES: sodium:proton antiporter [Vibrio harveyi group]	27.8	27.8	88%	74	75%	WP_050913765.1
sodium:proton antiporter [Vibrio hyugaensis]	27.8	27.8	88%	74	75%	WP_045496573.1
sodium:proton antiporter [Vibrio hyugaensis]	27.8	27.8	88%	74	75%	WP_045467026.1
sodium:proton antiporter [Vibrio owensii]	27.8	27.8	88%	74	75%	WP_042979970.1
sodium:proton antiporter [Vibrio owensii]	27.8	27.8	88%	74	75%	WP_039986405.1
sodium:proton antiporter [Vibrio owensii]	27.8	27.8	88%	74	75%	WP_038894996.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	AIV07905.1
MULTISPECIES: sodium:proton antiporter [Vibrio]	27.8	27.8	88%	74	75%	WP_032802832.1
sodium:proton antiporter [Vibrio mytili]	27.8	27.8	88%	74	75%	KIN11270.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
sodium:proton antiporter [Vibrio rotiferianus]	27.8	27.8	88%	74	75%	ASI94266.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	ARR08055.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_081233063.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_077262568.1
sodium:proton antiporter [Vibrio rotiferianus]	27.8	27.8	88%	74	75%	WP_071235792.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_012130312.1
sodium:proton antiporter [Vibrio owensii]	27.8	27.8	88%	74	75%	WP_052470696.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_051177495.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_051116799.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_050939852.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_050925041.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_050919558.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_050909301.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_050567807.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_053049925.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_045455744.1
sodium:proton antiporter [Vibrio jasicida]	27.8	27.8	88%	74	75%	WP_045424803.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_045416483.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_045399458.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_045371149.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_042600338.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_042605944.1
sodium:proton antiporter [Vibrio jasicida]	27.8	27.8	88%	74	75%	WP_039973794.1
MULTISPECIES: sodium:proton antiporter [Vibrio]	27.8	27.8	88%	74	75%	WP_038869787.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_045383113.1
LOW QUALITY PROTEIN: Na+/H+ antiporter NhaD type [Vibrio sp. JCM 19052]	27.8	27.8	88%	74	75%	GAK20940.1
Na+/H+ antiporter [Vibrio harveyi 1DA3]	27.8	27.8	88%	74	75%	EEZ89786.1
hypothetical protein [Vibrio azureus]	27.8	27.8	88%	74	75%	WP_021708347.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
sodium:proton antiporter [VIbrio owensii CAIM 1854 = LMG 25443]	27.8	27.8	88%	74	75%	KIF52610.1
hypothetical protein [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_005448978.1
na+/H+ antiporter, NhaD family protein [Vibrio sp. HENC-02]	27.8	27.8	88%	74	75%	EKM32656.1
MULTISPECIES: sodium:proton antiporter [Vibrio]	27.8	27.8	88%	74	75%	WP_009696610.1
sodium:proton antiporter [Vibrio rotiferianus]	27.8	27.8	88%	74	75%	WP_010453570.1
sodium:proton antiporter [Photobacterium ganghwense]	27.8	27.8	88%	74	75%	WP_084712508.1
sodium:proton antiporter [Vibrio mytili]	27.8	27.8	88%	74	75%	WP_052481516.1
sodium:proton antiporter [Photobacterium ganghwense]	27.8	27.8	88%	74	75%	KLV10310.1
hypothetical protein [Pedobacter antarcticus]	27.8	27.8	88%	74	88%	WP_074590314.1
RagB/SusD family nutrient uptake outer membrane protein [Pedobacter antarcticus]	27.8	27.8	88%	74	88%	WP_037442725.1
sodium:proton antiporter [Vibrio rotiferianus]	27.8	27.8	88%	74	75%	WP_088880238.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_086371344.1
sodium:proton antiporter [Vibrio campbellii]	27.8	27.8	88%	74	75%	WP_086028458.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_086028116.1
sodium:proton antiporter [Vibrio harveyi]	27.8	27.8	88%	74	75%	WP_086027667.1
sodium:proton antiporter [Vibrio rotiferianus]	27.8	27.8	88%	74	75%	WP_086026629.1
collagen-like protein [Mucilaginibacter lappiensis]	27.8	27.8	77%	74	86%	WP_076374400.1
hypothetical protein SAMN05216490_1271 [Mucilaginibacter mallensis]	27.8	27.8	77%	74	86%	SDS50341.1
hypothetical protein [Candidatus Jidaibacter acanthamoeba]	27.8	27.8	88%	76	88%	WP_039456822.1
erythronolide synthase Mycocerosate synthase [Ruminococcus sp. CAG:624]	27.4	27.4	77%	104	100%	CDF00653.1
error-prone DNA polymerase [Mitsuaria sp. 7]	27.4	27.4	77%	104	86%	WP_067276811.1
error-prone DNA polymerase [Variovorax sp. KK3]	27.4	27.4	77%	104	86%	WP_076999167.1
error-prone DNA polymerase [Delftia sp. JD2]	27.4	27.4	77%	104	86%	WP_065345913.1
error-prone DNA polymerase [Delftia sp. ZNC0008]	27.4	27.4	77%	104	86%	WP_047468722.1
error-prone DNA polymerase [Pelomonas sp. Root1444]	27.4	27.4	77%	104	86%	WP_056877515.1
error-prone DNA polymerase [Methylibium petroleiphilum]	27.4	27.4	77%	104	86%	WP_011831928.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein D187_008301 [Cystobacter fuscus DSM 2262]	27.4	27.4	100%	104	78%	EPX55740.1

Alignments

alpha-1-acid glycoprotein 2 precursor [Homo sapiens]
Sequence ID: **NP_000599.1** Length: 201 Number of Matches: 1

See 6 more title(s)
Range 1: 171 to 179

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.8 bits(77)	0.10()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    SDVMYTDWK  9
           SDVMYTDWK
Sbjct  171  SDVMYTDWK  179
```

ORM2 [Homo sapiens]
Sequence ID: **CAG33211.1** Length: 201 Number of Matches: 1
Range 1: 171 to 179

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.8 bits(77)	0.10()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    SDVMYTDWK  9
           SDVMYTDWK
Sbjct  171  SDVMYTDWK  179
```

alpha-1-acid glycoprotein 2 precursor [Homo sapiens]
Sequence ID: **CAA29873.2** Length: 201 Number of Matches: 1
Range 1: 171 to 179

Score	Expect	Method	Identities	Positives	Gaps	Frame

35.8 bits(77)	0.10()	9/9(100%)	9/9(100%)	0/9(0%)

Features:

```
Query  1    SDVMYTDWK  9
           SDVMYTDWK
Sbjct  171  SDVMYTDWK  179
```

ORM2, partial [synthetic construct]

Sequence ID: **AIC54853.1** Length: 201 Number of Matches: 1
Range 1: 171 to 179

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.8 bits(77)	0.10()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    SDVMYTDWK  9
           SDVMYTDWK
Sbjct  171  SDVMYTDWK  179
```

Orosomucoid 1 [Homo sapiens]

Sequence ID: **AAI43315.1** Length: 201 Number of Matches: 1
Range 1: 171 to 179

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.8 bits(77)	0.10()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    SDVMYTDWK  9
           SDVMYTDWK
Sbjct  171  SDVMYTDWK  179
```

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BLAST Results

Job title: P_ORM2_TEDTIFLR

RID S56CJAXV015 (Expires on 08-04 11:33 am)

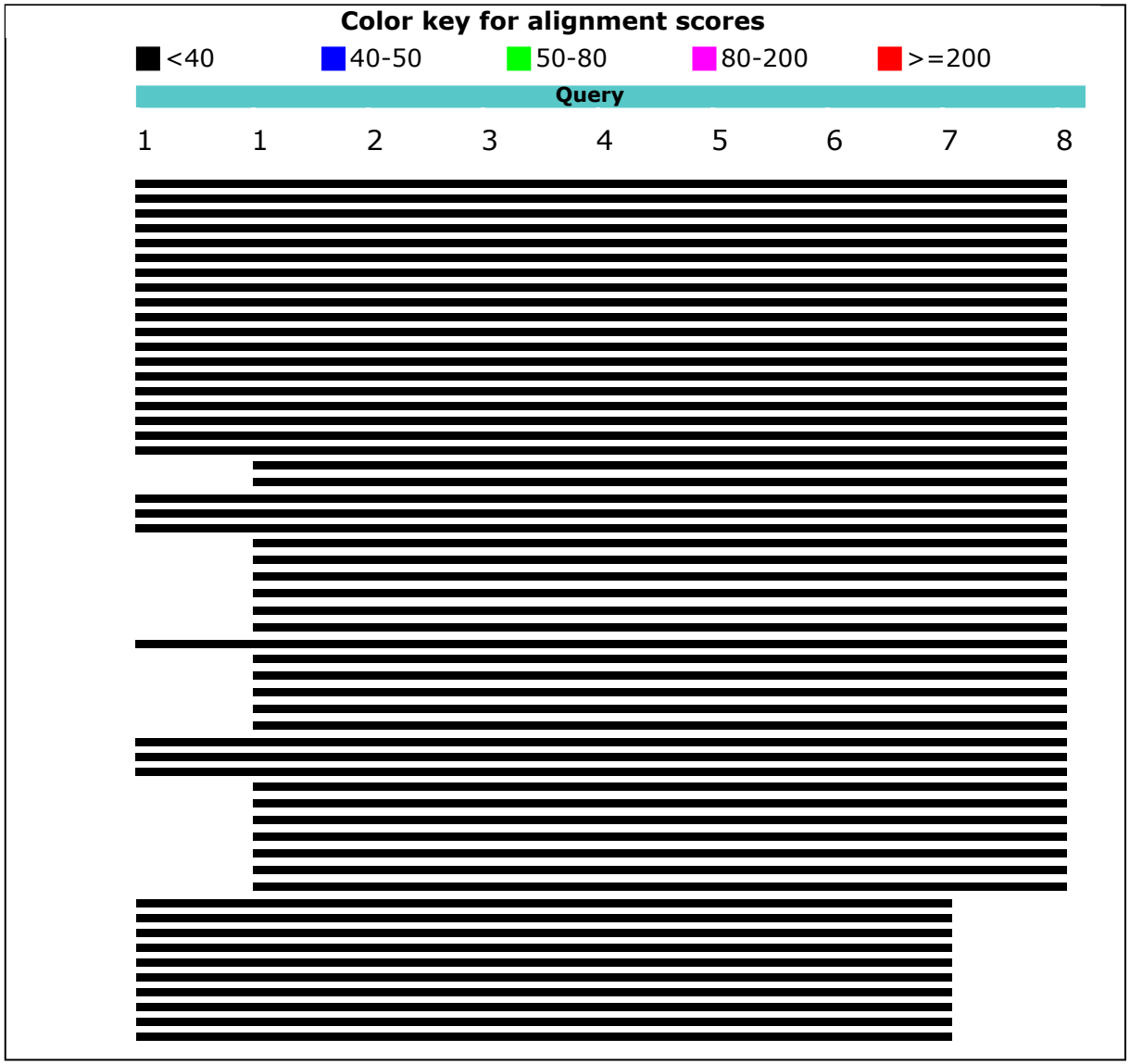
Query ID lcl|Query_242897
Description None
Molecule type amino acid
Query Length 8

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
orosomucoid 1 [synthetic construct]	29.5	29.5	100%	15	100%	AAV38575.1
orosomucoid 1 [synthetic construct]	29.5	29.5	100%	15	100%	AAV38574.1
Alpha-1-acid glycoprotein 1 [Macaca mulatta]	29.5	29.5	100%	15	100%	EHH23840.1
alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	29.5	29.5	100%	15	100%	NP_000599.1
alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	29.5	29.5	100%	15	100%	NP_000598.2
ORM2 [Homo sapiens]	29.5	29.5	100%	15	100%	CAG33211.1
alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	29.5	29.5	100%	15	100%	CAA29229.1
alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	29.5	29.5	100%	15	100%	CAA29873.2
RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Orosomucoid-1; Short=OMD 1; Flags: Precursor	29.5	29.5	100%	15	100%	P02763.1
ORM2 [synthetic construct]	29.5	29.5	100%	15	100%	AIC54853.1
ORM1 [synthetic construct]	29.5	29.5	100%	15	100%	AIC54852.1
Orosomucoid 1 [Homo sapiens]	29.5	29.5	100%	15	100%	AAI43315.1
unnamed protein product [Homo sapiens]	29.5	29.5	100%	15	100%	BAG35159.1
Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein	29.5	29.5	100%	15	100%	3KQ0_A
Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein	29.5	29.5	100%	15	100%	3BX6_A
Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid Glycoprotein	29.5	29.5	100%	15	100%	3APU_A
protein,alpha1 acid glyco	29.5	29.5	100%	15	100%	720005A
hypothetical protein [Hahella ganghwensis]	26.9	26.9	100%	118	88%	WP_020405326.1
hypothetical protein SCHCODRAFT_56496 [Schizophyllum commune H4-8]	26.9	26.9	100%	118	88%	EFI95932.1
unnamed protein product [Paramecium tetraurelia]	26.5	26.5	87%	167	100%	CAK74085.1
hypothetical protein [Carnobacterium inhibens]	26.5	26.5	87%	168	100%	WP_034536263.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
alpha-L-fucosidase 2 [Parafilimonas terrae]	26.5	26.5	100%	168	88%	SFP84514.1
hypothetical protein [Lutibacter flavus]	26.5	26.5	100%	168	88%	WP_089376527.1
Tyrosine-protein phosphatase non-receptor type 5 [Larimichthys crocea]	26.5	26.5	100%	169	88%	KKF26153.1
hypothetical protein BCV71DRAFT_268121 [Rhizopus microsporus]	26.5	26.5	87%	169	100%	ORE13678.1
hypothetical protein [Tistlia consotensis]	26.5	26.5	87%	169	100%	WP_085124477.1
peptide/nickel transport system substrate-binding protein [Tistlia consotensis USBA 355]	26.5	26.5	87%	169	100%	SMF52144.1
unnamed protein product [Tetraodon nigroviridis]	26.5	26.5	87%	169	100%	CAG04164.1
protein of unknown function [Prevotella sp. kh1p2]	26.5	26.5	87%	169	100%	SES86264.1
ROK family protein [Flexilinea flocculi]	26.5	26.5	87%	170	100%	WP_062283427.1
3,4-dihydroxyphenylacetate 2,3-dioxygenase [Aquimarina megaterium]	26.5	26.5	100%	170	88%	WP_025667728.1
3-keto-5-aminohexanoate cleavage protein [Novosphingobium sp. ST904]	26.5	26.5	87%	170	100%	WP_082370213.1
hypothetical protein ADT71_07475 [Novosphingobium sp. ST904]	26.5	26.5	87%	170	100%	KPH66181.1
anaerobic sulfite reductase subunit B [Clostridium fallax]	26.5	26.5	87%	170	100%	WP_072892434.1
hypothetical protein PENSOL_c003G11771 [Penicillium solitum]	26.5	26.5	87%	170	100%	OQE01913.1
hypothetical protein STEHIDRAFT_115916 [Stereum hirsutum FP-91666 SS1]	26.5	26.5	87%	171	100%	EIM80487.1
hypothetical protein [Pseudomonas lini]	26.5	26.5	100%	171	88%	WP_050683033.1
unnamed protein product [Tetraodon nigroviridis]	26.5	26.5	100%	171	88%	CAG13522.1
N-acetyltransferase [Gordonia soli]	26.5	26.5	100%	172	88%	WP_007620809.1
dihydroneopterin aldolase [Azoarcus toluclasticus]	26.5	26.5	87%	173	100%	WP_018989916.1
dihydroneopterin aldolase [Azoarcus sp. CIB]	26.5	26.5	87%	173	100%	AKU12023.1
dihydroneopterin aldolase [Azoarcus tolulyticus]	26.5	26.5	87%	173	100%	WP_076602941.1
dihydroneopterin aldolase [Azoarcus sp. CIB]	26.5	26.5	87%	173	100%	WP_050418331.1
hypothetical protein [Castellaniella defragrans]	26.5	26.5	87%	175	100%	WP_043681094.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein A2042_08565 [Candidatus Schekmanbacteria bacterium GWA2_38_11]	26.5	26.5	87%	178	100%	OGL41555.1
hypothetical protein BA871_08710 [Desulfuromonadales bacterium C00003096]	26.5	26.5	87%	178	100%	OEU54008.1
1ab [Wuhan nido-like virus 1]	26.1	26.1	87%	237	100%	YP_009345058.1
fibro-slime domain [Roseburia sp. CAG:197]	26.1	26.1	87%	238	100%	CDA24129.1
conserved Plasmodium protein, unknown function [Plasmodium chabaudi chabaudi]	26.1	26.1	87%	238	100%	SCM04749.1
conserved Plasmodium protein, unknown function [Plasmodium chabaudi adami]	26.1	26.1	87%	238	100%	SCM07566.1
conserved Plasmodium protein, unknown function [Plasmodium chabaudi chabaudi]	26.1	26.1	87%	238	100%	SCM02435.1
conserved Plasmodium protein, unknown function [Plasmodium chabaudi chabaudi]	26.1	26.1	87%	238	100%	CDU21694.1
GGDEF domain-containing protein [Clostridium homopropionicum]	26.1	26.1	87%	239	100%	WP_052222133.1
conserved hypothetical protein [Plasmodium chabaudi chabaudi]	26.1	26.1	87%	239	100%	CAH74638.1
hypothetical protein PENSTE_c008G02637 [Penicillium steckii]	26.1	26.1	87%	239	100%	OQE23787.1
UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Spirochaetes bacterium DG_61]	26.1	26.1	87%	240	100%	KPJ89705.1
ring-1,2-phenylacetyl-CoA epoxidase subunit PaaE [Bizionia paragorgiae]	26.1	26.1	87%	240	100%	SDZ80630.1
flavodoxin reductase [Lacinutrix venerupis]	26.1	26.1	87%	240	100%	WP_076731523.1
hypothetical protein SAMN03080617_00338 [Algoriphagus alkaliphilus]	26.1	26.1	87%	241	100%	SDA42025.1
hypothetical protein SAMN04489723_10998 [Algoriphagus aquimarinus]	26.1	26.1	87%	241	100%	SFB41059.1
hypothetical protein [Algoriphagus resistens]	26.1	26.1	87%	241	100%	WP_057938190.1
urease accessory protein UreG [Conexibacter woesei]	26.1	26.1	100%	241	88%	WP_081425405.1
hypothetical protein [Sporosarcina sp. EUR3 2.2.2]	26.1	26.1	100%	242	88%	WP_024535948.1
glutamate racemase [Myroides odoratus]	26.1	26.1	87%	242	100%	WP_060872651.1
glutamate racemase [Myroides odoratus]	26.1	26.1	87%	242	100%	WP_002989918.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
urease accessory protein UreG [Conexibacter woesei DSM 14684]	26.1	26.1	100%	242	88%	ADB51924.1
putative neutral zinc metallopeptidase [Clostridium sp. CAG:451]	26.1	26.1	87%	242	100%	CDE73270.1
MULTISPECIES: hypothetical protein [Atopobium]	26.1	26.1	100%	243	88%	WP_002562879.1
hypothetical protein SAMN02910339_01054 [Lachnospiraceae bacterium YSD2013]	26.1	26.1	87%	243	100%	SCX07362.1
DNA transformation protein [Vibrio cincinnatiensis]	26.1	26.1	100%	243	88%	WP_078924531.1
hypothetical protein [Stenotrophomonas maltophilia]	26.1	26.1	87%	246	100%	WP_080356462.1
DNA primase [Flavobacteria bacterium GWF1_32_7]	26.1	26.1	87%	247	100%	OGS63281.1
hypothetical protein [Flavobacterium gelidilacus]	26.1	26.1	87%	248	100%	WP_026715567.1
hypothetical protein [Flavobacterium sp. 316]	26.1	26.1	87%	249	100%	WP_045967293.1
hypothetical protein [Thioclava sp. EIOx9]	26.1	26.1	87%	256	100%	WP_083080471.1
hypothetical protein [Thioclava sp. F36-6]	26.1	26.1	87%	256	100%	WP_078547968.1
hypothetical protein BMI86_13240 [Thioclava sp. DLFJ5-1]	26.1	26.1	87%	256	100%	OOY19599.1
hypothetical protein BMG00_11150 [Thioclava marinus]	26.1	26.1	87%	256	100%	OOY11653.1
autotransporter domain-containing protein [Sphingobium ummariense]	25.7	25.7	100%	338	88%	WP_021320187.1
hypothetical protein [Nesterenkonia alba]	25.7	25.7	100%	339	88%	WP_022873143.1
hypothetical protein [Actinomyces naeslundii]	25.7	25.7	100%	341	88%	WP_076080648.1
hypothetical protein A2284_03835 [Deltaproteobacteria bacterium RIFOXYA12_FULL_61_11]	25.7	25.7	100%	342	88%	OGR03018.1
hypothetical protein [Ectothiorhodosinus mongolicus]	25.2	44.5	100%	478	88%	WP_076753973.1
hypothetical protein [Arcticibacter eurypsychrophilus]	25.2	25.2	100%	480	88%	WP_069660184.1
hypothetical protein [Arcticibacter svalbardensis]	25.2	25.2	100%	480	88%	WP_052017060.1
hypothetical protein ADIARSV_4144 [Arcticibacter svalbardensis MN12-7]	25.2	25.2	100%	480	88%	EOR92632.1
glycosyl transferase [Streptococcus mitis]	25.2	25.2	100%	481	89%	WP_061088360.1
hypothetical protein [Elizabethkingia miricola]	25.2	25.2	100%	481	89%	WP_078799185.1
hypothetical protein GLAREA_01465 [Glarea lozoyensis ATCC 20868]	25.2	25.2	100%	481	88%	EPE25553.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein ARALYDRAFT_333307 [Arabidopsis lyrata subsp. lyrata]	25.2	25.2	100%	484	88%	EFH38781.1
DUF3445 domain-containing protein [Rhizobium arenae]	25.2	25.2	100%	485	88%	WP_083637473.1
ring-1,2-phenylacetyl-CoA epoxidase subunit PaaC [Dokdonia pacifica]	25.2	25.2	100%	486	89%	SNR36147.1
16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase [Flavobacteriaceae bacterium TMED208]	25.2	25.2	100%	486	89%	OUW77580.1
phenylacetate-CoA oxygenase subunit PaaI [Dokdonia pacifica]	25.2	25.2	100%	487	89%	WP_089370731.1
phenylacetate-CoA oxygenase subunit PaaI [Flavobacterium aquatile]	25.2	25.2	100%	487	89%	WP_035123714.1
ring-1,2-phenylacetyl-CoA epoxidase subunit PaaC [Flavobacterium noncentrifugens]	25.2	25.2	100%	487	89%	SDJ14982.1
phenylacetate-CoA oxygenase subunit PaaI [Flavobacterium limnosediminis]	25.2	25.2	100%	487	89%	WP_023578396.1
phenylacetate-CoA oxygenase subunit PaaI [Flavobacterium enshiense]	25.2	25.2	100%	487	89%	WP_023573578.1
ring-1,2-phenylacetyl-CoA epoxidase subunit PaaC [Flavobacterium caeni]	25.2	25.2	100%	487	89%	SCY83339.1
LALA0S04e04720g1_1 [Lachancea lanzarotensis]	25.2	25.2	100%	488	88%	CEP61968.1

Alignments

orosomucoid 1, partial [synthetic construct]
Sequence ID: **AAV38575.1** Length: 202 Number of Matches: 1

See 4 more title(s)
Range 1: 74 to 81

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	15()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1   TEDTIFLR  8
           TEDTIFLR
Sbjct  74  TEDTIFLR  81
```

orosomucoid 1, partial [synthetic construct]

Sequence ID: **AAV38574.1** Length: 202 Number of Matches: 1

See 1 more title(s)

Range 1: 74 to 81

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	15()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1   TEDTIFLR  8
           TEDTIFLR
Sbjct  74  TEDTIFLR  81
```

Alpha-1-acid glycoprotein 1 [Macaca mulatta]

Sequence ID: **EHH23840.1** Length: 202 Number of Matches: 1

See 1 more title(s)

Range 1: 74 to 81

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	15()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1   TEDTIFLR  8
           TEDTIFLR
Sbjct  74  TEDTIFLR  81
```

alpha-1-acid glycoprotein 2 precursor [Homo sapiens]

Sequence ID: **NP_000599.1** Length: 201 Number of Matches: 1

See 6 more title(s)

Range 1: 74 to 81

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	15()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1   TEDTIFLR  8
           TEDTIFLR
```

```
Sbjct  74  TEDTIFLR  81
```

alpha-1-acid glycoprotein 1 precursor [Homo sapiens]
Sequence ID: **NP_000598.2** Length: 201 Number of Matches: 1

See 7 more title(s)
Range 1: 74 to 81

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	15()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1   TEDTIFLR  8
           TEDTIFLR
Sbjct  74  TEDTIFLR  81
```

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BLAST Results

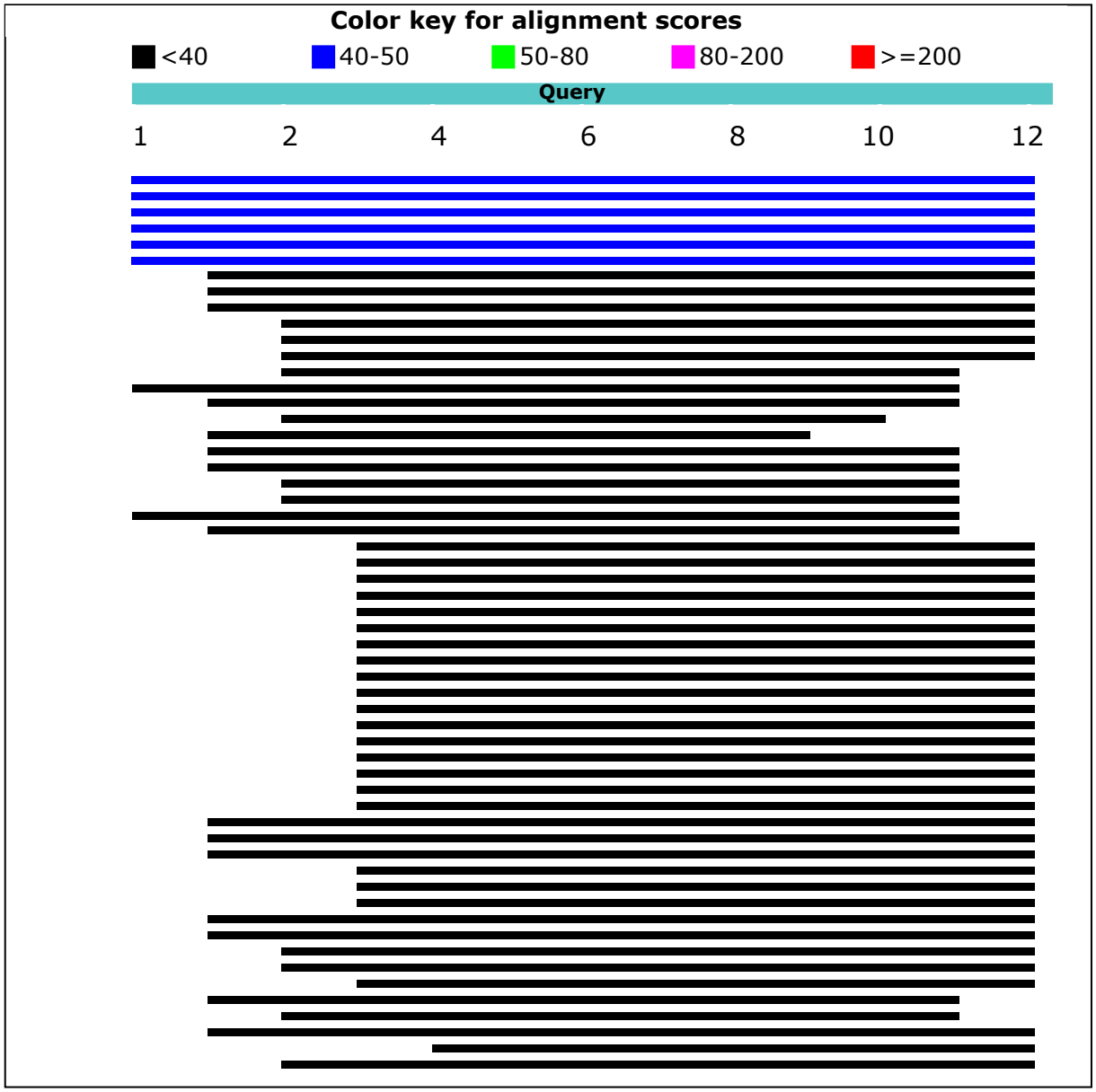
Job title: P_ORM2_TLMFGSYLDDEK

RID	S56CU1CS014 (Expires on 08-04 11:33 am)
Query ID	lcl|Query_35249
Description	None
Molecule type	amino acid
Query Length	12
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	43.1	43.1	100%	5e-04	100%	NP_000599.1
ORM2 [Homo sapiens]	43.1	43.1	100%	5e-04	100%	CAG33211.1
alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	43.1	43.1	100%	5e-04	100%	CAA29873.2
ORM2 [synthetic construct]	43.1	43.1	100%	5e-04	100%	AIC54853.1
unnamed protein product [Homo sapiens]	43.1	43.1	100%	5e-04	100%	BAG35159.1
Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid Glycoprotein	43.1	43.1	100%	5e-04	100%	3APU_A
endonuclease [Pedobacter sp. Leaf194]	33.3	33.3	91%	1.5	83%	WP_056872844.1
endonuclease [Pseudoxanthomonas sp. Root65]	33.3	33.3	91%	1.5	83%	WP_055941014.1
YeeE/YedE family protein [Vagococcus sp. D7T301]	32.9	32.9	91%	2.1	82%	WP_079345611.1
hypothetical protein [Bacteroides fragilis]	32.9	32.9	83%	2.1	90%	WP_080720174.1
hypothetical protein [Bacteroides timonensis]	32.9	32.9	83%	2.1	90%	WP_044271556.1
hypothetical protein EC81_0200540 [Bacteroides fragilis]	32.9	32.9	83%	2.1	90%	KER79639.1
membrane protein containing Beta-lactamase-like domain protein [Candidatus Magnetomorum sp. HK-1]	31.6	31.6	75%	5.9	89%	KPA16925.1
hypothetical protein YQE_09634 [Dendroctonus ponderosae]	30.8	61.5	91%	12	71%	ENN73765.1
ABC transporter ATP-binding protein [Burkholderia sp. E7m39]	30.8	30.8	83%	12	90%	WP_054926106.1
N-6 DNA methylase [Corynebacterium callunae]	30.8	30.8	66%	12	100%	WP_015650648.1
hypothetical protein AURANDRAFT_70682 [Aureococcus anophagefferens]	30.3	30.3	66%	17	100%	EGB11896.1
MHC class I antigen [Hypophthalmichthys molitrix]	30.3	30.3	83%	17	80%	AFP50363.1
sel1 repeat family protein [Helicobacter sp. MIT 05-5293]	29.9	29.9	83%	24	80%	WP_034369632.1
low molecular weight phosphotyrosine protein phosphatase [Rhodopirellula maiorica]	29.9	29.9	75%	24	89%	WP_081614310.1
Protein-tyrosine phosphatase, low molecular weight [Rhodopirellula maiorica SM1]	29.9	29.9	75%	24	89%	EMI17816.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Aminophospholipid translocase [Blumeria graminis f. sp. tritici 96224]	29.5	29.5	91%	34	75%	EPQ67156.1
ComEC/Rec2-like protein [Marinomonas sp. MWYL1]	29.5	29.5	83%	34	80%	WP_012069850.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057547418.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057570039.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057561897.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_055328730.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057536385.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057585422.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057555226.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057550788.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_055341932.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057566353.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057539575.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_055333489.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057564429.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_055331597.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057537767.1
sodium:neurotransmitter symporter [[Clostridium] sordellii]	29.5	29.5	75%	34	89%	CEK29816.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_057545023.1
SIR2 family protein [Leptospira alexanderi]	29.5	29.5	91%	34	73%	WP_078127481.1
SIR2 family protein [Leptospira weilii]	29.5	29.5	91%	34	73%	WP_061223379.1
SIR2 family protein [Leptospira weilii]	29.5	29.5	91%	34	73%	WP_004507891.1
hypothetical protein JGS6382_16291 [[Clostridium] sordellii]	29.5	29.5	75%	34	89%	CEK38297.1
sodium-dependent transporter [Paeniclostridium sordellii]	29.5	29.5	75%	34	89%	WP_055339481.1
neurotransmitter symporter family protein [[Clostridium] sordellii VPI 9048]	29.5	29.5	75%	34	89%	EPZ55964.1
SIR2 family protein [Leptospira alexanderi]	29.5	29.5	91%	34	73%	WP_078124808.1
SIR2-like domain protein [Leptospira alexanderi serovar Manhao 3 str. L 60]	29.5	29.5	91%	34	73%	EQA62859.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
C-5 sterol desaturase [Hyphomonas oceanitis]	29.5	29.5	83%	34	69%	WP_035535795.1
C-5 sterol desaturase [Hyphomonas chukchiensis]	29.5	29.5	83%	34	69%	WP_034737493.1
neurotransmitter symporter family protein [[Clostridium] sordellii ATCC 9714]	29.5	29.5	75%	34	89%	EPZ53995.1
predicted protein [Thalassiosira pseudonana CCMP1335]	29.1	29.1	83%	48	90%	EED86778.1
hypothetical protein [Thiomicrospira arctica]	29.1	29.1	75%	49	75%	WP_019555878.1
Dynein heavy chain 7, axonemal [Ooceraea biroi]	28.6	28.6	91%	68	73%	EZA60901.1
hypothetical protein BGO69_07650 [Bacteroidetes bacterium 46-16]	28.6	28.6	66%	68	100%	OJW84588.1
sigma-54-dependent Fis family transcriptional regulator [Clostridium lundense]	28.6	28.6	83%	68	80%	WP_051541917.1
polysaccharide biosynthesis protein [Candidatus Moduliflexus flocculans]	28.6	28.6	83%	68	82%	GAK51413.1
putative uncharacterized protein [Clostridium bolteae CAG:59]	28.6	28.6	83%	68	80%	CCY00941.1
sodium-dependent transporter [[Clostridium] bolteae]	28.6	28.6	83%	68	80%	WP_002569264.1
sodium-dependent transporter [[Clostridium] bolteae]	28.6	28.6	83%	68	80%	WP_002576991.1
sodium-dependent transporter [[Clostridium] bolteae]	28.6	28.6	83%	68	80%	WP_002573061.1
putative sodium symporter-family membrane transport protein [Chlamydia trachomatis]	28.6	28.6	83%	68	80%	CRH67613.1
hypothetical protein CLOBOL_04222 [[[Clostridium] bolteae ATCC BAA-613]	28.6	28.6	83%	68	80%	EDP15301.1
Sodium:neurotransmitter symporter family protein [Coriobacteriales bacterium DNF00809]	28.6	28.6	83%	68	80%	KXB53896.1
alpha/beta hydrolase [Chryseobacterium solincola]	28.6	28.6	100%	68	71%	WP_039341223.1
endonuclease [Pedobacter sp. Leaf176]	28.6	28.6	91%	68	75%	WP_056096943.1
ATP-dependent helicase DinG [Paenibacillus sp. Root52]	28.2	28.2	100%	96	67%	WP_056696789.1
TonB-dependent receptor [Cellvibrionales bacterium TMED122]	28.2	28.2	100%	96	83%	OUV59202.1
hypothetical protein BCR44DRAFT_1449593 [Catenaria anguillulae PL171]	28.2	28.2	75%	96	78%	ORZ29519.1
dNA topoisomerase [Eubacterium sp. CAG:274]	28.2	28.2	100%	96	48%	CDC18289.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein A2X45_15545 [Lentisphaerae bacterium GWF2_50_93]	28.2	28.2	100%	96	48%	OGV55306.1
DUF3131 domain-containing protein [Actibacterium atlanticum]	28.2	28.2	83%	96	80%	WP_035250104.1
hypothetical protein A3B81_00670 [Candidatus Muproteobacteria bacterium RIFCSPHIGHO2_02_FULL_65_16]	28.2	28.2	75%	96	78%	OGI49710.1
hypothetical protein A2637_05675 [Candidatus Muproteobacteria bacterium RIFCSPHIGHO2_01_FULL_65_16]	28.2	28.2	75%	96	78%	OGI45333.1
hypothetical protein EHEL_080100 [Encephalitozoon hellem ATCC 50504]	28.2	28.2	75%	97	78%	AFM98716.1
hypothetical protein NBO_623g0001 [Nosema bombycis CQ1]	28.2	28.2	75%	97	78%	EOB11940.1
CPBP family intramembrane metalloprotease [Aerococcus urinaeequi]	28.2	28.2	66%	97	88%	WP_069286469.1
CPBP family intramembrane metalloprotease [Streptomyces alboniger]	28.2	28.2	66%	97	88%	WP_059134875.1
hypothetical protein [Exiguobacterium sibiricum]	28.2	28.2	83%	97	64%	WP_051525145.1
hypothetical protein [Exiguobacterium sibiricum]	28.2	28.2	83%	97	64%	WP_012370305.1
conserved hypothetical protein [Pantoea sp. aB]	28.2	28.2	83%	99	70%	EFM17494.1
hypothetical protein SARC_02585 [Sphaeroforma arctica JP610]	27.8	27.8	83%	136	80%	KNC85207.1
hypothetical protein TP02_0020 [Theileria parva]	27.8	27.8	66%	136	88%	EAN32306.1
hypothetical protein TA11590 [Theileria annulata]	27.8	27.8	66%	136	88%	CAI74952.1
hybrid sensor histidine kinase/response regulator [Roseovarius marisflavi]	27.8	27.8	91%	136	73%	WP_084732841.1
elongation factor G [Klebsiella aerogenes]	27.8	27.8	75%	136	89%	WP_087876910.1
MULTISPECIES: TonB-dependent receptor [Acinetobacter]	27.8	27.8	100%	136	75%	WP_004646260.1
MULTISPECIES: membrane protein [Acinetobacter]	27.8	27.8	100%	136	75%	WP_044111636.1
membrane protein [Acinetobacter lwoffii]	27.8	27.8	100%	136	75%	WP_004279401.1
MULTISPECIES: TonB-dependent receptor [Acinetobacter]	27.8	27.8	100%	136	75%	WP_005104669.1
hypothetical protein [Parasitella parasitica]	27.8	27.8	83%	136	80%	CEP17924.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncharacterised protein [Dorea longicatena]	27.8	27.8	91%	136	73%	CUP17839.1
hypothetical protein [Leeuwenhoekiella sp. Hel_I_48]	27.8	27.8	83%	136	64%	WP_028377296.1
Na+-dependent transporters of the SNF family [uncultured Ruminococcus sp.]	27.8	27.8	91%	137	75%	SCH68496.1
transporter [Firmicutes bacterium CAG:145]	27.8	27.8	91%	137	75%	CDB03420.1
L-seryl-tRNA(Sec) selenium transferase [Finegoldia magna ATCC 53516]	27.8	27.8	100%	137	75%	EFH93000.1
L-selenocysteinyl-tRNA(Sec) synthase [Finegoldia magna]	27.8	27.8	100%	137	75%	WP_035109254.1
Na+-dependent transporters of the SNF family [uncultured Ruminococcus sp.]	27.8	27.8	91%	137	75%	SCH93947.1
sodium-dependent transporter [Coprococcus sp. CAG:131_42_139]	27.8	27.8	91%	137	75%	OKZ91760.1
sodium-dependent transporter [Coprococcus eutactus]	27.8	27.8	91%	137	75%	WP_055224294.1

Alignments

alpha-1-acid glycoprotein 2 precursor [Homo sapiens]
Sequence ID: **NP_000599.1** Length: 201 Number of Matches: 1

See 6 more title(s)
Range 1: 127 to 138

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	5e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    TLMFGSYLDDEK  12
           TLMFGSYLDDEK
Sbjct  127  TLMFGSYLDDEK  138
```

ORM2 [Homo sapiens]
Sequence ID: **CAG33211.1** Length: 201 Number of Matches: 1
Range 1: 127 to 138

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	5e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    TLMFGSYLDDEK  12
            TLMFGSYLDDEK
Sbjct  127  TLMFGSYLDDEK  138
```

alpha-1-acid glycoprotein 2 precursor [Homo sapiens]

Sequence ID: **CAA29873.2** Length: 201 Number of Matches: 1
Range 1: 127 to 138

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	5e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    TLMFGSYLDDEK  12
            TLMFGSYLDDEK
Sbjct  127  TLMFGSYLDDEK  138
```

ORM2, partial [synthetic construct]

Sequence ID: **AIC54853.1** Length: 201 Number of Matches: 1
Range 1: 127 to 138

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	5e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    TLMFGSYLDDEK  12
            TLMFGSYLDDEK
Sbjct  127  TLMFGSYLDDEK  138
```

unnamed protein product [Homo sapiens]

Sequence ID: **BAG35159.1** Length: 201 Number of Matches: 1
Range 1: 127 to 138

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	5e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    TLMFGSYLDDEK  12
           TLMFGSYLDDEK
Sbjct  127  TLMFGSYLDDEK  138
```

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BLAST Results

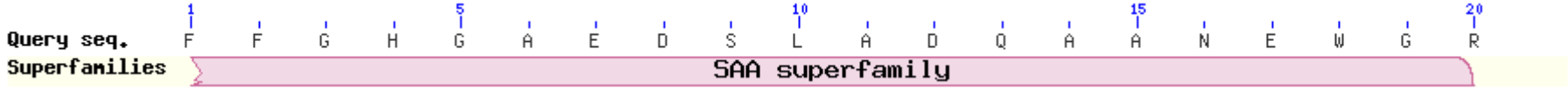
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RID S56D7NBW014 (Expires on 08-04 11:33 am)

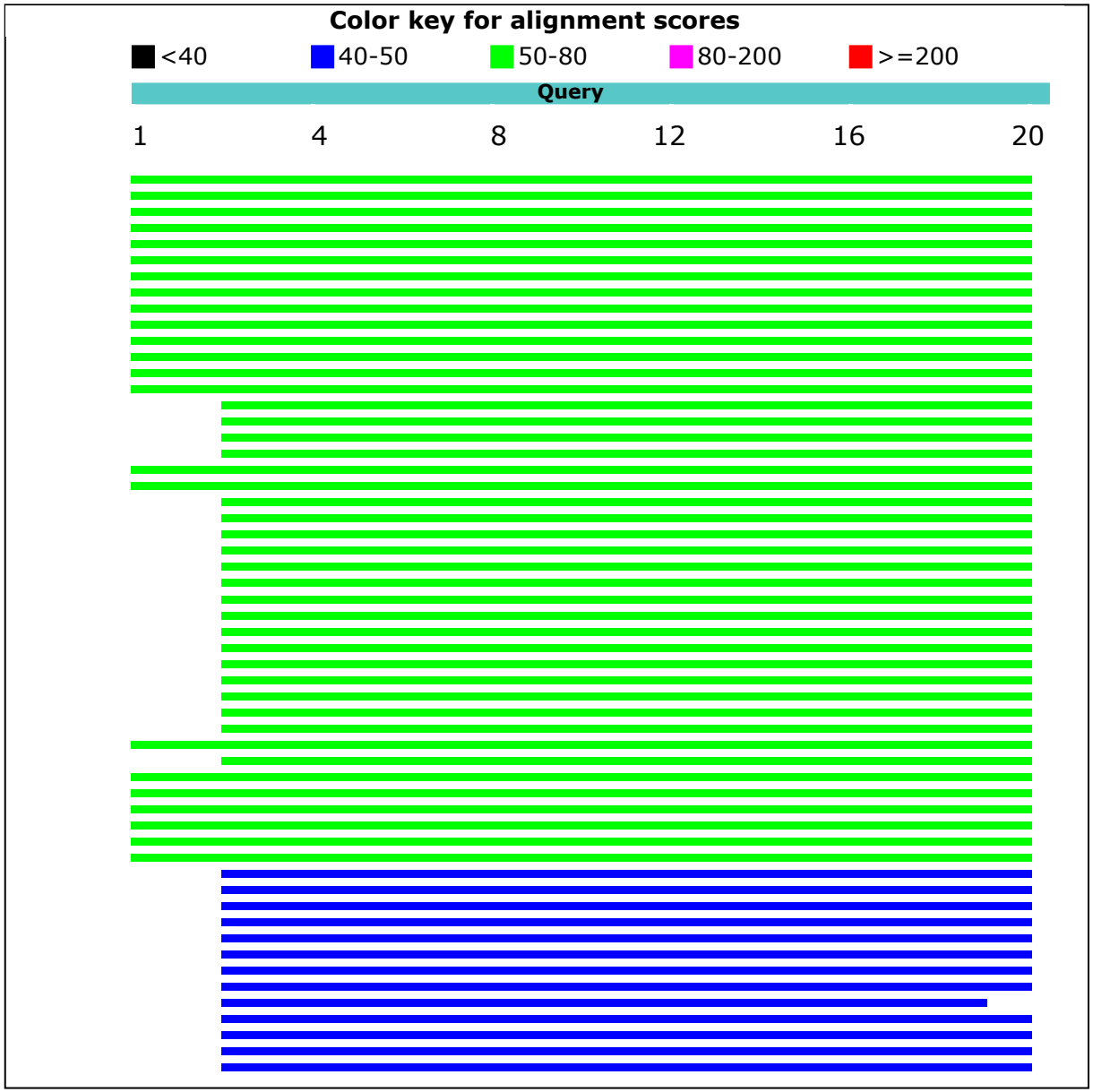
Query ID	lcl|Query_44576	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20	**Program**	BLASTP 2.6.1+

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
4
8
12
16
20

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
SAA protein partial (AA 1-52) [Homo sapiens]	67.2	67.2	100%	2e-12	100%	CAA35804.1
serum amyloid A [Homo sapiens]	67.2	67.2	100%	2e-12	100%	CAA35806.1
amyloid related serum protein SAA	67.2	67.2	100%	7e-12	100%	1405211B
Chain A, Structure Of Human Serum Amyloid A1	67.2	67.2	100%	7e-12	100%	4IP8_A
serum amyloid A1 [synthetic construct]	67.2	67.2	100%	7e-12	100%	AAX36983.1
human serum amyloid A [Homo sapiens]	67.2	67.2	100%	7e-12	100%	AAA60297.1
RecName: Full=Serum amyloid A-1 protein; Short=SAA; Contains: RecName: Full=Amyloid protein A; AltName: Full=Amyloid fibril protein AA; Contains: RecName: Full=Serum amyloid protein A(2-104); Contains: RecName: Full=Serum amyloid protein A(3-104); Contains: RecName: Full=Serum amyloid protein A(2-103); Contains: RecName: Full=Serum amyloid protein A(2-102); Contains: RecName: Full=Serum amyloid protein A(4-101); Flags: Precursor	67.2	67.2	100%	7e-12	100%	P0DJI8.1
serum amyloid A-1 protein preproprotein [Homo sapiens]	67.2	67.2	100%	7e-12	100%	NP_954630.1
serum amyloid A1, isoform CRA_a [Homo sapiens]	67.2	67.2	100%	7e-12	100%	EAW68408.1
Chain A, Structure Of Native Human Serum Amyloid A1	67.2	67.2	100%	7e-12	100%	4IP9_A
SAA1 protein [Homo sapiens]	64.7	64.7	100%	5e-11	95%	AAH07022.1
protein inflammatory disease	64.7	64.7	100%	5e-11	95%	0909229A
serum amyloid A protein beta des-Arg(pI5.6), SAA1 beta des-Arg pI5.6 [human, Peptide, 103 aa]	63.4	63.4	100%	1e-10	95%	AAB21773.1
serum amyloid A protein beta (pI6.1), SAA1 beta (pI6.1) [human, Peptide, 104 aa]	63.4	63.4	100%	1e-10	95%	AAB21774.1
hypothetical protein EGK_06437 [Macaca mulatta]	57.1	57.1	90%	3e-08	94%	EHH23059.1
serum amyloid A-1 protein precursor [Oryctolagus cuniculus]	57.1	57.1	90%	3e-08	94%	NP_001075796.1
serum amyloid A-2 protein precursor [Oryctolagus cuniculus]	57.1	57.1	90%	3e-08	94%	NP_001075861.1
serum amyloid A-2 protein precursor [Pongo abelii]	57.1	57.1	90%	3e-08	94%	NP_001127066.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
RecName: Full=Serum amyloid A protein; Short=SAA; Contains: RecName: Full=Amyloid protein A; AltName: Full=Amyloid fibril protein AA; Flags: Precursor	54.9	54.9	100%	1e-07	76%	P19707.2
serum amyloid A 1 [Acinonyx jubatus]	54.9	54.9	100%	1e-07	76%	BAG06986.1
serum amyloid A2-alpha [Homo sapiens]	54.5	54.5	90%	2e-07	94%	AAA64800.1
SAA precursor polypeptide (119 AA) [Homo sapiens]	54.5	54.5	90%	2e-07	94%	CAA35810.1
amyloid related serum protein SAA	54.5	54.5	90%	2e-07	94%	1405211A
SAA2 alpha [Homo sapiens]	54.5	54.5	90%	2e-07	94%	CAA39975.1
Serum amyloid A-3 protein [Tupaia chinensis]	54.1	54.1	90%	3e-07	94%	ELW70752.1
serum amyloid A protein [Oryctolagus cuniculus]	53.2	53.2	90%	5e-07	89%	CAA34450.1
serum amyloid A protein precursor [Canis lupus familiaris]	53.2	53.2	90%	6e-07	94%	NP_001300801.1
unknown [Oryctolagus cuniculus]	53.2	53.2	90%	6e-07	89%	CAA41560.1
serum amyloid A protein [Canis lupus familiaris]	53.2	53.2	90%	6e-07	94%	AAA62764.1
serum amyloid A protein [Canis lupus familiaris]	53.2	53.2	90%	6e-07	94%	AAA62762.1
serum amyloid A protein [Canis lupus familiaris]	53.2	53.2	90%	6e-07	94%	AAA51457.1
serum amyloid A protein [Canis lupus familiaris]	53.2	53.2	90%	6e-07	94%	AAA62765.1
serum amyloid A, SAA [rabbits, acute-phase serum, Peptide, 104 aa]	53.2	53.2	90%	6e-07	89%	AAB20537.1
serum amyloid A protein, SAA [rabbits, acute phase serum, Peptide Partial, 103 aa]	53.2	53.2	90%	6e-07	89%	AAB26155.1
Serum amyloid A protein [Macaca mulatta]	52.4	52.4	90%	1e-06	89%	EHH23058.1
hypothetical protein PANDA_022332 [Ailuropoda melanoleuca]	51.5	51.5	100%	2e-06	72%	EFB14467.1
Serum amyloid A-1 protein [Tupaia chinensis]	51.5	51.5	90%	2e-06	89%	ELW70751.1
hypothetical protein PANDA_018865 [Ailuropoda melanoleuca]	51.5	51.5	100%	2e-06	72%	EFB28776.1
serum amyloid A protein precursor [Felis catus]	51.5	51.5	100%	2e-06	72%	NP_001295969.1
serum amyloid A protein precursor [Felis catus]	51.5	51.5	100%	2e-06	72%	NP_001035288.1
serum amyloid A [Felis catus]	51.5	51.5	100%	2e-06	72%	BAE93427.1
serum amyloid A [Felis catus]	51.5	51.5	100%	2e-06	72%	BAE93425.1
serum amyloid A [Felis catus]	51.5	51.5	100%	2e-06	72%	AAD24489.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
SAA protein partial (AA 1-52) [Homo sapiens]	49.8	49.8	90%	6e-06	89%	CAA35805.1
Hermansky-Pudlak syndrome 5 protein isoform 1 [Camelus ferus]	49.8	97.1	90%	8e-06	89%	EQB79124.1
RecName: Full=Serum amyloid A-2 protein; Contains: RecName: Full=Amyloid protein A; AltName: Full=Amyloid fibril protein AA; Flags: Precursor	49.8	49.8	90%	9e-06	89%	P02739.2
RecName: Full=Serum amyloid A-1 protein; Flags: Precursor	49.8	49.8	90%	9e-06	89%	P18575.1
serum amyloid A-2 protein precursor [Mustela putorius furo]	49.8	49.8	90%	9e-06	89%	NP_001297109.1
amyloid A precursor [Homo sapiens]	49.8	49.8	90%	9e-06	89%	AAB59539.1
serum amyloid A-2 protein isoform a precursor [Homo sapiens]	49.8	49.8	90%	9e-06	89%	NP_110381.2
serum amyloid A, SAA [mink, Peptide, 114 aa]	49.8	49.8	90%	9e-06	89%	AAB27301.1
amyloid A protein	49.8	49.8	85%	9e-06	94%	1613169A
serum amyloid A protein precursor [Equus caballus]	49.0	49.0	90%	2e-05	89%	NP_001157364.1
serum amyloid A protein [Equus caballus]	49.0	49.0	90%	2e-05	89%	AAP78729.1
serum amyloid A protein precursor [Equus caballus]	48.6	48.6	90%	2e-05	89%	NP_001075322.1
RecName: Full=Serum amyloid A protein; Short=SAA; Contains: RecName: Full=Amyloid protein A; AltName: Full=Amyloid fibril protein AA	48.6	48.6	90%	2e-05	89%	P19857.2
serum amyloid A-3 [Mus musculus]	47.3	47.3	90%	4e-05	89%	CDI30254.1
hypothetical protein A6R68_19675 [Neotoma lepida]	47.3	47.3	90%	7e-05	89%	OBS77932.1
hypothetical protein A6R68_09367 [Neotoma lepida]	47.3	47.3	90%	7e-05	89%	OBS59504.1
serum amyloid A-3 protein precursor [Mus musculus]	47.3	47.3	90%	7e-05	89%	NP_035445.1
Serum amyloid A-1 protein [Fukomys damarensis]	47.3	47.3	90%	7e-05	89%	KFO18663.1
Serum amyloid A-3 protein [Heterocephalus glaber]	47.3	47.3	90%	7e-05	89%	EHA97364.1
serum amyloid A 3, isoform CRA_a [Mus musculus]	47.3	47.3	90%	7e-05	89%	EDL22935.1
Chain A, Crystal Structure Of Mouse Serum Amyloid A3	47.3	47.3	90%	7e-05	89%	4Q5G_A
serum amyloid A3 [Mus musculus]	47.3	47.3	90%	7e-05	89%	CAA27199.1
serum amyloid A (AA at 141) [Mus musculus]	47.3	47.3	90%	7e-05	89%	AAA40088.1
serum amyloid A-1-like protein [Mustela putorius furo]	46.4	46.4	90%	1e-04	83%	AKJ52175.1
serum amyloid A-3 protein precursor [Sus scrofa]	45.6	45.6	90%	3e-04	83%	NP_001038017.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
serum amyloid A protein precursor [Bos taurus]	45.6	45.6	90%	3e-04	83%	NP_001068728.1
TPA: serum amyloid A protein-like [Bos taurus]	45.6	45.6	90%	3e-04	83%	DAA13985.1
Serum amyloid A protein [Bos mutus]	45.6	45.6	90%	3e-04	83%	ELR52844.1
serum amyloid A [Epinephelus coioides]	45.6	45.6	90%	3e-04	83%	AFQ00087.1
serum amyloid A, SAA [cattle, serum, Peptide, 111 aa]	45.6	45.6	90%	3e-04	83%	AAB21386.1
serum amyloid A protein [Sus scrofa]	45.6	45.6	90%	3e-04	83%	ABN15150.1
Serum amyloid A protein [Pelecanus crispus]	42.6	42.6	90%	0.003	78%	KFQ51290.1
Serum amyloid A protein [Fulmarus glacialis]	42.6	42.6	90%	0.003	78%	KFV96126.1
Serum amyloid A protein [Mesitornis unicolor]	42.6	42.6	90%	0.003	78%	KFQ26810.1
Serum amyloid A protein [Haliaeetus albicilla]	42.6	42.6	90%	0.003	78%	KFP94150.1
Serum amyloid A protein, partial [Chlamydotis macqueenii]	42.6	42.6	90%	0.003	78%	KFP39350.1
Serum amyloid A protein [Cuculus canorus]	42.6	42.6	90%	0.003	78%	KFO71862.1
serum amyloid A [Sphenodon punctatus]	42.6	42.6	90%	0.003	78%	AAM46103.1
Serum amyloid A protein [Mizuhopecten yessoensis]	42.6	42.6	90%	0.003	78%	OWF44330.1
rCG53589, isoform CRA_a [Rattus norvegicus]	42.2	42.2	90%	0.004	83%	EDM07258.1
serum amyloid A-3 protein precursor [Oryctolagus cuniculus]	42.2	42.2	90%	0.004	78%	NP_001075771.1
rCG53589, isoform CRA_b [Rattus norvegicus]	42.2	42.2	90%	0.004	83%	EDM07259.1
Bq135360 [Rattus norvegicus]	42.2	42.2	90%	0.004	83%	AAP92660.1
Serum amyloid A-3 protein [Pteropus alecto]	41.8	41.8	90%	0.006	83%	ELK18831.1
serum amyloid A1 precursor [Canis lupus familiaris]	41.8	41.8	75%	0.006	93%	NP_001003050.1
serum amyloid A-2 protein-like precursor [Tursiops truncatus]	41.8	41.8	90%	0.006	83%	NP_001268733.1
mammary serum amyloid A3.2 precursor [Bos taurus]	41.8	41.8	70%	0.006	93%	NP_001229502.1
TPA: mammary serum amyloid A3.2-like [Bos taurus]	41.8	41.8	70%	0.006	93%	DAA13986.1
serum amyloid A3 [Bos taurus]	41.8	41.8	70%	0.006	93%	AHY20046.1
hypothetical protein [Streptomyces nanshensis]	40.9	40.9	90%	0.007	78%	WP_079163981.1
Serum amyloid A protein, partial [Balearica regulorum gibbericeps]	41.4	41.4	90%	0.008	72%	KFO04708.1
Serum amyloid A-3 protein [Cricetulus griseus]	40.9	40.9	100%	0.012	75%	EGW00379.1
Serum amyloid A-3 protein [Cricetulus griseus]	40.9	40.9	100%	0.012	75%	EGW00378.1
serum amyloid A [Bubalus bubalis]	40.9	40.9	90%	0.012	78%	AIP90360.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
serum amyloid A precursor [Bubalus bubalis]	40.9	40.9	90%	0.012	78%	AII78664.1
Serum amyloid A-2 protein [Calypte anna]	40.1	40.1	90%	0.023	72%	KFO96759.1
serum amyloid A [Perca flavescens]	40.1	40.1	90%	0.023	83%	AGH06149.1

Alignments

SAA protein partial (AA 1-52), partial [Homo sapiens]
Sequence ID: **CAA35804.1** Length: 50 Number of Matches: 1
Range 1: 14 to 33

Score	Expect	Method	Identities	Positives	Gaps	Frame
67.2 bits(151)	2e-12()		20/20(100%)	20/20(100%)	0/20(0%)	

Features:

```
Query  1   FFGHGAEDSLADQAANEWGR  20
           FFGHGAEDSLADQAANEWGR
Sbjct  14  FFGHGAEDSLADQAANEWGR  33
```

serum amyloid A, partial [Homo sapiens]
Sequence ID: **CAA35806.1** Length: 50 Number of Matches: 1

See 1 more title(s)
Range 1: 14 to 33

Score	Expect	Method	Identities	Positives	Gaps	Frame
67.2 bits(151)	2e-12()		20/20(100%)	20/20(100%)	0/20(0%)	

Features:

```
Query  1   FFGHGAEDSLADQAANEWGR  20
           FFGHGAEDSLADQAANEWGR
Sbjct  14  FFGHGAEDSLADQAANEWGR  33
```

amyloid related serum protein SAA
Sequence ID: **prf||1405211B** Length: 104 Number of Matches: 1
Range 1: 68 to 87

Score	Expect	Method	Identities	Positives	Gaps	Frame
67.2 bits(151)	7e-12()		20/20(100%)	20/20(100%)	0/20(0%)	

Features:

```
Query  1   FFGHGAEDSLADQAANEWGR  20
           FFGHGAEDSLADQAANEWGR
Sbjct  68  FFGHGAEDSLADQAANEWGR  87
```

Chain A, Structure Of Human Serum Amyloid A1

Sequence ID: **4IP8_A** Length: 105 Number of Matches: 1

See 3 more title(s)

Range 1: 69 to 88

Score	Expect	Method	Identities	Positives	Gaps	Frame
67.2 bits(151)	7e-12()		20/20(100%)	20/20(100%)	0/20(0%)	

Features:

```
Query  1   FFGHGAEDSLADQAANEWGR  20
           FFGHGAEDSLADQAANEWGR
Sbjct  69  FFGHGAEDSLADQAANEWGR  88
```

serum amyloid A1, partial [synthetic construct]

Sequence ID: **AAX36983.1** Length: 123 Number of Matches: 1

Range 1: 86 to 105

Score	Expect	Method	Identities	Positives	Gaps	Frame
67.2 bits(151)	7e-12()		20/20(100%)	20/20(100%)	0/20(0%)	

Features:

```
Query  1    FFGHGAEDSLADQAANEWGR  20
            FFGHGAEDSLADQAANEWGR
Sbjct  86   FFGHGAEDSLADQAANEWGR  105
```

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BLAST Results

Job title: P_SAA1_SFFSFLGEAFDGAR

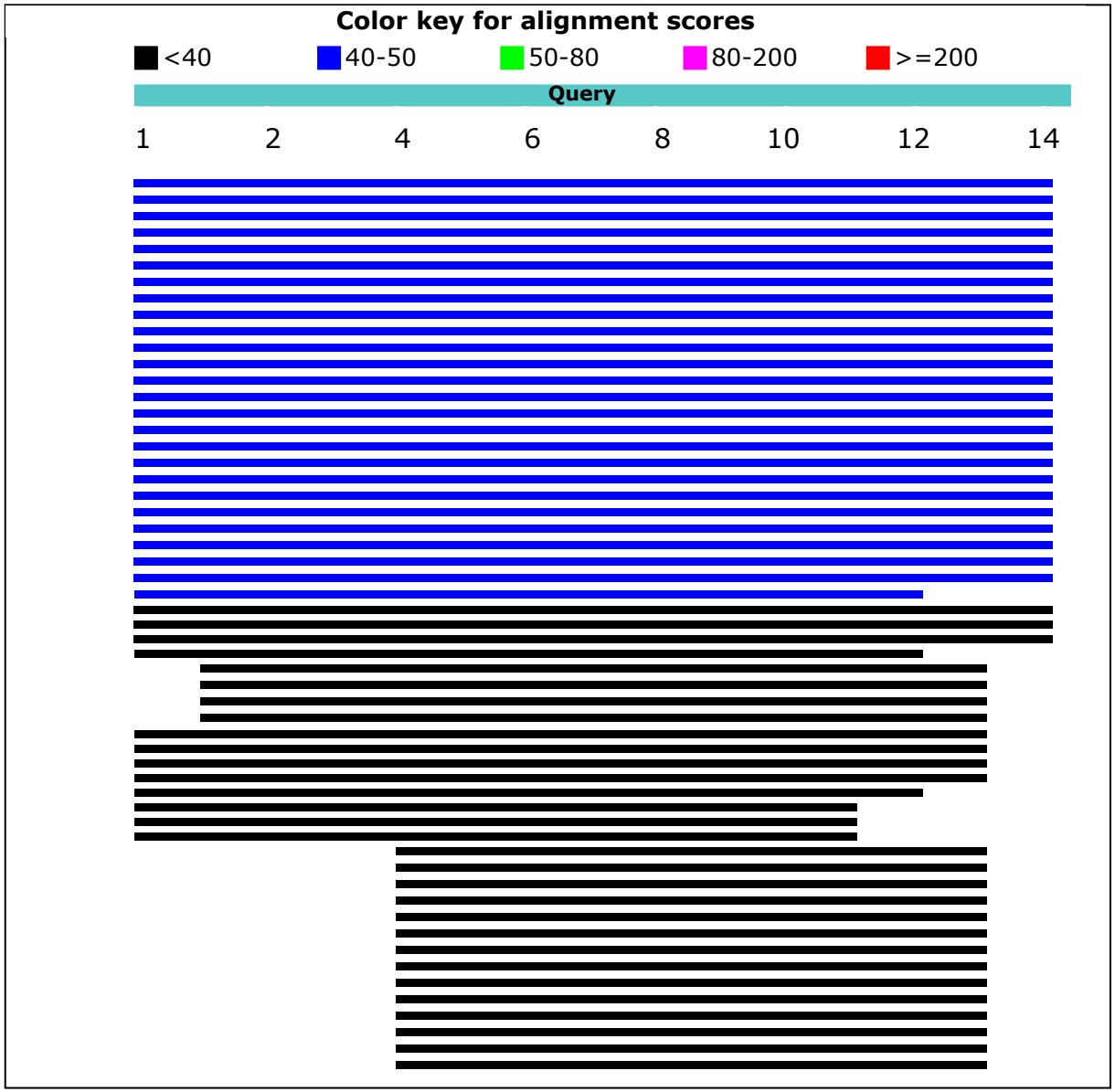
RID S56DE3W9014 (Expires on 08-04 11:34 am)

Query ID	lcl|Query_255596	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12
14

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
SAA precursor polypeptide (AA -18 to 37) [Homo sapiens]	46.9	46.9	100%	3e-05	100%	CAA35809.1
SAA2-SAA2 protein precursor [Homo sapiens]	46.9	46.9	100%	3e-05	100%	NP_001186673.1
SAA2-SAA3 isoform a [Homo sapiens]	46.9	46.9	100%	3e-05	100%	BAQ56008.1
SAA protein [Homo sapiens]	46.9	46.9	100%	3e-05	100%	CAA35808.1
serum amyloid A1 [synthetic construct]	46.9	46.9	100%	3e-05	100%	AAX36983.1
serum amyloid A2-alpha [Homo sapiens]	46.9	46.9	100%	3e-05	100%	AAA64800.1
human serum amyloid A [Homo sapiens]	46.9	46.9	100%	3e-05	100%	AAA60297.1
amyloid A precursor [Homo sapiens]	46.9	46.9	100%	3e-05	100%	AAB59539.1
SAA1 protein [Homo sapiens]	46.9	46.9	100%	3e-05	100%	AAH07022.1
serum amyloid A-2 protein isoform a precursor [Homo sapiens]	46.9	46.9	100%	3e-05	100%	NP_110381.2
RecName: Full=Serum amyloid A-1 protein; Short=SAA; Contains: RecName: Full=Amyloid protein A; AltName: Full=Amyloid fibril protein AA; Contains: RecName: Full=Serum amyloid protein A(2-104); Contains: RecName: Full=Serum amyloid protein A(3-104); Contains: RecName: Full=Serum amyloid protein A(2-103); Contains: RecName: Full=Serum amyloid protein A(2-102); Contains: RecName: Full=Serum amyloid protein A(4-101); Flags: Precursor	46.9	46.9	100%	3e-05	100%	P0DJI8.1
serum amyloid A-1 protein preproprotein [Homo sapiens]	46.9	46.9	100%	3e-05	100%	NP_954630.1
serum amyloid A1, isoform CRA_a [Homo sapiens]	46.9	46.9	100%	3e-05	100%	EAW68408.1
serum amyloid A-2 protein precursor [Pongo abelii]	46.9	46.9	100%	3e-05	100%	NP_001127066.1
SAA precursor polypeptide (119 AA) [Homo sapiens]	46.9	46.9	100%	3e-05	100%	CAA35810.1
serum amyloid A2, isoform CRA_a [Homo sapiens]	46.9	46.9	100%	3e-05	100%	EAW68412.1
Chain A, Structure Of Native Human Serum Amyloid A1	46.9	46.9	100%	3e-05	100%	4IP9_A
Chain A, Structure Of Human Serum Amyloid A1	46.9	46.9	100%	3e-05	100%	4IP8_A
amyloid related serum protein SAA	46.9	46.9	100%	3e-05	100%	1405211A
amyloid related serum protein SAA	46.9	46.9	100%	3e-05	100%	1405211B

Description	Max score	Total score	Query cover	E value	Ident	Accession
protein inflammatory disease	46.9	46.9	100%	3e-05	100%	0909229A
serum amyloid A protein beta (pI6.1), SAA1 beta (pI6.1) [human, Peptide, 104 aa]	46.9	46.9	100%	3e-05	100%	AAB21774.1
serum amyloid A protein beta des-Arg(pI5.6), SAA1 beta des-Arg pI5.6 [human, Peptide, 103 aa]	46.9	46.9	100%	3e-05	100%	AAB21773.1
serum amyloid A-2 protein isoform b precursor [Homo sapiens]	46.9	46.9	100%	4e-05	100%	NP_001120852.1
SAA2-SAA3 isoform b [Homo sapiens]	46.9	46.9	100%	4e-05	100%	BAQ56009.1
serum amyloid A1, isoform CRA_b [Homo sapiens]	40.9	40.9	85%	0.003	100%	EAW68410.1
hypothetical protein EGK_06437 [Macaca mulatta]	38.4	38.4	100%	0.034	86%	EHH23059.1
Serum amyloid A protein [Macaca mulatta]	38.4	38.4	100%	0.034	86%	EHH23058.1
RecName: Full=Amyloid protein A; AltName: Full=Amyloid fibril protein AA	38.4	38.4	100%	0.035	86%	P02738.1
Ab1-018 [Rattus norvegicus]	33.3	33.3	85%	2.1	83%	AAP92533.1
mCG144019 [Mus musculus]	33.3	33.3	85%	2.2	83%	EDL22939.1
serum amyloid A protein isoform 2 [Mus musculus]	33.3	33.3	85%	2.2	83%	AAB37250.1
serum amyloid A-2 protein precursor [Mus musculus]	33.3	33.3	85%	2.2	83%	NP_035444.1
serum amyloid A protein pI 5.9 isoform, apo-SAA (pI 5.9) [mice, SJL/J, Peptide, 103 aa]	33.3	33.3	85%	2.2	83%	AAB22172.1
type III secretion system effector protein exou [Pseudomonas fluorescens]	32.9	32.9	92%	3.0	77%	WP_043046223.1
type III secretion system effector protein exou [Pseudomonas fluorescens]	32.5	32.5	92%	4.3	77%	WP_068965657.1
type III secretion system effector protein exou [Pseudomonas sp. Root569]	32.5	32.5	92%	4.3	77%	WP_056846949.1
type III secretion system effector protein exou [Pseudomonas fluorescens]	32.5	32.5	92%	4.3	77%	WP_046069896.1
hypothetical protein [Pseudoalteromonas lipolytica]	31.6	31.6	85%	8.6	75%	WP_074989029.1
hypothetical protein UT47_C0001G0118 [candidate division CPR2 bacterium GW2011_GWC2_39_35]	31.2	31.2	78%	12	83%	KKR18728.1
hypothetical protein A2Y26_02575 [candidate division CPR2 bacterium GWD2_39_7]	31.2	31.2	78%	12	83%	OGB72832.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein A2Y27_01260 [candidate division CPR2 bacterium GWD1_39_7]	31.2	31.2	78%	12	83%	OGB56513.1
threonine synthase [Methylosinus sp. PW1]	30.8	30.8	64%	17	100%	WP_036294664.1
threonine synthase [Methylosinus sp. LW4]	30.8	30.8	64%	17	100%	WP_018266727.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_081196457.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_064973424.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_063280404.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_063281967.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_061777642.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_058225539.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_058209001.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_058219104.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_058204034.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_057719750.1
MIP family channel protein [Lactococcus lactis subsp. lactis]	30.8	30.8	64%	17	100%	KLK95205.1
MIP family channel protein [Lactococcus lactis subsp. cremoris]	30.8	30.8	64%	17	100%	KKW70644.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_046124201.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_043737220.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_012897073.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_010905238.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_011675282.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_032950855.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_021165796.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_014571958.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_014570367.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_021036633.1
hypothetical protein LLCRE1631_01370 [Lactococcus lactis subsp. lactis CNCM I-1631]	30.8	30.8	64%	17	100%	EHE93318.1
aquaporin family protein [Lactococcus lactis]	30.8	30.8	64%	17	100%	WP_038598844.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Glycerol uptake facilitator protein [Lactococcus lactis subsp. lactis]	30.8	30.8	64%	17	100%	KSU13518.1
hypothetical protein Celaphus_00013535 [Cervus elaphus hippelaphus]	30.8	30.8	71%	17	90%	OWK17284.1
Glycerol uptake facilitator protein [Lactococcus lactis subsp. lactis]	30.8	30.8	64%	17	100%	KST86044.1
hypothetical protein CANCADRAFT_93471 [Tortispora caseinolytica NRRL Y-17796]	29.9	29.9	71%	35	80%	ODV92797.1
hypothetical protein H072_5624 [Dactylellina haptotyla CBS 200.50]	29.5	29.5	78%	49	73%	EPS40525.1
hypothetical protein [Bdellovibrio exovorus]	29.5	29.5	100%	49	52%	WP_015470010.1
type III secretion system effector protein exou [Pseudomonas libanensis]	29.5	29.5	71%	49	80%	WP_057014135.1
two-component sensor histidine kinase [Lachnoclostridium phytofermentans]	29.5	29.5	64%	49	89%	WP_029502765.1
secretion system protein E [Thermodesulfobacterium geofontis]	29.5	29.5	64%	49	89%	WP_013909711.1
hypothetical protein [Sphingomonas sp. IBVSS2]	29.5	29.5	92%	49	77%	WP_086129439.1
metalloprotease [Haloterrigena turkmenica]	29.5	29.5	92%	49	77%	WP_058864873.1
peptidase M50 [Natronolimnobius innermongolicus]	29.5	29.5	92%	49	77%	WP_007259356.1
hypothetical protein AWC09_16575 [Mycobacterium hiberniae]	29.5	29.5	78%	49	82%	ORV67780.1
hypothetical protein [Mycobacterium hiberniae]	29.5	29.5	78%	49	82%	WP_085136490.1
GNAT family N-acetyltransferase [Afifella pfennigii]	29.5	29.5	78%	49	82%	WP_051630617.1
hypothetical protein B6I37_05395 [Desulfobacteraceae bacterium 4572_35.2]	29.5	29.5	92%	49	77%	OQY23400.1
unnamed protein product [Phytomonas sp. isolate Hart1]	29.5	29.5	64%	49	89%	CCW72307.1
serum amyloid A 1 [Mus musculus]	29.1	29.1	64%	60	89%	AAL83956.1
type III secretion system effector protein exou [Pseudomonas libanensis]	29.1	29.1	92%	70	69%	WP_059396631.1
secretion system protein E [Thermodesulfobacterium hveragerdense]	29.1	29.1	64%	70	89%	WP_028841174.1
secretion system protein E [Thermodesulfobacterium thermophilum]	29.1	29.1	64%	70	89%	WP_022855782.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
undecaprenyl-phosphate glucose phosphotransferase [Pseudoalteromonas ulvae]	29.1	29.1	64%	70	89%	WP_086742241.1
hypothetical protein [Acinetobacter baumannii]	29.1	29.1	71%	70	80%	WP_065725120.1
hypothetical protein [Acinetobacter baumannii]	29.1	29.1	71%	70	80%	WP_057689492.1
hypothetical protein [Acinetobacter baumannii]	29.1	29.1	71%	70	80%	WP_072618039.1
hypothetical protein [Acinetobacter baumannii]	29.1	29.1	71%	70	80%	WP_059212515.1
hypothetical protein [Acinetobacter junii]	29.1	29.1	71%	70	80%	WP_004909689.1
Ribonuclease III [Sporothrix insectorum RCEF 264]	28.6	28.6	92%	99	60%	OAA62582.1
hypothetical protein CHGG_06321 [Chaetomium globosum CBS 148.51]	28.6	28.6	85%	99	75%	EAQ89702.1
capsular biosynthesis protein [Pontibacter lucknowensis]	28.6	28.6	71%	99	80%	WP_076423137.1
hypothetical protein [Sandaracinus amylolyticus]	28.6	28.6	71%	99	80%	WP_053237236.1
Dipeptidyl aminopeptidase/acylaminoacyl peptidase [Alloactinosynnema iranicum]	28.6	28.6	71%	99	71%	SDC17235.1

Alignments

SAA precursor polypeptide (AA -18 to 37), partial [Homo sapiens]

Sequence ID: **CAA35809.1** Length: 55 Number of Matches: 1
Range 1: 20 to 33

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SFFSFLGEAFDGAR  14
           SFFSFLGEAFDGAR
Sbjct  20  SFFSFLGEAFDGAR  33
```

SAA2-SAA2 protein precursor [Homo sapiens]

Sequence ID: **NP_001186673.1** Length: 208 Number of Matches: 1
Range 1: 20 to 33

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SFFSFLGEAFDGAR  14
           SFFSFLGEAFDGAR
Sbjct  20  SFFSFLGEAFDGAR  33
```

SAA2-SAA3 isoform a [Homo sapiens]

Sequence ID: **BAQ56008.1** Length: 138 Number of Matches: 1
Range 1: 20 to 33

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SFFSFLGEAFDGAR  14
           SFFSFLGEAFDGAR
Sbjct  20  SFFSFLGEAFDGAR  33
```

SAA protein, partial [Homo sapiens]

Sequence ID: **CAA35808.1** Length: 64 Number of Matches: 1
Range 1: 13 to 26

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SFFSFLGEAFDGAR  14
           SFFSFLGEAFDGAR
Sbjct  13  SFFSFLGEAFDGAR  26
```

serum amyloid A1, partial [synthetic construct]

Sequence ID: **AAX36983.1** Length: 123 Number of Matches: 1
Range 1: 20 to 33

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.9 bits(103)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SFFSFLGEAFDGAR  14
           SFFSFLGEAFDGAR
Sbjct  20  SFFSFLGEAFDGAR  33
```

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BLAST Results

Job title: P_SAA4_EALQGVGDMGR

RID S56DX0H4014 (Expires on 08-04 11:34 am)

Query ID	lcl|Query_358754	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	11	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
SAA2-SAA2 protein precursor [Homo sapiens]	37.5	37.5	100%	0.038	100%	NP_001186673.1
serum amyloid A4 [synthetic construct]	37.5	37.5	100%	0.039	100%	AAX37106.1
serum amyloid A [Homo sapiens]	37.5	37.5	100%	0.039	100%	AAB24060.1
unnamed protein product [Homo sapiens]	37.5	37.5	100%	0.039	100%	BAG35115.1
serum amyloid A-4 protein precursor [Homo sapiens]	37.5	37.5	100%	0.039	100%	NP_006503.2
O-antigen translocase [Comamonadaceae bacterium A 288]	29.5	29.5	90%	28	90%	WP_088284872.1
Constitutively expressed serum amyloid A protein [Macaca mulatta]	29.5	29.5	100%	28	82%	EHH23060.1
kinase/pyrophosphorylase [Brachybacterium sp. P6-10-X1]	28.6	28.6	81%	56	89%	WP_076811276.1
hypothetical protein [Kushneria sp. YCWA18]	28.2	28.2	72%	79	100%	WP_084388004.1
hypothetical protein BH688_04460 [Kushneria sp. YCWA18]	28.2	28.2	72%	79	100%	OHV11935.1
hypothetical protein VFPPC_14781 [Pochonia chlamydosporia 170]	28.2	28.2	100%	79	73%	OAQ59484.1
hypothetical protein TI04_10935 [Achromatium sp. WMS2]	27.8	27.8	100%	112	82%	KOR28462.1
zinc transporter ZntB [Ruegeria pomeroyi]	27.8	27.8	81%	112	89%	WP_011241997.1
hypothetical protein COCHEDRAFT_1034479 [Bipolaris maydis C5]	27.8	27.8	90%	113	90%	EMD86707.1
hypothetical protein TI04_06615 [Achromatium sp. WMS2]	27.8	27.8	100%	113	82%	KOR30248.1
hypothetical protein TI04_12335 [Achromatium sp. WMS2]	27.8	27.8	100%	113	82%	KOR27879.1
hypothetical protein TI04_10350 [Achromatium sp. WMS2]	27.8	27.8	100%	114	82%	KOR28721.1
hypothetical protein TI04_12340 [Achromatium sp. WMS2]	27.8	27.8	100%	116	82%	KOR27880.1
Hypothetical protein AA314_02356 [Archangium gephyra]	27.8	27.8	100%	118	77%	AKJ00730.1
RecName: Full=AF4/FMR2 family member 4; AltName: Full=Protein lilliputian	27.4	27.4	90%	158	80%	Q29KG4.2
uncharacterized protein Dpse_GA21343, isoform E [Drosophila pseudoobscura pseudoobscura]	27.4	27.4	90%	158	80%	KRT04810.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
uncharacterized protein Dpse_GA21343, isoform D [Drosophila pseudoobscura pseudoobscura]	27.4	27.4	90%	158	80%	EAL33211.3
GL26297 [Drosophila persimilis]	27.4	27.4	90%	158	80%	EDW25655.1
DEAD/DEAH box helicase [Frankia sp. Iso899]	27.4	27.4	81%	159	89%	WP_022916108.1
ATP-binding protein [Amycolatopsis sp. MJM2582]	27.4	27.4	90%	159	90%	WP_052120991.1
type III secretion protein C [Pseudomonas sp. NFACC45]	27.4	27.4	100%	159	73%	SFG66450.1
APC family permease [Lentibacillus amyloliquefaciens]	27.4	27.4	90%	159	82%	WP_068446905.1
signal peptide peptidase SppA [Belnapia moabensis]	27.4	27.4	81%	160	90%	WP_043337075.1
hypothetical protein BU14_0266s0010 [Porphyra umbilicalis]	26.9	26.9	100%	225	75%	OSX74821.1
hypothetical protein BU14_0266s0019 [Porphyra umbilicalis]	26.9	26.9	100%	225	75%	OSX74830.1
PEP synthetase regulatory protein [Intrasporangium oryzae NRRL B-24470]	26.9	26.9	90%	227	80%	EWT02696.1
phosphoenolpyruvate synthase regulatory protein [Intrasporangium oryzae]	26.9	26.9	90%	227	80%	WP_034802485.1
hypothetical protein [Cystobacter ferrugineus]	26.9	26.9	100%	227	82%	WP_071897899.1
hypothetical protein [Cupriavidus sp. amp6]	26.9	26.9	90%	229	80%	WP_029044966.1
MULTISPECIES: hypothetical protein [Enterobacteriaceae]	26.9	26.9	81%	229	89%	WP_039265193.1
serum amyloid A3b [Cyprinus carpio]	26.9	26.9	100%	230	82%	ARO38308.1
hypothetical protein PSTG_01312 [Puccinia striiformis f. sp. tritici PST-78]	26.5	26.5	72%	319	88%	KNF05500.1
NLI interacting factor family phosphatase [Toxoplasma gondii GT1]	26.5	26.5	81%	319	89%	EPR62420.1
NLI interacting factor family phosphatase [Toxoplasma gondii ME49]	26.5	26.5	81%	319	89%	EPT27306.1
hypothetical protein [Salinimonas chungwhensis]	26.5	26.5	90%	319	80%	WP_083928636.1
thyroid hormone receptor-associated coactivator complex component [Aspergillus oryzae 3.042]	26.5	26.5	90%	319	80%	EIT72992.1
mediator of RNA polymerase II transcription subunit 14 [Aspergillus flavus AF70]	26.5	26.5	90%	319	80%	KOC16939.1
RecName: Full=Mediator of RNA polymerase II transcription subunit 14; AltName: Full=Mediator complex subunit 14	26.5	26.5	90%	319	80%	Q2UMJ1.2
Mediator complex subunit MED14 [Aspergillus parasiticus SU-1]	26.5	26.5	90%	319	80%	KJK63452.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Mediator complex, subunit Med14 [Aspergillus oryzae]	26.5	26.5	90%	319	80%	OOO04515.1
unnamed protein product [Aspergillus oryzae RIB40]	26.5	26.5	90%	319	80%	BAE57224.1
DNA mismatch repair protein MutS [Haemophilus paraphrohaemolyticus]	26.5	26.5	100%	320	73%	WP_005708108.1
DNA mismatch repair protein MutS [Haemophilus parahaemolyticus]	26.5	26.5	100%	320	73%	WP_005706410.1
MULTISPECIES: methyl-accepting chemotaxis protein [Methylobacterium]	26.5	26.5	100%	320	73%	WP_048430491.1
EscC/YscC/HrcC family type III secretion system outer membrane ring protein [Pseudomonas sp. 21C1]	26.5	26.5	100%	320	64%	WP_069522382.1
NLI interacting factor family phosphatase [Toxoplasma gondii MAS]	26.5	26.5	81%	320	89%	KFH10074.1
cytochrome-c oxidase, cbb3-type subunit I [Rubellimicrobium thermophilum]	26.5	26.5	100%	320	73%	WP_021097779.1
type II secretion system protein GspE [Teredinibacter turnerae]	26.5	26.5	90%	320	80%	WP_028875751.1
MULTISPECIES: type II secretion system protein GspE [Teredinibacter]	26.5	26.5	90%	320	80%	WP_018414630.1
type II secretion system protein GspE [Teredinibacter turnerae]	26.5	26.5	90%	320	80%	WP_018274977.1
type II secretion system protein GspE [Teredinibacter turnerae]	26.5	26.5	90%	320	80%	WP_015818660.1
type II secretion system protein GspE [Alteromonadaceae bacterium Bs31]	26.5	26.5	90%	320	80%	WP_085154191.1
type II secretion system protein GspE [Alteromonadales bacterium BS08]	26.5	26.5	90%	320	80%	WP_083608148.1
type II secretion system protein GspE [Alteromonadaceae bacterium Bs12]	26.5	26.5	90%	320	80%	WP_045856896.1
phospholipid/cholesterol/gamma-HCH transport system substrate-binding protein [Amycolatopsis marina]	26.5	26.5	100%	321	73%	SFB53480.1
MCE family protein [Amycolatopsis methanolica]	26.5	26.5	100%	321	73%	WP_017987800.1
MCE family protein [Frankia sp. BMG5.30]	26.5	26.5	100%	321	73%	WP_076843125.1
NLI interacting factor family phosphatase [Toxoplasma gondii FOU]	26.5	26.5	81%	321	89%	KFG52205.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ABC-type transport system involved in resistance to organic solvents, periplasmic component [Frankia sp. Dg2]	26.5	26.5	100%	321	73%	SBW22817.1
hypothetical protein A2133_06510 [Actinobacteria bacterium RBG_16_64_13]	26.5	26.5	100%	321	73%	OFW57426.1
NLI interacting factor family phosphatase [Toxoplasma gondii GAB2-2007-GAL-DOM2]	26.5	26.5	81%	321	89%	KFG44958.1
Methyltransferase domain-containing protein [Butyrivibrio sp. INIla14]	26.5	26.5	90%	322	70%	SCY43218.1
hypothetical protein [Mycobacterium abscessus]	26.5	26.5	81%	327	75%	WP_074354847.1
outer membrane adhesin-like protein [Pantoea sp. At-9b]	26.1	26.1	81%	453	89%	WP_013508603.1
hypothetical protein EGK_17965 [Macaca mulatta]	26.1	26.1	90%	453	90%	EHH27699.1
hypothetical protein [Staphylococcus sp. HMSC055C03]	26.1	26.1	81%	453	69%	WP_070501949.1
MULTISPECIES: hypothetical protein [Staphylococcus]	26.1	26.1	81%	453	69%	WP_070621488.1
hypothetical protein [Staphylococcus simulans]	26.1	26.1	81%	453	69%	WP_060804349.1
acriflavin resistance protein [Nostoc linckia NIES-25]	26.1	26.1	72%	454	88%	BAY75169.1
Methyltransferase domain [Rhizobiales bacterium HL-109]	26.1	26.1	100%	454	69%	KPQ10917.1
hypothetical protein [Rhizobiales bacterium HL-109]	26.1	26.1	100%	454	69%	WP_074444905.1
DNA mismatch repair protein MutS [Haemophilus parahaemolyticus]	26.1	26.1	90%	454	80%	WP_040217669.1
DNA mismatch repair protein MutS [Candidatus Lindowbacteria bacterium RIFCSPLOWO2_12_FULL_62_27]	26.1	26.1	100%	454	73%	OGH60663.1
hypothetical protein COLO4_02915 [Corchorus olitorius]	26.1	26.1	100%	454	73%	OMP12651.1
nuclear protein localization protein 4 [Tsuchiyaea wingfieldii CBS 7118]	26.1	26.1	81%	454	82%	ODO07176.1
nuclear protein localization protein 4 [Cryptococcus amylolentus CBS 6039]	26.1	26.1	81%	454	82%	ODN84567.1
putative ER-associated protein catabolism-related protein [Cutaneotrichosporon oleaginosus]	26.1	26.1	81%	454	82%	KLT42946.1
hydantoinase [Chromatiaceae bacterium 2141T.STBD.0c.01a]	26.1	26.1	72%	454	88%	WP_078121184.1
hypothetical protein COLO4_12684 [Corchorus olitorius]	26.1	26.1	100%	455	73%	OMP00445.1
DUF2972 domain-containing protein [Helicobacter sp. MIT 11-5569]	26.1	26.1	100%	455	73%	WP_081949852.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Rhodanobacter sp. FW510-R10]	26.1	26.1	90%	455	75%	WP_068098958.1
hypothetical protein RHOFW510R12_01140 [Rhodanobacter sp. FW510-R12]	26.1	26.1	90%	455	75%	KZC39879.1
hypothetical protein LS70_08345 [Helicobacter sp. MIT 11-5569]	26.1	26.1	100%	455	73%	KGL10590.1
hypothetical protein THITE_2119061 [Thielavia terrestris NRRL 8126]	26.1	26.1	90%	456	80%	AEO69064.1
hypothetical protein Francci3_0310 [Frankia casuarinae]	26.1	26.1	81%	456	89%	ABD09697.1
hypothetical protein [Frankia sp. KB5]	26.1	26.1	81%	456	89%	WP_085016350.1
MULTISPECIES: hypothetical protein [Frankia]	26.1	26.1	81%	456	89%	WP_035958315.1
phosphoenolpyruvate synthase regulatory protein [Terrabacter sp. 28]	26.1	26.1	90%	456	80%	WP_045190889.1
kinase/pyrophosphorylase [Monashia flava]	26.1	26.1	90%	457	80%	WP_076259457.1
hypothetical protein SAMN04488245_112124 [Yangia pacifica]	26.1	26.1	81%	457	78%	SDI09764.1
hypothetical protein [Yangia sp. CCB-MM3]	26.1	26.1	81%	457	78%	WP_066108786.1
hypothetical protein [Mameliella alba]	26.1	26.1	81%	457	82%	WP_052244889.1
hypothetical protein V490_07205 [Pseudogymnoascus sp. VKM F-3557]	25.7	25.7	63%	644	100%	KFX89144.1
hypothetical protein V495_05283 [Pseudogymnoascus sp. VKM F-4514 (FW-929)]	25.7	25.7	63%	644	100%	KFY40762.1
hypothetical protein PAXINDRAFT_48683 [Paxillus involutus ATCC 200175]	25.7	25.7	63%	644	100%	KIJ09179.1

Alignments

SAA2-SAA2 protein precursor [Homo sapiens]

Sequence ID: **NP_001186673.1** Length: 208 Number of Matches: 1
Range 1: 105 to 115

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.5 bits(81)	0.038()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    EALQGVGDMGR  11
            EALQGVGDMGR
Sbjct  105  EALQGVGDMGR  115
```

serum amyloid A4, partial [synthetic construct]

Sequence ID: **AAX37106.1** Length: 131 Number of Matches: 1
Range 1: 27 to 37

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.5 bits(81)	0.039()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    EALQGVGDMGR  11
            EALQGVGDMGR
Sbjct  27   EALQGVGDMGR  37
```

serum amyloid A [Homo sapiens]

Sequence ID: **AAB24060.1** Length: 130 Number of Matches: 1

See 6 more title(s)

Range 1: 27 to 37

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.5 bits(81)	0.039()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    EALQGVGDMGR  11
            EALQGVGDMGR
Sbjct  27   EALQGVGDMGR  37
```

unnamed protein product [Homo sapiens]

Sequence ID: **BAG35115.1** Length: 130 Number of Matches: 1
Range 1: 27 to 37

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.5 bits(81)	0.039()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    EALQGVGDMGR  11
            EALQGVGDMGR
Sbjct  27   EALQGVGDMGR  37
```

serum amyloid A-4 protein precursor [Homo sapiens]
Sequence ID: **NP_006503.2** Length: 130 Number of Matches: 1

See 1 more title(s)
Range 1: 27 to 37

Score	Expect	Method	Identities	Positives	Gaps	Frame
37.5 bits(81)	0.039()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1   EALQGVGDMGR  11
           EALQGVGDMGR
Sbjct  27  EALQGVGDMGR  37
```

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BLAST Results

Job title: P_SAA4_FRPDGLPK

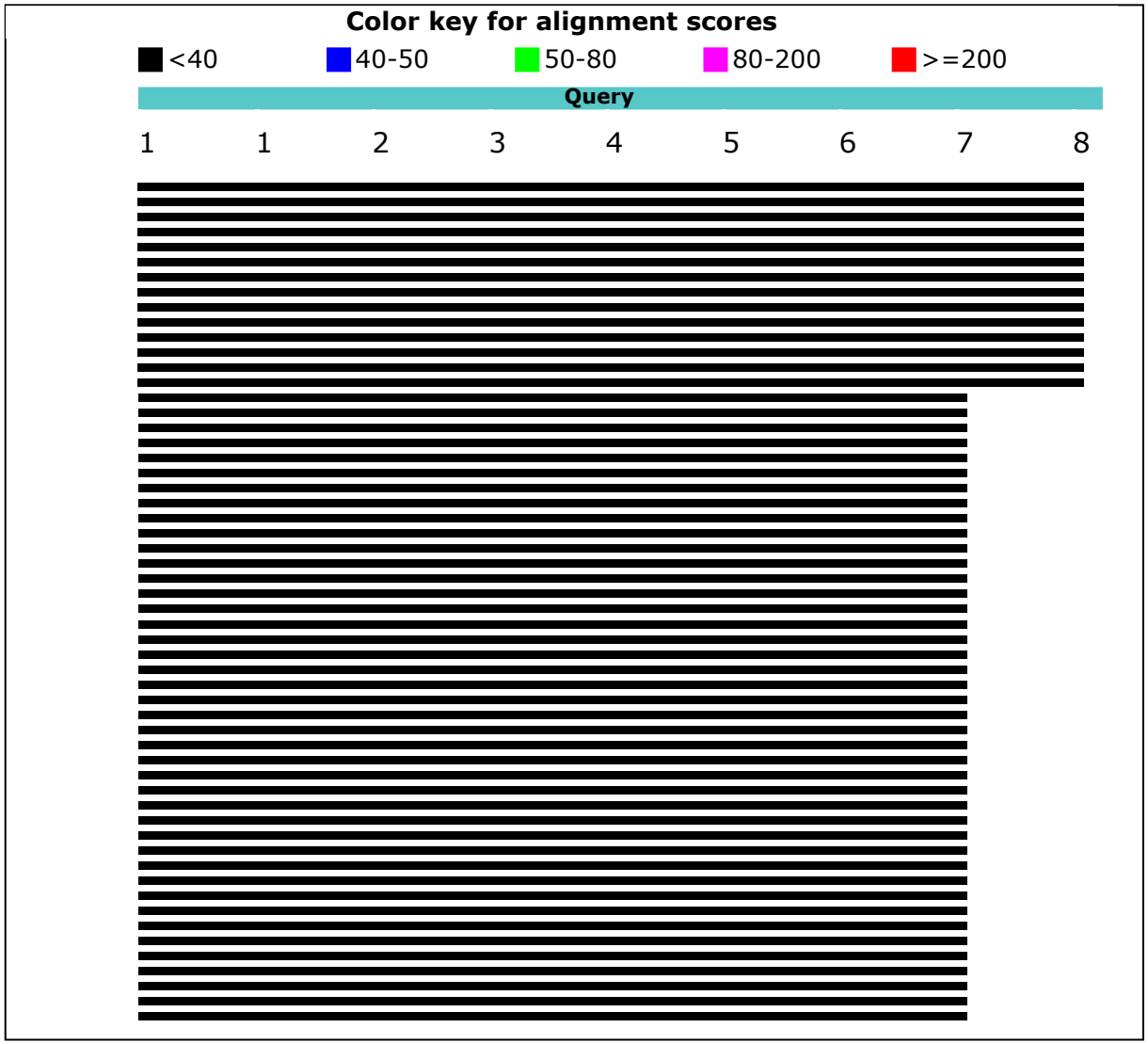
RID S56E490R014 (Expires on 08-04 11:34 am)

Query ID	lcl|Query_364502	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	8	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
SAA2-SAA2 protein precursor [Homo sapiens]	29.1	29.1	100%	21	100%	NP_001186673.1
serum amyloid A4 [synthetic construct]	29.1	29.1	100%	22	100%	AAX37106.1
serum amyloid A [Homo sapiens]	29.1	29.1	100%	22	100%	AAB24060.1
unnamed protein product [Homo sapiens]	29.1	29.1	100%	22	100%	BAG35115.1
serum amyloid A-4 protein precursor [Homo sapiens]	29.1	29.1	100%	22	100%	NP_006503.2
DNA gyrase subunit A [Oxalobacter formigenes]	26.5	26.5	100%	168	88%	WP_005879292.1
DNA gyrase subunit A [Oxalobacter formigenes]	26.5	26.5	100%	168	88%	WP_005878987.1
DNA gyrase subunit A [Betaproteobacteria bacterium UKL13-2]	26.5	26.5	100%	168	88%	AMS33785.1
hypothetical protein POPTR_0009s171801g [Populus trichocarpa]	26.5	26.5	100%	168	88%	ERP57174.1
hypothetical protein A3D92_13380 [Bacteroidetes bacterium RIFCSPHIGHO2_02_FULL_44_7]	26.5	26.5	100%	168	88%	OFZ57760.1
iduronate-2-sulfatase [Rikenella microfusus]	26.5	26.5	100%	169	88%	WP_027291842.1
iduronate-2-sulfatase [Millionella massiliensis]	26.5	26.5	100%	169	88%	WP_071135514.1
histidine kinase [Paenibacillus oryzae]	26.5	26.5	100%	169	88%	WP_068686014.1
SAA4 [Cervus elaphus hippelaphus]	26.5	26.5	100%	177	88%	OWK17211.1
conserved repeat domain-containing protein/fimbrial isopeptide formation D2 domain-containing protein [Stenotrophomonas sp. 92mfcol6.1]	26.1	26.1	87%	238	100%	SLM23583.1
hypothetical protein [Xanthomonas retroflexus]	26.1	26.1	87%	238	100%	WP_088100707.1
hypothetical protein [Stenotrophomonas sp. 92mfcol6.1]	26.1	26.1	87%	238	100%	WP_080149506.1
hypothetical protein [Stenotrophomonas maltophilia]	26.1	26.1	87%	238	100%	WP_032951782.1
hypothetical protein BSK19_03920 [Stenotrophomonas maltophilia]	26.1	26.1	87%	238	100%	OJH81580.1
hypothetical protein RJ55_07203 [Drechmeria coniospora]	26.1	26.1	87%	238	100%	ODA77574.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein NECHADRAFT_79968 [Nectria haematococca mpVI 77-13-4]	26.1	26.1	87%	238	100%	EEU42239.1
hypothetical protein FAVG1_06704 [Fusarium avenaceum]	26.1	26.1	87%	238	100%	KIL89967.1
probable Urea amidolyase [Zygosaccharomyces bailii]	26.1	26.1	87%	238	100%	SJM88884.1
hypothetical protein ZYGR_0U00120 [Zygosaccharomyces rouxii]	26.1	26.1	87%	238	100%	GAV50156.1
hypothetical protein ZYGR_0AS03840 [Zygosaccharomyces rouxii]	26.1	26.1	87%	238	100%	GAV55061.1
probable Urea amidolyase [Zygosaccharomyces bailii ISA1307]	26.1	26.1	87%	238	100%	CDH08854.1
probable Urea amidolyase [Zygosaccharomyces bailii ISA1307]	26.1	26.1	87%	238	100%	CDH14146.1
ZYBA0S08-00188g1_1 [Zygosaccharomyces bailii CLIB 213]	26.1	26.1	87%	238	100%	CDF90670.1
ZYRO0F08976p [Zygosaccharomyces rouxii]	26.1	26.1	87%	238	100%	CAR28654.1
hypothetical protein BABINDRAFT_161809 [Babjeviella inositovora NRRL Y-12698]	26.1	26.1	87%	238	100%	ODQ79407.1
urea amidolyase [Cyberlindnera jadinii NRRL Y-1542]	26.1	26.1	87%	238	100%	ODV76270.1
RecName: Full=Urea amidolyase; AltName: Full=Pyrimidine-degrading protein 13,15; AltName: Full=Uracil catabolism protein 3,5; Includes: RecName: Full=Urea carboxylase; Includes: RecName: Full=Allophanate hydrolase	26.1	26.1	87%	238	100%	A5H0J2.1
uahA [Cyberlindnera jadinii]	26.1	26.1	87%	238	100%	CEP20922.1
urea amidolyase	26.1	26.1	87%	238	100%	2009329A
Urea amidolyase [Fusarium oxysporum f. sp. cubense race 4]	26.1	26.1	87%	238	100%	EMT73320.1
hypothetical protein TDEL_0B03290 [Torulaspora delbrueckii]	26.1	26.1	87%	238	100%	CCE90458.1
Urea amidolyase [Cyberlindnera fabianii]	26.1	26.1	87%	238	100%	ONH69019.1
probable DUR1,2-urea amidolyase [Fusarium mangiferae]	26.1	26.1	87%	238	100%	CVL05539.1
probable DUR1,2-urea amidolyase [Fusarium proliferatum ET1]	26.1	26.1	87%	238	100%	CZR41530.1
probable DUR1,2-urea amidolyase [Fusarium proliferatum]	26.1	26.1	87%	238	100%	CVK97884.1
hypothetical protein PACTADRAFT_40561 [Pachysolen tannophilus NRRL Y-2460]	26.1	26.1	87%	238	100%	ODV95968.1
hypothetical protein DCS_06073 [Drechmeria coniospora]	26.1	26.1	87%	238	100%	KYK54116.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein FOXG_12848 [Fusarium oxysporum f. sp. lycopersici 4287]	26.1	26.1	87%	238	100%	KNB13302.1
hypothetical protein FOVG_11048 [Fusarium oxysporum f. sp. pisi HDV247]	26.1	26.1	87%	238	100%	EXA39530.1
hypothetical protein FOWG_04672 [Fusarium oxysporum f. sp. lycopersici MN25]	26.1	26.1	87%	238	100%	EWZ94337.1
hypothetical protein FOZG_14848 [Fusarium oxysporum Fo47]	26.1	26.1	87%	238	100%	EWZ31751.1
hypothetical protein FOYG_10772 [Fusarium oxysporum FOSC 3-a]	26.1	26.1	87%	238	100%	EWY86136.1
hypothetical protein FVEG_11593 [Fusarium verticillioides 7600]	26.1	26.1	87%	238	100%	EWG53096.1
putative DUR1,2-urea amidolyase [Fusarium fujikuroi]	26.1	26.1	87%	238	100%	KLP00584.1
putative DUR1,2-urea amidolyase [Fusarium fujikuroi]	26.1	26.1	87%	238	100%	KLO93230.1
unnamed protein product [Kluyveromyces dobzhanskii CBS 2104]	26.1	26.1	87%	238	100%	CDO94556.1
CYFA0S01e15346g1_1 [Cyberlindnera fabianii]	26.1	26.1	87%	238	100%	CDR37704.1
hypothetical protein FOTG_07010 [Fusarium oxysporum f. sp. vasinfectum 25433]	26.1	26.1	87%	238	100%	EXM26809.1
hypothetical protein FOIG_07637 [Fusarium oxysporum f. sp. cubense tropical race 4 54006]	26.1	26.1	87%	238	100%	EXM00677.1
hypothetical protein FOQG_05406 [Fusarium oxysporum f. sp. raphani 54005]	26.1	26.1	87%	238	100%	EXK93260.1
hypothetical protein FOMG_08652 [Fusarium oxysporum f. sp. melonis 26406]	26.1	26.1	87%	238	100%	EXK38224.1
probable DUR1,2-urea amidolyase [Fusarium fujikuroi IMI 58289]	26.1	26.1	87%	238	100%	CCT71624.1
Urea amidolyase [Fusarium oxysporum f. sp. cubense race 1]	26.1	26.1	87%	238	100%	ENH73015.1
hypothetical protein FOXB_06512 [Fusarium oxysporum Fo5176]	26.1	26.1	87%	238	100%	EGU82959.1
LAMI_0E06722g1_1 [Lachancea mirantina]	26.1	26.1	87%	238	100%	SCU91648.1
Urea amidolyase [Neonectria ditissima]	26.1	26.1	87%	238	100%	KPM40297.1
urea carboxylase [Wickerhamomyces ciferrii]	26.1	26.1	87%	238	100%	CCH43078.1
urea carboxylase [Conidiobolus coronatus NRRL 28638]	26.1	26.1	87%	238	100%	KXN66714.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein AC631_01977 [Debaryomyces fabryi]	26.1	26.1	87%	238	100%	KSA02241.1
DEHA2D07040p [Debaryomyces hansenii CBS767]	26.1	26.1	87%	238	100%	CAR65627.1
unnamed protein product [Kuraishia capsulata CBS 1993]	26.1	26.1	87%	238	100%	CDK27224.1
hypothetical protein FOZG_14848 [Fusarium oxysporum Fo47]	26.1	26.1	87%	238	100%	EWZ31752.1
hypothetical protein FOQG_05406 [Fusarium oxysporum f. sp. raphani 54005]	26.1	26.1	87%	238	100%	EXK93261.1
hypothetical protein FOYG_10772 [Fusarium oxysporum FOSC 3-a]	26.1	26.1	87%	238	100%	EWY86137.1
hypothetical protein FOIG_07637 [Fusarium oxysporum f. sp. cubense tropical race 4 54006]	26.1	26.1	87%	238	100%	EXM00678.1
hypothetical protein FOXG_12848 [Fusarium oxysporum f. sp. lycopersici 4287]	26.1	26.1	87%	238	100%	KNB13303.1
hypothetical protein FOMG_08652 [Fusarium oxysporum f. sp. melonis 26406]	26.1	26.1	87%	238	100%	EXK38225.1
hypothetical protein OIDMADRAFT_163795 [Oidiodendron maius Zn]	26.1	26.1	87%	238	100%	KIN01356.1
hypothetical protein A3F72_01990 [Bacteroidetes bacterium RIFCSPLOWO2_12_FULL_35_15]	26.1	26.1	87%	238	100%	OFY86953.1
hypothetical protein GNI_111010 [Gregarina niphandrodes]	26.1	26.1	87%	238	100%	EZG55555.1
ATP dependent DNA ligase domain-domain-containing protein [Absidia repens]	26.1	26.1	87%	238	100%	ORZ09615.1
DNA gyrase subunit A [Bordetella petrii]	26.1	26.1	87%	238	100%	WP_026640514.1
hypothetical protein BW38_01787 [Stenotrophomonas sp. RIT309]	26.1	26.1	87%	238	100%	EZP45644.1
histidine kinase [Microvirga massiliensis]	26.1	26.1	87%	238	100%	WP_082145790.1
UvrABC system protein C [uncultured Desulfovibrio sp.]	26.1	26.1	87%	239	100%	SCM73923.1
Excinuclease ABC subunit C [Desulfovibrio legallii]	26.1	26.1	87%	239	100%	SDF76451.1
uncharacterized protein RCO7_07260 [Rhynchosporium commune]	26.1	26.1	87%	239	100%	CZT07244.1
glycogen operon protein [Alloactinosynnema iranicum]	26.1	26.1	87%	239	100%	SDC61435.1
allophanate hydrolase [[Polyangium] brachysporum]	26.1	26.1	87%	239	100%	WP_047195308.1
allophanate hydrolase [Polaromonas glacialis]	26.1	26.1	87%	239	100%	WP_029525148.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
putative urea amidolyase [Enterobacter cloacae]	26.1	26.1	87%	239	100%	AAK11683.1
allophanate hydrolase [Magnetospirillum marisnigri]	26.1	26.1	87%	239	100%	WP_068496023.1
allophanate hydrolase [Dickeya chrysanthemi Ech1591]	26.1	26.1	87%	239	100%	ACT07573.1
allophanate hydrolase [Dechloromonas aromatica]	26.1	26.1	87%	239	100%	WP_011285844.1
allophanate hydrolase homologue [Oleomonas sagaranensis]	26.1	26.1	87%	239	100%	BAD16655.1
allophanate hydrolase [Dickeya chrysanthemi]	26.1	26.1	87%	239	100%	WP_040001681.1
allophanate hydrolase [Dickeya chrysanthemi]	26.1	26.1	87%	239	100%	WP_038927039.1
allophanate hydrolase [Dickeya chrysanthemi]	26.1	26.1	87%	239	100%	WP_033577601.1
allophanate hydrolase [Dickeya chrysanthemi]	26.1	26.1	87%	239	100%	WP_027712574.1
allophanate hydrolase [Polaromonas naphthalenivorans]	26.1	26.1	87%	239	100%	WP_011799471.1
allophanate hydrolase [Granulicella mallensis]	26.1	26.1	87%	239	100%	WP_014265490.1
MULTISPECIES: allophanate hydrolase [Enterobacteriaceae]	26.1	26.1	87%	239	100%	WP_044257532.1
allophanate hydrolase [Blastochloris viridis]	26.1	26.1	87%	239	100%	WP_055038432.1
allophanate hydrolase [Alphaproteobacteria bacterium RIFCSPHIGHO2_12_FULL_66_14]	26.1	26.1	87%	239	100%	OFX04937.1
allophanate hydrolase [Hydrogenophaga sp. A37]	26.1	26.1	87%	239	100%	WP_077333175.1

Alignments

SAA2-SAA2 protein precursor [Homo sapiens]
Sequence ID: **NP_001186673.1** Length: 208 Number of Matches: 1
Range 1: 199 to 206

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.1 bits(61)	21()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FRPDGLPK  8
            FRPDGLPK
Sbjct  199  FRPDGLPK  206
```

serum amyloid A4, partial [synthetic construct]

Sequence ID: **AAX37106.1** Length: 131 Number of Matches: 1
Range 1: 121 to 128

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.1 bits(61)	22()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FRPDGLPK  8
            FRPDGLPK
Sbjct  121  FRPDGLPK  128
```

serum amyloid A [Homo sapiens]

Sequence ID: **AAB24060.1** Length: 130 Number of Matches: 1

See 6 more title(s)

Range 1: 121 to 128

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.1 bits(61)	22()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FRPDGLPK  8
            FRPDGLPK
Sbjct  121  FRPDGLPK  128
```

unnamed protein product [Homo sapiens]

Sequence ID: **BAG35115.1** Length: 130 Number of Matches: 1
Range 1: 121 to 128

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.1 bits(61)	22()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FRPDGLPK  8
            FRPDGLPK
Sbjct  121  FRPDGLPK  128
```

serum amyloid A-4 protein precursor [Homo sapiens]

Sequence ID: **NP_006503.2** Length: 130 Number of Matches: 1

See 1 more title(s)

Range 1: 121 to 128

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.1 bits(61)	22()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    FRPDGLPK  8
           FRPDGLPK
Sbjct  121  FRPDGLPK  128
```

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BLAST Results

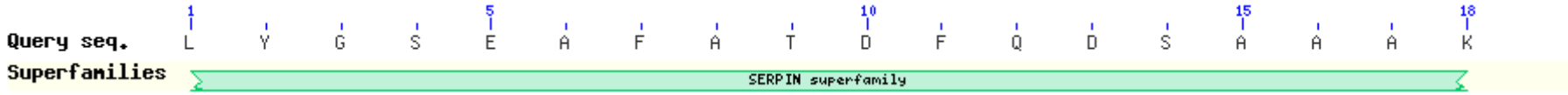
Job title: P_SERPINA3_LYGSEAFATDFQDSAAAK

RID	S56EMSVP014 (Expires on 08-04 11:34 am)
Query ID	lcl|Query_65510
Description	None
Molecule type	amino acid
Query Length	18

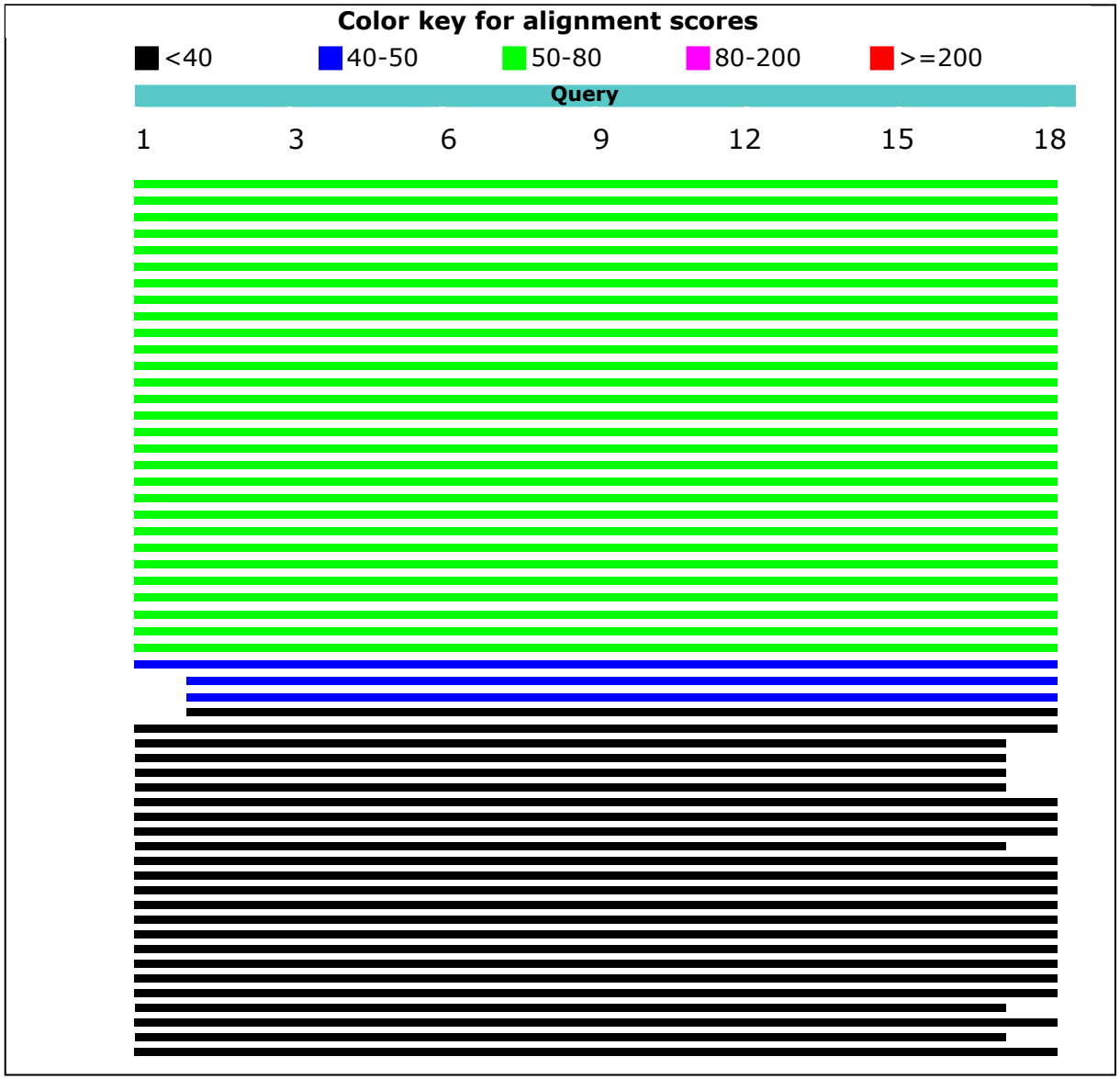
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
3
6
9
12
15
18

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
unnamed protein product [Homo sapiens]	57.9	57.9	100%	9e-09	100%	BAG52641.1
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3, isoform CRA_b [Homo sapiens]	57.9	57.9	100%	9e-09	100%	EAW81588.1
alpha1-antichymotrypsin [Homo sapiens]	57.9	57.9	100%	9e-09	100%	CAA48671.1
alpha-1-antichymotrypsin [Homo sapiens]	57.9	57.9	100%	9e-09	100%	AAA51543.1
chymotrypsin inhibitor	57.9	57.9	100%	9e-09	100%	1313184C
growth-inhibiting protein 24 [Homo sapiens]	57.9	57.9	100%	9e-09	100%	AAT08028.1
alpha-1-antichymotrypsin precursor [Pongo abelii]	57.9	57.9	100%	9e-09	100%	NP_001126852.1
alpha-1-antichymotrypsin precursor [Homo sapiens]	57.9	57.9	100%	9e-09	100%	NP_001076.2
SERPINA3 [synthetic construct]	57.9	57.9	100%	9e-09	100%	AKI69980.1
SERPINA3 [synthetic construct]	57.9	57.9	100%	9e-09	100%	AKI69978.1
SERPINA3 [synthetic construct]	57.9	57.9	100%	9e-09	100%	AKI69977.1
SERPINA3 [synthetic construct]	57.9	57.9	100%	9e-09	100%	AIC53935.1
unnamed protein product [Homo sapiens]	57.9	57.9	100%	9e-09	100%	BAG53869.1
Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 [Homo sapiens]	57.9	57.9	100%	9e-09	100%	AAH34554.1
Chain A, Antichymotrypsin	57.9	57.9	100%	9e-09	100%	3DLW_A
alpha-1-antichymotrypsin precursor [Homo sapiens]	57.9	57.9	100%	9e-09	100%	AAD08810.1
alpha-1-antichymotrypsin precursor [Homo sapiens]	57.9	57.9	100%	9e-09	100%	AAA51560.1
Chain A, Alpha1-Antichymotrypsin Serpin In The Delta Conformation (Partial Loop Insertion)	57.9	57.9	100%	9e-09	100%	1QMN_A
Chain A, Crystal Structure Of Cleaved Human Alpha1-antichymotrypsin At 2.7 Angstroms Resolution And Its Comparison With Other Serpins	57.9	57.9	100%	9e-09	100%	2ACH_A
Chain A, Cleaved Antichymotrypsin A349r	57.9	57.9	100%	9e-09	100%	1AS4_A
Chain A, Cleaved Antichymotrypsin T345r	57.9	57.9	100%	9e-09	100%	4CAA_A
Chain A, Cleaved Antichymotrypsin A347r	57.9	57.9	100%	9e-09	100%	3CAA_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
growth-inhibiting protein 25 [Homo sapiens]	57.9	57.9	100%	9e-09	100%	AAT08029.1
serine (or cysteine) proteinase inhibitor, clade A, member 3 precursor variant [Homo sapiens]	57.9	57.9	100%	9e-09	100%	BAD92297.1
alpha-1-antichymotrypsin isoform X1 [Papio anubis]	54.5	54.5	100%	1e-07	94%	XP_021797219.1
hypothetical protein EGM_16918 [Macaca fascicularis]	54.5	54.5	100%	1e-07	94%	EHH63863.1
hypothetical protein EGK_18506 [Macaca mulatta]	54.5	54.5	100%	1e-07	94%	EHH28145.1
alpha-1-antichymotrypsin precursor [Macaca mulatta]	54.5	54.5	100%	1e-07	94%	NP_001182279.1
alpha-1-antichymotrypsin isoform X2 [Papio anubis]	54.5	54.5	100%	1e-07	94%	XP_021797220.1
hypothetical protein PANDA_009263 [Ailuropoda melanoleuca]	46.4	46.4	100%	1e-04	78%	EFB15253.1
hypothetical protein XELAEV_18039576mg [Xenopus laevis]	40.5	40.5	94%	0.012	71%	OCT68278.1
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 L homeolog precursor [Xenopus laevis]	40.5	40.5	94%	0.012	71%	NP_001081358.1
LOC397792 protein [Xenopus laevis]	38.8	38.8	94%	0.048	71%	AAI70406.1
SERPINA3-5 [Cervus elaphus hippelaphus]	38.4	38.4	100%	0.067	67%	OWK09081.1
RecName: Full=Serpin A3-1; AltName: Full=Endopin-1A; AltName: Full=Muscle endopin-1A; Short=mEndopin-1A; Flags: Precursor	38.0	38.0	94%	0.095	71%	Q9TTE1.3
serpin A3-1 precursor [Bos taurus]	38.0	38.0	94%	0.095	71%	NP_777193.2
serpin A3-5 precursor [Bos taurus]	38.0	38.0	94%	0.095	71%	NP_001075213.1
serpin A3-2 precursor [Bos taurus]	38.0	38.0	94%	0.095	71%	NP_001139773.1
serpin A3-3 precursor [Bos taurus]	37.5	37.5	100%	0.13	67%	NP_001033293.1
RecName: Full=Serpin A3-4; Flags: Precursor	37.5	37.5	100%	0.13	67%	A2I7N0.1
serpin A3-6 precursor [Bos taurus]	37.5	37.5	100%	0.13	67%	NP_001139774.1
Alpha-1-antiproteinase [Chelonia mydas]	35.8	35.8	94%	0.53	65%	EMP32400.1
TPA: endopin 1b-like [Bos taurus]	35.4	35.4	100%	0.75	67%	DAA17365.1
TPA: endopin 1b-like [Bos taurus]	35.4	35.4	100%	0.75	67%	DAA24547.1
hypothetical protein M91_21718 [Bos mutus]	35.4	35.4	100%	0.75	67%	ELR44665.1
TPA: endopin 1b [Bos taurus]	35.4	35.4	100%	0.75	67%	DAA17336.1
TPA: serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 [Bos taurus]	35.4	35.4	100%	0.75	67%	DAA17343.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Serpin A3-3 [Bos mutus]	35.4	35.4	100%	0.75	67%	ELR45141.1
TPA: serpin A3-6 [Bos taurus]	35.4	35.4	100%	0.75	67%	DAA17272.1
SERPINA3-5 [Cervus elaphus hippelaphus]	35.0	35.0	100%	1.1	67%	OWK09077.1
RecName: Full=Alpha-1-antiproteinase; AltName: Full=Alpha-1-antitrypsin; AltName: Full=Alpha-1-proteinase inhibitor; Flags: Precursor	34.1	34.1	100%	2.1	67%	O54763.1
Alpha-1-antitrypsin [Pteropus alecto]	34.1	34.1	100%	2.1	67%	ELK01169.1
SERPINA3-6 [Cervus elaphus hippelaphus]	33.7	33.7	94%	3.0	65%	OWK08914.1
RecName: Full=Alpha-1-antiproteinase; AltName: Full=Alpha-1-antitrypsin; AltName: Full=Alpha-1-proteinase inhibitor; Flags: Precursor	33.7	33.7	100%	3.0	56%	Q03044.1
alpha-1-antichymotrypsin 2 precursor [Sus scrofa]	33.3	33.3	94%	4.3	71%	NP_998952.1
RecName: Full=Serpin A3-8; Flags: Precursor	33.3	33.3	100%	4.3	61%	A6QPQ2.1
TPA: SERPINA3-8 [Bos taurus]	33.3	33.3	100%	4.3	61%	DAA17297.1
serpin A3-8 precursor [Bos taurus]	33.3	33.3	100%	4.3	61%	NP_001075181.1
Alpha-1-antichymotrypsin [Fukomys damarensis]	33.3	33.3	100%	4.3	58%	KFO21354.1
alpha1 antitrypsin	32.9	32.9	100%	6.0	61%	1313184B
hypothetical protein PANDA_009257 [Ailuropoda melanoleuca]	32.9	32.9	100%	6.0	61%	EFB15247.1
Alpha-1-antiproteinase [Chelonia mydas]	32.9	32.9	94%	6.0	59%	EMP32399.1
Alpha-1-antichymotrypsin [Tupaia chinensis]	32.9	32.9	94%	6.0	59%	ELV12130.1
Transcription factor SFP1 [Phialophora attae]	32.9	32.9	61%	6.0	82%	KPI41101.1
endothelin-converting enzyme 1, metalloprotease family M13 [Achlya hypogyna]	32.9	32.9	66%	6.0	83%	OQR93662.1
RecName: Full=Corticosteroid-binding globulin; Short=CBG; AltName: Full=Serpin A6; AltName: Full=Transcortin	32.5	32.5	66%	8.5	83%	P23775.1
hypothetical protein M91_18313 [Bos mutus]	32.0	32.0	100%	12	56%	ELR45142.1
RecName: Full=Alpha-1-antitrypsin-like protein GS55-MS; Flags: Precursor	31.6	31.6	100%	17	61%	O54761.1
alpha-1-antitrypsin-like protein GS55-LT precursor [Ictidomys tridecemlineatus]	31.6	31.6	100%	17	61%	NP_001299613.1
LOC100145012 protein, partial [Xenopus tropicalis]	31.6	31.6	94%	17	59%	AAI58356.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein XENTR_v90021258mg [Xenopus tropicalis]	31.6	31.6	94%	17	59%	OCA25998.1
Alpha-1-antitrypsin precursor-like protein [Camelus ferus]	31.6	31.6	100%	17	61%	EPY81615.1
viron-encapsulated RNA polymerase [Vibrio phage phi 1]	31.6	53.0	72%	17	67%	YP_009198592.1
hypothetical protein [Actinopolyspora erythraea]	31.2	31.2	72%	24	69%	WP_043571347.1
hypothetical protein SAMN04487905_10918 [Actinopolyspora xinjiangensis]	31.2	31.2	72%	24	69%	SDP78514.1
hypothetical protein SAMN04487820_102286 [Actinopolyspora mzabensis]	31.2	31.2	72%	24	69%	SDJ83224.1
TIGR01777 family protein [Thiomicrospira sp. WB1]	31.2	31.2	55%	24	90%	WP_068583627.1
Uncharacterized conserved protein YkaA, UPF0111/DUF47 family [Halorientalis persicus]	30.8	30.8	77%	34	79%	SEN51845.1
short-chain dehydrogenase [Verminephrobacter aporrectodeae]	30.8	30.8	72%	34	77%	WP_029554640.1
Serpin A9 [Myotis davidii]	30.8	30.8	94%	34	65%	ELK27060.1
Na/Pi cotransporter family protein [[Clostridium] viride]	30.8	30.8	55%	34	90%	WP_027096299.1
hypothetical protein [Xanthomonas vesicatoria]	30.3	30.3	50%	47	100%	WP_080553084.1
hypothetical protein [Xanthomonas arboricola]	30.3	30.3	50%	47	100%	WP_049818005.1
MULTISPECIES: hypothetical protein [Xanthomonas]	30.3	30.3	50%	47	100%	WP_065032169.1
MULTISPECIES: hypothetical protein [Xanthomonas]	30.3	30.3	50%	47	100%	WP_046345592.1
hypothetical protein BJD12_15635 [Xanthomonas vesicatoria ATCC 35937]	30.3	30.3	50%	48	100%	APP76425.1
Alpha-1-antiproteinase 2 [Chelonia mydas]	30.3	30.3	94%	48	53%	EMP32397.1
rCG20944, isoform CRA_a [Rattus norvegicus]	30.3	30.3	100%	48	61%	EDL81802.1
alpha/beta hydrolase [Pimelobacter simplex]	30.3	30.3	94%	48	65%	WP_038682806.1
prephenate dehydratase [Streptacidiphilus carbonis]	30.3	30.3	94%	48	65%	WP_042403426.1
Serine (or cysteine) peptidase inhibitor, clade A, member 3N [Rattus norvegicus]	30.3	30.3	100%	48	61%	AAH78796.2
serine protease inhibitor A3N [Rattus norvegicus]	30.3	30.3	100%	48	61%	NP_113719.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
RecName: Full=Serine protease inhibitor A3N; Short=Serpin A3N; AltName: Full=CPI-26; AltName: Full=Contrapsin-like protease inhibitor 6; AltName: Full=SPI-2.2; AltName: Full=Serine protease inhibitor 3; Short=SPI-3; Flags: Precursor	30.3	30.3	100%	48	61%	P09006.3
RecName: Full=Serine protease inhibitor A3A; Short=Serpin A3A; Flags: Precursor	30.3	30.3	66%	48	75%	Q6P4P1.2
Serpina3a protein [Mus musculus]	30.3	30.3	66%	48	75%	AAH63325.1
serpina3n-like protein [Rattus norvegicus]	30.3	30.3	100%	48	61%	ADK91429.1
hypothetical protein GUITHDRAFT_115815 [Guillardia theta CCMP2712]	29.9	29.9	77%	68	60%	EKX38053.1
hypothetical protein MIMGU_mgv1a008238mg [Erythranthe guttata]	29.9	29.9	94%	68	46%	EYU33847.1
RecName: Full=Alpha-1-antitrypsin; AltName: Full=Alpha-1 protease inhibitor; AltName: Full=Alpha-1-antiproteinase; AltName: Full=Serpin A1; Flags: Precursor	29.9	29.9	100%	68	56%	O00394.1
RecName: Full=Alpha-1-antitrypsin; Short=AAT; AltName: Full=Alpha-1 protease inhibitor; AltName: Full=Alpha-1-antiproteinase; AltName: Full=Serpin A1; Flags: Precursor	29.9	29.9	100%	68	56%	P01010.1

Alignments

unnamed protein product [Homo sapiens]

Sequence ID: **BAG52641.1** Length: 448 Number of Matches: 1
Range 1: 185 to 202

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.9 bits(129)	9e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1    LYGSEAFATDFQDSAAAK  18
            LYGSEAFATDFQDSAAAK
Sbjct  185  LYGSEAFATDFQDSAAAK  202
```

serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3, isoform CRA_b [Homo sapiens]

Sequence ID: **EAW81588.1** Length: 448 Number of Matches: 1
Range 1: 185 to 202

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.9 bits(129)	9e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1    LYGSEAFATDFQDSAAAK  18
            LYGSEAFATDFQDSAAAK
Sbjct  185  LYGSEAFATDFQDSAAAK  202
```

alpha1-antichymotrypsin, partial [Homo sapiens]

Sequence ID: **CAA48671.1** Length: 442 Number of Matches: 1
Range 1: 179 to 196

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.9 bits(129)	9e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1    LYGSEAFATDFQDSAAAK  18
            LYGSEAFATDFQDSAAAK
Sbjct  179  LYGSEAFATDFQDSAAAK  196
```

alpha-1-antichymotrypsin [Homo sapiens]

Sequence ID: **AAA51543.1** Length: 433 Number of Matches: 1
Range 1: 160 to 177

Score	Expect	Method	Identities	Positives	Gaps	Frame
57.9 bits(129)	9e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1    LYGSEAFATDFQDSAAAK  18
            LYGSEAFATDFQDSAAAK
Sbjct  160  LYGSEAFATDFQDSAAAK  177
```

chymotrypsin inhibitor

Sequence ID: **prf||1313184C** Length: 433 Number of Matches: 1
Range 1: 160 to 177

Score	Expect	Method	Identities	Positives	Gaps	Frame

57.9 bits(129) 9e-09() 18/18(100%) 18/18(100%) 0/18(0%)

Features:

```
Query  1    LYGSEAFATDFQDSAAAK  18
           LYGSEAFATDFQDSAAAK
Sbjct  160  LYGSEAFATDFQDSAAAK  177
```

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BLAST Results

Job title: P_SERPINA3_MEEVEAMLLPETLK

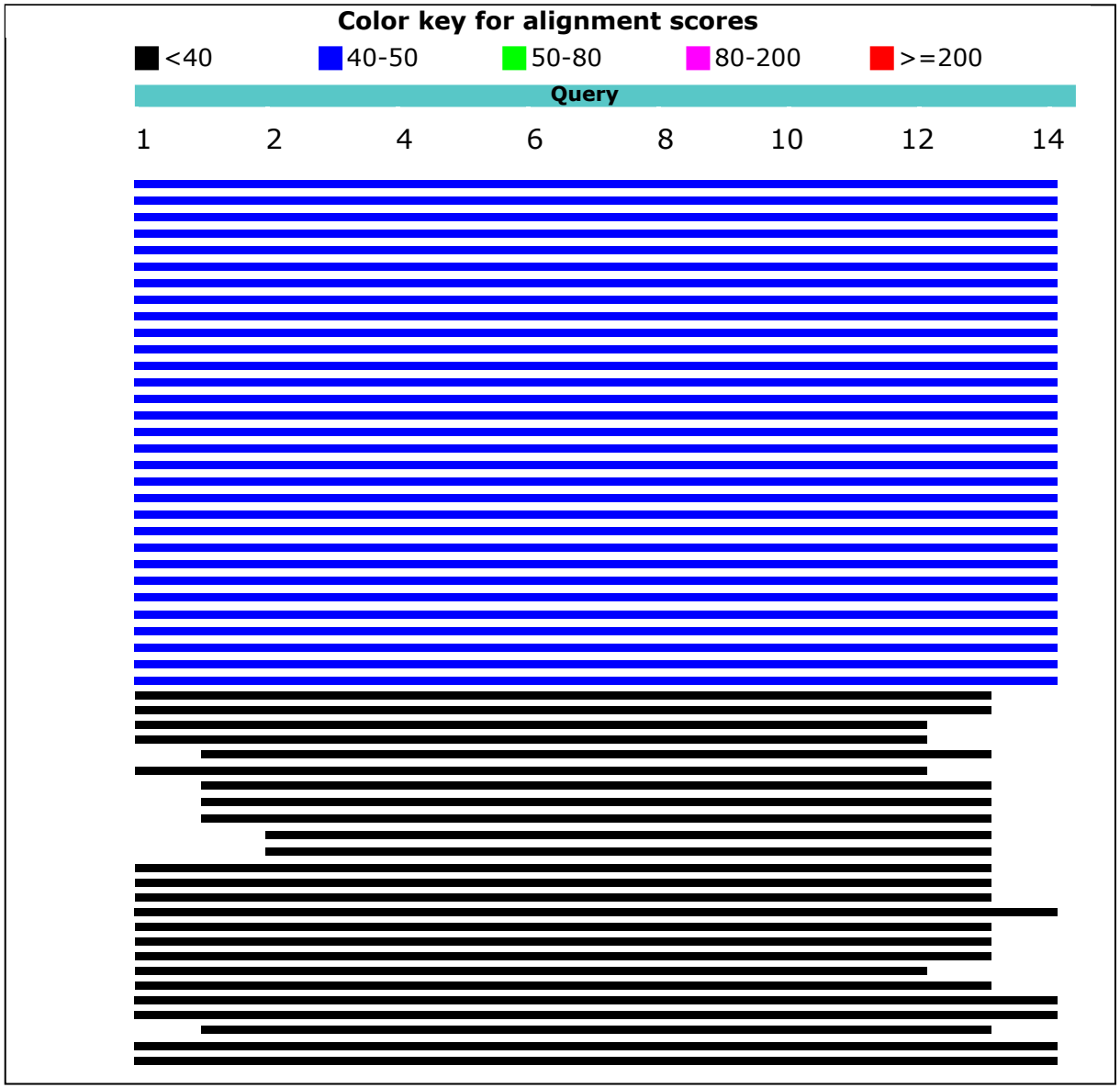
RID S56EXHBE014 (Expires on 08-04 11:34 am)

Query ID	lcl|Query_68942	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12
14

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
alpha-1-antichymotrypsin isoform X1 [Papio anubis]	49.8	49.8	100%	3e-06	100%	XP_021797219.1
unnamed protein product [Homo sapiens]	49.8	49.8	100%	3e-06	100%	BAG52641.1
hypothetical protein EGM_16918 [Macaca fascicularis]	49.8	49.8	100%	3e-06	100%	EHH63863.1
hypothetical protein EGK_18506 [Macaca mulatta]	49.8	49.8	100%	3e-06	100%	EHH28145.1
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3, isoform CRA_b [Homo sapiens]	49.8	49.8	100%	3e-06	100%	EAW81588.1
alpha1-antichymotrypsin [Homo sapiens]	49.8	49.8	100%	3e-06	100%	CAA48671.1
alpha-1-antichymotrypsin [Homo sapiens]	49.8	49.8	100%	3e-06	100%	AAA51543.1
chymotrypsin inhibitor	49.8	49.8	100%	3e-06	100%	1313184C
alpha-1-antichymotrypsin precursor [Macaca mulatta]	49.8	49.8	100%	3e-06	100%	NP_001182279.1
alpha-1-antichymotrypsin isoform X2 [Papio anubis]	49.8	49.8	100%	3e-06	100%	XP_021797220.1
growth-inhibiting protein 24 [Homo sapiens]	49.8	49.8	100%	3e-06	100%	AAT08028.1
alpha-1-antichymotrypsin precursor [Pongo abelii]	49.8	49.8	100%	3e-06	100%	NP_001126852.1
alpha-1-antichymotrypsin precursor [Homo sapiens]	49.8	49.8	100%	3e-06	100%	NP_001076.2
SERPINA3 [synthetic construct]	49.8	49.8	100%	3e-06	100%	AKI69980.1
SERPINA3 [synthetic construct]	49.8	49.8	100%	3e-06	100%	AKI69978.1
SERPINA3 [synthetic construct]	49.8	49.8	100%	3e-06	100%	AKI69977.1
SERPINA3 [synthetic construct]	49.8	49.8	100%	3e-06	100%	AIC53935.1
unnamed protein product [Homo sapiens]	49.8	49.8	100%	3e-06	100%	BAG53869.1
Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 [Homo sapiens]	49.8	49.8	100%	3e-06	100%	AAH34554.1
Chain A, Antichymotrypsin	49.8	49.8	100%	3e-06	100%	3DLW_A
alpha-1-antichymotrypsin precursor [Homo sapiens]	49.8	49.8	100%	3e-06	100%	AAD08810.1
alpha-1-antichymotrypsin precursor [Homo sapiens]	49.8	49.8	100%	3e-06	100%	AAA51560.1
Chain A, Alpha1-Antichymotrypsin Serpin In The Delta Conformation (Partial Loop Insertion)	49.8	49.8	100%	3e-06	100%	1QMN_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, Crystal Structure Of Cleaved Human Alpha1-antichymotrypsin At 2.7 Angstroms Resolution And Its Comparison With Other Serpins	49.8	49.8	100%	3e-06	100%	2ACH_A
Chain A, Cleaved Antichymotrypsin A349r	49.8	49.8	100%	3e-06	100%	1AS4_A
Chain A, Cleaved Antichymotrypsin T345r	49.8	49.8	100%	3e-06	100%	4CAA_A
Chain A, Cleaved Antichymotrypsin A347r	49.8	49.8	100%	3e-06	100%	3CAA_A
growth-inhibiting protein 25 [Homo sapiens]	49.8	49.8	100%	3e-06	100%	AAT08029.1
unnamed protein product [Homo sapiens]	49.8	49.8	100%	3e-06	100%	CAA25459.1
serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3, isoform CRA_a [Homo sapiens]	49.8	49.8	100%	3e-06	100%	EAW81587.1
SERPINA3 protein [Homo sapiens]	49.8	49.8	100%	3e-06	100%	AAH13189.1
hypothetical protein PANDA_009263 [Ailuropoda melanoleuca]	38.0	38.0	92%	0.047	85%	EFB15253.1
serpin A3-8 precursor [Camelus ferus]	37.1	37.1	92%	0.094	85%	EPY81608.1
ABC transporter [Flammeovirga sp. SJP92]	35.4	35.4	85%	0.38	83%	WP_062614826.1
ABC transporter [Flammeovirga sp. OC4]	35.4	35.4	85%	0.38	83%	WP_044201662.1
hypothetical protein [Yangia sp. CCB-MM3]	34.1	34.1	85%	1.1	65%	WP_083191472.1
ABC transporter [Flammeovirga pacifica]	33.3	33.3	85%	2.1	75%	WP_044223829.1
thiosulfate sulfurtransferase [Diplodia corticola]	33.3	33.3	85%	2.1	83%	OJD35136.1
hypothetical protein UCDDS831_g03326 [Diplodia seriata]	33.3	33.3	85%	2.1	83%	KKY22892.1
hypothetical protein MPH_01047 [Macrophomina phaseolina MS6]	33.3	33.3	85%	2.1	83%	EKG21613.1
helicase, RecD/TraA family [Haliangium ochraceum DSM 14365]	32.9	32.9	78%	3.0	82%	ACY18225.1
ATP-dependent RecD-like DNA helicase [Haliangium ochraceum]	32.9	32.9	78%	3.0	82%	WP_045119489.1
tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG [Bdellovibrio bacteriovorus]	32.9	32.9	92%	3.0	77%	WP_061834287.1
hypothetical protein BGO09_16065 [Bacteroidetes bacterium 47-18]	32.9	32.9	92%	3.0	77%	OJU76438.1
alpha-1-antichymotrypsin 2 precursor [Sus scrofa]	32.9	32.9	92%	3.0	77%	NP_998952.1
serine protease [Bradyrhizobium yuanmingense]	32.9	32.9	100%	3.0	79%	WP_050995937.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
alpha-1-antichymotrypsin 2 [Sus scrofa]	32.9	32.9	92%	3.0	77%	CAC06755.1
alpha-1-antichymotrypsin 1 [Sus scrofa]	32.9	32.9	92%	3.0	77%	CAC06757.1
alpha-1-antichymotrypsin 3 [Sus scrofa]	32.9	32.9	92%	3.1	77%	CAC06756.1
hypothetical protein [Flexithrix dorotheae]	32.5	32.5	85%	4.3	75%	WP_020530565.1
hypothetical protein PANDA_009258 [Ailuropoda melanoleuca]	32.5	32.5	92%	4.3	77%	EFB15248.1
hypothetical protein AK812_SmicGene29065 [Symbiodinium microadriaticum]	32.0	32.0	100%	6.1	71%	OLP89467.1
hypothetical protein PPL_04626 [Polysphondylium pallidum PN500]	32.0	32.0	100%	6.1	73%	EFA82203.1
AAA ATPase [Candidatus Gottesmanbacteria bacterium GW2011_GWA2_41_12]	32.0	32.0	85%	6.1	83%	KKR88413.1
serine protease inhibitor A3M precursor [Rattus norvegicus]	32.0	32.0	100%	6.1	71%	NP_001257911.1
RecName: Full=Serine protease inhibitor A3M; Short=Serpin A3M; AltName: Full=Serine protease inhibitor 2.4; Short=SPI-2.4; Flags: Precursor	32.0	32.0	100%	6.1	71%	Q63556.1
rCG20922 [Rattus norvegicus]	32.0	32.0	100%	6.1	71%	EDL81798.1
FAD-binding oxidoreductase [Dethiosulfatarculus sandiegensis]	31.6	31.6	71%	8.6	90%	WP_044351910.1
hypothetical protein AUK25_13585 [Desulfobacteraceae bacterium CG2_30_51_40]	31.6	31.6	71%	8.6	90%	OIP38007.1
hypothetical protein [Methanobrevibacter ruminantium]	31.6	31.6	92%	8.6	69%	WP_012956700.1
VWA domain-containing protein [Hyphomonas johnsonii]	31.6	31.6	100%	8.6	58%	WP_035617508.1
toxin subunit [Sorangium cellulosum]	31.2	31.2	85%	12	83%	WP_012241170.1
hypothetical protein [Pseudomonas fluorescens]	31.2	31.2	57%	12	100%	WP_050572396.1
AcrB/AcrD/AcrF family protein [Endozoicomonas sp. S-B4-1U]	31.2	31.2	71%	12	80%	WP_087107342.1
hypothetical protein I350_00687 [Cryptococcus amylolentus CBS 6273]	31.2	31.2	57%	12	100%	ODO11903.1
hypothetical protein L202_00242 [Cryptococcus amylolentus CBS 6039]	31.2	31.2	57%	12	100%	ODN84253.1
Bcr/CflA family drug resistance efflux transporter [Nesterenkonia sp. PF2B19]	31.2	31.2	71%	12	90%	WP_085437515.1
ABC transporter [Flammeovirga sp. MY04]	31.2	31.2	85%	12	75%	WP_066208034.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Nucleobindin-1 [Stegodyphus mimosarum]	31.2	31.2	71%	12	90%	KFM74056.1
hypothetical protein [Hahella ganghwensis]	31.2	31.2	85%	12	60%	WP_020407713.1
subtype II CRISPR-associated endonuclease Cas1 [Bacteroides fragilis]	31.2	31.2	85%	12	77%	WP_032571476.1
IclR family transcriptional regulator [Saccharopolyspora erythraea]	31.2	31.2	71%	12	77%	WP_009946408.1
coat protein [Varroa Tymo-like virus]	31.2	31.2	100%	12	75%	YP_009159827.1
hypothetical protein [Mesonia phycicola]	31.2	31.2	100%	12	64%	WP_073153820.1
Inositol polyphosphate 5-phosphatase and related proteins [Plasmopara halstedii]	30.8	30.8	92%	17	77%	CEG36092.1
hypothetical protein F441_01709 [Phytophthora parasitica CJ01A1]	30.8	30.8	92%	17	77%	ETP25373.1
hypothetical protein F444_01744 [Phytophthora parasitica P1976]	30.8	30.8	92%	17	77%	ETO84330.1
hypothetical protein PPTG_06857 [Phytophthora parasitica INRA-310]	30.8	30.8	92%	17	77%	ETN15619.1
hypothetical protein L917_01601 [Phytophthora parasitica]	30.8	30.8	92%	17	77%	ETM01845.1
hypothetical protein F443_01743 [Phytophthora parasitica P1569]	30.8	30.8	92%	17	77%	ETI55569.1
hypothetical protein PHYSODRAFT_559294 [Phytophthora sojae]	30.8	30.8	92%	17	77%	EGZ18540.1
diguanylate cyclase [Pseudomonas xanthomarina]	30.8	30.8	100%	17	67%	WP_065983070.1
putative nucleolar MIF4G domain-containing protein 1 [Lucilia cuprina]	30.8	30.8	92%	17	77%	KNC31706.1
sigma-54-dependent Fis family transcriptional regulator [Pseudacidovorax intermedius]	30.8	30.8	92%	17	69%	WP_043119012.1
sigma-54-dependent Fis family transcriptional regulator [Pelomonas puraquae]	30.8	30.8	92%	17	69%	WP_088485845.1
fumarylacetoacetase [Desulfobacterales bacterium SG8_35_2]	30.8	30.8	71%	17	90%	KPK28976.1
fumarylacetoacetase [Polaribacter sp. Hel_I_88]	30.8	30.8	71%	17	90%	WP_026777605.1
Serpin A11 [Bos mutus]	30.8	30.8	100%	17	71%	ELR56059.1
SERPINA11 [Cervus elaphus hippelaphus]	30.8	30.8	100%	17	71%	OWK09124.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
serpin A11 precursor [Bos taurus]	30.8	30.8	100%	17	71%	NP_001092553.1
elongation factor P lysine(34) lysyltransferase [Alteromonas macleodii]	30.8	30.8	92%	17	77%	WP_080590378.1
putative uncharacterized protein [uncultured microorganism]	30.8	30.8	85%	17	77%	BAM62607.1
elongation factor P lysine(34) lysyltransferase [Alteromonas macleodii]	30.8	30.8	92%	17	77%	WP_061439490.1
lysyl-tRNA synthetase [Alteromonas macleodii str. 'English Channel 673']	30.8	30.8	92%	17	77%	AFT73286.1
class I SAM-dependent methyltransferase [Streptomyces sp. JHA19]	30.8	30.8	100%	17	69%	WP_055621526.1
sulfur carrier protein ThiS adenylyltransferase [Dethiobacter alkaliphilus]	30.8	30.8	64%	17	89%	WP_008515160.1
RNA polymerase sigma-70 factor [Bacteroides sp. Marseille-P3132]	30.8	30.8	78%	17	59%	WP_073347423.1
hypothetical protein [Bacteroides acidifaciens]	30.8	30.8	78%	17	59%	WP_052662366.1
hypothetical protein AOL_s00081g302 [Arthrobotrys oligospora ATCC 24927]	30.3	30.3	92%	24	79%	EGX47975.1
multidrug efflux RND transporter permease subunit [Vibrio alginolyticus]	30.3	30.3	78%	24	69%	WP_054576391.1

Alignments

alpha-1-antichymotrypsin isoform X1 [Papio anubis]
Sequence ID: **XP_021797219.1** Length: 448 Number of Matches: 1
Range 1: 309 to 322

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.8 bits(110)	3e-06()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MEEVEAMLLPETLK  14
            MEEVEAMLLPETLK
Sbjct  309  MEEVEAMLLPETLK  322
```

unnamed protein product [Homo sapiens]

Sequence ID: **BAG52641.1** Length: 448 Number of Matches: 1
Range 1: 309 to 322

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.8 bits(110)	3e-06()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MEEVEAMLLPETLK  14
            MEEVEAMLLPETLK
Sbjct  309  MEEVEAMLLPETLK  322
```

hypothetical protein EGM_16918 [Macaca fascicularis]

Sequence ID: **EHH63863.1** Length: 448 Number of Matches: 1
Range 1: 309 to 322

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.8 bits(110)	3e-06()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MEEVEAMLLPETLK  14
            MEEVEAMLLPETLK
Sbjct  309  MEEVEAMLLPETLK  322
```

hypothetical protein EGK_18506 [Macaca mulatta]

Sequence ID: **EHH28145.1** Length: 448 Number of Matches: 1
Range 1: 309 to 322

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.8 bits(110)	3e-06()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MEEVEAMLLPETLK  14
            MEEVEAMLLPETLK
Sbjct  309  MEEVEAMLLPETLK  322
```

serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3, isoform CRA_b [Homo sapiens]

Sequence ID: **EAW81588.1** Length: 448 Number of Matches: 1
Range 1: 309 to 322

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.8 bits(110)	3e-06()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1    MEEVEAMLLPETLK  14
            MEEVEAMLLPETLK
Sbjct  309  MEEVEAMLLPETLK  322
```

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BLAST Results

Job title: P_TLN1_NCGQMSEIEAK

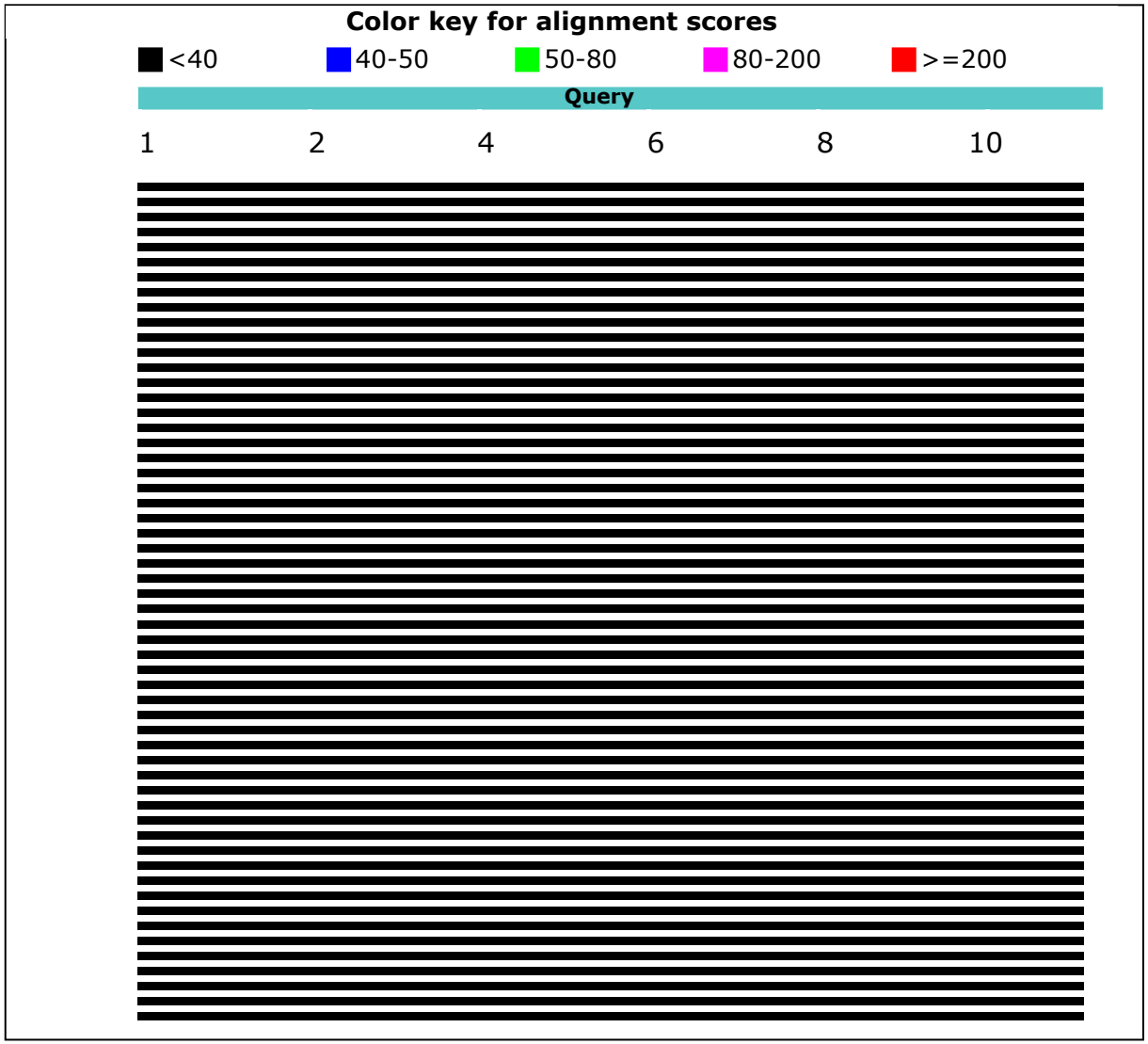
RID S56FCDV4015 (Expires on 08-04 11:35 am)

Query ID	lcl|Query_287666	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	11	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
rCG55135, isoform CRA_a [Rattus norvegicus]	39.7	39.7	100%	0.007	100%	EDL98751.1
mKIAA1027 protein [Mus musculus]	39.7	39.7	100%	0.007	100%	BAC65702.4
talin-1 [Homo sapiens]	39.7	39.7	100%	0.007	100%	AQN67632.1
Talin-1 [Bos mutus]	39.7	39.7	100%	0.007	100%	ELR52791.1
talin 1, isoform CRA_b [Mus musculus]	39.7	39.7	100%	0.007	100%	EDL02466.1
talin [Homo sapiens]	39.7	39.7	100%	0.007	100%	AAD13152.1
talin [Homo sapiens]	39.7	39.7	100%	0.007	100%	AAF23322.1
unnamed protein product [Mus musculus]	39.7	39.7	100%	0.007	100%	BAE27781.1
talin-1 [Homo sapiens]	39.7	39.7	100%	0.007	100%	NP_006280.3
talin	39.7	39.7	100%	0.007	100%	1617167A
talin-1 isoform X1 [Papio anubis]	39.7	39.7	100%	0.007	100%	XP_003911573.2
hypothetical protein PANDA_007476 [Ailuropoda melanoleuca]	39.7	39.7	100%	0.007	100%	EFB15370.1
talin [Mus musculus]	39.7	39.7	100%	0.007	100%	CAA39588.1
Talin-1 [Macaca mulatta]	39.7	39.7	100%	0.007	100%	EHH23990.1
talin-1 [Bos taurus]	39.7	39.7	100%	0.007	100%	NP_001192357.2
talin-1 [Mus musculus]	39.7	39.7	100%	0.007	100%	NP_035732.2
talin 1, isoform CRA_b [Homo sapiens]	39.7	39.7	100%	0.007	100%	EAW58353.1
talin-1 [Rattus norvegicus]	39.7	39.7	100%	0.007	100%	NP_001034114.2
Talin 1 [Homo sapiens]	39.7	39.7	100%	0.007	100%	AAH42923.1
talin [Homo sapiens]	39.7	39.7	100%	0.007	100%	AAF27330.1
Talin-1 [Fukomys damarensis]	39.7	39.7	100%	0.007	100%	KFO35373.1
Talin-1 [Heterocephalus glaber]	39.7	39.7	100%	0.007	100%	EHB09959.1
talin-1 isoform 1 [Cricetulus griseus]	39.7	39.7	100%	0.007	100%	ERE83219.1
Talin-1 [Myotis brandtii]	39.7	39.7	100%	0.007	100%	EPQ18776.1
talin-1 isoform 2 [Camelus ferus]	39.7	39.7	100%	0.007	100%	EPY78578.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
talin-1 isoform X2 [Papio anubis]	39.7	39.7	100%	0.007	100%	XP_021783085.1
Talin-1 [Tupaia chinensis]	39.7	39.7	100%	0.007	100%	ELW70306.1
talin-1 isoform X3 [Papio anubis]	39.7	39.7	100%	0.007	100%	XP_021783086.1
Talin-1 [Cricetulus griseus]	39.7	39.7	100%	0.007	100%	EGW07880.1
Talin-1 [Pteropus alecto]	39.7	39.7	100%	0.007	100%	ELK09027.1
TLN1 protein [Bos taurus]	39.7	39.7	100%	0.007	100%	AAI22767.1
Chain A, Crystal Structure Of The Talin Head Ferm Domain	39.7	39.7	100%	0.007	100%	3IVF_A
unnamed protein product [Mus musculus]	39.7	39.7	100%	0.007	100%	BAC30516.1
Chain A, Crystal Structure Of Talin Autoinhibition Complex	39.7	39.7	100%	0.007	100%	4F7G_A
Chain B, Structural Basis For Phosphatidylinositol Phosphate Kinase Type I- Gamma Binding To Talin At Focal Adhesions	39.7	39.7	100%	0.007	100%	1Y19_B
Talin-2 [Heterocephalus glaber]	36.7	36.7	100%	0.074	91%	EHB01326.1
Talin-2 [Fukomys damarensis]	36.7	36.7	100%	0.074	91%	KFO26023.1
mCG141703, isoform CRA_c [Mus musculus]	36.7	36.7	100%	0.074	91%	EDL26154.1
mCG141703, isoform CRA_a [Mus musculus]	36.7	36.7	100%	0.074	91%	EDL26152.1
hypothetical protein EGM_16033 [Macaca fascicularis]	36.7	36.7	100%	0.074	91%	EHH63127.1
Tln2 protein [Mus musculus]	36.7	36.7	100%	0.074	91%	AAI58058.1
talin-2 [Homo sapiens]	36.7	36.7	100%	0.074	91%	NP_055874.2
talin-2 [Mus musculus]	36.7	36.7	100%	0.074	91%	NP_001074711.2
Talin-2 [Cricetulus griseus]	36.7	36.7	100%	0.074	91%	EGW07150.1
TPA: talin 2 [Bos taurus]	36.7	36.7	100%	0.074	91%	DAA25364.1
talin 2 [Homo sapiens]	36.7	36.7	100%	0.074	91%	AAM73764.1
Talin-1 [Chaetura pelagica]	36.7	36.7	100%	0.074	91%	KFU87202.1
talin 2, isoform CRA_c [Homo sapiens]	36.7	36.7	100%	0.074	91%	EAW77617.1
RecName: Full=Talin-2	36.7	36.7	100%	0.074	91%	Q71LX4.3
talin 2 [Mus musculus]	36.7	36.7	100%	0.074	91%	AAQ05019.1
talin-2 isoform 1 [Camelus ferus]	36.7	36.7	100%	0.074	91%	EPY81739.1
talin-2-like protein [Cricetulus griseus]	36.7	36.7	100%	0.074	91%	ERE74589.1
talin-2-like protein [Cricetulus griseus]	36.7	36.7	100%	0.074	91%	ERE74590.1
talin-2-like protein [Cricetulus griseus]	36.7	36.7	100%	0.074	91%	ERE74591.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein A6R68_07157 [Neotoma lepida]	36.7	36.7	100%	0.074	91%	OBS64302.1
unnamed protein product [Mus musculus]	36.7	36.7	100%	0.075	91%	BAE38220.1
unnamed protein product [Mus musculus]	36.7	36.7	100%	0.075	91%	BAE39153.1
Chain A, Crystal Structure Of Talin2 F2-f3 In Complex With The Integrin Beta1d Cytoplasmic Tail	36.7	36.7	100%	0.076	91%	3G9W_A
Talin-1 [Chlamydotis macqueenii]	35.4	35.4	100%	0.21	91%	KFP42152.1
hypothetical protein H355_006584 [Colinus virginianus]	35.0	35.0	100%	0.30	91%	OXB79125.1
hypothetical protein ASZ78_013077 [Callipepla squamata]	35.0	35.0	100%	0.30	91%	OXB66686.1
Talin-1 [Pygoscelis adeliae]	35.0	35.0	100%	0.30	91%	KFW62869.1
talin-1 [Patagioenas fasciata monilis]	35.0	35.0	100%	0.30	91%	OPJ75460.1
Talin-1 [Struthio camelus australis]	35.0	35.0	100%	0.30	91%	KFV84240.1
Talin-1 [Aptenodytes forsteri]	35.0	35.0	100%	0.30	91%	KFM11569.1
talin 1 [Coturnix japonica]	35.0	35.0	100%	0.30	91%	NP_001310165.1
talin-1 [Gallus gallus]	35.0	35.0	100%	0.30	91%	NP_989854.1
Talin-1 [Manacus vitellinus]	35.0	35.0	100%	0.30	91%	KFW87779.1
Talin-1 [Cuculus canorus]	35.0	35.0	100%	0.30	91%	KFO73905.1
Talin-1 [Pterocles gutturalis]	35.0	35.0	100%	0.30	91%	KFV10056.1
Talin-1 [Corvus brachyrhynchos]	35.0	35.0	100%	0.30	91%	KFO52801.1
Talin-1 [Buceros rhinoceros silvestris]	35.0	35.0	100%	0.30	91%	KFO88453.1
Talin-1 [Chelonia mydas]	35.0	35.0	100%	0.30	91%	EMP24898.1
Talin-1 [Myotis davidii]	35.0	35.0	100%	0.30	91%	ELK34248.1
Chain A, Crystal Structure Of A Ferm Domain Of Talin	35.0	35.0	100%	0.30	91%	1MIX_A
Chain B, Crystal Structure Of An Integrin Beta3-Talin Chimera	35.0	35.0	100%	0.31	91%	1MIZ_B
Chain B, Crystal Structure Of An Integrin Beta3-Talin Chimera	35.0	35.0	100%	0.31	91%	1MK7_B
Chain A, Nmr Solution Structure Of The F2 Subdomain Of Talin	35.0	35.0	100%	0.31	91%	2HRJ_A
unnamed protein product [Tetraodon nigroviridis]	34.1	34.1	100%	0.60	82%	CAG02348.1
Talin-1 [Picoides pubescens]	34.1	34.1	100%	0.60	91%	KFV65621.1
hypothetical protein XELAEV_18018012mg [Xenopus laevis]	34.1	34.1	100%	0.60	82%	OCT89391.1
hypothetical protein XELAEV_18020799mg [Xenopus laevis]	34.1	34.1	100%	0.60	82%	OCT87107.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein XENTR_v900085562mg [Xenopus tropicalis]	34.1	34.1	100%	0.60	82%	OCA41499.1
Talin-2 [Lonchura striata domestica]	34.1	34.1	100%	0.60	82%	OWK58873.1
talin-2 [Patagioenas fasciata monilis]	34.1	34.1	100%	0.60	82%	OPJ70141.1
hypothetical protein Y1Q_0001590 [Alligator mississippiensis]	34.1	34.1	100%	0.60	82%	KYO21362.1
Talin-2 [Larimichthys crocea]	34.1	34.1	100%	0.60	82%	KKF12598.1
Talin-2 [Nipponia nippon]	34.1	34.1	100%	0.60	82%	KFR02123.1
Talin-2 [Aptenodytes forsteri]	34.1	34.1	100%	0.60	82%	KFM03965.1
Talin-2 [Charadrius vociferus]	34.1	34.1	100%	0.60	82%	KGL94689.1
Talin-2, partial [Antrostomus carolinensis]	34.1	34.1	100%	0.60	82%	KFZ61778.1
Talin-2 [Struthio camelus australis]	34.1	34.1	100%	0.60	82%	KFV84748.1
Talin-2 [Picoides pubescens]	34.1	34.1	100%	0.60	82%	KFV61064.1
Talin-2 [Tauraco erythrolophus]	34.1	34.1	100%	0.60	82%	KFV12397.1
Talin-2 [Opisthocomus hoazin]	34.1	34.1	100%	0.60	82%	KFR17588.1
Talin-2 [Egretta garzetta]	34.1	34.1	100%	0.60	82%	KFP20122.1
Talin-2 [Cuculus canorus]	34.1	34.1	100%	0.60	82%	KFO74139.1
Talin-2 [Haliaeetus albicilla]	34.1	34.1	100%	0.60	82%	KFQ02099.1
Talin-2 [Corvus brachyrhynchos]	34.1	34.1	100%	0.60	82%	KFO53373.1
Talin-2 [Calypte anna]	34.1	34.1	100%	0.60	82%	KFO96706.1

Alignments

rCG55135, isoform CRA_a [Rattus norvegicus]

Sequence ID: **EDL98751.1** Length: 2577 Number of Matches: 1

Range 1: 321 to 331

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.7 bits(86)	0.007()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    NCGQMSEIEAK  11
            NCGQMSEIEAK
```

```
Sbjct  321  NCGQMSEIEAK  331
```

mKIAA1027 protein, partial [Mus musculus]

Sequence ID: **BAC65702.4** Length: 2564 Number of Matches: 1
Range 1: 308 to 318

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.7 bits(86)	0.007()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    NCGQMSEIEAK  11
            NCGQMSEIEAK
Sbjct  308  NCGQMSEIEAK  318
```

talin-1 [Homo sapiens]

Sequence ID: **AQN67632.1** Length: 2558 Number of Matches: 1
Range 1: 285 to 295

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.7 bits(86)	0.007()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    NCGQMSEIEAK  11
            NCGQMSEIEAK
Sbjct  285  NCGQMSEIEAK  295
```

Talin-1, partial [Bos mutus]

Sequence ID: **ELR52791.1** Length: 2553 Number of Matches: 1
Range 1: 294 to 304

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.7 bits(86)	0.007()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    NCGQMSEIEAK  11
            NCGQMSEIEAK
Sbjct  294  NCGQMSEIEAK  304
```

talin 1, isoform CRA_b [Mus musculus]

Sequence ID: **EDL02466.1** Length: 2541 Number of Matches: 1

See 1 more title(s)

Range 1: 285 to 295

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.7 bits(86)	0.007()		11/11(100%)	11/11(100%)	0/11(0%)	

Features:

```
Query  1    NCGQMSEIEAK  11
           NCGQMSEIEAK
Sbjct  285  NCGQMSEIEAK  295
```

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BLAST Results

Job title: P_TLN1_SAQPASAEPR

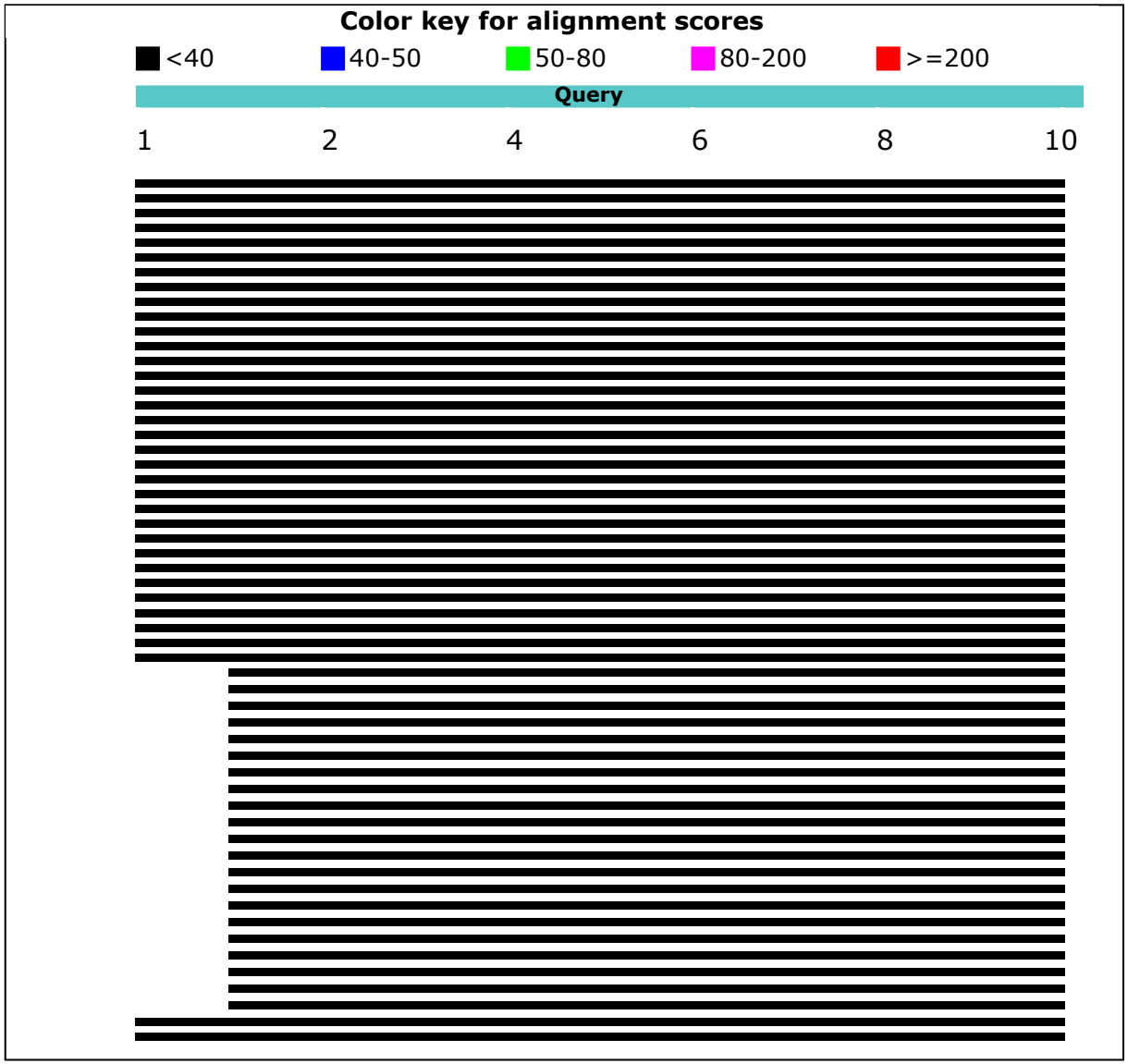
RID S56FS9KN015 (Expires on 08-04 11:35 am)

Query ID	lcl|Query_25784	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	10	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 103 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
rCG55135, isoform CRA_a [Rattus norvegicus]	32.9	32.9	100%	1.4	100%	EDL98751.1
mKIAA1027 protein [Mus musculus]	32.9	32.9	100%	1.4	100%	BAC65702.4
talin-1 [Homo sapiens]	32.9	32.9	100%	1.4	100%	AQN67632.1
Talin-1 [Bos mutus]	32.9	32.9	100%	1.4	100%	ELR52791.1
talin 1, isoform CRA_b [Mus musculus]	32.9	32.9	100%	1.4	100%	EDL02466.1
talin [Homo sapiens]	32.9	32.9	100%	1.4	100%	AAD13152.1
talin [Homo sapiens]	32.9	32.9	100%	1.4	100%	AAF23322.1
unnamed protein product [Mus musculus]	32.9	32.9	100%	1.4	100%	BAE27781.1
talin-1 [Homo sapiens]	32.9	32.9	100%	1.4	100%	NP_006280.3
talin	32.9	32.9	100%	1.4	100%	1617167A
talin-1 isoform X1 [Papio anubis]	32.9	32.9	100%	1.4	100%	XP_003911573.2
hypothetical protein PANDA_007476 [Ailuropoda melanoleuca]	32.9	32.9	100%	1.4	100%	EFB15370.1
talin [Mus musculus]	32.9	32.9	100%	1.4	100%	CAA39588.1
Talin-1 [Macaca mulatta]	32.9	32.9	100%	1.4	100%	EHH23990.1
talin-1 [Bos taurus]	32.9	32.9	100%	1.4	100%	NP_001192357.2
talin-1 [Mus musculus]	32.9	32.9	100%	1.4	100%	NP_035732.2
talin 1, isoform CRA_b [Homo sapiens]	32.9	32.9	100%	1.4	100%	EAW58353.1
talin-1 [Rattus norvegicus]	32.9	32.9	100%	1.4	100%	NP_001034114.2
Talin 1 [Homo sapiens]	32.9	32.9	100%	1.4	100%	AAH42923.1
talin [Homo sapiens]	32.9	32.9	100%	1.4	100%	AAF27330.1
Talin-1 [Fukomys damarensis]	32.9	32.9	100%	1.4	100%	KFO35373.1
Talin-1 [Heterocephalus glaber]	32.9	32.9	100%	1.4	100%	EHB09959.1
Talin-1 [Myotis brandtii]	32.9	32.9	100%	1.4	100%	EPQ18776.1
talin-1 isoform 2 [Camelus ferus]	32.9	32.9	100%	1.4	100%	EPY78578.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
talin-1 isoform X2 [Papio anubis]	32.9	32.9	100%	1.4	100%	XP_021783085.1
Talin-1 [Tupaia chinensis]	32.9	32.9	100%	1.4	100%	ELW70306.1
talin-1 isoform X3 [Papio anubis]	32.9	32.9	100%	1.4	100%	XP_021783086.1
rCG55135, isoform CRA_c [Rattus norvegicus]	32.9	32.9	100%	1.4	100%	EDL98753.1
talin 1, isoform CRA_a [Mus musculus]	32.9	32.9	100%	1.4	100%	EDL02465.1
Talin-1 [Myotis davidii]	32.9	32.9	100%	1.4	100%	ELK34248.1
Talin-1 [Pteropus alecto]	32.9	32.9	100%	1.4	100%	ELK09027.1
Chain A, Crystal Structure Of Talin Residues 482-789	32.9	32.9	100%	1.4	100%	1SJ8_A
Chain A, Crystal Structure Of Talin Rod 482-655	32.9	32.9	100%	1.4	100%	1SJ7_A
hypothetical protein H355_006584 [Colinus virginianus]	30.3	30.3	90%	11	100%	OXB79125.1
hypothetical protein ASZ78_013077 [Callipepla squamata]	30.3	30.3	90%	11	100%	OXB66686.1
Talin-1 [Pygoscelis adeliae]	30.3	30.3	90%	11	100%	KFW62869.1
Talin-1 [Picoides pubescens]	30.3	30.3	90%	11	100%	KFV65621.1
talin-1 [Patagioenas fasciata monilis]	30.3	30.3	90%	11	100%	OPJ75460.1
talin-1 [Amazona aestiva]	30.3	30.3	90%	11	100%	KQK82883.1
Talin-1 [Struthio camelus australis]	30.3	30.3	90%	11	100%	KFV84240.1
Talin-1 [Chlamydotis macqueenii]	30.3	30.3	90%	11	100%	KFP42152.1
Talin-1 [Aptenodytes forsteri]	30.3	30.3	90%	11	100%	KFM11569.1
talin 1 [Coturnix japonica]	30.3	30.3	90%	11	100%	NP_001310165.1
talin-1 [Gallus gallus]	30.3	30.3	90%	11	100%	NP_989854.1
Talin-1 [Manacus vitellinus]	30.3	30.3	90%	11	100%	KFW87779.1
Talin-1 [Cuculus canorus]	30.3	30.3	90%	11	100%	KFO73905.1
Talin-1 [Lonchura striata domestica]	30.3	30.3	90%	11	100%	OWK58725.1
Talin-1 [Pterocles gutturalis]	30.3	30.3	90%	11	100%	KFV10056.1
Talin-1 [Corvus brachyrhynchos]	30.3	30.3	90%	11	100%	KFO52801.1
Talin-1 [Buceros rhinoceros silvestris]	30.3	30.3	90%	11	100%	KFO88453.1
Talin-1 [Chelonia mydas]	30.3	30.3	90%	11	100%	EMP24898.1
talin-2 [Alligator mississippiensis]	30.3	30.3	90%	11	100%	KYO20875.1
DNA translocase FtsK [Chelativorans sp. BNC1]	30.3	30.3	90%	11	100%	WP_011581214.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Acidovorax sp. CF316]	30.3	30.3	90%	11	100%	WP_007853364.1
talin-1 isoform 1 [Cricetulus griseus]	29.9	29.9	100%	16	90%	ERE83219.1
Talin-1 [Cricetulus griseus]	29.9	29.9	100%	16	90%	EGW07880.1
PPE family protein [Mycobacterium genavense]	29.9	29.9	100%	16	90%	WP_025736587.1
hypothetical protein [Ponticaulis koreensis]	29.5	29.5	90%	22	100%	WP_022694423.1
biopolymer transporter ExbB [Agrobacterium sp. SUL3]	29.5	51.3	100%	23	100%	KNY32446.1
tonB-system energizer ExbB [Agrobacterium sp. SUL3]	29.5	51.3	100%	23	100%	WP_082178963.1
type VII secretion-associated protein [Rhodococcus fascians]	29.5	53.4	90%	23	100%	WP_037106789.1
hypothetical protein [Nocardiopsis sp. NRRL B-16309]	28.6	28.6	100%	46	90%	WP_053618350.1
other/FunK1 protein kinase [Coprinopsis cinerea okayama7#130]	27.8	27.8	80%	91	100%	EAU87390.2
MULTISPECIES: hypothetical protein [Bradyrhizobium]	27.8	27.8	90%	91	89%	WP_028154024.1
putative CCR4-NOT transcription complex [Rosellinia necatrix]	27.8	27.8	90%	91	89%	GAP83282.1
hypothetical protein [Bradyrhizobium japonicum]	27.8	27.8	90%	91	89%	WP_038976523.1
hypothetical protein [Bradyrhizobium japonicum]	27.8	27.8	90%	91	89%	WP_038953946.1
hypothetical protein [Bradyrhizobium japonicum]	27.8	27.8	90%	91	89%	WP_038945437.1
gamma-glutamyltransferase [Thermocrispum agreste]	27.8	27.8	90%	91	89%	WP_038045023.1
MSHA biogenesis protein MshL [Alkalimonas amylolytica]	27.8	27.8	80%	91	100%	SEB00387.1
Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains) [Arthrobacter sp. ok909]	27.8	27.8	90%	91	89%	SDP66958.1
LysM repeat-containing protein [Arthrobacter sp. ov118]	27.8	27.8	90%	91	89%	SFU09083.1
lytic transglycosylase [Arthrobacter sp. 9MFCol3.1]	27.8	27.8	90%	91	89%	WP_026538794.1
hypothetical protein [Arthrobacter sp. 131MFCol6.1]	27.8	27.8	90%	91	89%	WP_018772331.1
Flp pilus assembly protein TadG [Mesorhizobium qingshengii]	27.8	27.8	100%	91	90%	SDA54633.1
hypothetical protein [Mesorhizobium sp. WSM3626]	27.8	27.8	100%	91	90%	WP_027145143.1
conjugal transfer protein TrbI [Bradyrhizobium sp. CCH5-F6]	27.8	27.8	90%	91	89%	WP_061027597.1
hypothetical protein SLNWT_2013 [Streptomyces albus]	27.8	27.8	80%	92	100%	AJE82389.1
DUF72 domain-containing protein [Paraburkholderia sp. SOS3]	27.8	27.8	80%	92	100%	WP_075155902.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
branched-chain amino acid aminotransferase [Mycobacterium sp. E796]	27.8	27.8	100%	92	90%	WP_068140519.1
hypothetical protein SNOG_14171 [Parastagonospora nodorum SN15]	27.8	27.8	90%	92	89%	EAT78408.2
hypothetical protein A2Z83_02855 [Omnitrophica bacterium GWA2_52_8]	27.8	27.8	80%	93	100%	OGW77993.1
transcriptional regulator [Porphyrobacter sp. AAP82]	27.8	27.8	90%	93	89%	WP_017663957.1
hypothetical protein AYO46_09925 [Betaproteobacteria bacterium SCGC AG-212-J23]	27.8	27.8	90%	93	89%	OAI50519.1
hypothetical protein A3I61_02015 [Acidobacteria bacterium RIFCSPLOWO2_02_FULL_68_18]	27.8	27.8	80%	93	100%	OFW03702.1
Hypothetical protein Achr_8380 [Azotobacter chroococcum NCIMB 8003]	27.8	27.8	90%	94	89%	AJE20326.1
hypothetical protein [Azotobacter chroococcum]	27.8	27.8	90%	94	89%	WP_052264003.1
unnamed protein product [Tetraodon nigroviridis]	27.4	27.4	90%	129	89%	CAF93389.1
hypothetical protein XELAEV_18004235mg [Xenopus laevis]	27.4	27.4	90%	129	89%	OCT56929.1
talin-1-like [Scleropages formosus]	27.4	27.4	90%	129	89%	KPP73766.1
hypothetical protein XELAEV_18008634mg [Xenopus laevis]	27.4	27.4	90%	129	89%	OCU02863.1
ATPase [Micromonospora purpureochromogenes]	27.4	27.4	100%	129	90%	WP_088964029.1
hypothetical protein CY34DRAFT_797435 [Suillus luteus UH-Slu-Lm8-n1]	27.4	27.4	100%	129	80%	KIK49052.1
gamma-glutamyltransferase [Glutamicibacter arilaitensis]	27.4	27.4	100%	129	90%	WP_013347648.1
hypothetical protein cypCar_00045025 [Cyprinus carpio]	27.4	27.4	90%	130	89%	KTF79747.1
hypothetical protein [beta proteobacterium AAP51]	27.4	27.4	90%	130	89%	WP_054155767.1
TAP complex multifunctional esterase [Nitrospira sp. OLB3]	27.4	27.4	100%	131	80%	KXK01897.1
hypothetical protein SAMN04489726_5910 [Allokutzneria albata]	27.4	27.4	90%	131	89%	SDN29186.1
hypothetical protein [Pseudomonas syringae]	27.4	27.4	90%	131	89%	WP_080115845.1
Uncharacterised protein [Bordetella pertussis]	27.4	27.4	100%	137	80%	CFN79844.1

Alignments

rCG55135, isoform CRA_a [Rattus norvegicus]

Sequence ID: **EDL98751.1** Length: 2577 Number of Matches: 1
Range 1: 661 to 670

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.9 bits(70)	1.4()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    SAQPASAEPR  10
           SAQPASAEPR
Sbjct  661  SAQPASAEPR  670
```

mKIAA1027 protein, partial [Mus musculus]

Sequence ID: **BAC65702.4** Length: 2564 Number of Matches: 1
Range 1: 648 to 657

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.9 bits(70)	1.4()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    SAQPASAEPR  10
           SAQPASAEPR
Sbjct  648  SAQPASAEPR  657
```

talin-1 [Homo sapiens]

Sequence ID: **AQN67632.1** Length: 2558 Number of Matches: 1
Range 1: 625 to 634

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.9 bits(70)	1.4()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    SAQPASAEPR  10
           SAQPASAEPR
Sbjct  625  SAQPASAEPR  634
```

Talin-1, partial [Bos mutus]

Sequence ID: **ELR52791.1** Length: 2553 Number of Matches: 1
Range 1: 634 to 643

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.9 bits(70)	1.4()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    SAQPASAEPR  10
           SAQPASAEPR
Sbjct  634  SAQPASAEPR  643
```

talin 1, isoform CRA_b [Mus musculus]

Sequence ID: **EDL02466.1** Length: 2541 Number of Matches: 1

See 1 more title(s)

Range 1: 625 to 634

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.9 bits(70)	1.4()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    SAQPASAEPR  10
           SAQPASAEPR
Sbjct  625  SAQPASAEPR  634
```

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BLAST Results

Job title: P_TLN1_TLAESALQLLYTAK

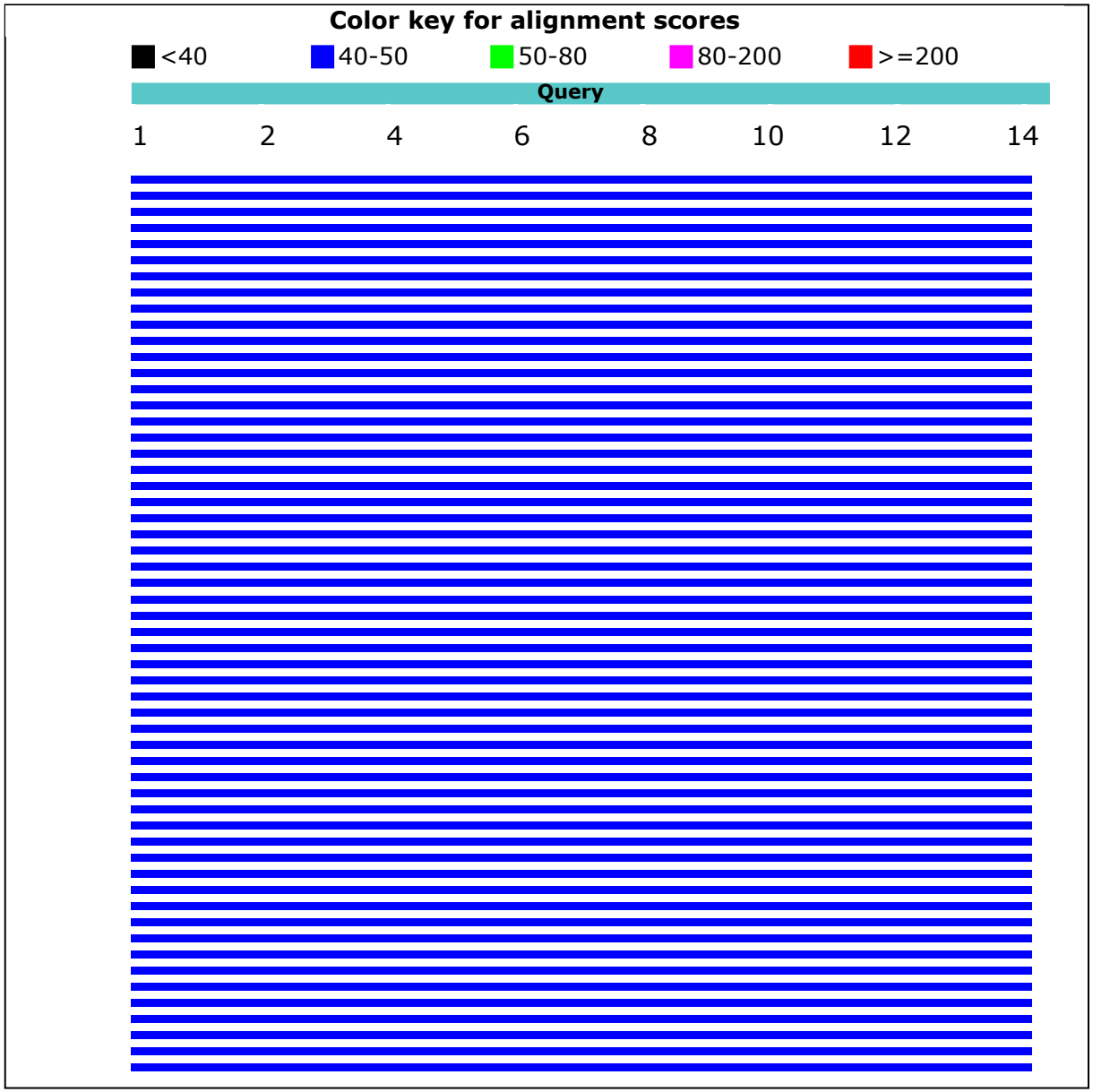
RID S56G1TX3014 (Expires on 08-04 11:35 am)

Query ID	lcl|Query_85412	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12
14

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
rCG55135, isoform CRA_a [Rattus norvegicus]	45.2	45.2	100%	1e-04	100%	EDL98751.1
mKIAA1027 protein [Mus musculus]	45.2	45.2	100%	1e-04	100%	BAC65702.4
talin-1 [Homo sapiens]	45.2	45.2	100%	1e-04	100%	AQN67632.1
Talin-1 [Bos mutus]	45.2	45.2	100%	1e-04	100%	ELR52791.1
talin 1, isoform CRA_b [Mus musculus]	45.2	45.2	100%	1e-04	100%	EDL02466.1
talin [Homo sapiens]	45.2	45.2	100%	1e-04	100%	AAD13152.1
talin [Homo sapiens]	45.2	45.2	100%	1e-04	100%	AAF23322.1
unnamed protein product [Mus musculus]	45.2	45.2	100%	1e-04	100%	BAE27781.1
talin-1 [Homo sapiens]	45.2	45.2	100%	1e-04	100%	NP_006280.3
talin	45.2	45.2	100%	1e-04	100%	1617167A
talin-1 isoform X1 [Papio anubis]	45.2	45.2	100%	1e-04	100%	XP_003911573.2
hypothetical protein PANDA_007476 [Ailuropoda melanoleuca]	45.2	45.2	100%	1e-04	100%	EFB15370.1
talin [Mus musculus]	45.2	45.2	100%	1e-04	100%	CAA39588.1
Talin-1 [Macaca mulatta]	45.2	45.2	100%	1e-04	100%	EHH23990.1
talin-1 [Bos taurus]	45.2	45.2	100%	1e-04	100%	NP_001192357.2
talin-1 [Mus musculus]	45.2	45.2	100%	1e-04	100%	NP_035732.2
talin 1, isoform CRA_b [Homo sapiens]	45.2	45.2	100%	1e-04	100%	EAW58353.1
talin-1 [Rattus norvegicus]	45.2	45.2	100%	1e-04	100%	NP_001034114.2
Talin 1 [Homo sapiens]	45.2	45.2	100%	1e-04	100%	AAH42923.1
talin [Homo sapiens]	45.2	45.2	100%	1e-04	100%	AAF27330.1
Talin-1 [Fukomys damarensis]	45.2	45.2	100%	1e-04	100%	KFO35373.1
Talin-1 [Heterocephalus glaber]	45.2	45.2	100%	1e-04	100%	EHB09959.1
talin-1 isoform 1 [Cricetulus griseus]	45.2	45.2	100%	1e-04	100%	ERE83219.1
Talin-1 [Myotis brandtii]	45.2	45.2	100%	1e-04	100%	EPQ18776.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
talin-1 isoform 2 [Camelus ferus]	45.2	45.2	100%	1e-04	100%	EPY78578.1
talin-1 isoform X2 [Papio anubis]	45.2	45.2	100%	1e-04	100%	XP_021783085.1
Talin-1 [Tupaia chinensis]	45.2	45.2	100%	1e-04	100%	ELW70306.1
talin-1 isoform X3 [Papio anubis]	45.2	45.2	100%	1e-04	100%	XP_021783086.1
rCG55135, isoform CRA_c [Rattus norvegicus]	45.2	45.2	100%	1e-04	100%	EDL98753.1
talin 1, isoform CRA_a [Mus musculus]	45.2	45.2	100%	1e-04	100%	EDL02465.1
Talin-1 [Cricetulus griseus]	45.2	45.2	100%	1e-04	100%	EGW07880.1
talin-2 [Alligator mississippiensis]	45.2	45.2	100%	1e-04	100%	KYO20875.1
Tln1 protein [Rattus norvegicus]	45.2	45.2	100%	1e-04	100%	AAI00263.1
Tln1 protein [Mus musculus]	45.2	45.2	100%	1e-04	100%	AAI21788.1
hypothetical protein Celaphus_00018421 [Cervus elaphus hippelaphus]	45.2	45.2	100%	1e-04	100%	OWK01031.1
unnamed protein product [Mus musculus]	45.2	45.2	100%	1e-04	100%	BAE42391.1
Talin-1 [Pteropus alecto]	45.2	45.2	100%	1e-04	100%	ELK09031.1
Tln1 protein [Mus musculus]	45.2	45.2	100%	1e-04	100%	AAH18557.1
Chain A, Structural Analysis Of A Talin Triple Domain Module, E1794y, E1797y, Q1801y Mutant	45.2	45.2	100%	1e-04	100%	5IC1_A
Chain A, Structural Analysis Of A Talin Triple Domain Module	45.2	45.2	100%	1e-04	100%	5IC0_A
Chain B, Crystal Structure Of Talin Autoinhibition Complex	45.2	45.2	100%	1e-04	100%	4F7G_B
Chain A, Nmr Structure Of The Talin Rod Domain, 1655-1822	45.2	45.2	100%	1e-04	100%	2KBB_A
hypothetical protein H355_006584 [Colinus virginianus]	42.6	42.6	100%	0.001	93%	OXB79125.1
hypothetical protein ASZ78_013077 [Callipepla squamata]	42.6	42.6	100%	0.001	93%	OXB66686.1
Talin-1 [Pygoscelis adeliae]	42.6	42.6	100%	0.001	93%	KFW62869.1
Talin-1 [Picoides pubescens]	42.6	42.6	100%	0.001	93%	KFV65621.1
talin-1-like [Scleropages formosus]	42.6	42.6	100%	0.001	93%	KPP73766.1
talin-1 [Patagioenas fasciata monilis]	42.6	42.6	100%	0.001	93%	OPJ75460.1
talin-1 [Amazona aestiva]	42.6	42.6	100%	0.001	93%	KQK82883.1
Talin-1 [Struthio camelus australis]	42.6	42.6	100%	0.001	93%	KFV84240.1
Talin-1 [Chlamydotis macqueenii]	42.6	42.6	100%	0.001	93%	KFP42152.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Talin-1 [Aptenodytes forsteri]	42.6	42.6	100%	0.001	93%	KFM11569.1
talin 1 [Coturnix japonica]	42.6	42.6	100%	0.001	93%	NP_001310165.1
talin-1 [Gallus gallus]	42.6	42.6	100%	0.001	93%	NP_989854.1
Talin-1 [Manacus vitellinus]	42.6	42.6	100%	0.001	93%	KFW87779.1
talin-1 [Danio rerio]	42.6	42.6	100%	0.001	93%	NP_001009560.1
Talin-1 [Cuculus canorus]	42.6	42.6	100%	0.001	93%	KFO73905.1
Talin-1 [Lonchura striata domestica]	42.6	42.6	100%	0.001	93%	OWK58725.1
Talin-1 [Pterocles gutturalis]	42.6	42.6	100%	0.001	93%	KFV10056.1
Talin-1 [Corvus brachyrhynchos]	42.6	42.6	100%	0.001	93%	KFO52801.1
Talin-1 [Buceros rhinoceros silvestris]	42.6	42.6	100%	0.001	93%	KFO88453.1
hypothetical protein XELAEV_18008634mg [Xenopus laevis]	42.6	42.6	100%	0.001	93%	OCU02863.1
Talin-1 [Pelecanus crispus]	42.6	42.6	100%	0.001	93%	KFQ62766.1
Talin-1, partial [Antrostomus carolinensis]	42.6	42.6	100%	0.001	93%	KFZ54815.1
talin-related protein [Homo sapiens]	41.4	41.4	100%	0.003	93%	AAB62679.1
unnamed protein product [Tetraodon nigroviridis]	40.1	40.1	100%	0.008	86%	CAF93389.1
hypothetical protein XELAEV_18004235mg [Xenopus laevis]	40.1	40.1	100%	0.008	86%	OCT56929.1
Talin-1 [Chelonia mydas]	40.1	40.1	100%	0.008	86%	EMP24898.1
hypothetical protein XENTR_v900303562mg, partial [Xenopus tropicalis]	40.1	40.1	100%	0.008	86%	OCA15211.1
hypothetical protein cypCar_00028015 [Cyprinus carpio]	39.7	39.7	100%	0.012	86%	KTF74906.1
hypothetical protein cypCar_00042682 [Cyprinus carpio]	39.7	39.7	100%	0.012	86%	KTF79748.1
Talin-1 [Larimichthys crocea]	39.7	39.7	100%	0.012	86%	KKF18162.1
unnamed protein product [Oncorhynchus mykiss]	39.7	39.7	100%	0.012	86%	CDQ89317.1
Talin-1 [Anas platyrhynchos]	39.7	39.7	100%	0.012	86%	EOA93682.1
Talin-2 [Heterocephalus glaber]	39.2	39.2	100%	0.017	86%	EHB01326.1
Talin-2 [Fukomys damarensis]	39.2	39.2	100%	0.017	86%	KFO26023.1
mCG141703, isoform CRA_c [Mus musculus]	39.2	39.2	100%	0.017	86%	EDL26154.1
Talin-2 [Myotis davidii]	39.2	39.2	100%	0.017	86%	ELK31332.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
mCG141703, isoform CRA_a [Mus musculus]	39.2	39.2	100%	0.017	86%	EDL26152.1
hypothetical protein EGM_16033 [Macaca fascicularis]	39.2	39.2	100%	0.017	86%	EHH63127.1
hypothetical protein XELAEV_18018012mg [Xenopus laevis]	39.2	39.2	100%	0.017	86%	OCT89391.1
hypothetical protein XELAEV_18020799mg [Xenopus laevis]	39.2	39.2	100%	0.017	86%	OCT87107.1
hypothetical protein XENTR_v900085562mg [Xenopus tropicalis]	39.2	39.2	100%	0.017	86%	OCA41499.1
talin-2 [Danio rerio]	39.2	39.2	100%	0.017	86%	NP_957487.2
talin-2 [Patagioenas fasciata monilis]	39.2	39.2	100%	0.017	86%	OPJ70141.1
Tln2 protein [Mus musculus]	39.2	39.2	100%	0.017	86%	AAI58058.1
hypothetical protein Y1Q_0001590 [Alligator mississippiensis]	39.2	39.2	100%	0.017	86%	KYO21362.1
Talin-2 [Larimichthys crocea]	39.2	39.2	100%	0.017	86%	KKF12598.1
Talin-2 [Nipponia nippon]	39.2	39.2	100%	0.017	86%	KFR02123.1
Talin-2 [Aptenodytes forsteri]	39.2	39.2	100%	0.017	86%	KFM03965.1
Talin-2 [Cricetulus griseus]	39.2	39.2	100%	0.017	86%	EGW07150.1
TPA: talin 2 [Bos taurus]	39.2	39.2	100%	0.017	86%	DAA25364.1
Talin-2 [Charadrius vociferus]	39.2	39.2	100%	0.017	86%	KGL94689.1
Talin-2, partial [Antrostomus carolinensis]	39.2	39.2	100%	0.017	86%	KFZ61778.1
Talin-2 [Struthio camelus australis]	39.2	39.2	100%	0.017	86%	KFV84748.1
Talin-2 [Picoides pubescens]	39.2	39.2	100%	0.017	86%	KFV61064.1
Talin-2 [Tauraco erythrolophus]	39.2	39.2	100%	0.017	86%	KFV12397.1
Talin-2 [Opisthocomus hoazin]	39.2	39.2	100%	0.017	86%	KFR17588.1
Talin-2 [Egretta garzetta]	39.2	39.2	100%	0.017	86%	KFP20122.1
Talin-2 [Cuculus canorus]	39.2	39.2	100%	0.017	86%	KFO74139.1

Alignments

rCG55135, isoform CRA_a [Rattus norvegicus]

Sequence ID: **EDL98751.1** Length: 2577 Number of Matches: 1
Range 1: 1803 to 1816

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1     TLAESALQLLYTAK  14
            TLAESALQLLYTAK
Sbjct  1803  TLAESALQLLYTAK  1816
```

mKIAA1027 protein, partial [Mus musculus]

Sequence ID: **BAC65702.4** Length: 2564 Number of Matches: 1
Range 1: 1790 to 1803

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1     TLAESALQLLYTAK  14
            TLAESALQLLYTAK
Sbjct  1790  TLAESALQLLYTAK  1803
```

talin-1 [Homo sapiens]

Sequence ID: **AQN67632.1** Length: 2558 Number of Matches: 1
Range 1: 1784 to 1797

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1     TLAESALQLLYTAK  14
            TLAESALQLLYTAK
Sbjct  1784  TLAESALQLLYTAK  1797
```

Talin-1, partial [Bos mutus]

Sequence ID: **ELR52791.1** Length: 2553 Number of Matches: 1
Range 1: 1779 to 1792

Score	Expect	Method	Identities	Positives	Gaps	Frame

45.2 bits(99)	1e-04()	14/14(100%)	14/14(100%)	0/14(0%)

Features:

```
Query  1     TLAESALQLLYTAK  14
             TLAESALQLLYTAK
Sbjct  1779  TLAESALQLLYTAK  1792
```

talin 1, isoform CRA_b [Mus musculus]

Sequence ID: **EDL02466.1** Length: 2541 Number of Matches: 1

See 1 more title(s)

Range 1: 1767 to 1780

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.2 bits(99)	1e-04()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1     TLAESALQLLYTAK  14
             TLAESALQLLYTAK
Sbjct  1767  TLAESALQLLYTAK  1780
```

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BLAST Results

Job title: NCBI BlastP_TTR_GSPAINVAVHVFR

RID S54K4EAZ014 (Expires on 08-04 11:03 am)

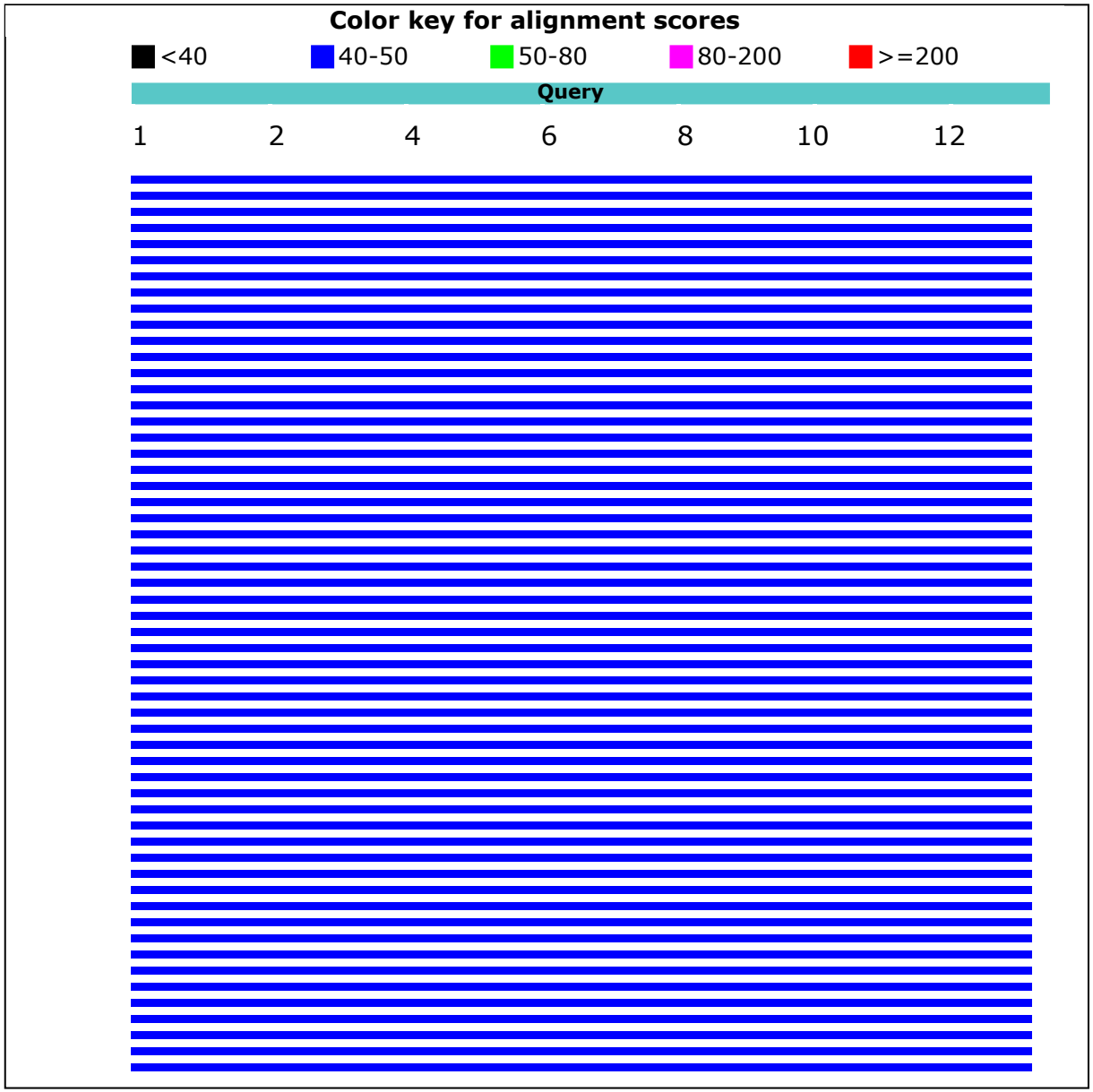
Query ID lcl|Query_230897
Description None
Molecule type amino acid
Query Length 13

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
transthyretin [Homo sapiens]	43.5	43.5	100%	4e-04	100%	AAD14098.1
transthyretin [Homo sapiens]	43.5	43.5	100%	4e-04	100%	AAB36045.1
transthyretin amyloidosis variant D38V [Homo sapiens]	43.5	43.5	100%	4e-04	100%	AAL92042.1
transthyretin [Homo sapiens]	43.5	43.5	100%	5e-04	100%	ABI63345.1
Chain A, Crystal Structure Of Human Transthyretin	43.5	43.5	100%	5e-04	100%	4N85_A
Homo sapiens transthyretin (prealbumin, amyloidosis type I) [synthetic construct]	43.5	43.5	100%	5e-04	100%	AAP36542.1
prealbumin [Homo sapiens]	43.5	43.5	100%	5e-04	100%	AAA98771.1
TTR [synthetic construct]	43.5	43.5	100%	5e-04	100%	AKI71139.1
TTR [synthetic construct]	43.5	43.5	100%	5e-04	100%	AKI71138.1
TTR [synthetic construct]	43.5	43.5	100%	5e-04	100%	AKI71136.1
transthyretin precursor [Homo sapiens]	43.5	43.5	100%	5e-04	100%	NP_000362.1
TTR [Homo sapiens]	43.5	43.5	100%	5e-04	100%	CAG33189.1
transthyretin (prealbumin, amyloidosis type I), isoform CRA_b [Homo sapiens]	43.5	43.5	100%	5e-04	100%	EAX01265.1
transthyretin [Homo sapiens]	43.5	43.5	100%	5e-04	100%	ABI63351.1
Chain A, Human Transthyretin (ttr) Complexed With (2,7-dichloro-fluoren-9- Ylideneaminooxy)-acetic Acid	43.5	43.5	100%	5e-04	100%	5E4A_A
Chain A, X-ray Structure Of Ttr Mutant - T119m At 1.22a Resolution	43.5	43.5	100%	5e-04	100%	5CLZ_A
Chain A, X-ray Structure Of Perdeuterated Ttr Mutant - S52p At 1.28a Resolution	43.5	43.5	100%	5e-04	100%	5CLX_A
Chain A, X-ray Structure Of Human Transthyretin (ttr) At Room Temperature To 1.9a Resolution	43.5	43.5	100%	5e-04	100%	4PVL_A
Chain A, Complex Of Ttr And Rbp4 And Oleic Acid	43.5	43.5	100%	5e-04	100%	2WQA_A
Chain A, Crystal Structure Of Dacm F87m/I110m Transthyretin Mutant	43.5	43.5	100%	5e-04	100%	5LLV_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, V122i Transthyretin Structure In Complex With Tolcalpone	43.5	43.5	100%	5e-04	100%	5A6I_A
Chain A, Crystal Structure Of Human Transthyretin With Bound Iodide	43.5	43.5	100%	5e-04	100%	1ZCR_A
Chain A, Solution Structure Of The T119m Variant Of Transthyretin In Its Monomeric State	43.5	43.5	100%	5e-04	100%	2NBP_A
Chain A, Structure Of Human Transthyretin Mutant A108v	43.5	43.5	100%	5e-04	100%	5FW6_A
Chain A, Structure Of Human Transthyretin Mutant A109v	43.5	43.5	100%	5e-04	100%	5FW7_A
Chain A, Structure Of Human Transthyretin Mutant E89k	43.5	43.5	100%	5e-04	100%	5FW8_A
Chain A, Structure Of Human Transthyretin Mutant A108i	43.5	43.5	100%	5e-04	100%	5FO2_A
Chain A, The X-Ray Crystallographic Structure Of The Amyloidogenic Variant Ttr Tyr78phe	43.5	43.5	100%	5e-04	100%	1X7S_A
Chain A, Structure Of Ttr R104h: A Non-Amyloidogenic Variant With Protective Clinical Effects	43.5	43.5	100%	5e-04	100%	1X7T_A
Chain A, Crystal Structure Of The Transthyretin Mutant A108yL110E SOLVED IN Space Group P21212	43.5	43.5	100%	5e-04	100%	1SOK_A
Chain A, Crystal Structure Of The Transthyretin Mutant Ttr C10aY114C	43.5	43.5	100%	5e-04	100%	1IJN_A
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	43.5	43.5	100%	5e-04	100%	1BZE_A
Chain A, Leu 55 Pro Transthyretin Crystal Structure	43.5	43.5	100%	5e-04	100%	5TTR_A
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	43.5	43.5	100%	5e-04	100%	2TRH_A
Chain A, The X-Ray Crystal Structure Refinements Of Normal Human Transthyretin And The Amyloidogenic Val30met Variant To 1.7 Angstroms Resolution	43.5	43.5	100%	5e-04	100%	1TTA_A
Chain A, High Resolution Crystal Structure Of Human Transthyretin Bound To Ligand And Conjugates Of 3-(5-(3,5-dichloro-4-hydroxyphenyl)-1,3,4- Oxadiazol-2-yl)phenyl Fluorosulfate	43.5	43.5	100%	5e-04	100%	4YDM_A
Chain A, Crystal Structure Of The Transthyretin Mutant Ttr Y114c-data Collected At Room Temperature	43.5	43.5	100%	5e-04	100%	1III_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	43.5	43.5	100%	5e-04	100%	1TSH_A
Chain A, Crystal Structure Of Human Transthyretin (e54k)	43.5	43.5	100%	5e-04	100%	3A4F_A
Chain A, Crystal Structure Of Human Transthyretin (e54g)	43.5	43.5	100%	5e-04	100%	3A4E_A
Chain A, Crystal Structure Of Transthyretin Variant V20s	43.5	43.5	100%	5e-04	100%	3BT0_A
Chain A, An Engineered Transthyretin Monomer That Is Non-Amyloidogenic - Unless Partially Denatured	43.5	43.5	100%	5e-04	100%	1GKO_A
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	43.5	43.5	100%	5e-04	100%	1BZD_A
Chain A, Transthyretin-V122I CARDIOMYOPATHIC MUTANT	43.5	43.5	100%	5e-04	100%	1TTR_A
Chain A, Crystal Structure Of The Highly Amyloidogenic Transthyretin Mutant Ttr G53sE54DL55S	43.5	43.5	100%	5e-04	100%	1G1O_A
Chain A, The X-Ray Crystal Structure Refinements Of Normal Human Transthyretin And The Amyloidogenic Val30met Variant To 1.7 Angstroms Resolution	43.5	43.5	100%	5e-04	100%	1TTB_A
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	43.5	43.5	100%	5e-04	100%	2TRY_A
Chain A, Structure Of Prealbumin, Secondary, Tertiary And Quaternary Interactions Determined By Fourier Refinement At 1.8 Angstroms	43.5	43.5	100%	5e-04	100%	2PAB_A
Chain A, Crystal Structure Of Transthyretin Variant L58h At Neutral Ph	43.5	43.5	100%	5e-04	100%	3DJR_A
Chain A, Crystal Structure Of Transthyretin Variant Y114h	43.5	43.5	100%	5e-04	100%	3CXF_A
Chain A, Crystal Structure Of Transthyretin Mutant I84a At Low Ph	43.5	43.5	100%	5e-04	100%	2G3Z_A
Chain A, Crystal Structure Of Cys10 Sulfonated Transthyretin	43.5	43.5	100%	5e-04	100%	2H4E_A
Chain A, Crystal Structure Of Transthyretin Mutant I84s At Acidic Ph	43.5	43.5	100%	5e-04	100%	2G3X_A
Chain A, Crystal Structure Of H88y Mutated Human Transthyretin	43.5	43.5	100%	5e-04	100%	5H0Y_A
Chain A, Crystal Structure Of H88a Mutated Human Transthyretin	43.5	43.5	100%	5e-04	100%	5H0V_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, Crystal Structure Of P113a Mutated Human Transthyretin	43.5	43.5	100%	5e-04	100%	5H0Z_A
Chain A, Crystal Structure Of H88f Mutated Human Transthyretin	43.5	43.5	100%	5e-04	100%	5H0W_A
Chain B, Crystal Structure Of H88s Mutated Human Transthyretin	43.5	43.5	100%	5e-04	100%	5H0X_B
Chain A, Transthyretin (Del Val122)	43.5	43.5	100%	5e-04	100%	1BZ8_A
Chain A, Human Transthyretin Ser52pro Mutant	43.5	43.5	100%	5e-04	100%	4MRC_A
Chain A, Crystal Structure Of Human Transthyretin Thr119met Mutant	43.5	43.5	100%	5e-04	100%	4TNG_A
Chain A, Crystal Structure Of Human Transthyretin Lys15trp Mutant	43.5	43.5	100%	5e-04	100%	4TNF_A
Chain A, Crystal Structure Of Human Transthyretin Ala108trp Mutant	43.5	43.5	100%	5e-04	100%	4TLU_A
Chain A, Crystal Structure Of Human Transthyretin Thr119tyr Mutant	43.5	43.5	100%	5e-04	100%	4TNE_A
Chain A, Crystal Structure Of Human Transthyretin Thr119trp Mutant	43.5	43.5	100%	5e-04	100%	4TM9_A
Chain A, Crystal Structure Of Human Transthyretin	43.5	43.5	100%	5e-04	100%	4TLT_A
Chain A, Crystal Structure Of Human Transthyretin Glu92pro Mutant	43.5	43.5	100%	5e-04	100%	4TLS_A
Chain A, Crystal Structure Of Human Transthyretin Ser85pro/glu92pro Mutant	43.5	43.5	100%	5e-04	100%	4TLK_A
Chain A, Crystal Structure Of Human Transthyretin Ser85pro Mutant	43.5	43.5	100%	5e-04	100%	4TL5_A
Chain A, Crystal Structure Of Human Transthyretin Leu55pro Mutant	43.5	43.5	100%	5e-04	100%	4TKW_A
Chain A, Crystal Structure Of Transthyretin In Complex With Iododiflunisal-Betaalaome	43.5	43.5	100%	5e-04	100%	3FC8_A
Chain A, Crystal Structure Of Human Transthyretin In Complex With Diclofenac	43.5	43.5	100%	5e-04	100%	1DVX_A
Chain A, Human Transthyretin (ttr) Complexed With 4-hydroxy-chalcone	43.5	43.5	100%	5e-04	100%	5EZP_A
Chain A, Human Transthyretin (ttr) Complexed With Ferulic Acid And Curcumin	43.5	43.5	100%	5e-04	100%	4PME_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, Crystal Structure Of The Apo Form Of Human Wild-Type Transthyretin	43.5	43.5	100%	5e-04	100%	3CFM_A
Chain A, Human Transthyretin (ttr) Complexed With (z)-((3,4-dichloro-phenyl)- Methyleneaminooxy)-acetic Acid	43.5	43.5	100%	5e-04	100%	5E4O_A
Chain A, Human Transthyretin (ttr) Complexed With Curcumin	43.5	43.5	100%	5e-04	100%	4PMF_A
Chain A, Crystal Structure Of The Wild Type Ttr Binding Naringenin (Ttrwt:nar)	43.5	43.5	100%	5e-04	100%	4DEU_A
Chain A, A Covalent Dimer Of Transthyretin That Affects The Amyloid Pathway	43.5	43.5	100%	5e-04	100%	1QWH_A
Chain A, X-Ray Crystal Structure Of Human Transthyretin At Room Temperature	43.5	43.5	100%	5e-04	100%	3U2I_A
Chain A, Transthyretin Natural Mutant A19d	43.5	43.5	100%	5e-04	100%	5DEJ_A
Chain A, Crystal Structure Of Ttr/resveratrol/t4 Complex	43.5	43.5	100%	5e-04	100%	5CR1_A
Chain A, Crystal Structure Of Human Transthyretin - Wild Type	43.5	43.5	100%	5e-04	100%	3I9P_A
Chain A, Transthyretin Thr119met Protein Stabilisation	43.5	43.5	100%	5e-04	100%	1F86_A
Chain A, Crystal Structure Of Human Transthyretin Variant A25t - #1	40.5	40.5	100%	0.006	92%	3I9A_A
Chain A, Crystal Structure Of Human Transthyretin Variant A25t - #2	40.5	40.5	100%	0.006	92%	3I9I_A
Chain A, Crystal Structure Of V30m Mutant Human Transthyretin Complexed With Glabridin	40.1	40.1	100%	0.008	92%	4N87_A
PREDICTED: transthyretin [Pan paniscus]	40.1	40.1	92%	0.008	100%	XP_003830303.1
transthyretin precursor [Pan troglodytes]	40.1	40.1	92%	0.008	100%	NP_001009137.1
prealbumin [Homo sapiens]	40.1	40.1	100%	0.008	92%	BAA00059.1
Chain A, The X-Ray Crystal Structure Refinements Of Normal Human Transthyretin And The Amyloidogenic Val30met Variant To 1.7 Angstroms Resolution	40.1	40.1	100%	0.008	92%	1TTC_A
prealbumin variant	40.1	40.1	100%	0.008	92%	1008142A
Chain A, Crystal Structure Of Human Transthyretin Val30met Mutant	40.1	40.1	100%	0.008	92%	4TL4_A
transthyretin [Pan troglodytes]	40.1	40.1	92%	0.008	100%	AAV74330.1
Chain A, V30m Mutant Human Transthyretin (Ttr) Complexed With Gc-1 (V30m:gc-1)	40.1	40.1	100%	0.008	92%	3NES_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain 1, The X-Ray Crystal Structure Refinements Of Normal Human Transthyretin And The Amyloidogenic Val 30-->met Variant To 1.7 Angstroms Resolution	39.2	39.2	100%	0.016	93%	1ETA_1
Chain A, Transthyretin Stability As A Key Factor In Amyloidogenesis	39.2	39.2	100%	0.016	93%	1FH2_A
transthyretin amyloidosis variant F33V [Homo sapiens]	38.4	38.4	100%	0.026	92%	AAL92043.1
transthyretin [Homo sapiens]	38.4	38.4	100%	0.030	92%	AAD14937.2
PREDICTED: transthyretin isoform X1 [Colobus angolensis palliatus]	36.3	36.3	92%	0.18	92%	XP_011788672.1

Alignments

transthyretin, partial [Homo sapiens]

Sequence ID: **AAD14098.1** Length: 44 Number of Matches: 1
Range 1: 19 to 31

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	4e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   GSPAINVAVHVFR  13
           GSPAINVAVHVFR
Sbjct  19  GSPAINVAVHVFR  31
```

transthyretin, partial [Homo sapiens]

Sequence ID: **AAB36045.1** Length: 44 Number of Matches: 1
Range 1: 19 to 31

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	4e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   GSPAINVAVHVFR  13
           GSPAINVAVHVFR
Sbjct  19  GSPAINVAVHVFR  31
```

transthyretin amyloidosis variant D38V, partial [Homo sapiens]

Sequence ID: **AAL92042.1** Length: 46 Number of Matches: 1
Range 1: 21 to 33

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	4e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   GSPAINVAVHVFR  13
           GSPAINVAVHVFR
Sbjct  21  GSPAINVAVHVFR  33
```

transthyretin [Homo sapiens]

Sequence ID: **ABI63345.1** Length: 184 Number of Matches: 1
Range 1: 42 to 54

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	5e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   GSPAINVAVHVFR  13
           GSPAINVAVHVFR
Sbjct  42  GSPAINVAVHVFR  54
```

Chain A, Crystal Structure Of Human Transthyretin

Sequence ID: **4N85_A** Length: 159 Number of Matches: 1

See 5 more title(s)

Range 1: 54 to 66

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	5e-04()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   GSPAINVAVHVFR  13
           GSPAINVAVHVFR
Sbjct  54  GSPAINVAVHVFR  66
```

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Job title: NCBI BlastP_TTR_TSESGELHGLTTEEEFVEGIYK

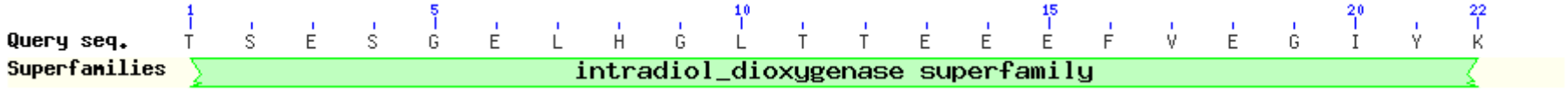
RID S54KJGRS015 (Expires on 08-04 11:03 am)

Query ID	lcl|Query_115664	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	22	**Program**	BLASTP 2.6.1+

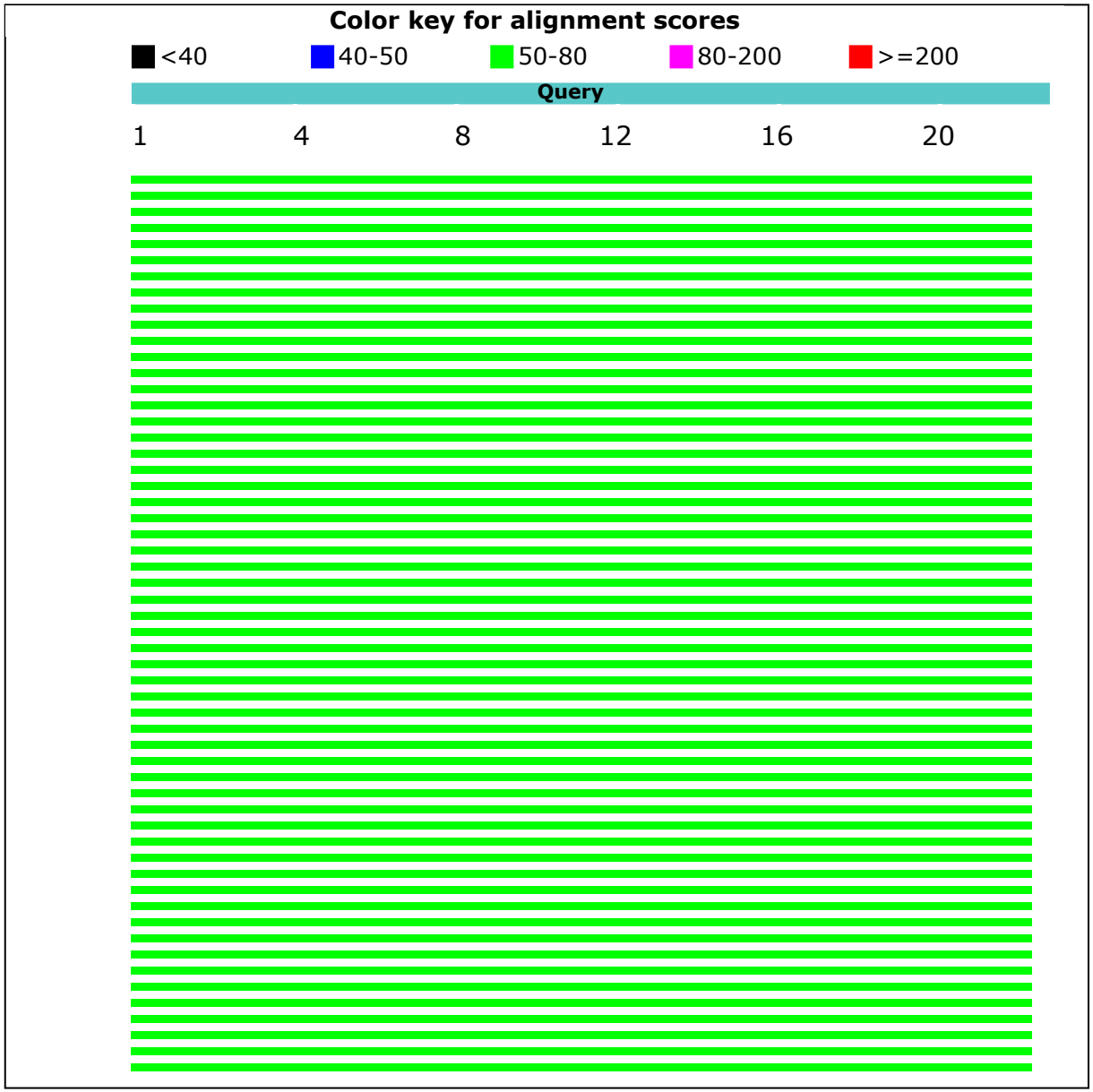
New Analyze your query with SmartBLAST

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
4
8
12
16
20

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
transthyretin [Homo sapiens]	72.3	72.3	100%	2e-13	100%	ABI63345.1
Chain A, Crystal Structure Of V30m Mutant Human Transthyretin Complexed With Glabridin	72.3	72.3	100%	2e-13	100%	4N87_A
Chain A, Crystal Structure Of Human Transthyretin	72.3	72.3	100%	2e-13	100%	4N85_A
PREDICTED: transthyretin isoform X1 [Colobus angolensis palliatus]	72.3	72.3	100%	2e-13	100%	XP_011788672.1
PREDICTED: transthyretin isoform X2 [Colobus angolensis palliatus]	72.3	72.3	100%	2e-13	100%	XP_011788673.1
Homo sapiens transthyretin (prealbumin, amyloidosis type I) [synthetic construct]	72.3	72.3	100%	2e-13	100%	AAP36542.1
PREDICTED: transthyretin [Pan paniscus]	72.3	72.3	100%	2e-13	100%	XP_003830303.1
PREDICTED: transthyretin [Rhinopithecus bieti]	72.3	72.3	100%	2e-13	100%	XP_017713537.1
prealbumin [Homo sapiens]	72.3	72.3	100%	2e-13	100%	AAA98771.1
transthyretin precursor [Pongo abelii]	72.3	72.3	100%	2e-13	100%	NP_001127064.1
transthyretin precursor [Pan troglodytes]	72.3	72.3	100%	2e-13	100%	NP_001009137.1
transthyretin [Macaca fascicularis]	72.3	72.3	100%	2e-13	100%	BAC20609.1
TTR [synthetic construct]	72.3	72.3	100%	2e-13	100%	AKI71139.1
TTR [synthetic construct]	72.3	72.3	100%	2e-13	100%	AKI71138.1
TTR [synthetic construct]	72.3	72.3	100%	2e-13	100%	AKI71136.1
PREDICTED: transthyretin [Cercocebus atys]	72.3	72.3	100%	2e-13	100%	XP_011930274.1
PREDICTED: transthyretin isoform X3 [Colobus angolensis palliatus]	72.3	72.3	100%	2e-13	100%	XP_011788674.1
PREDICTED: transthyretin [Rhinopithecus roxellana]	72.3	72.3	100%	2e-13	100%	XP_010379114.1
PREDICTED: transthyretin [Chlorocebus sabaeus]	72.3	72.3	100%	2e-13	100%	XP_007972558.1
PREDICTED: transthyretin [Gorilla gorilla gorilla]	72.3	72.3	100%	2e-13	100%	XP_004059337.1
transthyretin precursor [Homo sapiens]	72.3	72.3	100%	2e-13	100%	NP_000362.1
prealbumin [Homo sapiens]	72.3	72.3	100%	2e-13	100%	BAA00059.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
transthyretin [Chlorocebus aethiops]	72.3	72.3	100%	2e-13	100%	BAL44623.1
transthyretin [Chlorocebus aethiops]	72.3	72.3	100%	2e-13	100%	BAL44398.1
transthyretin [Macaca fuscata]	72.3	72.3	100%	2e-13	100%	BAL44395.1
transthyretin precursor [Macaca mulatta]	72.3	72.3	100%	2e-13	100%	NP_001248608.1
TTR [Homo sapiens]	72.3	72.3	100%	2e-13	100%	CAG33189.1
transthyretin (prealbumin, amyloidosis type I), isoform CRA_b [Homo sapiens]	72.3	72.3	100%	2e-13	100%	EAX01265.1
transthyretin [Homo sapiens]	72.3	72.3	100%	2e-13	100%	ABI63351.1
Chain A, Human Transthyretin (ttr) Complexed With (2,7-dichloro-fluoren-9- Ylideneaminooxy)-acetic Acid	72.3	72.3	100%	2e-13	100%	5E4A_A
Chain A, Transthyretin Thr119met Protein Stabilisation	72.3	72.3	100%	2e-13	100%	1F86_A
Chain A, X-ray Structure Of Ttr Mutant - T119m At 1.22a Resolution	72.3	72.3	100%	2e-13	100%	5CLZ_A
Chain A, X-ray Structure Of Human Transthyretin (ttr) At Room Temperature To 1.9a Resolution	72.3	72.3	100%	2e-13	100%	4PVL_A
Chain A, Transthyretin Natural Mutant A19d	72.3	72.3	100%	2e-13	100%	5DEJ_A
Chain A, Crystal Structure Of Ttr/resveratrol/t4 Complex	72.3	72.3	100%	2e-13	100%	5CR1_A
Chain A, Crystal Structure Of Human Transthyretin - Wild Type	72.3	72.3	100%	2e-13	100%	3I9P_A
Chain A, Crystal Structure Of Human Transthyretin Variant A25t - #2	72.3	72.3	100%	2e-13	100%	3I9I_A
Chain A, V30m Mutant Human Transthyretin (Ttr) Complexed With Gc-1 (V30m:gc-1)	72.3	72.3	100%	2e-13	100%	3NES_A
Chain A, Transthyretin Stability As A Key Factor In Amyloidogenesis	72.3	72.3	100%	2e-13	100%	1FH2_A
hypothetical protein [Escherichia coli]	72.3	72.3	100%	2e-13	100%	WP_072794633.1
Chain A, Complex Of Ttr And Rbp4 And Oleic Acid	72.3	72.3	100%	2e-13	100%	2WQA_A
Chain A, Crystal Structure Of Dacm F87m/I110m Transthyretin Mutant	72.3	72.3	100%	2e-13	100%	5LLV_A
Chain A, V122i Transthyretin Structure In Complex With Tolcalpone	72.3	72.3	100%	2e-13	100%	5A6I_A
Chain A, Crystal Structure Of Human Transthyretin With Bound Iodide	72.3	72.3	100%	2e-13	100%	1ZCR_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain 1, The X-Ray Crystal Structure Refinements Of Normal Human Transthyretin And The Amyloidogenic Val 30-->met Variant To 1.7 Angstroms Resolution	72.3	72.3	100%	2e-13	100%	1ETA_1
Chain A, Human Transthyretin (ttr) Complexed With (z)-((3,4-dichloro-phenyl)- Methyleneaminooxy)-acetic Acid	72.3	72.3	100%	2e-13	100%	5E4O_A
Chain A, Human Transthyretin (ttr) Complexed With Curcumin	72.3	72.3	100%	2e-13	100%	4PMF_A
Chain A, Crystal Structure Of The Wild Type Ttr Binding Naringenin (Ttrwt:nar)	72.3	72.3	100%	2e-13	100%	4DEU_A
Chain A, A Covalent Dimer Of Transthyretin That Affects The Amyloid Pathway	72.3	72.3	100%	2e-13	100%	1QWH_A
Chain A, X-Ray Crystal Structure Of Human Transthyretin At Room Temperature	72.3	72.3	100%	2e-13	100%	3U2I_A
Chain A, Solution Structure Of The T119m Variant Of Transthyretin In Its Monomeric State	72.3	72.3	100%	2e-13	100%	2NBP_A
Chain A, Structure Of Human Transthyretin Mutant A108v	72.3	72.3	100%	2e-13	100%	5FW6_A
Chain A, Structure Of Human Transthyretin Mutant A109v	72.3	72.3	100%	2e-13	100%	5FW7_A
Chain A, Structure Of Human Transthyretin Mutant E89k	72.3	72.3	100%	2e-13	100%	5FW8_A
Chain A, Structure Of Human Transthyretin Mutant A108i	72.3	72.3	100%	2e-13	100%	5FO2_A
Chain A, The X-Ray Crystallographic Structure Of The Amyloidogenic Variant Ttr Tyr78phe	72.3	72.3	100%	2e-13	100%	1X7S_A
Chain A, Structure Of Ttr R104h: A Non-Amyloidogenic Variant With Protective Clinical Effects	72.3	72.3	100%	2e-13	100%	1X7T_A
Chain A, Crystal Structure Of The Transthyretin Mutant A108yL110E SOLVED IN Space Group P21212	72.3	72.3	100%	2e-13	100%	1SOK_A
Chain A, Crystal Structure Of The Transthyretin Mutant Ttr C10aY114C	72.3	72.3	100%	2e-13	100%	1IJN_A
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	72.3	72.3	100%	2e-13	100%	1BZE_A
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	72.3	72.3	100%	2e-13	100%	2TRH_A
Chain A, The X-Ray Crystal Structure Refinements Of Normal Human Transthyretin And The Amyloidogenic Val30met Variant To 1.7 Angstroms Resolution	72.3	72.3	100%	2e-13	100%	1TTA_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, The X-Ray Crystal Structure Refinements Of Normal Human Transthyretin And The Amyloidogenic Val30met Variant To 1.7 Angstroms Resolution	72.3	72.3	100%	2e-13	100%	1TTC_A
Chain A, High Resolution Crystal Structure Of Human Transthyretin Bound To Ligand And Conjugates Of 3-(5-(3,5-dichloro-4-hydroxyphenyl)-1,3,4- Oxadiazol-2-yl)phenyl Fluorosulfate	72.3	72.3	100%	2e-13	100%	4YDM_A
Chain A, Crystal Structure Of The Transthyretin Mutant Ttr Y114c-data Collected At Room Temperature	72.3	72.3	100%	2e-13	100%	1III_A
Chain A, Crystal Structure Of Transthyretin Variant V20s	72.3	72.3	100%	2e-13	100%	3BT0_A
Chain A, An Engineered Transthyretin Monomer That Is Non-Amyloidogenic - Unless Partially Denatured	72.3	72.3	100%	2e-13	100%	1GKO_A
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	72.3	72.3	100%	2e-13	100%	1BZD_A
Chain A, Transthyretin-V122I CARDIOMYOPATHIC MUTANT	72.3	72.3	100%	2e-13	100%	1TTR_A
Chain A, The X-Ray Crystal Structure Refinements Of Normal Human Transthyretin And The Amyloidogenic Val30met Variant To 1.7 Angstroms Resolution	72.3	72.3	100%	2e-13	100%	1TTB_A
Chain A, Tertiary Structures Of Three Amyloidogenic Transthyretin Variants And Implications For Amyloid Fibril Formation	72.3	72.3	100%	2e-13	100%	2TRY_A
Chain A, Crystal Structure Of Human Transthyretin Variant A25t - #1	72.3	72.3	100%	2e-13	100%	3I9A_A
Chain A, Crystal Structure Of Transthyretin Variant Y114h	72.3	72.3	100%	2e-13	100%	3CXF_A
Chain A, Crystal Structure Of Transthyretin Mutant I84a At Low Ph	72.3	72.3	100%	2e-13	100%	2G3Z_A
Chain A, Crystal Structure Of Cys10 Sulfonated Transthyretin	72.3	72.3	100%	2e-13	100%	2H4E_A
Chain A, Crystal Structure Of Transthyretin Mutant I84s At Acidic Ph	72.3	72.3	100%	2e-13	100%	2G3X_A
Chain A, Human Transthyretin (ttr) Complexed With Ferulic Acid And Curcumin	72.3	72.3	100%	2e-13	100%	4PME_A
Chain A, Crystal Structure Of The Apo Form Of Human Wild-Type Transthyretin	72.3	72.3	100%	2e-13	100%	3CFM_A
Chain A, Crystal Structure Of H88y Mutated Human Transthyretin	72.3	72.3	100%	2e-13	100%	5H0Y_A

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, Crystal Structure Of H88a Mutated Human Transthyretin	72.3	72.3	100%	2e-13	100%	5H0V_A
Chain A, Crystal Structure Of P113a Mutated Human Transthyretin	72.3	72.3	100%	2e-13	100%	5H0Z_A
Chain A, Crystal Structure Of H88f Mutated Human Transthyretin	72.3	72.3	100%	2e-13	100%	5H0W_A
Chain B, Crystal Structure Of H88s Mutated Human Transthyretin	72.3	72.3	100%	2e-13	100%	5H0X_B
Chain A, Transthyretin (Del Val122)	72.3	72.3	100%	2e-13	100%	1BZ8_A
Chain A, Crystal Structure Of Human Transthyretin Thr119met Mutant	72.3	72.3	100%	2e-13	100%	4TNG_A
Chain A, Crystal Structure Of Human Transthyretin Lys15trp Mutant	72.3	72.3	100%	2e-13	100%	4TNF_A
Chain A, Crystal Structure Of Human Transthyretin Ala108trp Mutant	72.3	72.3	100%	2e-13	100%	4TLU_A
Chain A, Crystal Structure Of Human Transthyretin Thr119tyr Mutant	72.3	72.3	100%	2e-13	100%	4TNE_A
Chain A, Crystal Structure Of Human Transthyretin Thr119trp Mutant	72.3	72.3	100%	2e-13	100%	4TM9_A
Chain A, Crystal Structure Of Human Transthyretin	72.3	72.3	100%	2e-13	100%	4TLT_A
Chain A, Crystal Structure Of Human Transthyretin Glu92pro Mutant	72.3	72.3	100%	2e-13	100%	4TLS_A
Chain A, Crystal Structure Of Human Transthyretin Ser85pro/glu92pro Mutant	72.3	72.3	100%	2e-13	100%	4TLK_A
Chain A, Crystal Structure Of Human Transthyretin Ser85pro Mutant	72.3	72.3	100%	2e-13	100%	4TL5_A
Chain A, Crystal Structure Of Human Transthyretin Val30met Mutant	72.3	72.3	100%	2e-13	100%	4TL4_A
Chain A, Crystal Structure Of Transthyretin In Complex With Iododiflunisal-Betaalaome	72.3	72.3	100%	2e-13	100%	3FC8_A
transthyretin [Pan troglodytes]	72.3	72.3	100%	2e-13	100%	AAV74330.1
Chain A, Human Transthyretin (ttr) Complexed With 4-hydroxy-chalcone	72.3	72.3	100%	2e-13	100%	5EZP_A
PREDICTED: transthyretin [Nomascus leucogenys]	69.8	69.8	100%	1e-12	95%	XP_003262011.1
transthyretin [Chiropotes satanas]	69.4	69.4	95%	2e-12	100%	BAL44396.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, Structure Of Prealbumin, Secondary, Tertiary And Quaternary Interactions Determined By Fourier Refinement At 1.8 Angstroms	69.4	69.4	100%	2e-12	95%	2PAB_A

Alignments

transthyretin [Homo sapiens]

Sequence ID: **ABI63345.1** Length: 184 Number of Matches: 1
Range 1: 69 to 90

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.3 bits(163)	2e-13()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1   TSESGELHGLTTEEEFVEGIYK  22
           TSESGELHGLTTEEEFVEGIYK
Sbjct  69  TSESGELHGLTTEEEFVEGIYK  90
```

Chain A, Crystal Structure Of V30m Mutant Human Transthyretin Complexed With Glabridin

Sequence ID: **4N87_A** Length: 159 Number of Matches: 1

See 27 more title(s)

Range 1: 81 to 102

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.3 bits(163)	2e-13()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1    TSESGELHGLTTEEEFVEGIYK  22
            TSESGELHGLTTEEEFVEGIYK
Sbjct  81   TSESGELHGLTTEEEFVEGIYK  102
```

Chain A, Crystal Structure Of Human Transthyretin

Sequence ID: **4N85_A** Length: 159 Number of Matches: 1

See 5 more title(s)

Range 1: 81 to 102

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.3 bits(163)	2e-13()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1    TSESGELHGLTTEEEFVEGIYK  22
           TSESGELHGLTTEEEFVEGIYK
Sbjct  81   TSESGELHGLTTEEEFVEGIYK  102
```

PREDICTED: transthyretin isoform X1 [Colobus angolensis palliatus]

Sequence ID: **XP_011788672.1** Length: 150 Number of Matches: 1
Range 1: 69 to 90

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.3 bits(163)	2e-13()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1   TSESGELHGLTTEEEFVEGIYK  22
           TSESGELHGLTTEEEFVEGIYK
Sbjct  69  TSESGELHGLTTEEEFVEGIYK  90
```

PREDICTED: transthyretin isoform X2 [Colobus angolensis palliatus]

Sequence ID: **XP_011788673.1** Length: 149 Number of Matches: 1
Range 1: 71 to 92

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.3 bits(163)	2e-13()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1   TSESGELHGLTTEEEFVEGIYK  22
           TSESGELHGLTTEEEFVEGIYK
Sbjct  71  TSESGELHGLTTEEEFVEGIYK  92
```

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BLAST Results

Job title: NCBI BlastP_VTN_DVWGIEGPIDAAFTR

RID S54KZ08X015 (Expires on 08-04 11:03 am)

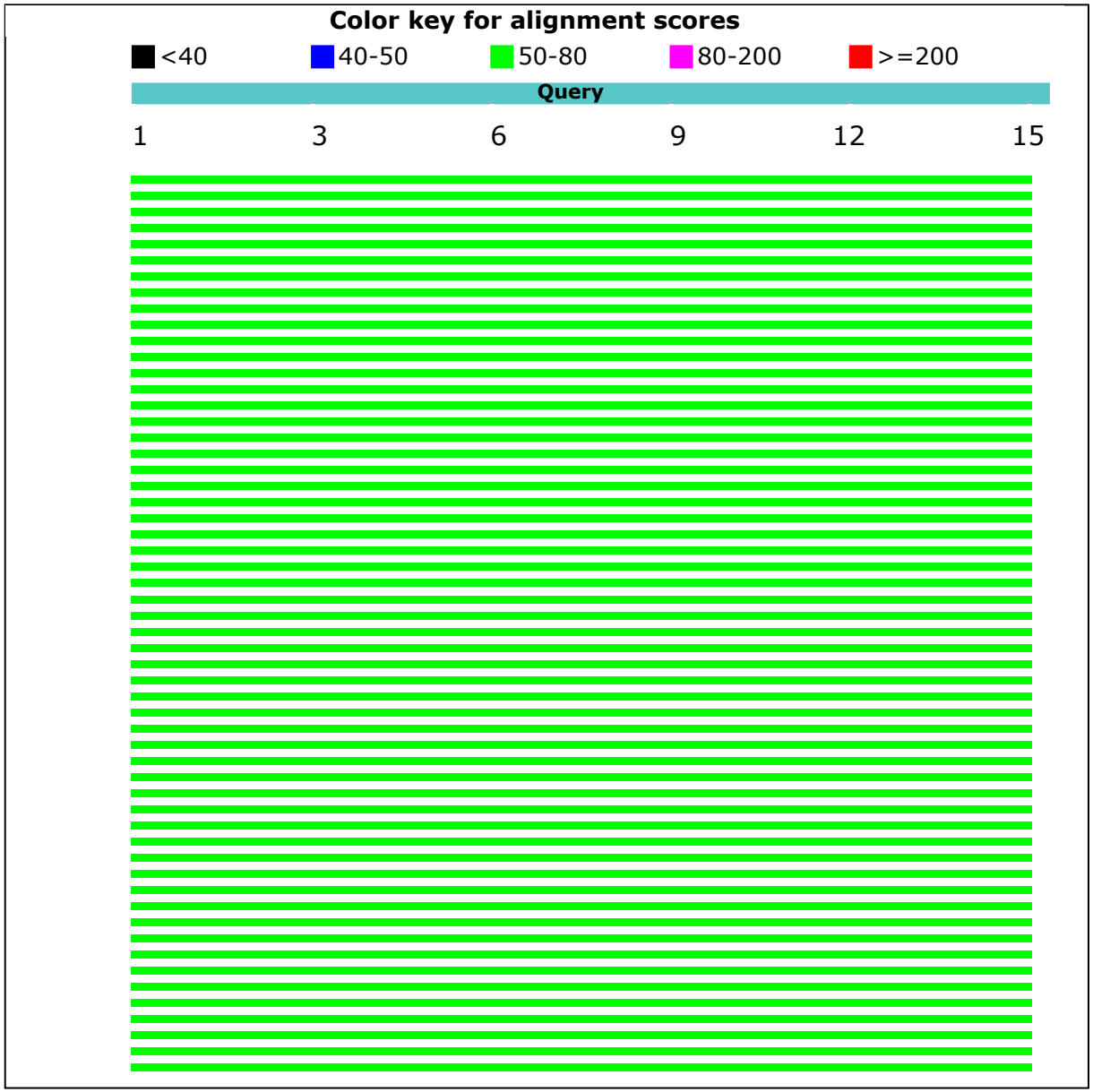
Query ID lcl|Query_245279
Description None
Molecule type amino acid
Query Length 15

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 102 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
3
6
9
12
15

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
VTN [Lycalopex culpaeus]	52.4	52.4	100%	5e-07	100%	ABB48172.1
vitronectin [Cricetulus griseus]	52.4	52.4	100%	5e-07	100%	ERE67884.1
Vitronectin [Cricetulus griseus]	52.4	52.4	100%	5e-07	100%	EGV94342.1
vitronectin [Cricetulus griseus]	52.4	52.4	100%	5e-07	100%	ERE67885.1
PREDICTED: vitronectin [Apteryx australis mantelli]	52.4	104	100%	5e-07	100%	XP_013797930.1
Vitronectin [Heterocephalus glaber]	52.4	52.4	100%	5e-07	100%	EHB13304.1
PREDICTED: vitronectin isoform X1 [Balaenoptera acutorostrata scammoni]	52.4	52.4	100%	5e-07	100%	XP_007183959.1
PREDICTED: vitronectin isoform X1 [Lipotes vexillifer]	52.4	52.4	100%	5e-07	100%	XP_007452469.1
PREDICTED: vitronectin [Tursiops truncatus]	52.4	52.4	100%	5e-07	100%	XP_004314075.2
PREDICTED: vitronectin [Cynoglossus semilaevis]	52.4	52.4	100%	5e-07	100%	XP_008307351.1
PREDICTED: vitronectin isoform X2 [Balaenoptera acutorostrata scammoni]	52.4	52.4	100%	5e-07	100%	XP_007183960.1
PREDICTED: vitronectin-like [Nothobranchius furzeri]	52.4	52.4	100%	5e-07	100%	XP_015807112.1
PREDICTED: vitronectin isoform X3 [Balaenoptera acutorostrata scammoni]	52.4	52.4	100%	5e-07	100%	XP_007183961.1
vitronectin [Heterocephalus glaber]	52.4	52.4	100%	5e-07	100%	XP_004857038.3
vitronectin [Odobenus rosmarus]	52.4	52.4	100%	5e-07	100%	AAZ83645.1
Vitronectin [Myotis brandtii]	52.4	52.4	100%	5e-07	100%	EPQ14351.1
PREDICTED: vitronectin isoform X1 [Nannospalax galili]	52.4	52.4	100%	5e-07	100%	XP_017650703.1
vitronectin precursor [Camelus ferus]	52.4	52.4	100%	5e-07	100%	EQB78383.1
PREDICTED: vitronectin isoform X1 [Ovis aries]	52.4	52.4	100%	5e-07	100%	XP_004013271.1
Aa1018 [Rattus norvegicus]	52.4	52.4	100%	5e-07	100%	AAP85374.1
Serum-spreading factor [Macaca fascicularis]	52.4	52.4	100%	5e-07	100%	EHH57817.1
Serum-spreading factor [Macaca mulatta]	52.4	52.4	100%	5e-07	100%	EHH24628.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: vitronectin [Equus asinus]	52.4	52.4	100%	5e-07	100%	XP_014717595.1
vitronectin [Castor canadensis]	52.4	52.4	100%	5e-07	100%	XP_020038091.1
vitronectin [Mesocricetus auratus]	52.4	52.4	100%	5e-07	100%	XP_005077063.1
PREDICTED: vitronectin [Echinops telfairi]	52.4	52.4	100%	5e-07	100%	XP_004706989.1
PREDICTED: vitronectin [Fukomys damarensis]	52.4	52.4	100%	5e-07	100%	XP_010640628.1
PREDICTED: vitronectin [Equus przewalskii]	52.4	52.4	100%	5e-07	100%	XP_008525973.1
PREDICTED: vitronectin [Peromyscus maniculatus bairdii]	52.4	52.4	100%	5e-07	100%	XP_006977542.1
PREDICTED: vitronectin [Lepisosteus oculatus]	52.4	75.9	100%	5e-07	100%	XP_006641129.1
PREDICTED: LOW QUALITY PROTEIN: vitronectin [Equus caballus]	52.4	52.4	100%	5e-07	100%	XP_001504173.3
vitronectin [Carlito syrichta]	52.4	52.4	100%	5e-07	100%	XP_008064906.1
hypothetical protein A6R68_04065 [Neotoma lepida]	52.4	52.4	100%	5e-07	100%	OBS67363.1
PREDICTED: vitronectin isoform X2 [Cricetulus griseus]	52.4	52.4	100%	5e-07	100%	XP_007642160.1
PREDICTED: vitronectin [Erinaceus europaeus]	52.4	52.4	100%	5e-07	100%	XP_007530777.1
PREDICTED: vitronectin [Cavia porcellus]	52.4	52.4	100%	5e-07	100%	XP_003469615.1
PREDICTED: vitronectin [Ochotona princeps]	52.4	52.4	100%	5e-07	100%	XP_012784917.1
PREDICTED: vitronectin isoform X2 [Lipotes vexillifer]	52.4	52.4	100%	5e-07	100%	XP_007452470.1
PREDICTED: vitronectin isoform X1 [Chinchilla lanigera]	52.4	52.4	100%	5e-07	100%	XP_005402814.1
PREDICTED: vitronectin [Orcinus orca]	52.4	52.4	100%	5e-07	100%	XP_004267189.1
VTN [Cervus elaphus hippelaphus]	52.4	52.4	100%	5e-07	100%	OWK14767.1
PREDICTED: vitronectin isoform X2 [Nannospalax galili]	52.4	52.4	100%	5e-07	100%	XP_008819803.1
PREDICTED: vitronectin [Tupaia chinensis]	52.4	52.4	100%	5e-07	100%	XP_006165500.1
vitronectin [Phascolarctos cinereus]	52.4	52.4	100%	5e-07	100%	XP_020819034.1
PREDICTED: vitronectin [Cercocebus atys]	52.4	52.4	100%	5e-07	100%	XP_011927770.1
PREDICTED: vitronectin [Macaca nemestrina]	52.4	52.4	100%	5e-07	100%	XP_011730114.1
PREDICTED: vitronectin isoform X1 [Mandrillus leucophaeus]	52.4	52.4	100%	5e-07	100%	XP_011852916.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: vitronectin [Macaca fascicularis]	52.4	52.4	100%	5e-07	100%	XP_015293529.1
vitronectin [Papio anubis]	52.4	52.4	100%	5e-07	100%	XP_003912541.1
PREDICTED: vitronectin [Macaca mulatta]	52.4	52.4	100%	5e-07	100%	XP_001106884.1
vitronectin [Meriones unguiculatus]	52.4	52.4	100%	5e-07	100%	XP_021495454.1
vitronectin [Mus caroli]	52.4	52.4	100%	5e-07	100%	XP_021033609.1
vitronectin [Mus pahari]	52.4	52.4	100%	5e-07	100%	XP_021068694.1
vitronectin isoform X1 [Odocoileus virginianus texanus]	52.4	52.4	100%	5e-07	100%	XP_020740434.1
PREDICTED: vitronectin [Rhinopithecus bieti]	52.4	52.4	100%	5e-07	100%	XP_017744404.1
vitronectin [Mus musculus]	52.4	52.4	100%	5e-07	100%	AAL34534.1
vitronectin [Rattus norvegicus]	52.4	52.4	100%	5e-07	100%	AAB01090.1
vitronectin precursor [Rattus norvegicus]	52.4	52.4	100%	5e-07	100%	NP_062029.2
PREDICTED: LOW QUALITY PROTEIN: vitronectin [Anser cygnoides domesticus]	52.4	52.4	100%	5e-07	100%	XP_013056806.1
vitronectin precursor [Mus musculus]	52.4	52.4	100%	5e-07	100%	NP_035837.1
PREDICTED: vitronectin [Colobus angolensis palliatus]	52.4	52.4	100%	5e-07	100%	XP_011796165.1
PREDICTED: vitronectin [Rhinopithecus roxellana]	52.4	52.4	100%	5e-07	100%	XP_010370618.1
PREDICTED: vitronectin isoform X1 [Pongo abelii]	52.4	52.4	100%	5e-07	100%	XP_009249687.1
PREDICTED: vitronectin [Chlorocebus sabaeus]	52.4	52.4	100%	5e-07	100%	XP_008008964.1
PREDICTED: vitronectin [Gorilla gorilla gorilla]	52.4	52.4	100%	5e-07	100%	XP_004042098.1
unnamed protein product [Homo sapiens]	52.4	52.4	100%	5e-07	100%	CAA28659.1
vitronectin precursor [Homo sapiens]	52.4	52.4	100%	5e-07	100%	NP_000629.3
unnamed protein product [Homo sapiens]	52.4	52.4	100%	5e-07	100%	CAA26933.1
PREDICTED: vitronectin [Pan paniscus]	52.4	52.4	100%	5e-07	100%	XP_003812709.1
PREDICTED: vitronectin [Pan troglodytes]	52.4	52.4	100%	5e-07	100%	XP_001146856.1
Vitronectin [Homo sapiens]	52.4	52.4	100%	5e-07	100%	AAH05046.1
vitronectin precursor [Pongo abelii]	52.4	52.4	100%	5e-07	100%	NP_001127063.1
Vitronectin [Mus musculus]	52.4	52.4	100%	5e-07	100%	AAH12690.1
unnamed protein product [Mus musculus]	52.4	52.4	100%	5e-07	100%	BAB27809.1
PREDICTED: vitronectin [Bos indicus]	52.4	52.4	100%	5e-07	100%	XP_019837935.1
vitronectin [Mus musculus]	52.4	52.4	100%	5e-07	100%	AAA40558.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
vitronectin precursor [Bos taurus]	52.4	52.4	100%	5e-07	100%	NP_001030222.1
PREDICTED: vitronectin [Bison bison bison]	52.4	52.4	100%	5e-07	100%	XP_010859725.1
PREDICTED: vitronectin [Bubalus bubalis]	52.4	52.4	100%	5e-07	100%	XP_006042264.1
PREDICTED: vitronectin [Bos mutus]	52.4	52.4	100%	5e-07	100%	XP_005907308.1
PREDICTED: vitronectin [Hipposideros armiger]	52.4	52.4	100%	5e-07	100%	XP_019502671.1
vitronectin precursor [Oryctolagus cuniculus]	52.4	52.4	100%	5e-07	100%	NP_001075761.1
PREDICTED: vitronectin isoform X2 [Ovis aries musimon]	52.4	52.4	100%	5e-07	100%	XP_011998146.1
PREDICTED: vitronectin [Myotis lucifugus]	52.4	52.4	100%	5e-07	100%	XP_006095579.1
PREDICTED: vitronectin [Myotis brandtii]	52.4	52.4	100%	5e-07	100%	XP_005876966.1
PREDICTED: vitronectin [Capra hircus]	52.4	52.4	100%	5e-07	100%	XP_005693309.1
PREDICTED: vitronectin [Octodon degus]	52.4	52.4	100%	5e-07	100%	XP_004635479.1
PREDICTED: vitronectin [Dasypus novemcinctus]	52.4	52.4	100%	5e-07	100%	XP_004450014.1
PREDICTED: vitronectin [Myotis davidii]	52.4	52.4	100%	5e-07	100%	XP_006768075.1
PREDICTED: vitronectin [Eptesicus fuscus]	52.4	52.4	100%	5e-07	100%	XP_008146023.1
PREDICTED: vitronectin [Jaculus jaculus]	52.4	52.4	100%	5e-07	100%	XP_004664567.1
PREDICTED: vitronectin [Elephantulus edwardii]	52.4	52.4	100%	5e-07	100%	XP_006891135.1
PREDICTED: vitronectin [Sorex araneus]	52.4	52.4	100%	5e-07	100%	XP_004605088.1
vitronectin [Neomonachus schauinslandi]	52.4	52.4	100%	5e-07	100%	XP_021559839.1
PREDICTED: vitronectin [Canis lupus familiaris]	52.4	52.4	100%	5e-07	100%	XP_854040.1
PREDICTED: vitronectin [Chrysochloris asiatica]	52.4	52.4	100%	5e-07	100%	XP_006874275.1
vitronectin isoform X1 [Ictidomys tridecemlineatus]	52.4	52.4	100%	5e-07	100%	XP_005327870.1
PREDICTED: vitronectin [Mustela putorius furo]	52.4	52.4	100%	5e-07	100%	XP_004747069.1
PREDICTED: vitronectin [Ceratotherium simum simum]	52.4	52.4	100%	5e-07	100%	XP_004433444.1
PREDICTED: vitronectin [Otolemur garnettii]	52.4	52.4	100%	5e-07	100%	XP_003797209.1

Alignments

VTN, partial [Lycalopex culpaeus]

Sequence ID: **ABB48172.1** Length: 64 Number of Matches: 1
Range 1: 5 to 19

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.4 bits(116)	5e-07()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1   DVWGIEGPIDAAFTR  15
           DVWGIEGPIDAAFTR
Sbjct  5   DVWGIEGPIDAAFTR  19
```

vitronectin [Cricetulus griseus]

Sequence ID: **ERE67884.1** Length: 876 Number of Matches: 1
Range 1: 199 to 213

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.4 bits(116)	5e-07()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    DVWGIEGPIDAAFTR  15
            DVWGIEGPIDAAFTR
Sbjct  199  DVWGIEGPIDAAFTR  213
```

Vitronectin [Cricetulus griseus]

Sequence ID: **EGV94342.1** Length: 876 Number of Matches: 1
Range 1: 199 to 213

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.4 bits(116)	5e-07()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    DVWGIEGPIDAAFTR  15
            DVWGIEGPIDAAFTR
Sbjct  199  DVWGIEGPIDAAFTR  213
```

vitronectin [Cricetulus griseus]

Sequence ID: **ERE67885.1** Length: 672 Number of Matches: 1
Range 1: 199 to 213

Score	Expect	Method	Identities	Positives	Gaps	Frame

52.4 bits(116)	5e-07()	15/15(100%)	15/15(100%)	0/15(0%)

Features:

```
Query  1    DVWGIEGPIDAAFTR  15
            DVWGIEGPIDAAFTR
Sbjct  199  DVWGIEGPIDAAFTR  213
```

PREDICTED: vitronectin [Apteryx australis mantelli]

Sequence ID: **XP_013797930.1** Length: 641 Number of Matches: 2
Range 1: 191 to 205

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.4 bits(116)	5e-07()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    DVWGIEGPIDAAFTR  15
            DVWGIEGPIDAAFTR
Sbjct  191  DVWGIEGPIDAAFTR  205
```

Range 2: 384 to 398

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.4 bits(116)	5e-07()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    DVWGIEGPIDAAFTR  15
            DVWGIEGPIDAAFTR
Sbjct  384  DVWGIEGPIDAAFTR  398
```

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BLAST Results

Job title: NCBI BlastP_VTN_FEDGVLDPDYPR

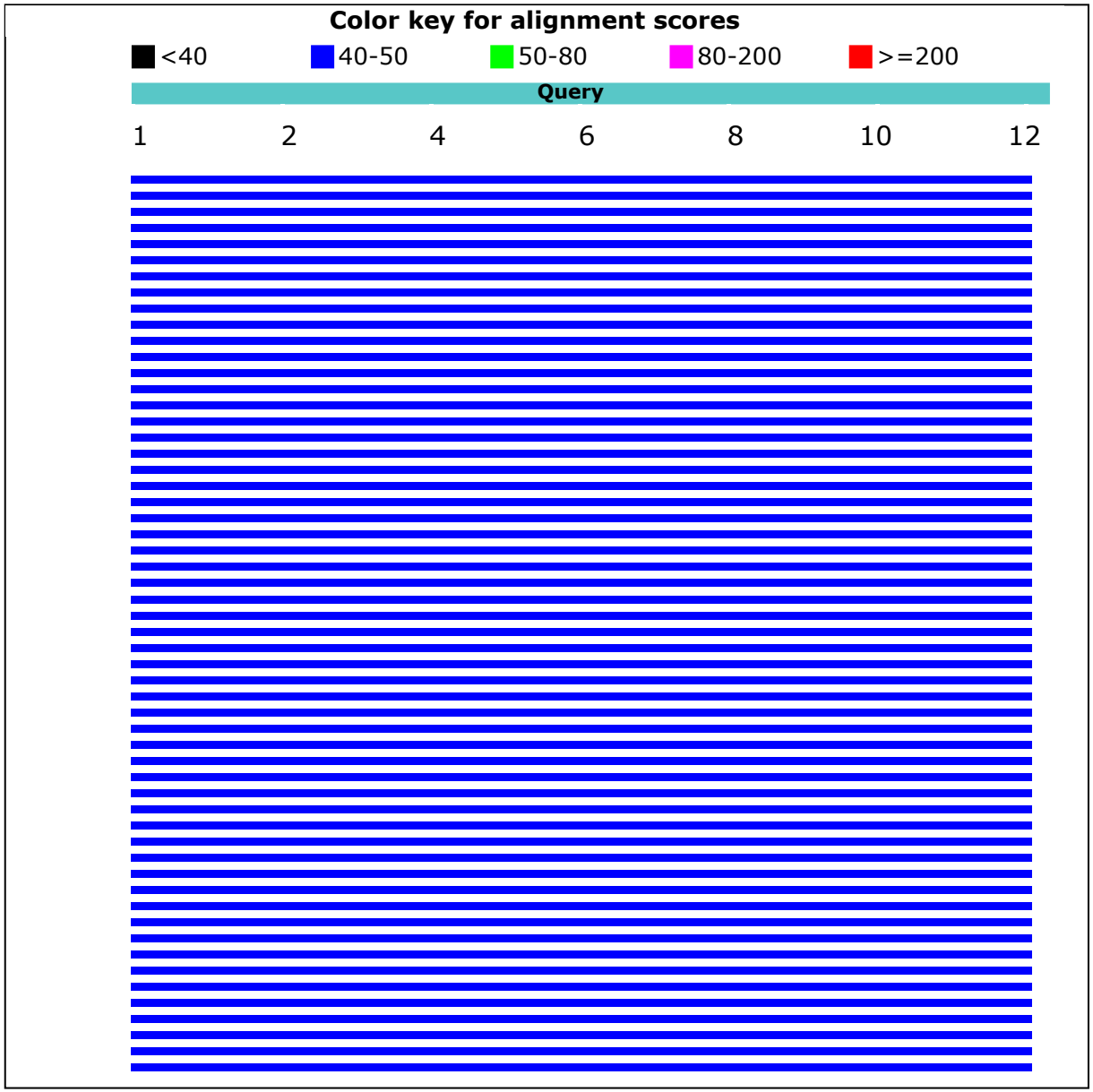
RID S54MHTMZ015 (Expires on 08-04 11:03 am)

Query ID	lcl|Query_253793	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	12	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Vitronectin [Myotis brandtii]	43.5	43.5	100%	4e-04	100%	EPQ14351.1
vitronectin precursor [Camelus ferus]	43.5	43.5	100%	4e-04	100%	EQB78383.1
Aa1018 [Rattus norvegicus]	43.5	43.5	100%	4e-04	100%	AAP85374.1
Serum-spreading factor [Macaca fascicularis]	43.5	43.5	100%	4e-04	100%	EHH57817.1
Serum-spreading factor [Macaca mulatta]	43.5	43.5	100%	4e-04	100%	EHH24628.1
PREDICTED: vitronectin [Equus asinus]	43.5	43.5	100%	4e-04	100%	XP_014717595.1
PREDICTED: vitronectin [Galeopterus variegatus]	43.5	43.5	100%	4e-04	100%	XP_008578016.1
vitronectin [Castor canadensis]	43.5	43.5	100%	4e-04	100%	XP_020038091.1
PREDICTED: vitronectin [Equus przewalskii]	43.5	43.5	100%	4e-04	100%	XP_008525973.1
PREDICTED: LOW QUALITY PROTEIN: vitronectin [Equus caballus]	43.5	43.5	100%	4e-04	100%	XP_001504173.3
vitronectin [Carlito syrichta]	43.5	43.5	100%	4e-04	100%	XP_008064906.1
PREDICTED: vitronectin [Ochotona princeps]	43.5	43.5	100%	4e-04	100%	XP_012784917.1
PREDICTED: vitronectin [Cercocebus atys]	43.5	43.5	100%	4e-04	100%	XP_011927770.1
PREDICTED: vitronectin [Macaca nemestrina]	43.5	43.5	100%	4e-04	100%	XP_011730114.1
PREDICTED: vitronectin isoform X1 [Mandrillus leucophaeus]	43.5	43.5	100%	4e-04	100%	XP_011852916.1
PREDICTED: vitronectin [Macaca fascicularis]	43.5	43.5	100%	4e-04	100%	XP_015293529.1
vitronectin [Papio anubis]	43.5	43.5	100%	4e-04	100%	XP_003912541.1
PREDICTED: vitronectin [Macaca mulatta]	43.5	43.5	100%	4e-04	100%	XP_001106884.1
PREDICTED: vitronectin [Rhinopithecus bieti]	43.5	43.5	100%	4e-04	100%	XP_017744404.1
vitronectin [Rattus norvegicus]	43.5	43.5	100%	4e-04	100%	AAB01090.1
vitronectin precursor [Rattus norvegicus]	43.5	43.5	100%	4e-04	100%	NP_062029.2
PREDICTED: vitronectin [Colobus angolensis palliatus]	43.5	43.5	100%	4e-04	100%	XP_011796165.1
PREDICTED: vitronectin [Rhinopithecus roxellana]	43.5	43.5	100%	4e-04	100%	XP_010370618.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: vitronectin isoform X1 [Pongo abelii]	43.5	43.5	100%	4e-04	100%	XP_009249687.1
PREDICTED: vitronectin [Chlorocebus sabaeus]	43.5	43.5	100%	4e-04	100%	XP_008008964.1
PREDICTED: vitronectin [Gorilla gorilla gorilla]	43.5	43.5	100%	4e-04	100%	XP_004042098.1
unnamed protein product [Homo sapiens]	43.5	43.5	100%	4e-04	100%	CAA28659.1
vitronectin precursor [Homo sapiens]	43.5	43.5	100%	4e-04	100%	NP_000629.3
unnamed protein product [Homo sapiens]	43.5	43.5	100%	4e-04	100%	CAA26933.1
PREDICTED: vitronectin [Pan paniscus]	43.5	43.5	100%	4e-04	100%	XP_003812709.1
PREDICTED: vitronectin [Pan troglodytes]	43.5	43.5	100%	4e-04	100%	XP_001146856.1
Vitronectin [Homo sapiens]	43.5	43.5	100%	4e-04	100%	AAH05046.1
vitronectin precursor [Pongo abelii]	43.5	43.5	100%	4e-04	100%	NP_001127063.1
PREDICTED: vitronectin [Hipposideros armiger]	43.5	43.5	100%	4e-04	100%	XP_019502671.1
PREDICTED: vitronectin [Myotis lucifugus]	43.5	43.5	100%	4e-04	100%	XP_006095579.1
PREDICTED: vitronectin [Myotis brandtii]	43.5	43.5	100%	4e-04	100%	XP_005876966.1
PREDICTED: vitronectin [Myotis davidii]	43.5	43.5	100%	4e-04	100%	XP_006768075.1
PREDICTED: vitronectin [Microtus ochrogaster]	43.5	43.5	100%	4e-04	100%	XP_005349504.1
PREDICTED: vitronectin [Jaculus jaculus]	43.5	43.5	100%	4e-04	100%	XP_004664567.1
PREDICTED: vitronectin [Elephantulus edwardii]	43.5	43.5	100%	4e-04	100%	XP_006891135.1
PREDICTED: vitronectin [Canis lupus familiaris]	43.5	43.5	100%	4e-04	100%	XP_854040.1
PREDICTED: vitronectin [Chrysochloris asiatica]	43.5	43.5	100%	4e-04	100%	XP_006874275.1
PREDICTED: vitronectin [Ceratotherium simum simum]	43.5	43.5	100%	4e-04	100%	XP_004433444.1
PREDICTED: vitronectin [Vicugna pacos]	43.5	43.5	100%	4e-04	100%	XP_015101299.1
PREDICTED: vitronectin [Camelus ferus]	43.5	43.5	100%	4e-04	100%	XP_006195736.2
PREDICTED: vitronectin [Panthera pardus]	43.5	43.5	100%	4e-04	100%	XP_019279353.1
PREDICTED: vitronectin [Miniopterus natalensis]	43.5	43.5	100%	4e-04	100%	XP_016057381.1
PREDICTED: vitronectin [Rousettus aegyptiacus]	43.5	43.5	100%	4e-04	100%	XP_015974682.1
PREDICTED: vitronectin [Acinonyx jubatus]	43.5	43.5	100%	4e-04	100%	XP_014936904.1
PREDICTED: vitronectin [Panthera tigris altaica]	43.5	43.5	100%	4e-04	100%	XP_007076107.1
PREDICTED: vitronectin [Felis catus]	43.5	43.5	100%	4e-04	100%	XP_003996546.1
PREDICTED: vitronectin [Rhinolophus sinicus]	43.5	43.5	100%	4e-04	100%	XP_019587033.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: vitronectin [Pteropus vampyrus]	43.5	43.5	100%	4e-04	100%	XP_011358379.1
PREDICTED: vitronectin [Trichechus manatus latirostris]	43.5	43.5	100%	4e-04	100%	XP_004385502.1
PREDICTED: vitronectin [Condylura cristata]	43.5	43.5	100%	4e-04	100%	XP_004685209.1
PREDICTED: vitronectin [Pteropus alecto]	43.5	43.5	100%	4e-04	100%	XP_006925231.1
PREDICTED: LOW QUALITY PROTEIN: vitronectin [Camelus dromedarius]	43.5	43.5	100%	4e-04	100%	XP_010977288.1
PREDICTED: LOW QUALITY PROTEIN: vitronectin [Camelus bactrianus]	43.5	43.5	100%	4e-04	100%	XP_010956585.1
unnamed protein product [Homo sapiens]	43.5	43.5	100%	4e-04	100%	BAH12789.1
vitronectin [Atelocynus microtis]	43.5	43.5	100%	4e-04	100%	AAX82456.1
vitronectin [Vulpes lagopus]	43.5	43.5	100%	4e-04	100%	AAX82455.1
VTN [Vulpes rueppellii]	43.5	43.5	100%	4e-04	100%	ABB48178.1
VTN [Vulpes cana]	43.5	43.5	100%	4e-04	100%	ABB48176.1
vitronectin [Otocyon megalotis]	43.5	43.5	100%	4e-04	100%	AAX82472.1
vitronectin [Urocyon cinereoargenteus]	43.5	43.5	100%	4e-04	100%	AAX82474.1
VTN [Vulpes chama]	43.5	43.5	100%	4e-04	100%	ABB48177.1
PREDICTED: vitronectin [Erinaceus europaeus]	41.4	41.4	100%	0.002	92%	XP_007530777.1
vitronectin precursor [Oryctolagus cuniculus]	41.4	41.4	100%	0.002	92%	NP_001075761.1
PREDICTED: vitronectin isoform X1 [Nannospalax galili]	40.9	40.9	100%	0.003	92%	XP_017650703.1
PREDICTED: vitronectin [Echinops telfairi]	40.9	40.9	100%	0.003	92%	XP_004706989.1
PREDICTED: vitronectin isoform X2 [Nannospalax galili]	40.9	40.9	100%	0.003	92%	XP_008819803.1
vitronectin [Mus caroli]	40.9	40.9	100%	0.003	92%	XP_021033609.1
PREDICTED: vitronectin [Eptesicus fuscus]	40.9	40.9	100%	0.003	92%	XP_008146023.1
PREDICTED: vitronectin [Otolemur garnettii]	40.9	40.9	100%	0.003	92%	XP_003797209.1
Vitronectin [Heterocephalus glaber]	40.1	40.1	100%	0.007	92%	EHB13304.1
PREDICTED: vitronectin isoform X1 [Lipotes vexillifer]	40.1	40.1	100%	0.007	92%	XP_007452469.1
PREDICTED: vitronectin [Tursiops truncatus]	40.1	40.1	100%	0.007	92%	XP_004314075.2
vitronectin [Heterocephalus glaber]	40.1	40.1	100%	0.007	92%	XP_004857038.3
PREDICTED: vitronectin [Fukomys damarensis]	40.1	40.1	100%	0.007	92%	XP_010640628.1
PREDICTED: vitronectin isoform X2 [Lipotes vexillifer]	40.1	40.1	100%	0.007	92%	XP_007452470.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: vitronectin [Orcinus orca]	40.1	40.1	100%	0.007	92%	XP_004267189.1
PREDICTED: vitronectin [Physeter catodon]	40.1	40.1	100%	0.007	92%	XP_007121821.1
vitronectin [Meriones unguiculatus]	40.1	40.1	100%	0.007	92%	XP_021495454.1
vitronectin [Neomonachus schauinslandi]	40.1	40.1	100%	0.007	92%	XP_021559839.1
PREDICTED: vitronectin [Ursus maritimus]	40.1	40.1	100%	0.007	92%	XP_008693573.1
PREDICTED: vitronectin [Mustela putorius furo]	40.1	40.1	100%	0.007	92%	XP_004747069.1
PREDICTED: vitronectin [Ailuropoda melanoleuca]	40.1	40.1	100%	0.007	92%	XP_002912420.1
hypothetical protein PANDA_000124 [Ailuropoda melanoleuca]	40.1	40.1	100%	0.007	92%	EFB26139.1
vitronectin [Microcebus murinus]	40.1	40.1	100%	0.007	92%	XP_012596125.1
PREDICTED: vitronectin [Propithecus coquereli]	40.1	40.1	100%	0.007	92%	XP_012503738.1
PREDICTED: vitronectin [Leptonychotes weddellii]	40.1	40.1	100%	0.007	92%	XP_006731638.1
PREDICTED: vitronectin [Gekko japonicus]	40.1	40.1	100%	0.007	92%	XP_015277378.1
PREDICTED: LOW QUALITY PROTEIN: vitronectin [Odobenus rosmarus divergens]	40.1	40.1	100%	0.007	92%	XP_004417761.1
PREDICTED: LOW QUALITY PROTEIN: vitronectin [Orycteropus afer afer]	40.1	40.1	100%	0.007	92%	XP_007935554.1
vitronectin [Conepatus sp.]	40.1	40.1	100%	0.007	92%	AIW43032.1
vitronectin [Conepatus sp.]	40.1	40.1	100%	0.007	92%	AIW43029.1
vitronectin [Conepatus sp.]	40.1	40.1	100%	0.007	92%	AIW43026.1
vitronectin [Mirounga angustirostris]	40.1	40.1	100%	0.007	92%	AAZ83644.1
vitronectin [Ailuropoda melanoleuca]	40.1	40.1	100%	0.007	92%	AAZ83643.1
vitronectin [Ursus americanus]	40.1	40.1	100%	0.007	92%	AAX82478.1

Alignments

Vitronectin [Myotis brandtii]

Sequence ID: **EPQ14351.1** Length: 500 Number of Matches: 1
Range 1: 253 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame

43.5 bits(95)	4e-04()	12/12(100%)	12/12(100%)	0/12(0%)

Features:

```
Query  1    FEDGVLDPDYPR  12
            FEDGVLDPDYPR
Sbjct  253  FEDGVLDPDYPR  264
```

vitronectin precursor [Camelus ferus]

Sequence ID: **EQB78383.1** Length: 490 Number of Matches: 1
Range 1: 241 to 252

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	4e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    FEDGVLDPDYPR  12
            FEDGVLDPDYPR
Sbjct  241  FEDGVLDPDYPR  252
```

Aa1018 [Rattus norvegicus]

Sequence ID: **AAP85374.1** Length: 490 Number of Matches: 1
Range 1: 237 to 248

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	4e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    FEDGVLDPDYPR  12
            FEDGVLDPDYPR
Sbjct  237  FEDGVLDPDYPR  248
```

Serum-spreading factor [Macaca fascicularis]

Sequence ID: **EHH57817.1** Length: 489 Number of Matches: 1
Range 1: 235 to 246

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	4e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    FEDGVLDPDYPR  12
            FEDGVLDPDYPR
Sbjct  235  FEDGVLDPDYPR  246
```

Serum-spreading factor [Macaca mulatta]

Sequence ID: **EHH24628.1** Length: 489 Number of Matches: 1
Range 1: 235 to 246

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(95)	4e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    FEDGVLDPDYPR  12
            FEDGVLDPDYPR
Sbjct  235  FEDGVLDPDYPR  246
```

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BLAST Results

Job title: NCBI BlastP_FLNA#_ENGVYLIDVK

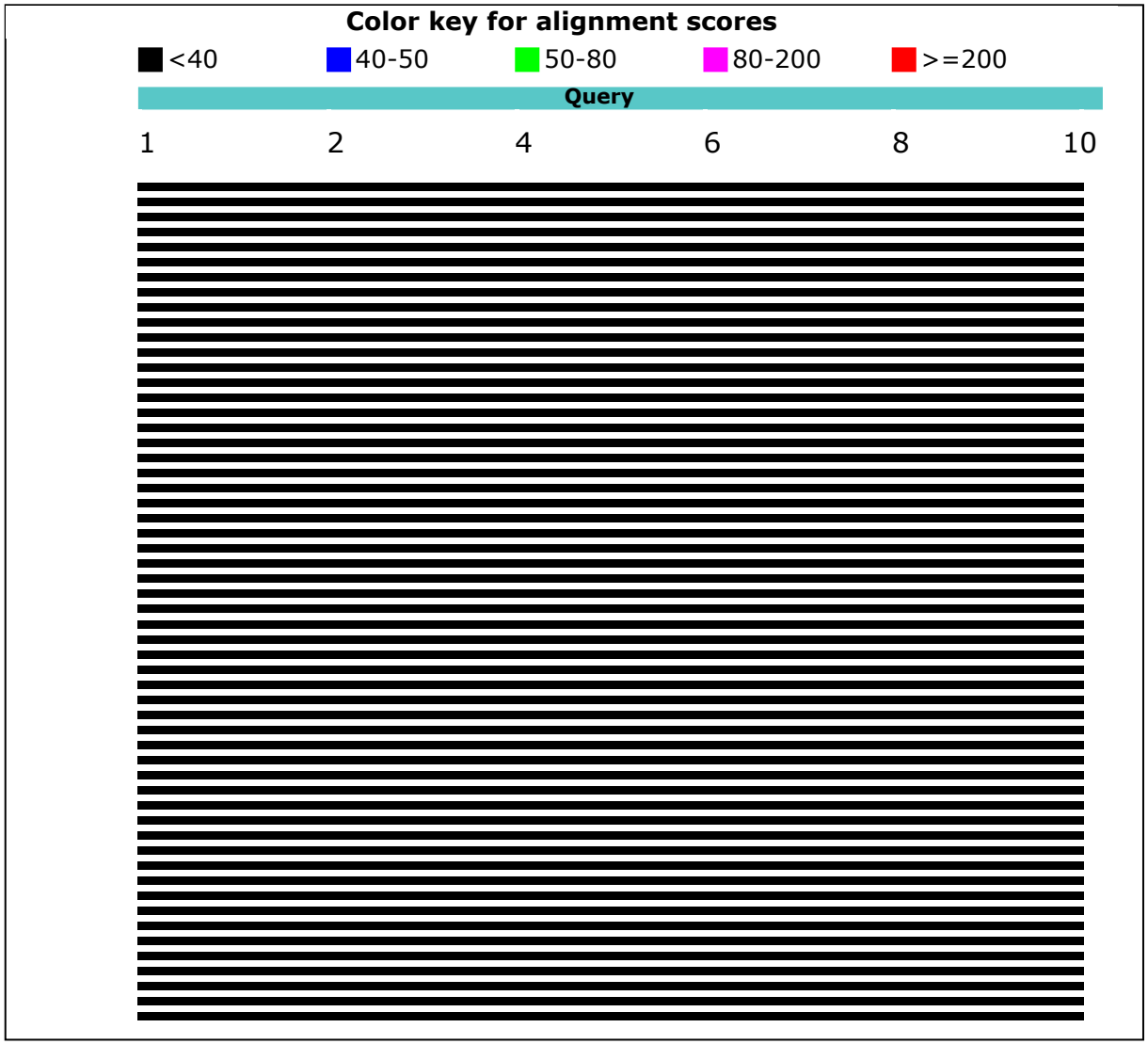
RID S54VB0Y7015 (Expires on 08-04 11:07 am)

Query ID	lcl|Query_36500	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	10	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
filamin-A isoform 2 [Homo sapiens]	35.4	35.4	100%	0.17	100%	NP_001104026.1
unnamed protein product [Homo sapiens]	35.4	35.4	100%	0.17	100%	CAA37495.1
filamin A, alpha isoform 2 (predicted) [Otolemur garnettii]	35.4	35.4	100%	0.17	100%	ACH53071.1
filamin A, alpha isoform 2 (predicted) [Dasypus novemcinctus]	35.4	35.4	100%	0.17	100%	ACO95345.1
filamin A, alpha isoform 2 (predicted) [Callithrix jacchus]	35.4	35.4	100%	0.17	100%	ABZ10487.1
filamin-A [Rattus norvegicus]	35.4	35.4	100%	0.17	100%	NP_001128071.1
filamin A alpha [synthetic construct]	35.4	35.4	100%	0.17	100%	BAG72555.2
filamin-A [Papio anubis]	35.4	35.4	100%	0.17	100%	NP_001162272.1
filamin-A isoform 1 [Homo sapiens]	35.4	35.4	100%	0.17	100%	NP_001447.2
filamin A, alpha isoform 2 (predicted) [Rhinolophus ferrumequinum]	35.4	35.4	100%	0.17	100%	ACC68902.1
filamin A [Homo sapiens]	35.4	35.4	100%	0.17	100%	BAD52436.1
filamin-A isoform X3 [Papio anubis]	35.4	35.4	100%	0.17	100%	XP_021788085.1
filamin A [Homo sapiens]	35.4	35.4	100%	0.17	100%	BAD52435.1
hypothetical protein EGM_19347 [Macaca fascicularis]	35.4	35.4	100%	0.17	100%	EHH61351.1
filamin-A isoform X4 [Papio anubis]	35.4	35.4	100%	0.17	100%	XP_021788086.1
filamin, alpha (predicted), isoform CRA_b [Rattus norvegicus]	35.4	35.4	100%	0.17	100%	EDL84990.1
hypothetical protein EGK_21101 [Macaca mulatta]	35.4	35.4	100%	0.17	100%	EHH31213.1
Filamin-A [Myotis brandtii]	35.4	35.4	100%	0.17	100%	EPQ20180.1
Filamin-A [Tupaia chinensis]	35.4	35.4	100%	0.17	100%	ELV11387.1
filamin-A isoform X5 [Papio anubis]	35.4	35.4	100%	0.17	100%	XP_021788087.1
Filamin-A [Myotis davidii]	35.4	35.4	100%	0.17	100%	ELK27817.1
hypothetical protein PANDA_022175 [Ailuropoda melanoleuca]	35.4	35.4	100%	0.17	100%	EFB12904.1
filamin A [Homo sapiens]	35.4	35.4	100%	0.17	100%	BAG48306.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
FLJ00119 protein [Homo sapiens]	35.4	35.4	100%	0.17	100%	BAB84874.1
FLNA protein (predicted) [Plecturocebus moloch]	35.4	35.4	100%	0.17	100%	ACB21220.1
FLNA protein [Homo sapiens]	35.4	35.4	100%	0.17	100%	AAH67111.1
FLNA protein [Homo sapiens]	35.4	35.4	100%	0.17	100%	AAH14654.1
unnamed protein product [Homo sapiens]	35.4	35.4	100%	0.17	100%	BAG65121.1
unnamed protein product [Homo sapiens]	35.4	35.4	100%	0.17	100%	BAG61947.1
Filamin-A [Fukomys damarensis]	33.3	33.3	100%	0.97	90%	KFO35178.1
RecName: Full=Filamin-A; Short=FLN-A; AltName: Full=Actin-binding protein 280; Short=ABP-280; AltName: Full=Alpha-filamin; AltName: Full=Endothelial actin-binding protein; AltName: Full=Filamin-1; AltName: Full=Non-muscle filamin	33.3	33.3	100%	0.97	90%	Q8BTM8.5
Filamin-A [Pteropus alecto]	33.3	33.3	100%	0.97	90%	ELK09744.1
filamin-A [Bos taurus]	33.3	33.3	100%	0.97	90%	NP_001193443.1
filamin-A [Oryctolagus cuniculus]	33.3	33.3	100%	0.97	90%	NP_001164842.1
Filamin-A [Bos mutus]	33.3	33.3	100%	0.97	90%	ELR49471.1
Flna [Castor fiber]	33.3	33.3	100%	0.97	90%	APD32923.1
mCG21234, isoform CRA_b [Mus musculus]	33.3	33.3	100%	0.97	90%	EDL29839.1
filamin-A isoform 1 [Mus musculus]	33.3	33.3	100%	0.97	90%	NP_034357.2
filamin-A [Cricetulus griseus]	33.3	33.3	100%	0.97	90%	ERE63086.1
Filamin-A [Heterocephalus glaber]	33.3	33.3	100%	0.97	90%	EHB00999.1
filamin-A [Cricetulus griseus]	33.3	33.3	100%	0.97	90%	ERE63085.1
mCG21234, isoform CRA_c [Mus musculus]	33.3	33.3	100%	0.97	90%	EDL29840.1
TPA: filamin A, alpha [Bos taurus]	33.3	33.3	100%	0.97	90%	DAA13210.1
filamin, alpha [Mus musculus]	33.3	33.3	100%	0.97	90%	CAT00729.1
hypothetical protein A6R68_21406 [Neotoma lepida]	33.3	33.3	100%	0.97	90%	OBS80380.1
Filamin-A [Cricetulus griseus]	33.3	33.3	100%	0.97	90%	EGW11368.1
filamin-A isoform 1 [Camelus ferus]	33.3	33.3	100%	0.97	90%	EPY72663.1
mCG21234, isoform CRA_a [Mus musculus]	33.3	33.3	100%	0.97	90%	EDL29838.1
filamin-A isoform 2 [Mus musculus]	33.3	33.3	100%	0.97	90%	NP_001277350.1
mFLJ00343 protein [Mus musculus]	33.3	33.3	100%	0.97	90%	BAD21429.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
filamin A, alpha isoform 2 (predicted) [Sorex araneus]	33.3	33.3	100%	0.97	90%	ACE79063.1
filamin, alpha [synthetic construct]	33.3	33.3	100%	0.98	90%	AAI72827.1
FLNA protein [Oryctolagus cuniculus]	33.3	33.3	100%	0.98	90%	NP_001164844.1
Flna protein [Mus musculus]	33.3	33.3	100%	0.98	90%	AAH04061.1
filamin-A-like [Scleropages formosus]	33.3	33.3	100%	0.99	90%	KPP57744.1
Flna protein [Mus musculus]	33.3	33.3	100%	0.99	90%	AAH99506.1
MULTISPECIES: phosphoribosyl-ATP pyrophosphohydrolase [Lysinibacillus]	32.5	32.5	90%	2.1	100%	WP_036122750.1
unnamed protein product [Tetraodon nigroviridis]	31.6	31.6	100%	3.9	90%	CAF93177.1
Filamin-A [Larimichthys crocea]	31.6	31.6	100%	3.9	90%	KKF31673.1
filamin-A-like [Scleropages formosus]	31.6	31.6	100%	3.9	90%	KPP74783.1
hypothetical protein cypCar_00003514 [Cyprinus carpio]	31.6	31.6	100%	3.9	90%	KTG45199.1
hypothetical protein cypCar_00005607 [Cyprinus carpio]	31.6	31.6	100%	3.9	90%	KTG42782.1
Filamin-A [Salmo salar]	31.6	31.6	100%	4.0	90%	ACN58728.1
filamin A [Paralichthys olivaceus]	31.6	31.6	100%	4.0	90%	BAE48215.1
filamin-A [Oncorhynchus mykiss]	31.6	31.6	100%	4.1	90%	AIZ75054.1
unnamed protein product [Oncorhynchus mykiss]	31.6	31.6	100%	4.1	90%	CDQ90711.1
conserved Plasmodium protein, unknown function [Plasmodium malariae]	30.8	30.8	100%	7.9	80%	SCN12623.1
conserved Plasmodium protein, unknown function [Plasmodium malariae]	30.8	30.8	100%	7.9	80%	SBT71203.1
conserved Plasmodium protein, unknown function [Plasmodium malariae]	30.8	30.8	100%	7.9	80%	SBS85214.1
rhodanese domain-containing protein [Thecamonas trahens ATCC 50062]	29.9	29.9	90%	16	89%	KNC46055.1
hypothetical protein UT05_C0010G0036 [Parcubacteria group bacterium GW2011_GWF2_38_76]	29.9	29.9	90%	16	89%	KKQ81702.1
hypothetical protein A3A94_03320 [Candidatus Portnoybacteria bacterium RIFCSPLOWO2_01_FULL_43_11]	29.5	29.5	100%	22	90%	OGZ38922.1
hypothetical protein PRSY57_1411400 [Plasmodium reichenowi]	29.5	29.5	100%	22	90%	KYN93781.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
conserved Plasmodium protein, unknown function [Plasmodium reichenowi]	29.5	29.5	100%	22	90%	CDO66605.1
hypothetical protein PGSY75_1412100 [Plasmodium gaboni]	29.5	29.5	100%	22	90%	KYN95734.1
hypothetical protein [Ekhidna lutea]	29.5	29.5	80%	22	100%	WP_089355698.1
filamin A [Bos taurus]	29.5	29.5	100%	23	80%	AAL66773.1
ribonuclease D [gamma proteobacterium IMCC1989]	29.5	29.5	80%	23	100%	WP_009669040.1
filamin-A [Gallus gallus]	29.1	29.1	100%	32	90%	NP_989905.1
hybrid sensor histidine kinase/response regulator [Flammeovirga pacifica]	29.1	29.1	80%	32	100%	WP_071397273.1
hypothetical protein NH26_22885 [Flammeovirga pacifica]	29.1	29.1	80%	32	100%	OHX64436.1
hypothetical protein H355_011795 [Colinus virginianus]	29.1	29.1	100%	32	90%	OXB78777.1
Filamin-A [Lonchura striata domestica]	29.1	29.1	100%	32	90%	OWK49688.1
peptidase [Haloplasma contractile]	29.1	29.1	90%	32	89%	WP_008825095.1
hypothetical protein [Arcobacter sp. LPB0137]	29.1	29.1	100%	32	80%	WP_076087996.1
anaerobic sulfite reductase subunit A [Desulfosporosinus sp. FKB]	29.1	29.1	100%	32	90%	WP_088228226.1
hypothetical protein [Peptostreptococcaceae bacterium VA2]	28.6	28.6	100%	45	80%	WP_082209554.1
hypothetical protein [Pseudomonas alcaligenes]	28.6	28.6	80%	45	100%	WP_021702518.1
hypothetical protein [Pseudomonas stutzeri]	28.6	28.6	80%	45	100%	WP_068506757.1
hypothetical protein BM557_04740 [Flavobacterium sp. MedPE-SWcel]	28.6	28.6	100%	45	80%	OIQ21067.1
class I SAM-dependent rRNA methyltransferase [Lachnospiraceae bacterium AC2014]	28.6	28.6	100%	45	82%	WP_031543551.1
putative 23S rRNA methyltransferase [[[Clostridium] symbiosum ATCC 14940]	28.6	28.6	100%	45	82%	ERI77365.1
Ribosomal RNA large subunit methyltransferase I [uncultured Roseburia sp.]	28.6	28.6	100%	45	82%	SCJ13589.1
putative uncharacterized protein [Clostridium sp. CAG:43]	28.6	28.6	100%	45	82%	CDD59467.1
sAM-dependent methyltransferase [Clostridium sp. CAG:299]	28.6	28.6	100%	45	82%	CDD44909.1
class I SAM-dependent rRNA methyltransferase [[Clostridium] symbiosum]	28.6	28.6	100%	45	82%	WP_044902539.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
MULTISPECIES: class I SAM-dependent rRNA methyltransferase [Clostridiales]	28.6	28.6	100%	45	82%	WP_003506691.1
class I SAM-dependent rRNA methyltransferase [[Clostridium] symbiosum]	28.6	28.6	100%	45	82%	WP_003501401.1
class I SAM-dependent rRNA methyltransferase [[Clostridium] saccharolyticum]	28.6	28.6	100%	45	82%	WP_015573529.1
class I SAM-dependent rRNA methyltransferase [Clostridium sp. M62/1]	28.6	28.6	100%	45	82%	WP_008395570.1

Alignments

filamin-A isoform 2 [Homo sapiens]
Sequence ID: **NP_001104026.1** Length: 2647 Number of Matches: 1

See 5 more title(s)
Range 1: 2396 to 2405

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1     ENGVYLIDVK  10
             ENGVYLIDVK
Sbjct  2396  ENGVYLIDVK  2405
```

unnamed protein product [Homo sapiens]
Sequence ID: **CAA37495.1** Length: 2647 Number of Matches: 1
Range 1: 2396 to 2405

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1     ENGVYLIDVK  10
             ENGVYLIDVK
Sbjct  2396  ENGVYLIDVK  2405
```

filamin A, alpha isoform 2 (predicted) [Otolemur garnettii]

Sequence ID: **ACH53071.1** Length: 2647 Number of Matches: 1
Range 1: 2396 to 2405

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1     ENGVYLIDVK  10
             ENGVYLIDVK
Sbjct  2396  ENGVYLIDVK  2405
```

filamin A, alpha isoform 2 (predicted) [Dasypus novemcinctus]

Sequence ID: **ACO95345.1** Length: 2647 Number of Matches: 1
Range 1: 2397 to 2406

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1     ENGVYLIDVK  10
             ENGVYLIDVK
Sbjct  2397  ENGVYLIDVK  2406
```

filamin A, alpha isoform 2 (predicted) [Callithrix jacchus]

Sequence ID: **ABZ10487.1** Length: 2647 Number of Matches: 1
Range 1: 2396 to 2405

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.17()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1     ENGVYLIDVK  10
             ENGVYLIDVK
Sbjct  2396  ENGVYLIDVK  2405
```

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BLAST Results

Job title: P_ITIH3_DYIFGNYIER

RID S568HBSK015 (Expires on 08-04 11:31 am)

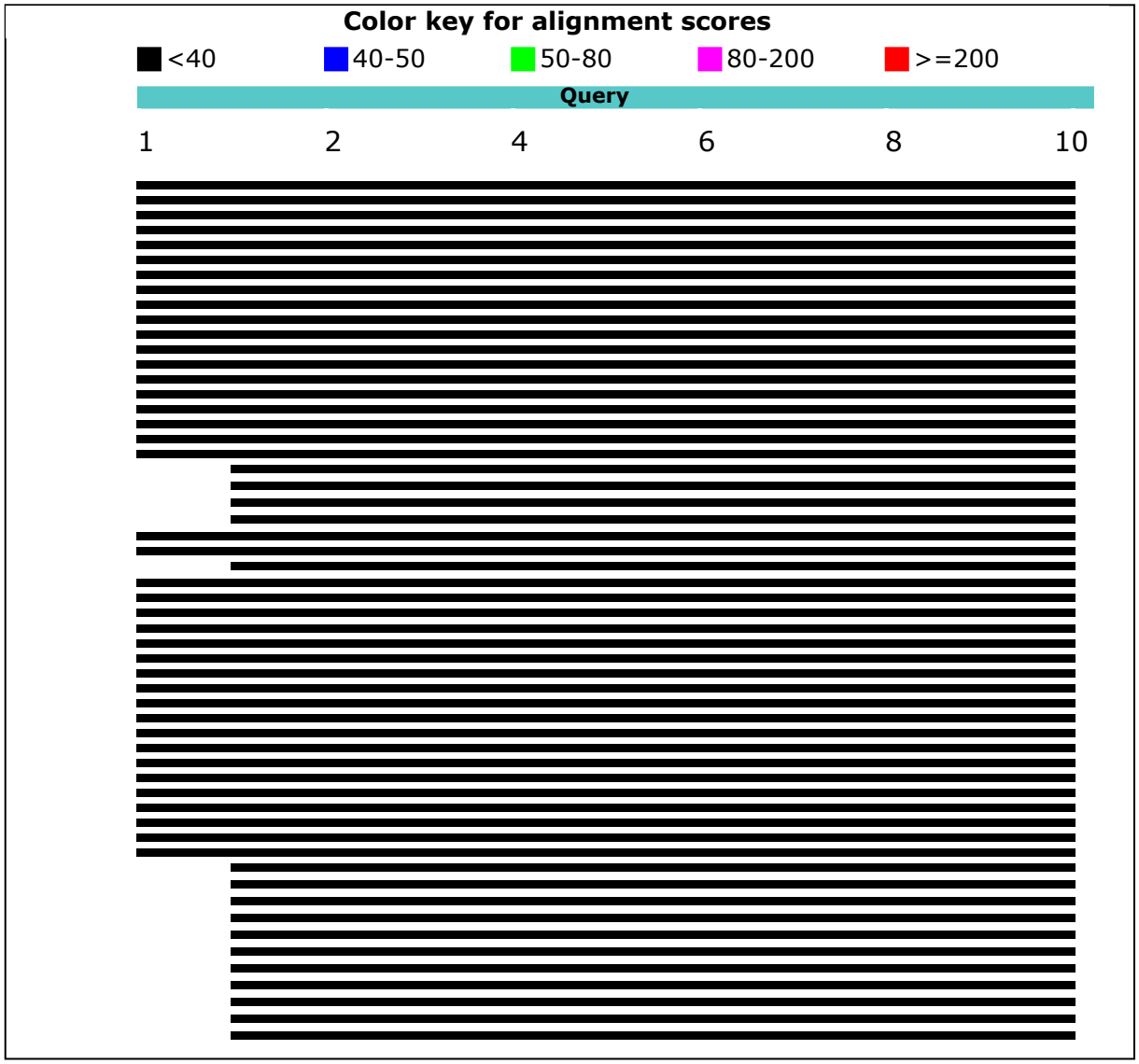
Query ID lcl|Query_267032
Description None
Molecule type amino acid
Query Length 10

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 104 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein EGM_10594 [Macaca fascicularis]	38.4	38.4	100%	0.015	100%	EHH51254.1
hypothetical protein EGK_11565 [Macaca mulatta]	38.4	38.4	100%	0.015	100%	EHH16301.1
inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Homo sapiens]	38.4	38.4	100%	0.015	100%	NP_002208.3
inter-alpha (globulin) inhibitor H3, isoform CRA_b [Homo sapiens]	38.4	38.4	100%	0.015	100%	EAW65263.1
inter-alpha (globulin) inhibitor H3 variant [Homo sapiens]	38.4	38.4	100%	0.015	100%	BAD96477.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Sus scrofa]	38.4	38.4	100%	0.015	100%	NP_001193278.1
inter-alpha-trypsin inhibitor heavy chain H3 [Homo sapiens]	38.4	38.4	100%	0.015	100%	CAC79611.1
inter-alpha-trypsin inhibitor heavy chain H3 [Homo sapiens]	38.4	38.4	100%	0.015	100%	CAA47439.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Pongo abelii]	38.4	38.4	100%	0.015	100%	NP_001125590.1
RecName: Full=Inter-alpha-trypsin inhibitor heavy chain H3; Short=ITI heavy chain H3; Short=ITI-HC3; Short=Inter-alpha-inhibitor heavy chain 3; Flags: Precursor	38.4	38.4	100%	0.015	100%	Q5RB37.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Pteropus alecto]	38.4	38.4	100%	0.015	100%	ELK07821.1
hypothetical protein PANDA_007565 [Ailuropoda melanoleuca]	38.4	38.4	100%	0.015	100%	EFB13610.1
inter-alpha (globulin) inhibitor H3, isoform CRA_a [Homo sapiens]	38.4	38.4	100%	0.015	100%	EAW65262.1
lambda HuHITI-13 [Homo sapiens]	38.4	38.4	100%	0.015	100%	CAA32821.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Oryctolagus cuniculus]	35.8	35.8	100%	0.12	90%	NP_001075477.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Bos taurus]	35.8	35.8	100%	0.12	90%	NP_001095368.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Bos mutus]	35.8	35.8	100%	0.12	90%	ELR55870.1
inter-alpha (globulin) inhibitor H3 [Bos taurus]	35.8	35.8	100%	0.12	90%	ABG67028.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
inter-alpha-trypsin inhibitor heavy chain H3 [Camelus ferus]	35.8	35.8	100%	0.12	90%	EPY76914.1
hypothetical protein A6R68_08945 [Neotoma lepida]	35.0	35.0	90%	0.24	100%	OBS59914.1
inter-alpha-trypsin inhibitor heavy chain H3-like protein [Cricetulus griseus]	35.0	35.0	90%	0.24	100%	ERE91861.1
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster	35.0	35.0	90%	0.24	100%	JC5576
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Mesocricetus auratus]	35.0	35.0	90%	0.24	100%	NP_001268279.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Heterocephalus glaber]	35.0	35.0	100%	0.24	90%	EHB12994.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Fukomys damarensis]	35.0	35.0	100%	0.24	90%	KFO25196.1
inter-alpha-trypsin inhibitor heavy chain H3-like protein [Cricetulus griseus]	35.0	35.0	90%	0.24	100%	ERE91860.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Myotis davidii]	35.0	35.0	100%	0.24	90%	ELK32299.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Myotis davidii]	35.0	35.0	100%	0.25	90%	ELK35385.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Myotis brandtii]	35.0	35.0	100%	0.25	90%	EPQ20720.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Anas platyrhynchos]	33.3	33.3	100%	0.98	80%	EOA97231.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Haliaeetus albicilla]	33.3	33.3	100%	0.98	80%	KFP93734.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Phalacrocorax carbo]	33.3	33.3	100%	0.98	80%	KFW95239.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Pygoscelis adeliae]	33.3	33.3	100%	0.98	80%	KFW65616.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Leptosomus discolor]	33.3	33.3	100%	0.98	80%	KFQ06491.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Egretta garzetta]	33.3	33.3	100%	0.98	80%	KFP16383.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Buceros rhinoceros silvestris]	33.3	33.3	100%	0.98	80%	KFO87688.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Pterocles gutturalis]	33.3	33.3	100%	0.98	80%	KFV08108.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Cuculus canorus]	33.3	33.3	100%	0.98	80%	KFO82367.1
Inter-alpha-trypsin inhibitor heavy chain H3, partial [Chlamydotis macqueenii]	33.3	33.3	100%	0.98	80%	KFP42279.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Inter-alpha-trypsin inhibitor heavy chain H3 [Nipponia nippon]	33.3	33.3	100%	0.98	80%	KFQ93546.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Calypte anna]	33.3	33.3	100%	0.98	80%	KFP04871.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Chelonia mydas]	33.3	33.3	100%	0.98	80%	EMP39757.1
ITIH3 [Cervus elaphus hippelaphus]	33.3	33.3	100%	0.98	80%	OWK02650.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Phoenicopterus ruber ruber]	33.3	33.3	100%	0.98	80%	KFQ74268.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Chelonia mydas]	33.3	33.3	100%	0.98	80%	EMP39755.1
inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Mus musculus]	32.5	32.5	90%	2.0	89%	NP_032433.2
inter-alpha-trypsin inhibitor heavy chain H3 [Patagioenas fasciata monilis]	32.5	32.5	90%	2.0	89%	OPJ80829.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Rattus norvegicus]	32.5	32.5	90%	2.0	89%	NP_059047.1
inter-alpha trypsin inhibitor, heavy chain 3 [Rattus norvegicus]	32.5	32.5	90%	2.0	89%	EDL88977.1
inter-alpha trypsin inhibitor, heavy chain 3 [Mus musculus]	32.5	32.5	90%	2.0	89%	EDL24773.1
inter-alpha-inhibitor H3 chain [Mus musculus]	32.5	32.5	90%	2.0	89%	CAA49843.1
Inter-alpha trypsin inhibitor, heavy chain 3 [Mus musculus]	32.5	32.5	90%	2.0	89%	AAH15276.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Columba livia]	32.5	32.5	90%	2.0	89%	EMC85223.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Tinamus guttatus]	32.5	32.5	90%	2.0	89%	KGL75413.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Charadrius vociferus]	32.5	32.5	90%	2.0	89%	KGL98256.1
Inter-alpha-trypsin inhibitor heavy chain H4 [Chelonia mydas]	31.6	31.6	90%	3.9	89%	EMP39756.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Cariama cristata]	31.6	31.6	100%	3.9	80%	KFP68729.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Manacus vitellinus]	31.6	31.6	100%	3.9	80%	KFW74679.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Cathartes aura]	31.6	31.6	100%	3.9	80%	KFP56831.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Phaethon lepturus]	31.6	31.6	100%	3.9	80%	KFQ73894.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Apaloderma vittatum]	31.6	31.6	100%	3.9	80%	KFP89411.1
inter-alpha-trypsin inhibitor heavy chain H4 isoform A [Patagioenas fasciata monilis]	31.6	31.6	90%	3.9	89%	OPJ80830.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Inter-alpha-trypsin inhibitor heavy chain H4 [Lonchura striata domestica]	31.6	31.6	90%	3.9	89%	OWK63483.1
inter-alpha-trypsin inhibitor heavy chain H3 [Amazona aestiva]	31.6	31.6	100%	3.9	80%	KQK84618.1
inter-alpha-trypsin inhibitor heavy chain H4 isoform B [Patagioenas fasciata monilis]	31.6	31.6	90%	3.9	89%	OPJ80831.1
inter-alpha-trypsin inhibitor heavy chain H4 [Amazona aestiva]	31.6	31.6	90%	3.9	89%	KQK84619.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Acanthisitta chloris]	31.6	31.6	100%	3.9	80%	KFP75441.1
Inter-alpha-trypsin inhibitor heavy chain H4 [Pygoscelis adeliae]	31.6	31.6	90%	3.9	89%	KFW65617.1
Inter-alpha-trypsin inhibitor heavy chain H4, partial [Chlamydotis macqueenii]	31.6	31.6	90%	3.9	89%	KFP42280.1
Inter-alpha-trypsin inhibitor heavy chain H4 [Cuculus canorus]	31.6	31.6	90%	3.9	89%	KFO82366.1
Inter-alpha-trypsin inhibitor heavy chain H4 [Columba livia]	31.6	31.6	90%	3.9	89%	EMC85224.1
Inter-alpha-trypsin inhibitor heavy chain H4 [Anas platyrhynchos]	31.6	31.6	90%	3.9	89%	EOA97223.1
GTPase-activating protein, putative [Plasmodium malariae]	30.8	50.9	100%	7.9	80%	SBT87727.1
GTPase-activating protein, putative [Plasmodium malariae]	30.8	50.9	100%	7.9	80%	SBT70848.1
GTPase-activating protein, putative [Plasmodium malariae]	30.8	50.9	100%	7.9	80%	SBS83618.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Corvus brachyrhynchos]	30.8	30.8	90%	7.9	89%	KFO57970.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Tyto alba]	30.8	30.8	90%	7.9	89%	KFV54080.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Lonchura striata domestica]	30.8	30.8	90%	7.9	89%	OWK63482.1
hypothetical protein [Campylobacter rectus]	30.8	30.8	100%	7.9	80%	WP_004320826.1
hypothetical protein [Campylobacter concisus]	30.8	30.8	100%	7.9	80%	WP_087576632.1
transcriptional regulator [Bacillus lentus]	30.8	30.8	80%	8.0	100%	WP_066145319.1
hypothetical protein HMPREF9108_01894 [Leptotrichia sp. oral taxon 225 str. F0581]	30.8	30.8	80%	8.1	100%	ERL25348.1
glycosyltransferase family 2 protein [Butyrivibrio sp. FC2001]	30.3	30.3	100%	11	80%	WP_051205866.1
glycosyltransferase family 2 protein [Butyrivibrio sp. XPD2002]	30.3	30.3	100%	11	80%	WP_051201190.1
N-acetyltransferase [Paenibacillus camerounensis]	30.3	30.3	100%	11	75%	WP_042200046.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein H355_016419 [Colinus virginianus]	29.9	29.9	100%	16	70%	OXB73239.1
hypothetical protein ASZ78_011534 [Callipepla squamata]	29.9	29.9	100%	16	70%	OXB60694.1
AAA family ATPase [Methanobacterium congolense]	29.5	29.5	90%	23	78%	WP_071907370.1
ATPase AAA [Methanobacterium sp. SMA-27]	29.5	29.5	90%	23	78%	WP_048192690.1
phenylacetic acid degradation protein PaaN [Sphingobacteriales bacterium TSM_CSS]	29.5	29.5	90%	23	69%	WP_088746345.1
hypothetical protein [Lactobacillus reuteri]	29.5	52.6	90%	23	78%	WP_003664492.1
peptidase M16 [Colwellia sp. 39_35_sub15_T18]	29.1	29.1	80%	32	88%	OUR61995.1
peptidase M16 [Colwellia chukchiensis]	29.1	29.1	80%	32	88%	WP_085282557.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Tupaia chinensis]	29.1	29.1	90%	32	78%	ELV10372.1
unnamed protein product [Oncorhynchus mykiss]	29.1	29.1	100%	32	70%	CDQ92156.1
hypothetical protein [Sporocytophaga myxococcoides]	29.1	29.1	80%	32	88%	WP_028978614.1
Inter-alpha-trypsin inhibitor heavy chain H4 [Aptenodytes forsteri]	29.1	29.1	90%	32	78%	KFM04443.1
Inter-alpha-trypsin inhibitor heavy chain H4 [Calypte anna]	29.1	29.1	90%	32	78%	KFP04870.1
Inter-alpha-trypsin inhibitor heavy chain H4 [Corvus brachyrhynchos]	29.1	29.1	90%	32	78%	KFO57969.1
AI-2E family transporter [Lachnospiraceae bacterium AD3010]	29.1	29.1	80%	32	88%	WP_051543627.1

Alignments

hypothetical protein EGM_10594 [Macaca fascicularis]
Sequence ID: **EHH51254.1** Length: 891 Number of Matches: 1
Range 1: 561 to 570

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.4 bits(83)	0.015()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DYIFGNYIER  10
            DYIFGNYIER
Sbjct  561  DYIFGNYIER  570
```

hypothetical protein EGK_11565 [Macaca mulatta]
Sequence ID: **EHH16301.1** Length: 891 Number of Matches: 1
Range 1: 561 to 570

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.4 bits(83)	0.015()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DYIFGNYIER  10
            DYIFGNYIER
Sbjct  561  DYIFGNYIER  570
```

inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Homo sapiens]
Sequence ID: **NP_002208.3** Length: 890 Number of Matches: 1

See 7 more title(s)
Range 1: 547 to 556

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.4 bits(83)	0.015()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DYIFGNYIER  10
            DYIFGNYIER
Sbjct  547  DYIFGNYIER  556
```

inter-alpha (globulin) inhibitor H3, isoform CRA_b [Homo sapiens]
Sequence ID: **EAW65263.1** Length: 890 Number of Matches: 1
Range 1: 547 to 556

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.4 bits(83)	0.015()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DYIFGNYIER  10
            DYIFGNYIER
Sbjct  547  DYIFGNYIER  556
```

inter-alpha (globulin) inhibitor H3 variant, partial [Homo sapiens]

Sequence ID: **BAD96477.1** Length: 890 Number of Matches: 1

See 1 more title(s)

Range 1: 547 to 556

Score	Expect	Method	Identities	Positives	Gaps	Frame
38.4 bits(83)	0.015()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DYIFGNYIER  10
           DYIFGNYIER
Sbjct  547  DYIFGNYIER  556
```

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BLAST Results

Job title: P_ITIH3_EVSFDVELPK

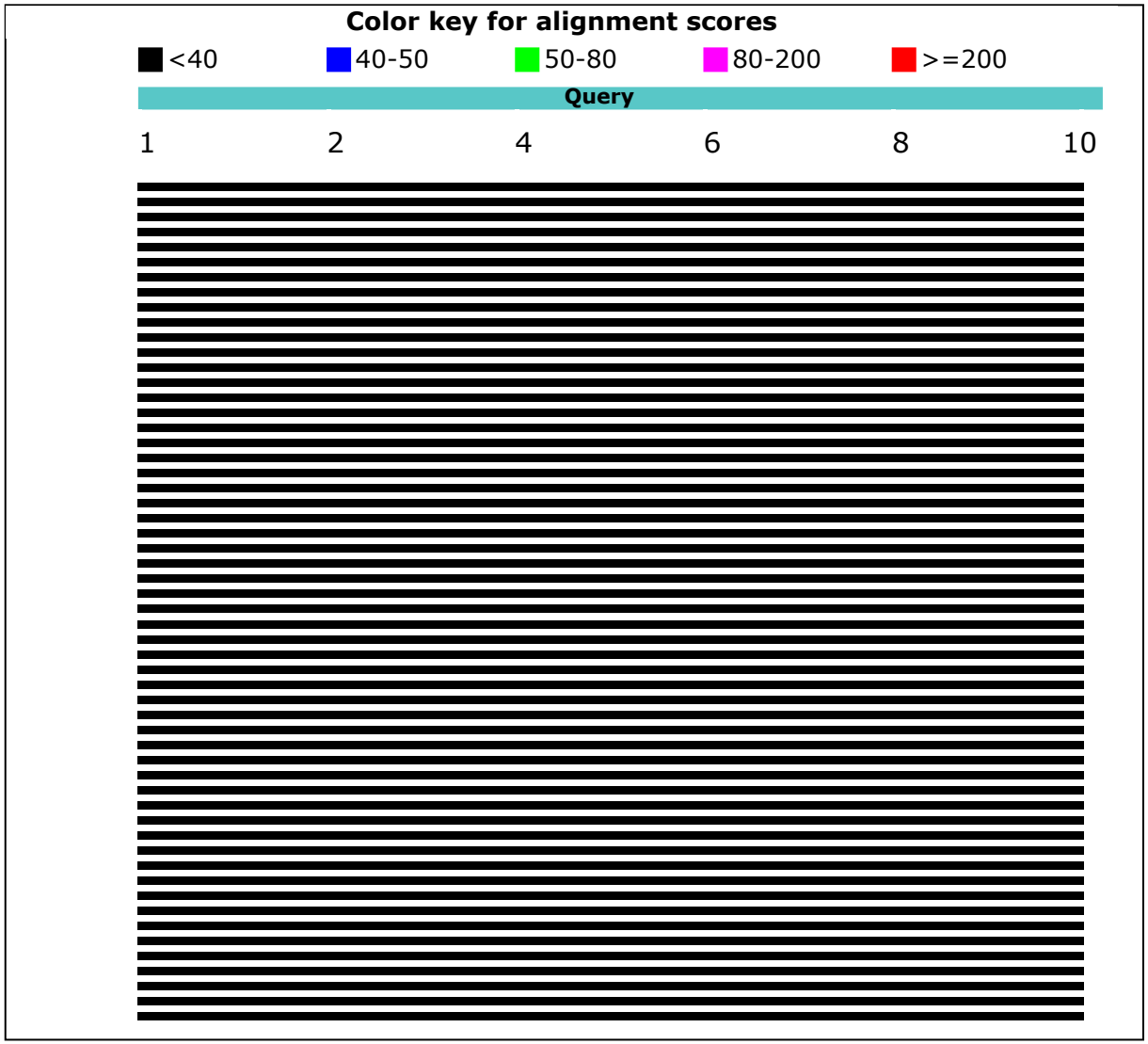
RID S568UG03015 (Expires on 08-04 11:31 am)

Query ID	lcl|Query_177620	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	10	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein A6R68_08945 [Neotoma lepida]	35.0	64.1	100%	0.24	100%	OBS59914.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Oryctolagus cuniculus]	35.0	35.0	100%	0.24	100%	NP_001075477.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Bos taurus]	35.0	35.0	100%	0.24	100%	NP_001095368.1
inter-alpha-trypsin inhibitor heavy chain H3-like protein [Cricetulus griseus]	35.0	35.0	100%	0.24	100%	ERE91861.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Bos mutus]	35.0	35.0	100%	0.24	100%	ELR55870.1
hypothetical protein EGM_10594 [Macaca fascicularis]	35.0	35.0	100%	0.24	100%	EHH51254.1
hypothetical protein EGK_11565 [Macaca mulatta]	35.0	35.0	100%	0.24	100%	EHH16301.1
inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Homo sapiens]	35.0	35.0	100%	0.24	100%	NP_002208.3
inter-alpha (globulin) inhibitor H3, isoform CRA_b [Homo sapiens]	35.0	35.0	100%	0.24	100%	EAW65263.1
inter-alpha (globulin) inhibitor H3 variant [Homo sapiens]	35.0	35.0	100%	0.24	100%	BAD96477.1
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster	35.0	35.0	100%	0.24	100%	JC5576
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Sus scrofa]	35.0	35.0	100%	0.24	100%	NP_001193278.1
inter-alpha-trypsin inhibitor heavy chain H3 preproprotein [Mus musculus]	35.0	35.0	100%	0.24	100%	NP_032433.2
inter-alpha (globulin) inhibitor H3 [Bos taurus]	35.0	35.0	100%	0.24	100%	ABG67028.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Rattus norvegicus]	35.0	35.0	100%	0.24	100%	NP_059047.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Mesocricetus auratus]	35.0	35.0	100%	0.24	100%	NP_001268279.1
inter-alpha trypsin inhibitor, heavy chain 3 [Rattus norvegicus]	35.0	35.0	100%	0.24	100%	EDL88977.1
inter-alpha trypsin inhibitor, heavy chain 3 [Mus musculus]	35.0	35.0	100%	0.24	100%	EDL24773.1
inter-alpha-trypsin inhibitor heavy chain H3 [Homo sapiens]	35.0	35.0	100%	0.24	100%	CAC79611.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
inter-alpha-inhibitor H3 chain [Mus musculus]	35.0	35.0	100%	0.24	100%	CAA49843.1
Inter-alpha trypsin inhibitor, heavy chain 3 [Mus musculus]	35.0	35.0	100%	0.24	100%	AAH15276.1
inter-alpha-trypsin inhibitor heavy chain H3 [Homo sapiens]	35.0	35.0	100%	0.24	100%	CAA47439.1
inter-alpha-trypsin inhibitor heavy chain H3 precursor [Pongo abelii]	35.0	35.0	100%	0.24	100%	NP_001125590.1
RecName: Full=Inter-alpha-trypsin inhibitor heavy chain H3; Short=ITI heavy chain H3; Short=ITI-HC3; Short=Inter-alpha-inhibitor heavy chain 3; Flags: Precursor	35.0	35.0	100%	0.24	100%	Q5RB37.1
inter-alpha-trypsin inhibitor heavy chain H3-like protein [Cricetulus griseus]	35.0	35.0	100%	0.24	100%	ERE91860.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Pteropus alecto]	35.0	35.0	100%	0.24	100%	ELK07821.1
hypothetical protein PANDA_007565 [Ailuropoda melanoleuca]	35.0	35.0	100%	0.24	100%	EFB13610.1
ITIH3 [Cervus elaphus hippelaphus]	35.0	35.0	100%	0.24	100%	OWK02650.1
unnamed protein product [Homo sapiens]	35.0	35.0	100%	0.24	100%	BAG60666.1
inter-alpha (globulin) inhibitor H3, isoform CRA_a [Homo sapiens]	35.0	35.0	100%	0.24	100%	EAW65262.1
LOC594926 protein, partial [Xenopus tropicalis]	32.5	32.5	100%	2.0	90%	AAH92555.1
hypothetical protein cypCar_00046118 [Cyprinus carpio]	32.5	32.5	100%	2.0	90%	KTF71724.1
inter-alpha-trypsin inhibitor heavy chain H3 [Camelus ferus]	32.5	32.5	100%	2.0	90%	EPY76914.1
hypothetical protein XELAEV_18001873mg [Xenopus laevis]	32.5	32.5	100%	2.0	90%	OCT58731.1
hypothetical protein XELAEV_18002612mg [Xenopus laevis]	32.5	32.5	100%	2.0	90%	OCT58117.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Myotis brandtii]	32.5	32.5	100%	2.0	90%	EPQ10204.1
inter-alpha (globulin) inhibitor H3 [Carassius auratus]	32.5	32.5	100%	2.0	90%	AGO58869.1
unnamed protein product [Tetraodon nigroviridis]	30.3	30.3	100%	11	80%	CAG02026.1
unnamed protein product [Tetraodon nigroviridis]	30.3	30.3	100%	11	80%	CAG02027.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Anas platyrhynchos]	29.9	29.9	100%	16	90%	EOA97231.1
inter-alpha-trypsin inhibitor heavy chain H3 [Patagioenas fasciata monilis]	29.9	29.9	100%	16	90%	OPJ80829.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Haliaeetus albicilla]	29.9	29.9	100%	16	90%	KFP93734.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Inter-alpha-trypsin inhibitor heavy chain H3 [Phalacrocorax carbo]	29.9	29.9	100%	16	90%	KFW95239.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Pygoscelis adeliae]	29.9	29.9	100%	16	90%	KFW65616.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Cariama cristata]	29.9	29.9	100%	16	90%	KFP68729.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Egretta garzetta]	29.9	29.9	100%	16	90%	KFP16383.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Manacus vitellinus]	29.9	29.9	100%	16	90%	KFW74679.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Pterocles gutturalis]	29.9	29.9	100%	16	90%	KFV08108.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Cuculus canorus]	29.9	29.9	100%	16	90%	KFO82367.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Cathartes aura]	29.9	29.9	100%	16	90%	KFP56831.1
Inter-alpha-trypsin inhibitor heavy chain H3, partial [Chlamydotis macqueenii]	29.9	29.9	100%	16	90%	KFP42279.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Apaloderma vittatum]	29.9	29.9	100%	16	90%	KFP89411.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Corvus brachyrhynchos]	29.9	29.9	100%	16	90%	KFO57970.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Columba livia]	29.9	29.9	100%	16	90%	EMC85223.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Tinamus guttatus]	29.9	29.9	100%	16	90%	KGL75413.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Tyto alba]	29.9	29.9	100%	16	90%	KFV54080.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Nipponia nippon]	29.9	29.9	100%	16	90%	KFQ93546.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Charadrius vociferus]	29.9	29.9	100%	16	90%	KGL98256.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Lonchura striata domestica]	29.9	29.9	100%	16	90%	OWK63482.1
hypothetical protein H355_016419 [Colinus virginianus]	29.9	29.9	100%	16	90%	OXB73239.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Phoenicopterus ruber ruber]	29.9	29.9	100%	16	90%	KFQ74268.1
inter-alpha-trypsin inhibitor heavy chain H3-like [Scleropages formosus]	29.9	29.9	100%	16	90%	KPP66971.1
hypothetical protein ASZ78_011534 [Callipepla squamata]	29.9	29.9	100%	16	90%	OXB60694.1
hypothetical protein [Pseudoalteromonas luteoviolacea]	29.9	29.9	100%	16	80%	WP_063367048.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Pseudoalteromonas luteoviolacea]	29.9	29.9	100%	16	80%	WP_039608597.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Mesitornis unicolor]	29.9	29.9	100%	16	90%	KFQ40317.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Leptosomus discolor]	29.5	29.5	100%	22	90%	KFQ06491.1
Inter-alpha-trypsin inhibitor heavy chain H3 [Phaethon lepturus]	29.5	29.5	100%	22	90%	KFQ73894.1
16S rRNA (guanine(966)-N(2))-methyltransferase RsmD [Bacillus sp. OV166]	29.5	29.5	100%	23	90%	SMQ70162.1
16S rRNA (guanine(966)-N(2))-methyltransferase RsmD [Bacillus sp. OV166]	29.5	29.5	100%	23	90%	WP_088086283.1
16S rRNA (guanine(966)-N(2))-methyltransferase RsmD [Bacillus drentensis]	29.5	29.5	100%	23	90%	WP_066252545.1
16S rRNA (guanine(966)-N(2))-methyltransferase RsmD [Bacillus vireti]	29.5	29.5	100%	23	90%	WP_034724340.1
16S rRNA (guanine(966)-N(2))-methyltransferase RsmD [Bacillus sp. UNC41MFS5]	29.5	29.5	100%	23	90%	WP_026566349.1
putative methyltransferase [Bacillus vireti LMG 21834]	29.5	29.5	100%	23	90%	ETI67958.1
RecName: Full=Inter-alpha-trypsin inhibitor heavy chain H1; Short=ITI heavy chain H1; Short=ITI-HC1; Short=Inter-alpha-inhibitor heavy chain 1; Flags: Precursor	29.1	29.1	100%	32	80%	P97278.1
inter-alpha-trypsin inhibitor heavy chain H1 isoform 2 precursor [Mus musculus]	29.1	29.1	100%	32	80%	NP_001293007.1
Inter-alpha-trypsin inhibitor heavy chain H1 [Tupaia chinensis]	29.1	29.1	100%	32	80%	ELV10373.1
hypothetical protein EGM_10595 [Macaca fascicularis]	29.1	29.1	100%	32	80%	EHH51255.1
hypothetical protein EGK_11566 [Macaca mulatta]	29.1	29.1	100%	32	80%	EHH16302.1
Itih1 protein [Mus musculus]	29.1	29.1	100%	32	80%	AAH28814.1
inter-alpha trypsin inhibitor, heavy chain 1 [Mus musculus]	29.1	29.1	100%	32	80%	AAH13465.1
Inter-alpha-trypsin inhibitor heavy chain H1 [Bos mutus]	29.1	29.1	100%	32	80%	ELR55871.1
inter-alpha-trypsin inhibitor heavy chain H1 isoform 1 preproprotein [Mus musculus]	29.1	29.1	100%	32	80%	NP_032432.2
inter-alpha-inhibitor H1 chain [Mus musculus]	29.1	29.1	100%	32	80%	CAA49841.1
TPA: inter-alpha-trypsin inhibitor heavy chain H1 precursor [Bos taurus]	29.1	29.1	100%	32	80%	DAA16905.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
inter-alpha-trypsin inhibitor heavy chain H1 precursor [Oryctolagus cuniculus]	29.1	29.1	100%	32	80%	NP_001076115.1
inter-alpha-trypsin inhibitor heavy chain H1 precursor [Bos taurus]	29.1	29.1	100%	32	80%	NP_001068821.1
inter-alpha-trypsin inhibitor heavy chain H1 precursor [Rattus norvegicus]	29.1	29.1	100%	32	80%	NP_001100761.2
inter-alpha-trypsin inhibitor heavy chain H1 precursor [Sus scrofa]	29.1	29.1	100%	32	80%	NP_999089.2
RecName: Full=Inter-alpha-trypsin inhibitor heavy chain H1; Short=ITI heavy chain H1; Short=ITI-HC1; Short=Inter-alpha-inhibitor heavy chain 1; Flags: Precursor	29.1	29.1	100%	32	80%	Q29052.1
inter-alpha trypsin inhibitor, heavy chain 1 (predicted), isoform CRA_b [Rattus norvegicus]	29.1	29.1	100%	32	80%	EDL88975.1
inter-alpha-trypsin inhibitor heavy chain H1-like protein [Cricetulus griseus]	29.1	29.1	100%	32	80%	ERE91862.1
hypothetical protein PANDA_007566 [Ailuropoda melanoleuca]	29.1	29.1	100%	32	80%	EFB13611.1
inter-alpha trypsin inhibitor, heavy chain 1, isoform CRA_c [Mus musculus]	29.1	29.1	100%	32	80%	EDL24776.1
inter-alpha trypsin inhibitor, heavy chain 1, isoform CRA_d [Mus musculus]	29.1	29.1	100%	32	80%	EDL24777.1
inter-alpha trypsin inhibitor, heavy chain 1, isoform CRA_b [Mus musculus]	29.1	29.1	100%	32	80%	EDL24775.1
ITIH1 [Cervus elaphus hippelaphus]	29.1	29.1	100%	33	80%	OWK02409.1
inter-alpha trypsin inhibitor, heavy chain 1 (predicted), isoform CRA_c [Rattus norvegicus]	29.1	29.1	100%	33	80%	EDL88976.1
hypothetical protein [Flammeovirga pacifica]	28.6	28.6	80%	45	100%	WP_044227366.1
hypothetical protein [Flammeovirga sp. MY04]	28.6	28.6	80%	45	100%	WP_066211579.1

Alignments

hypothetical protein A6R68_08945 [Neotoma lepida]
Sequence ID: **OBS59914.1** Length: 1581 Number of Matches: 2
Range 1: 770 to 779

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.0 bits(75)	0.24()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    EVSFDVELPK  10
            EVSFDVELPK
Sbjct  770  EVSFDVELPK  779
```

Range 2: 53 to 62

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.1 bits(61)	32()		8/10(80%)	8/10(80%)	0/10(0%)	

Features:

```
Query  1   EVSFDVELPK  10
           EV FDVE PK
Sbjct  53  EVAFDVEIPK  62
```

inter-alpha-trypsin inhibitor heavy chain H3 precursor [Oryctolagus cuniculus]
Sequence ID: **NP_001075477.1** Length: 903 Number of Matches: 1

See 2 more title(s)
Range 1: 76 to 85

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.0 bits(75)	0.24()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   EVSFDVELPK  10
           EVSFDVELPK
Sbjct  76  EVSFDVELPK  85
```

inter-alpha-trypsin inhibitor heavy chain H3 precursor [Bos taurus]
Sequence ID: **NP_001095368.1** Length: 891 Number of Matches: 1

See 3 more title(s)
Range 1: 76 to 85

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.0 bits(75)	0.24()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   EVSFDVELPK  10
           EVSFDVELPK
Sbjct  76  EVSFDVELPK  85
```

inter-alpha-trypsin inhibitor heavy chain H3-like protein [Cricetulus griseus]

Sequence ID: **ERE91861.1** Length: 891 Number of Matches: 1
Range 1: 76 to 85

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.0 bits(75)	0.24()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   EVSFDVELPK  10
           EVSFDVELPK
Sbjct  76  EVSFDVELPK  85
```

Inter-alpha-trypsin inhibitor heavy chain H3 [Bos mutus]

Sequence ID: **ELR55870.1** Length: 891 Number of Matches: 1
Range 1: 76 to 85

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.0 bits(75)	0.24()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   EVSFDVELPK  10
           EVSFDVELPK
Sbjct  76  EVSFDVELPK  85
```

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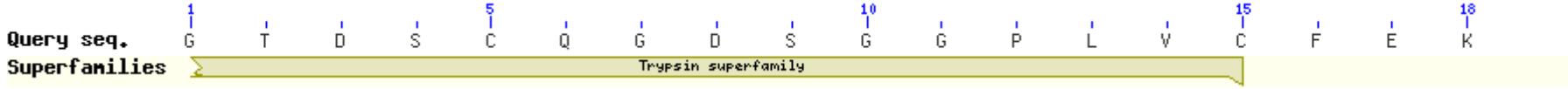
BLAST Results

Job title: NCBI BlastP_LPA_GTDSCQGDSGGPLVCFEK

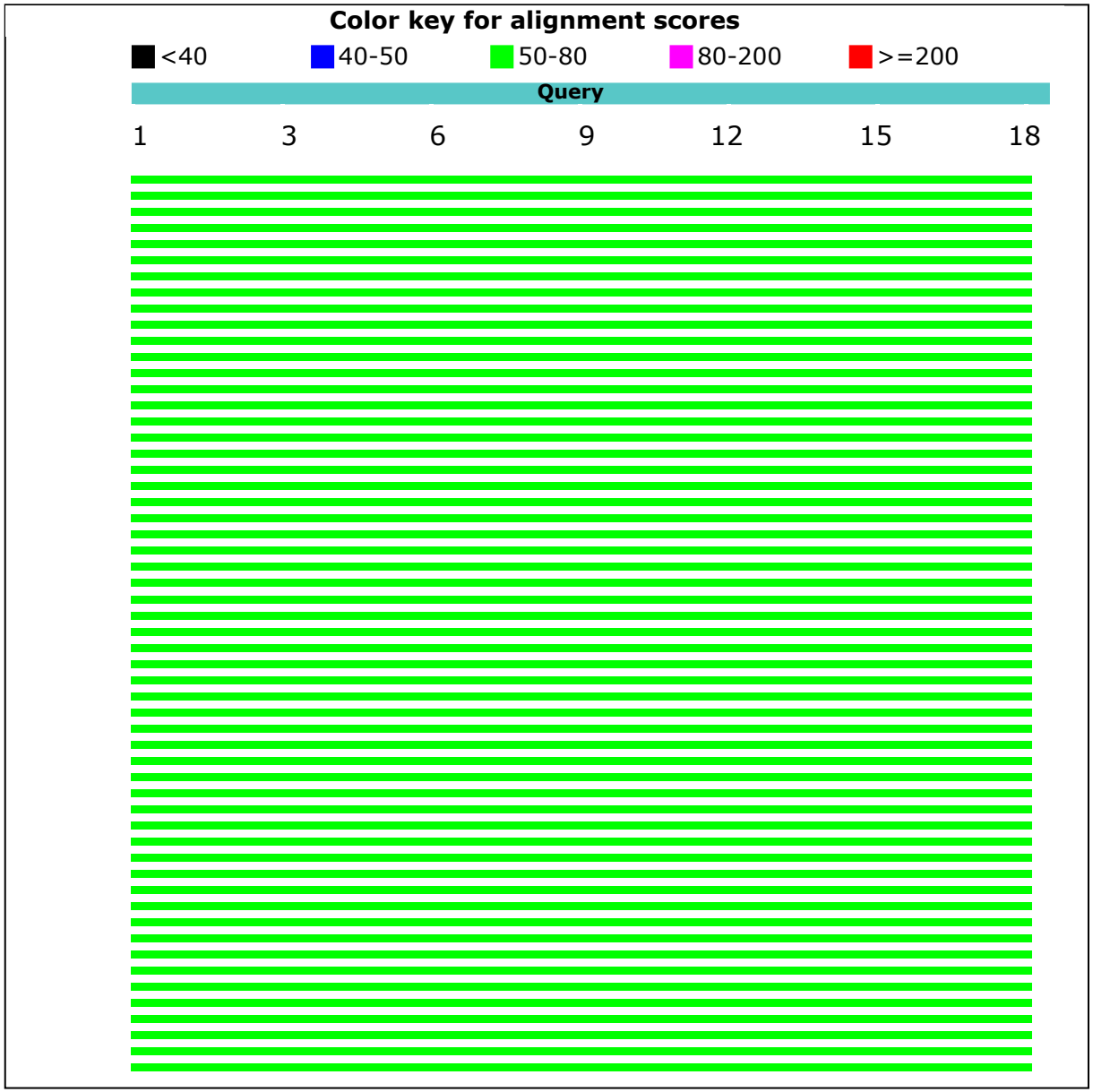
RID	S54HB2V7014 (Expires on 08-04 11:02 am)
Query ID	lcl|Query_197840
Description	None
Molecule type	amino acid
Query Length	18
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
3
6
9
12
15
18

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
plasminogen [Canis lupus familiaris]	59.6	59.6	100%	1e-09	100%	AAT44581.1
RecName: Full=Apolipoprotein(a); Short=Apo(a); Short=Lp(a); Flags: Precursor	59.6	59.6	100%	3e-09	100%	P08519.1
apolipoprotein a	59.6	59.6	100%	3e-09	100%	1313352A
PREDICTED: apolipoprotein(a) [Gorilla gorilla gorilla]	59.6	59.6	100%	3e-09	100%	XP_018884409.1
lipoprotein, Lp(a) [Homo sapiens]	59.6	59.6	100%	3e-09	100%	ABF47086.1
apolipoprotein(a) precursor [Homo sapiens]	59.6	59.6	100%	3e-09	100%	NP_005568.2
PREDICTED: apolipoprotein(a) [Pan paniscus]	59.6	59.6	100%	3e-09	100%	XP_008957511.1
PREDICTED: plasminogen [Sorex araneus]	59.6	59.6	100%	3e-09	100%	XP_012787754.1
lipoprotein, Lp(a) [Homo sapiens]	59.6	59.6	100%	3e-09	100%	EAW47596.1
PREDICTED: plasminogen [Pan troglodytes]	59.6	59.6	100%	3e-09	100%	XP_016810272.1
plasminogen isoform X1 [Heterocephalus glaber]	59.6	59.6	100%	3e-09	100%	XP_004869056.3
plasminogen isoform X2 [Heterocephalus glaber]	59.6	59.6	100%	3e-09	100%	XP_004869057.3
PREDICTED: plasminogen isoform X1 [Camelus dromedarius]	59.6	59.6	100%	3e-09	100%	XP_010975053.1
PREDICTED: plasminogen [Camelus bactrianus]	59.6	59.6	100%	3e-09	100%	XP_010964083.1
Plasminogen [Heterocephalus glaber]	59.6	59.6	100%	3e-09	100%	EHB06864.1
PREDICTED: plasminogen isoform X1 [Colobus angolensis palliatus]	59.6	59.6	100%	3e-09	100%	XP_011790378.1
PREDICTED: plasminogen isoform X1 [Mandrillus leucophaeus]	59.6	59.6	100%	3e-09	100%	XP_011831301.1
PREDICTED: plasminogen [Pteropus alecto]	59.6	59.6	100%	3e-09	100%	XP_015447353.1
PREDICTED: plasminogen isoform X1 [Rousettus aegyptiacus]	59.6	59.6	100%	3e-09	100%	XP_016008225.1
PREDICTED: plasminogen isoform X1 [Otolemur garnettii]	59.6	59.6	100%	3e-09	100%	XP_012662186.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: LOW QUALITY PROTEIN: plasminogen [Panthera tigris altaica]	59.6	59.6	100%	3e-09	100%	XP_007097297.1
PREDICTED: plasminogen isoform X1 [Tupaia chinensis]	59.6	59.6	100%	3e-09	100%	XP_006152311.2
PREDICTED: plasminogen [Galeopterus variegatus]	59.6	59.6	100%	3e-09	100%	XP_008572823.1
hypothetical protein A6R68_19482 [Neotoma lepida]	59.6	59.6	100%	3e-09	100%	OBS78129.1
PREDICTED: plasminogen isoform X1 [Marmota marmota marmota]	59.6	59.6	100%	3e-09	100%	XP_015354097.1
PREDICTED: plasminogen isoform X1 [Chinchilla lanigera]	59.6	59.6	100%	3e-09	100%	XP_005390756.2
plasminogen isoform X1 [Ictidomys tridecemlineatus]	59.6	59.6	100%	3e-09	100%	XP_005321483.1
plasminogen isoform X1 [Neomonachus schauinslandi]	59.6	59.6	100%	3e-09	100%	XP_021548734.1
PREDICTED: plasminogen [Panthera pardus]	59.6	59.6	100%	3e-09	100%	XP_019268263.1
plasminogen precursor [Canis lupus familiaris]	59.6	59.6	100%	3e-09	100%	NP_001273889.1
PREDICTED: plasminogen [Felis catus]	59.6	59.6	100%	3e-09	100%	XP_006932192.1
PREDICTED: plasminogen-like isoform X1 [Leptonychotes weddellii]	59.6	59.6	100%	3e-09	100%	XP_006734343.1
PREDICTED: plasminogen isoform X1 [Odobenus rosmarus divergens]	59.6	59.6	100%	3e-09	100%	XP_012418086.1
PREDICTED: plasminogen isoform X2 [Octodon degus]	59.6	59.6	100%	3e-09	100%	XP_012372001.1
PREDICTED: plasminogen [Ailuropoda melanoleuca]	59.6	59.6	100%	3e-09	100%	XP_011225084.1
PREDICTED: plasminogen [Ursus maritimus]	59.6	59.6	100%	3e-09	100%	XP_008686708.1
PREDICTED: plasminogen-like isoform X3 [Pantholops hodgsonii]	59.6	59.6	100%	3e-09	100%	XP_005980473.1
PREDICTED: plasminogen isoform X1 [Octodon degus]	59.6	59.6	100%	3e-09	100%	XP_004639490.1
plasminogen precursor [Bos taurus]	59.6	59.6	100%	3e-09	100%	NP_776376.1
TPA: plasminogen precursor [Bos taurus]	59.6	59.6	100%	3e-09	100%	DAA25966.1
plasminogen isoform X2 [Ictidomys tridecemlineatus]	59.6	59.6	100%	3e-09	100%	XP_021579553.1
PREDICTED: plasminogen [Oryctolagus cuniculus]	59.6	59.6	100%	3e-09	100%	XP_017200963.1
PREDICTED: LOW QUALITY PROTEIN: plasminogen [Acinonyx jubatus]	59.6	59.6	100%	3e-09	100%	XP_014938731.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: plasminogen isoform X2 [Chinchilla lanigera]	59.6	59.6	100%	3e-09	100%	XP_005390757.2
PREDICTED: plasminogen isoform X2 [Otolemur garnettii]	59.6	59.6	100%	3e-09	100%	XP_012662187.1
PREDICTED: plasminogen [Fukomys damarensis]	59.6	59.6	100%	3e-09	100%	XP_010629347.1
PREDICTED: plasminogen [Microtus ochrogaster]	59.6	59.6	100%	3e-09	100%	XP_005363435.1
PREDICTED: plasminogen [Saimiri boliviensis boliviensis]	59.6	59.6	100%	3e-09	100%	XP_003933830.1
plasminogen isoform X2 [Neomonachus schauinslandi]	59.6	59.6	100%	3e-09	100%	XP_021548735.1
plasminogen [Papio anubis]	59.6	59.6	100%	3e-09	100%	XP_009204619.2
PREDICTED: plasminogen [Manis javanica]	59.6	59.6	100%	3e-09	100%	XP_017525539.1
PREDICTED: plasminogen isoform X1 [Cebus capucinus imitator]	59.6	59.6	100%	3e-09	100%	XP_017393509.1
PREDICTED: plasminogen isoform X2 [Rousettus aegyptiacus]	59.6	59.6	100%	3e-09	100%	XP_016008226.1
plasminogen [Homo sapiens]	59.6	59.6	100%	3e-09	100%	AAA60113.1
plasminogen [Homo sapiens]	59.6	59.6	100%	3e-09	100%	AAA36451.1
PREDICTED: plasminogen-like isoform X2 [Leptonychotes weddellii]	59.6	59.6	100%	3e-09	100%	XP_006734344.1
plasminogen isoform 1 precursor [Homo sapiens]	59.6	59.6	100%	3e-09	100%	NP_000292.1
plasminogen precursor [Macaca mulatta]	59.6	59.6	100%	3e-09	100%	NP_001036540.1
PLG [synthetic construct]	59.6	59.6	100%	3e-09	100%	AKI72407.1
PLG [synthetic construct]	59.6	59.6	100%	3e-09	100%	AKI72406.1
PLG [synthetic construct]	59.6	59.6	100%	3e-09	100%	AKI72405.1
PREDICTED: LOW QUALITY PROTEIN: plasminogen [Nomascus leucogenys]	59.6	59.6	100%	3e-09	100%	XP_012361543.1
plasminogen [Aotus nancymaae]	59.6	59.6	100%	3e-09	100%	XP_012306596.1
PREDICTED: plasminogen [Macaca nemestrina]	59.6	59.6	100%	3e-09	100%	XP_011749269.1
PREDICTED: plasminogen [Cercocebus atys]	59.6	59.6	100%	3e-09	100%	XP_011933449.1
PREDICTED: plasminogen isoform X2 [Colobus angolensis palliatus]	59.6	59.6	100%	3e-09	100%	XP_011790379.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: plasminogen isoform X2 [Mandrillus leucophaeus]	59.6	59.6	100%	3e-09	100%	XP_011831302.1
PREDICTED: plasminogen [Rhinopithecus roxellana]	59.6	59.6	100%	3e-09	100%	XP_010371459.1
plasminogen [Carlito syrichta]	59.6	59.6	100%	3e-09	100%	XP_008066085.1
PREDICTED: plasminogen [Chlorocebus sabaeus]	59.6	59.6	100%	3e-09	100%	XP_008005937.1
unnamed protein product [Homo sapiens]	59.6	59.6	100%	3e-09	100%	BAG35805.1
Plasminogen [Homo sapiens]	59.6	59.6	100%	3e-09	100%	AAH60513.1
PREDICTED: plasminogen isoform X1 [Peromyscus maniculatus bairdii]	59.6	59.6	100%	3e-09	100%	XP_006978086.1
PREDICTED: plasminogen-like isoform X2 [Pantholops hodgsonii]	59.6	59.6	100%	3e-09	100%	XP_005980472.1
PREDICTED: plasminogen-like isoform X1 [Pantholops hodgsonii]	59.6	59.6	100%	3e-09	100%	XP_005980471.1
PREDICTED: plasminogen [Macaca fascicularis]	59.6	59.6	100%	3e-09	100%	XP_005551555.1
PREDICTED: plasminogen [Mustela putorius furo]	59.6	59.6	100%	3e-09	100%	XP_004770898.1
PREDICTED: plasminogen [Condylura cristata]	59.6	59.6	100%	3e-09	100%	XP_004674018.1
PREDICTED: plasminogen isoform X3 [Octodon degus]	59.6	59.6	100%	3e-09	100%	XP_004639491.1
PREDICTED: plasminogen isoform X2 [Odobenus rosmarus divergens]	59.6	59.6	100%	3e-09	100%	XP_004401166.1
PREDICTED: plasminogen isoform X1 [Trichechus manatus latirostris]	59.6	59.6	100%	3e-09	100%	XP_004368848.1
PREDICTED: plasminogen isoform X1 [Pan paniscus]	59.6	59.6	100%	3e-09	100%	XP_003820290.1
plasminogen precursor [Pongo abelii]	59.6	59.6	100%	3e-09	100%	NP_001126035.1
PREDICTED: plasminogen isoform X2 [Marmota marmota marmota]	59.6	59.6	100%	3e-09	100%	XP_015354098.1
PREDICTED: plasminogen isoform X1 [Ovis aries musimon]	59.6	59.6	100%	3e-09	100%	XP_011982597.1
PREDICTED: plasminogen isoform X1 [Ovis aries]	59.6	59.6	100%	3e-09	100%	XP_012038601.1
PREDICTED: plasminogen-like isoform X5 [Pantholops hodgsonii]	59.6	59.6	100%	3e-09	100%	XP_005980475.1
PREDICTED: plasminogen [Capra hircus]	59.6	59.6	100%	3e-09	100%	XP_005685011.1
plasminogen [Mesocricetus auratus]	59.6	59.6	100%	3e-09	100%	XP_021078698.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: plasminogen [Rhinolophus sinicus]	59.6	59.6	100%	3e-09	100%	XP_019605319.1
PREDICTED: plasminogen isoform X1 [Bos mutus]	59.6	59.6	100%	3e-09	100%	XP_014335153.1
PREDICTED: plasminogen [Dipodomys ordii]	59.6	59.6	100%	3e-09	100%	XP_012880042.1
PREDICTED: plasminogen isoform X2 [Peromyscus maniculatus bairdii]	59.6	59.6	100%	3e-09	100%	XP_015852227.1
PREDICTED: plasminogen isoform X2 [Bos mutus]	59.6	59.6	100%	3e-09	100%	XP_005900461.1
PREDICTED: plasminogen isoform X2 [Trichechus manatus latirostris]	59.6	59.6	100%	3e-09	100%	XP_004368849.1
PREDICTED: plasminogen isoform X3 [Bos mutus]	59.6	59.6	100%	3e-09	100%	XP_005900460.1
PREDICTED: plasminogen [Bison bison bison]	59.6	59.6	100%	3e-09	100%	XP_010839202.1
PREDICTED: plasminogen isoform X5 [Bos mutus]	59.6	59.6	100%	3e-09	100%	XP_005900459.1
PREDICTED: LOW QUALITY PROTEIN: plasminogen [Bos indicus]	59.6	59.6	100%	3e-09	100%	XP_019823222.1
Plasminogen [Bos mutus]	59.6	59.6	100%	3e-09	100%	ELR53056.1

Alignments

plasminogen, partial [Canis lupus familiaris]
Sequence ID: **AAT44581.1** Length: 54 Number of Matches: 1
Range 1: 26 to 43

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.6 bits(133)	1e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1   GTDSCQGDSGGPLVCFEK  18
           GTDSCQGDSGGPLVCFEK
Sbjct  26  GTDSCQGDSGGPLVCFEK  43
```

RecName: Full=Apolipoprotein(a); Short=Apo(a); Short=Lp(a); Flags: Precursor
Sequence ID: **P08519.1** Length: 4548 Number of Matches: 1

See 1 more title(s)

Range 1: 4490 to 4507

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.6 bits(133)	3e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1     GTDSCQGDSGGPLVCFEK  18
            GTDSCQGDSGGPLVCFEK
Sbjct  4490  GTDSCQGDSGGPLVCFEK  4507
```

apolipoprotein a

Sequence ID: **prf||1313352A** Length: 4548 Number of Matches: 1
Range 1: 4490 to 4507

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.6 bits(133)	3e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1     GTDSCQGDSGGPLVCFEK  18
            GTDSCQGDSGGPLVCFEK
Sbjct  4490  GTDSCQGDSGGPLVCFEK  4507
```

PREDICTED: apolipoprotein(a) [Gorilla gorilla gorilla]

Sequence ID: **XP_018884409.1** Length: 2203 Number of Matches: 1
Range 1: 2145 to 2162

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.6 bits(133)	3e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1     GTDSCQGDSGGPLVCFEK  18
            GTDSCQGDSGGPLVCFEK
Sbjct  2145  GTDSCQGDSGGPLVCFEK  2162
```

lipoprotein, Lp(a) [Homo sapiens]

Sequence ID: **ABF47086.1** Length: 2040 Number of Matches: 1
Range 1: 1982 to 1999

Score	Expect	Method	Identities	Positives	Gaps	Frame
59.6 bits(133)	3e-09()		18/18(100%)	18/18(100%)	0/18(0%)	

Features:

```
Query  1     GTDSCQGDSGGPLVCFEK  18
             GTDSCQGDSGGPLVCFEK
Sbjct  1982  GTDSCQGDSGGPLVCFEK  1999
```

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BLAST Results

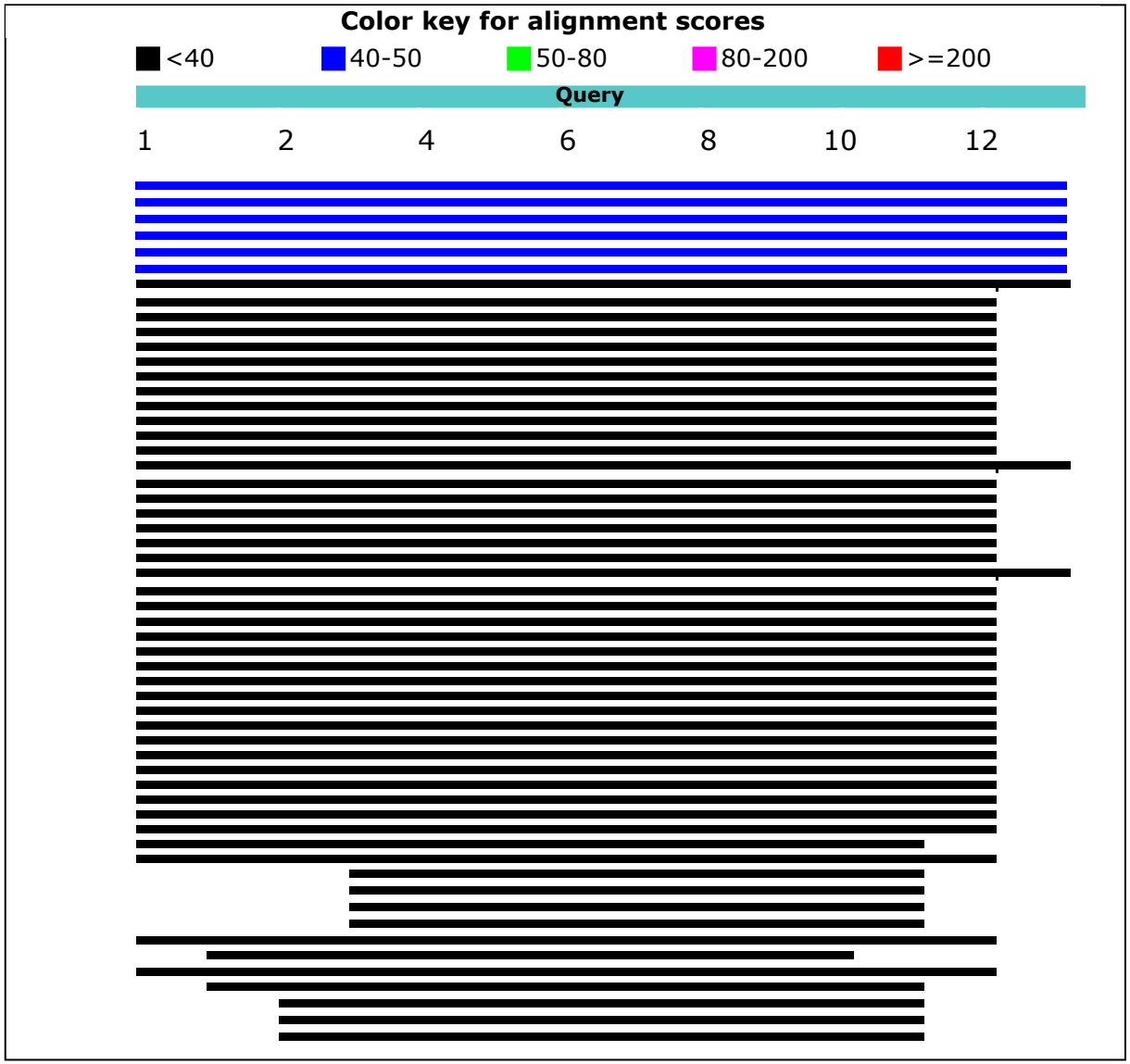
Job title: NCBI BlastP_LPA_NPDAVAAPYCYTR

RID	S54HUGGC015 (Expires on 08-04 11:02 am)
Query ID	lcl|Query_86903
Description	None
Molecule type	amino acid
Query Length	13
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 329 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
RecName: Full=Apolipoprotein(a); Short=Apo(a); Short=Lp(a); Flags: Precursor	46.4	1467	100%	4e-05	100%	P08519.1
apolipoprotein a	46.4	1460	100%	4e-05	100%	1313352A
lipoprotein, Lp(a) [Homo sapiens]	46.4	446	100%	4e-05	100%	ABF47086.1
apolipoprotein(a) precursor [Homo sapiens]	46.4	446	100%	4e-05	100%	NP_005568.2
lipoprotein, Lp(a) [Homo sapiens]	46.4	124	100%	4e-05	100%	EAW47596.1
PREDICTED: apolipoprotein(a) [Gorilla gorilla gorilla]	43.1	346	100%	7e-04	92%	XP_018884409.1
PREDICTED: LOW QUALITY PROTEIN: apolipoprotein(a) [Pan troglodytes]	39.7	376	100%	0.011	92%	XP_016812070.1
PREDICTED: apolipoprotein(a) [Chlorocebus sabaeus]	39.7	334	92%	0.011	92%	XP_008006112.1
PREDICTED: apolipoprotein(a) [Mandrillus leucophaeus]	39.7	268	92%	0.011	92%	XP_011831359.1
PREDICTED: apolipoprotein(a) isoform X1 [Macaca fascicularis]	39.7	212	92%	0.011	92%	XP_015304003.1
apolipoprotein(a) isoform X1 [Papio anubis]	39.7	252	92%	0.011	92%	XP_017813932.1
PREDICTED: apolipoprotein(a) isoform X2 [Macaca fascicularis]	39.7	212	92%	0.011	92%	XP_015304004.1
apolipoprotein(a) isoform X2 [Papio anubis]	39.7	252	92%	0.011	92%	XP_017813933.1
PREDICTED: apolipoprotein(a) isoform X1 [Macaca mulatta]	39.7	252	92%	0.011	92%	XP_014993121.1
PREDICTED: apolipoprotein(a) isoform X3 [Macaca fascicularis]	39.7	212	92%	0.011	92%	XP_015304005.1
PREDICTED: apolipoprotein(a) isoform X2 [Macaca mulatta]	39.7	252	92%	0.011	92%	XP_014993122.1
PREDICTED: apolipoprotein(a) isoform X4 [Macaca fascicularis]	39.7	212	92%	0.011	92%	XP_015304006.1
PREDICTED: apolipoprotein(a) isoform X3 [Macaca mulatta]	39.7	212	92%	0.011	92%	XP_014993123.1
PREDICTED: apolipoprotein(a) [Pan paniscus]	39.7	221	100%	0.011	92%	XP_008957511.1
PREDICTED: apolipoprotein(a) isoform X4 [Macaca mulatta]	39.7	252	92%	0.011	92%	XP_014993124.1
RecName: Full=Apolipoprotein(a); Short=Apo(a); Short=Lp(a)	39.7	172	92%	0.011	92%	P14417.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein(a) isoform X5 [Macaca mulatta]	39.7	252	92%	0.011	92%	XP_014993125.1
apolipoprotein(a) isoform X3 [Papio anubis]	39.7	172	92%	0.011	92%	XP_003898415.3
PREDICTED: apolipoprotein(a) isoform X4 [Cercocebus atys]	39.7	133	92%	0.011	92%	XP_011905764.1
PREDICTED: apolipoprotein(a) isoform X1 [Cercocebus atys]	39.7	133	92%	0.011	92%	XP_011905761.1
PREDICTED: apolipoprotein(a) [Pongo abelii]	39.7	157	100%	0.011	92%	XP_002817599.2
PREDICTED: LOW QUALITY PROTEIN: apolipoprotein(a) [Macaca nemestrina]	39.7	133	92%	0.011	92%	XP_011757132.1
PREDICTED: apolipoprotein(a) isoform X3 [Cercocebus atys]	39.7	93.5	92%	0.011	92%	XP_011905763.1
PREDICTED: apolipoprotein(a) isoform X2 [Cercocebus atys]	39.7	133	92%	0.011	92%	XP_011905762.1
PREDICTED: apolipoprotein(a) isoform X5 [Cercocebus atys]	39.7	133	92%	0.011	92%	XP_011905765.1
hypothetical protein EGK_15486 [Macaca mulatta]	39.7	112	92%	0.011	92%	EHH18817.1
PREDICTED: apolipoprotein(a) [Rhinopithecus roxellana]	39.7	73.0	92%	0.011	92%	XP_010368310.1
PREDICTED: uncharacterized protein LOC100988253 [Pan paniscus]	39.7	39.7	92%	0.011	92%	XP_003820297.1
PREDICTED: apolipoprotein(a)-like isoform X1 [Cercocebus atys]	39.7	39.7	92%	0.011	92%	XP_011933444.1
PREDICTED: apolipoprotein(a)-like isoform X2 [Cercocebus atys]	39.7	39.7	92%	0.011	92%	XP_011933445.1
apolipoprotein(a)-like [Papio anubis]	39.7	79.3	92%	0.011	92%	XP_009196879.1
PREDICTED: apolipoprotein(a)-like [Macaca nemestrina]	39.7	39.7	92%	0.011	92%	XP_011749267.1
PREDICTED: apolipoprotein(a)-like isoform X4 [Cercocebus atys]	39.7	39.7	92%	0.011	92%	XP_011933448.1
PREDICTED: apolipoprotein(a)-like [Pongo abelii]	39.7	39.7	92%	0.011	92%	XP_009240688.1
putative apolipoprotein(a)-like protein 2 [Papio anubis]	39.7	39.7	92%	0.012	92%	XP_003919010.2
apolipoprotein[a] [Macaca fascicularis]	39.7	39.7	92%	0.012	92%	AAD14312.1
PREDICTED: apolipoprotein(a) [Colobus angolensis palliatus]	36.3	90.1	92%	0.18	83%	XP_011790481.1
PREDICTED: apolipoprotein(a) [Rhinopithecus bieti]	33.3	33.3	92%	2.1	83%	XP_017718856.1
aspartate aminotransferase family protein [Bacillus sp. SJS]	30.8	30.8	84%	17	82%	WP_035406281.1
hypothetical protein H072_2597 [Dactylellina haptotyla CBS 200.50]	30.3	30.3	92%	24	75%	XP_011108584.1
N(6)-acetyl-beta-lysine transaminase precursor [Fictibacillus solisalsi]	29.9	29.9	61%	33	100%	SDM67866.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
aspartate aminotransferase family protein [Bacillus sp. NC2-31]	29.9	29.9	61%	33	100%	WP_070119627.1
aspartate aminotransferase family protein [Bacillus oryziterrae]	29.9	29.9	61%	33	100%	WP_017754752.1
BA14K-like protein [Bradyrhizobium sp. Gha]	29.9	29.9	61%	34	100%	SFK06451.1
PREDICTED: plasminogen-like [Branchiostoma belcheri]	29.5	70.6	92%	47	75%	XP_019627269.1
hypothetical protein SPPG_05293 [Spizellomyces punctatus DAOM BR117]	29.5	29.5	69%	47	89%	XP_016607961.1
hypothetical protein BRAFLDRAFT_59252 [Branchiostoma floridae]	29.5	50.1	92%	47	75%	XP_002590082.1
nematode cuticle collagen domain protein [Dictyocaulus viviparus]	29.5	29.5	76%	47	75%	KJH45113.1
adenosine monophosphate-protein transferase [Rhodopseudomonas palustris]	29.5	29.5	69%	47	89%	WP_011662148.1
adenosine monophosphate-protein transferase [Parvibaculum lavamentivorans]	29.5	29.5	69%	47	89%	WP_011995226.1
adenosine monophosphate-protein transferase [Rhodopseudomonas palustris]	29.5	29.5	69%	47	89%	WP_011440879.1
PREDICTED: LOW QUALITY PROTEIN: sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 [Callorhinchus milii]	29.1	29.1	69%	67	89%	XP_007902176.1
MULTISPECIES: pectate lyase [Achromobacter]	29.1	29.1	76%	67	82%	WP_088599612.1
pectate lyase [Bordetella sp. N]	29.1	29.1	76%	67	82%	ALM86481.1
pectate lyase [Bordetella sp. N]	29.1	29.1	76%	67	82%	WP_082621922.1
pectate lyase [Achromobacter sp. MFA1 R4]	29.1	29.1	76%	67	82%	WP_076517492.1
pectate lyase [Bordetella genomosp. 9]	29.1	29.1	76%	67	82%	WP_086071740.1
pectate lyase [Bordetella genomosp. 9]	29.1	29.1	76%	67	82%	WP_086059259.1
pectate lyase [Bordetella genomosp. 9]	29.1	29.1	76%	67	82%	ARP92510.1
pectate lyase [Bordetella genomosp. 9]	29.1	29.1	76%	67	82%	ARP88544.1
glycosyl transferase family 2 [Staphylothermus hellenicus]	29.1	29.1	100%	67	62%	WP_013143205.1
PREDICTED: zonadhesin-like [Crassostrea gigas]	28.6	28.6	92%	95	75%	XP_011456641.2
Zonadhesin [Crassostrea gigas]	28.6	28.6	92%	95	75%	EKC36393.1
glycosyl transferase [Mycobacterium litorale]	28.6	28.6	100%	95	58%	WP_078021337.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
glycosyl transferase [Actinokineospora bangkokensis]	28.6	28.6	100%	95	58%	WP_075974204.1
glycosyl transferase [Mycobacterium sp. SWH-M5]	28.6	28.6	100%	95	58%	WP_073676294.1
glycosyl transferase [Mycobacterium wolinskyi]	28.6	28.6	100%	95	58%	WP_067853011.1
isochorismate synthase [Bacillus cereus]	28.6	28.6	76%	95	69%	WP_088030104.1
hypothetical protein AUK63_974 [bacterium P3]	28.6	28.6	92%	95	83%	KWW30322.1
PREDICTED: plasminogen [Crassostrea gigas]	28.6	28.6	92%	95	75%	XP_011451343.1
hypothetical protein BRAFLDRAFT_250118 [Branchiostoma floridae]	28.6	81.7	92%	95	75%	XP_002590959.1
Plasminogen [Crassostrea gigas]	28.6	28.6	92%	95	75%	EKC22374.1
PREDICTED: LOW QUALITY PROTEIN: phosphoinositide-3-kinase-interacting protein 1 [Crocodylus porosus]	28.6	28.6	100%	95	69%	XP_019394948.1
PREDICTED: plasminogen [Crassostrea gigas]	28.6	28.6	92%	95	75%	XP_011443863.1
Plasminogen [Crassostrea gigas]	28.6	28.6	92%	95	75%	EKC22363.1
PREDICTED: phosphoinositide-3-kinase-interacting protein 1 [Gavialis gangeticus]	28.6	28.6	100%	95	69%	XP_019362181.1
hypothetical protein [Rhizobium tropici]	28.6	28.6	76%	95	64%	WP_047636963.1
type VI secretion protein IcmF [Sphingomonas hankookensis]	28.2	28.2	100%	134	69%	WP_066688972.1
type VI secretion protein IcmF [Sphingomonas sp. Leaf23]	28.2	28.2	100%	134	69%	WP_055758089.1
MULTISPECIES: type VI secretion protein IcmF [Sphingomonas]	28.2	28.2	100%	134	69%	WP_055788385.1
MULTISPECIES: type VI secretion protein IcmF [Sphingomonas]	28.2	28.2	100%	134	69%	WP_055818248.1
Succinyl-diaminopimelate desuccinylase [Arthrobacter saudimassiliensis]	28.2	28.2	61%	134	100%	CEA08514.1
RagB/SusD family nutrient uptake outer membrane protein [Chitinophaga sancti]	28.2	28.2	76%	134	69%	WP_083571799.1
SusD family protein [Chitinophaga sancti]	28.2	28.2	76%	134	69%	SFW84349.1
MULTISPECIES: peptidase [Nocardioides]	28.2	28.2	61%	134	100%	WP_011757815.1
hypothetical protein CYLTODRAFT_483269 [Cylindrobasidium torrendii FP15055 ss-10]	28.2	28.2	61%	134	100%	KIY60730.1
hypothetical protein IQ07DRAFT_506574 [Pyrenochaeta sp. DS3sAY3a]	28.2	28.2	84%	135	69%	OAL51848.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Sphingomonas sp. MCT13]	28.2	28.2	61%	135	100%	WP_069321718.1
N-acetylmuramoyl-L-alanine amidase [Nocardiopsis gilva]	28.2	28.2	84%	135	77%	WP_017620573.1
hypothetical protein SNOG_14864 [Parastagonospora nodorum SN15]	28.2	28.2	84%	135	69%	XP_001805034.1
isopentenyl-diphosphate delta-isomerase [Flavisolibacter sp. LCS9]	28.2	28.2	92%	135	75%	WP_066406979.1
PREDICTED: uncharacterized protein LOC106086986 [Stomoxys calcitrans]	27.8	27.8	100%	190	50%	XP_013107293.1
PREDICTED: plasminogen [Sorex araneus]	27.8	27.8	92%	190	75%	XP_012787754.1
hypothetical protein [Catenuloplanes japonicus]	27.8	27.8	84%	190	82%	WP_033344630.1
plasminogen [Microcebus murinus]	27.8	27.8	92%	190	75%	XP_012615092.1

Alignments

RecName: Full=Apolipoprotein(a); Short=Apo(a); Short=Lp(a); Flags: Precursor
Sequence ID: **P08519.1** Length: 4548 Number of Matches: 33

See 1 more title(s)

Range 1: 79 to 91

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   NPDAVAAPYCYTR  13
           NPDAVAAPYCYTR
Sbjct  79  NPDAVAAPYCYTR  91
```

Range 2: 193 to 205

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
```

```
Sbjct  193  NPDAVAAPYCYTR  205
```

Range 3: 307 to 319

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  307  NPDAVAAPYCYTR  319
```

Range 4: 421 to 433

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  421  NPDAVAAPYCYTR  433
```

Range 5: 535 to 547

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  535  NPDAVAAPYCYTR  547
```

Range 6: 649 to 661

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  649  NPDAVAAPYCYTR  661
```

Range 7: 763 to 775

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  763  NPDAVAAPYCYTR  775
```

Range 8: 877 to 889

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  877  NPDAVAAPYCYTR  889
```

Range 9: 991 to 1003

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  991  NPDAVAAPYCYTR  1003
```

Range 10: 1105 to 1117

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  1105 NPDAVAAPYCYTR  1117
```

Range 11: 1219 to 1231

Score	Expect	Method	Identities	Positives	Gaps	Frame

46.4 bits(102)	4e-05()	13/13(100%)	13/13(100%)	0/13(0%)

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1219  NPDAVAAPYCYTR  1231
```

Range 12: 1333 to 1345

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1333  NPDAVAAPYCYTR  1345
```

Range 13: 1447 to 1459

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1447  NPDAVAAPYCYTR  1459
```

Range 14: 1561 to 1573

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1561  NPDAVAAPYCYTR  1573
```

Range 15: 1675 to 1687

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1675  NPDAVAAPYCYTR  1687
```

Range 16: 1789 to 1801

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1789  NPDAVAAPYCYTR  1801
```

Range 17: 1903 to 1915

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1903  NPDAVAAPYCYTR  1915
```

Range 18: 2017 to 2029

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2017  NPDAVAAPYCYTR  2029
```

Range 19: 2131 to 2143

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2131  NPDAVAAPYCYTR  2143
```

Range 20: 2245 to 2257

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2245  NPDAVAAPYCYTR  2257
```

Range 21: 2359 to 2371

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2359  NPDAVAAPYCYTR  2371
```

Range 22: 2473 to 2485

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2473  NPDAVAAPYCYTR  2485
```

Range 23: 2587 to 2599

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2587  NPDAVAAPYCYTR  2599
```

Range 24: 2701 to 2713

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2701  NPDAVAAPYCYTR  2713
```

Range 25: 2815 to 2827

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2815  NPDAVAAPYCYTR  2827
```

Range 26: 2929 to 2941

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2929  NPDAVAAPYCYTR  2941
```

Range 27: 3043 to 3055

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  3043  NPDAVAAPYCYTR  3055
```

Range 28: 3157 to 3169

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  3157  NPDAVAAPYCYTR  3169
```

Range 29: 3271 to 3283

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  3271  NPDAVAAPYCYTR  3283
```

Range 30: 3385 to 3397

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	7e-04()		12/13(92%)	12/13(92%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPD VAAPYCYTR
Sbjct  3385  NPDPVAAPYCYTR  3397
```

Range 31: 3499 to 3510

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.3 bits(71)	2.0()		10/12(83%)	10/12(83%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPD VAAP CYT
Sbjct  3499  NPDPVAAPWCYT  3510
```

Range 32: 3727 to 3738

Score	Expect	Method	Identities	Positives	Gaps	Frame
24.0 bits(49)	4460()		8/12(67%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPDA   P CYT
```

```
Sbjct  3727  NPDAEISPWCYT  3738
```

Range 33: 4175 to 4186

Score	Expect	Method	Identities	Positives	Gaps	Frame
20.6 bits(41)	74850()		7/12(58%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPDA   P C+T
Sbjct  4175  NPDADTGPWCFT  4186
```

apolipoprotein a

Sequence ID: **prf||1313352A** Length: 4548 Number of Matches: 33
Range 1: 79 to 91

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   NPDAVAAPYCYTR  13
           NPDAVAAPYCYTR
Sbjct  79  NPDAVAAPYCYTR  91
```

Range 2: 193 to 205

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  193  NPDAVAAPYCYTR  205
```

Range 3: 307 to 319

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
```

```
Sbjct  307  NPDAVAAPYCYTR  319
```

Range 4: 421 to 433

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  421  NPDAVAAPYCYTR  433
```

Range 5: 535 to 547

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  535  NPDAVAAPYCYTR  547
```

Range 6: 649 to 661

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  649  NPDAVAAPYCYTR  661
```

Range 7: 763 to 775

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  763  NPDAVAAPYCYTR  775
```

Range 8: 877 to 889

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  877  NPDAVAAPYCYTR  889
```

Range 9: 991 to 1003

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  991  NPDAVAAPYCYTR  1003
```

Range 10: 1105 to 1117

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  1105 NPDAVAAPYCYTR  1117
```

Range 11: 1219 to 1231

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  1219 NPDAVAAPYCYTR  1231
```

Range 12: 1333 to 1345

Score	Expect	Method	Identities	Positives	Gaps	Frame

46.4 bits(102)	4e-05()	13/13(100%)	13/13(100%)	0/13(0%)

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1333  NPDAVAAPYCYTR  1345
```

Range 13: 1447 to 1459

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1447  NPDAVAAPYCYTR  1459
```

Range 14: 1561 to 1573

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1561  NPDAVAAPYCYTR  1573
```

Range 15: 1675 to 1687

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1675  NPDAVAAPYCYTR  1687
```

Range 16: 1789 to 1801

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1789  NPDAVAAPYCYTR  1801
```

Range 17: 1903 to 1915

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  1903  NPDAVAAPYCYTR  1915
```

Range 18: 2017 to 2029

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2017  NPDAVAAPYCYTR  2029
```

Range 19: 2131 to 2143

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2131  NPDAVAAPYCYTR  2143
```

Range 20: 2359 to 2371

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2359  NPDAVAAPYCYTR  2371
```

Range 21: 2473 to 2485

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2473  NPDAVAAPYCYTR  2485
```

Range 22: 2587 to 2599

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2587  NPDAVAAPYCYTR  2599
```

Range 23: 2701 to 2713

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2701  NPDAVAAPYCYTR  2713
```

Range 24: 2815 to 2827

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2815  NPDAVAAPYCYTR  2827
```

Range 25: 2929 to 2941

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  2929  NPDAVAAPYCYTR  2941
```

Range 26: 3043 to 3055

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  3043  NPDAVAAPYCYTR  3055
```

Range 27: 3157 to 3169

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  3157  NPDAVAAPYCYTR  3169
```

Range 28: 3271 to 3283

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDAVAAPYCYTR
Sbjct  3271  NPDAVAAPYCYTR  3283
```

Range 29: 3385 to 3397

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	7e-04()		12/13(92%)	12/13(92%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPD VAAPYCYTR
Sbjct  3385  NPDPVAAPYCYTR  3397
```

Range 30: 2245 to 2257

Score	Expect	Method	Identities	Positives	Gaps	Frame
39.2 bits(85)	0.016()		11/13(85%)	11/13(84%)	0/13(0%)	

Features:

```
Query  1     NPDAVAAPYCYTR  13
             NPDA  APYCYTR
Sbjct  2245  NPDAAVAPYCYTR  2257
```

Range 31: 3499 to 3510

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.3 bits(71)	2.0()		10/12(83%)	10/12(83%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPD VAAP CYT
Sbjct  3499  NPDPVAAPWCYT  3510
```

Range 32: 3727 to 3738

Score	Expect	Method	Identities	Positives	Gaps	Frame
24.0 bits(49)	4460()		8/12(67%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPDA   P CYT
Sbjct  3727  NPDAEISPWCYT  3738
```

Range 33: 4175 to 4186

Score	Expect	Method	Identities	Positives	Gaps	Frame
20.6 bits(41)	74850()		7/12(58%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPDA   P C+T
```

```
Sbjct  4175  NPDADTGPWCFT  4186
```

lipoprotein, Lp(a) [Homo sapiens]

Sequence ID: **ABF47086.1** Length: 2040 Number of Matches: 11
Range 1: 79 to 91

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   NPDAVAAPYCYTR  13
           NPDAVAAPYCYTR
Sbjct  79  NPDAVAAPYCYTR  91
```

Range 2: 193 to 205

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  193  NPDAVAAPYCYTR  205
```

Range 3: 307 to 319

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  307  NPDAVAAPYCYTR  319
```

Range 4: 421 to 433

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
```

```
Sbjct  421  NPDAVAAPYCYTR  433
```

Range 5: 535 to 547

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  535  NPDAVAAPYCYTR  547
```

Range 6: 649 to 661

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  649  NPDAVAAPYCYTR  661
```

Range 7: 763 to 775

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  763  NPDAVAAPYCYTR  775
```

Range 8: 877 to 889

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	7e-04()		12/13(92%)	12/13(92%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPD VAAPYCYTR
Sbjct  877  NPDPVAAPYCYTR  889
```

Range 9: 991 to 1002

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.3 bits(71)	2.0()		10/12(83%)	10/12(83%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPD VAAP CYT
Sbjct  991   NPDPVAAPWCYT  1002
```

Range 10: 1219 to 1230

Score	Expect	Method	Identities	Positives	Gaps	Frame
24.0 bits(49)	4460()		8/12(67%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPDA   P CYT
Sbjct  1219  NPDAEISPWCYT  1230
```

Range 11: 1667 to 1678

Score	Expect	Method	Identities	Positives	Gaps	Frame
20.6 bits(41)	74822()		7/12(58%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPDA   P C+T
Sbjct  1667  NPDADTGPWCFT  1678
```

apolipoprotein(a) precursor [Homo sapiens]

Sequence ID: **NP_005568.2** Length: 2040 Number of Matches: 11
Range 1: 79 to 91

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   NPDAVAAPYCYTR  13
           NPDAVAAPYCYTR
Sbjct  79  NPDAVAAPYCYTR  91
```

Range 2: 193 to 205

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  193  NPDAVAAPYCYTR  205
```

Range 3: 307 to 319

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  307  NPDAVAAPYCYTR  319
```

Range 4: 421 to 433

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  421  NPDAVAAPYCYTR  433
```

Range 5: 535 to 547

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  535  NPDAVAAPYCYTR  547
```

Range 6: 649 to 661

Score	Expect	Method	Identities	Positives	Gaps	Frame

46.4 bits(102)	4e-05()	13/13(100%)	13/13(100%)	0/13(0%)

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  649  NPDAVAAPYCYTR  661
```

Range 7: 763 to 775

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPDAVAAPYCYTR
Sbjct  763  NPDAVAAPYCYTR  775
```

Range 8: 877 to 889

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	7e-04()		12/13(92%)	12/13(92%)	0/13(0%)	

Features:

```
Query  1    NPDAVAAPYCYTR  13
            NPD VAAPYCYTR
Sbjct  877  NPDPVAAPYCYTR  889
```

Range 9: 991 to 1002

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.3 bits(71)	2.0()		10/12(83%)	10/12(83%)	0/12(0%)	

Features:

```
Query  1    NPDAVAAPYCYT  12
            NPD VAAP CYT
Sbjct  991  NPDPVAAPWCYT  1002
```

Range 10: 1219 to 1230

Score	Expect	Method	Identities	Positives	Gaps	Frame
24.0 bits(49)	4460()		8/12(67%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPDA   P CYT
Sbjct  1219  NPDAEISPWCYT  1230
```

Range 11: 1667 to 1678

Score	Expect	Method	Identities	Positives	Gaps	Frame
20.6 bits(41)	74822()		7/12(58%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1     NPDAVAAPYCYT  12
             NPDA   P C+T
Sbjct  1667  NPDADTGPWCFT  1678
```

lipoprotein, Lp(a) [Homo sapiens]

Sequence ID: **EAW47596.1** Length: 1169 Number of Matches: 4

Range 1: 6 to 18

Score	Expect	Method	Identities	Positives	Gaps	Frame
46.4 bits(102)	4e-05()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1   NPDAVAAPYCYTR  13
           NPDAVAAPYCYTR
Sbjct  6   NPDAVAAPYCYTR  18
```

Range 2: 120 to 131

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.3 bits(71)	2.0()		10/12(83%)	10/12(83%)	0/12(0%)	

Features:

```
Query  1    NPDAVAAPYCYT  12
            NPD VAAP CYT
Sbjct  120  NPDPVAAPWCYT  131
```

Range 3: 348 to 359

Score	Expect	Method	Identities	Positives	Gaps	Frame
24.0 bits(49)	4459()		8/12(67%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1    NPDAVAAPYCYT  12
            NPDA   P CYT
Sbjct  348  NPDAEISPWCYT  359
```

Range 4: 796 to 807

Score	Expect	Method	Identities	Positives	Gaps	Frame
20.6 bits(41)	74784()		7/12(58%)	8/12(66%)	0/12(0%)	

Features:

```
Query  1    NPDAVAAPYCYT  12
            NPDA   P C+T
Sbjct  796  NPDADTGPWCFT  807
```

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BLAST Results

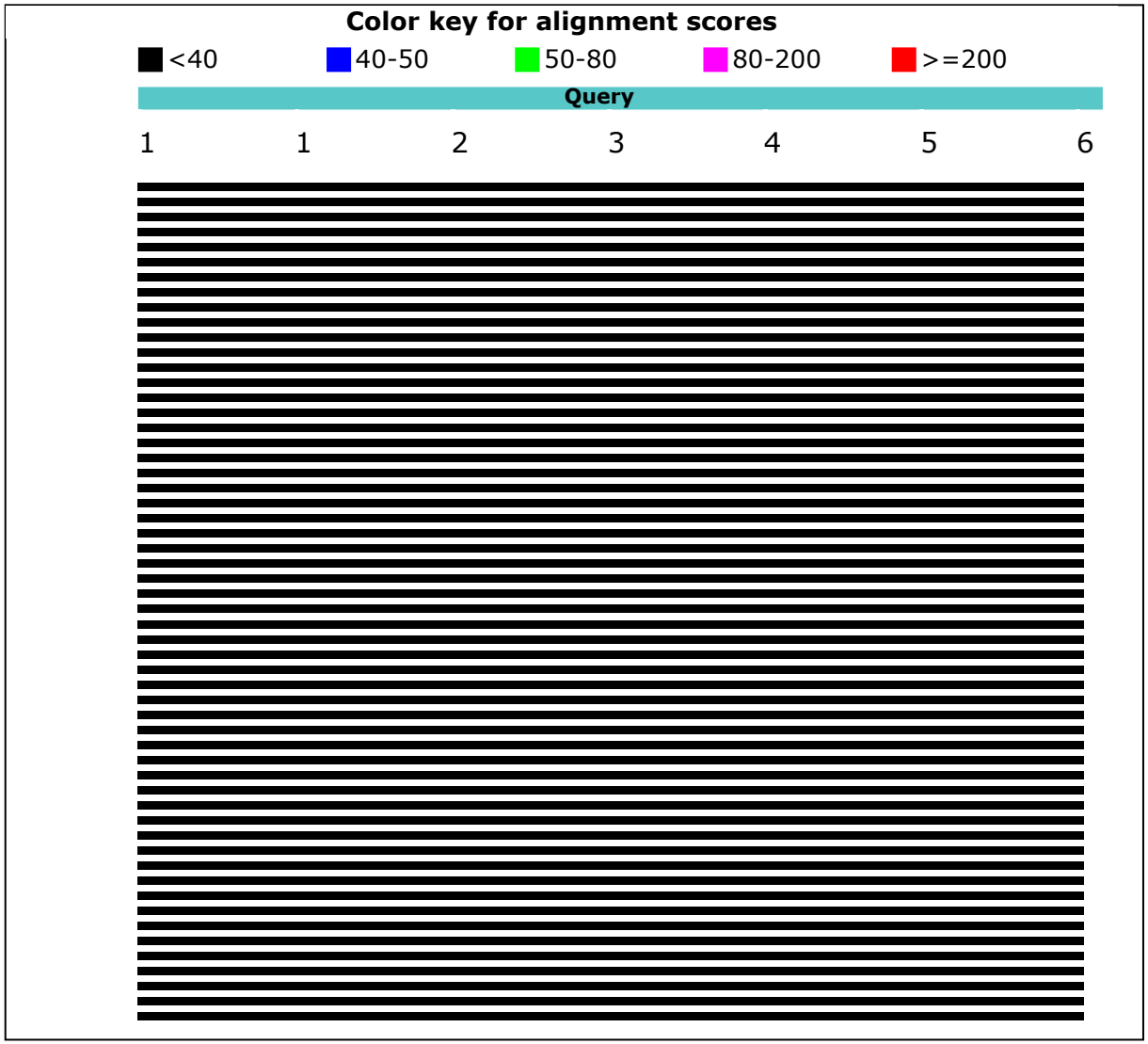
Job title: NCBI BlastP_CRP_AFVFPK

RID	S54TZ16E014 (Expires on 08-04 11:06 am)
Query ID	lcl|Query_4157
Description	None
Molecule type	amino acid
Query Length	6
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
conserved hypothetical protein [Leishmania major strain Friedlin]	22.7	22.7	100%	2413	100%	CAJ02748.1
hypothetical protein PICMEDRAFT_74862 [Pichia membranifaciens NRRL Y-2026]	22.7	22.7	100%	2414	100%	ODQ44257.1
hypothetical protein AN3443.2 [Aspergillus nidulans FGSC A4]	22.7	22.7	100%	2414	100%	EAA62983.1
AMP deaminase, putative [Trypanosoma brucei gambiense DAL972]	22.7	22.7	100%	2416	100%	CBH14311.1
adenosine monophosphate deaminase, putative [Trypanosoma brucei brucei TREU927]	22.7	22.7	100%	2416	100%	EAN76744.1
LADA_0E07250g1_1 [Lachancea dasiensis CBS 10888]	22.7	22.7	100%	2416	100%	SCU87953.1
restriction endonuclease [Actinomadura rubrobrunea]	22.7	22.7	100%	2418	100%	WP_067911976.1
hypothetical protein AEM38_01330 [Hyphomonadaceae bacterium UKL13-1]	22.7	22.7	100%	2419	100%	AMS28443.1
hypothetical protein ACHHYP_12779 [Achlya hypogyna]	22.7	22.7	100%	2420	100%	OQR84822.1
hypothetical protein TRFO_07441 [Tritrichomonas foetus]	22.7	22.7	100%	2420	100%	OHT01860.1
hypothetical protein [Cloacibacillus evryensis]	22.7	22.7	100%	2422	100%	WP_034443220.1
hypothetical protein [Synergistes sp. 3_1_syn1]	22.7	22.7	100%	2422	100%	WP_008712073.1
hypothetical protein PRIPAC_5420 [Pristionchus pacificus]	22.7	22.7	100%	2422	100%	KKA74937.1
glutamate receptor 2.8-like [Prunus avium]	22.7	22.7	100%	2422	100%	XP_021805259.1
hypothetical protein PRUPE_1G399700 [Prunus persica]	22.7	22.7	100%	2422	100%	ONI33012.1
glutamate receptor 2.1-like [Prunus avium]	22.7	22.7	100%	2422	100%	XP_021805272.1
putative mitochondrial proton motive ATPase [Leptomonas pyrrhocoris]	22.7	22.7	100%	2422	100%	KPA75612.1
hypothetical protein AK812_SmicGene3392 [Symbiodinium microadriaticum]	22.7	22.7	100%	2422	100%	OLQ12666.1
hypothetical protein PRUPE_1G400600 [Prunus persica]	22.7	22.7	100%	2422	100%	ONI33021.1
hypothetical protein PRUPE_1G399900 [Prunus persica]	22.7	22.7	100%	2422	100%	ONI33014.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein OsI_26456 [Oryza sativa Indica Group]	22.7	43.3	100%	2422	100%	EEC82261.1
glutamate receptor 2.8-like [Prunus avium]	22.7	22.7	100%	2422	100%	XP_021805298.1
hypothetical protein PRUPE_1G399800 [Prunus persica]	22.7	22.7	100%	2422	100%	ONI33013.1
glutamate receptor 2.8 [Nicotiana attenuata]	22.7	22.7	100%	2422	100%	OIT38033.1
glutamate receptor 2.7-like [Prunus avium]	22.7	22.7	100%	2423	100%	XP_021805269.1
hypothetical protein MIMGU_mgv1a023751mg [Erythranthe guttata]	22.7	22.7	100%	2423	100%	EYU45932.1
hypothetical protein POPTR_0018s03170g [Populus trichocarpa]	22.7	22.7	100%	2423	100%	EEF02926.2
hypothetical protein MIMGU_mgv1a025791mg [Erythranthe guttata]	22.7	22.7	100%	2423	100%	EYU21240.1
hypothetical protein A2790_02695 [Phenylobacterium sp. RIFCSPHIGHO2_01_FULL_69_31]	22.7	22.7	100%	2423	100%	OHB31740.1
hypothetical protein MIMGU_mgv1a023982mg, partial [Erythranthe guttata]	22.7	22.7	100%	2423	100%	EYU21236.1
hypothetical protein MIMGU_mgv1a025842mg, partial [Erythranthe guttata]	22.7	22.7	100%	2424	100%	EYU21241.1
hypothetical protein MIMGU_mgv1a001132mg [Erythranthe guttata]	22.7	22.7	100%	2424	100%	EYU21238.1
hypothetical protein UT04_C0016G0010 [Candidatus Daviesbacteria bacterium GW2011_GWF2_38_7]	22.7	22.7	100%	2424	100%	KKQ84389.1
hypothetical protein [Phenylobacterium sp. CCH12-B4]	22.7	22.7	100%	2424	100%	WP_082765689.1
hypothetical protein [Actinoplanes globisporus]	22.7	22.7	100%	2424	100%	WP_026205540.1
glutamate receptor 2.8-like [Dorcoceras hygrometricum]	22.7	22.7	100%	2424	100%	KZV41622.1
hypothetical protein [Flexithrix dorotheae]	22.7	22.7	100%	2424	100%	WP_020527118.1
Uncharacterized protein conserved in bacteria [uncultured Ruminococcus sp.]	22.7	22.7	100%	2424	100%	SCI57037.1
hypothetical protein PRUPE_2G105100 [Prunus persica]	22.7	22.7	100%	2425	100%	ONI22072.1
hypothetical protein AK812_SmicGene36561 [Symbiodinium microadriaticum]	22.7	22.7	100%	2425	100%	OLP82758.1
Uncharacterised protein [uncultured Eubacterium sp.]	22.7	22.7	100%	2425	100%	SCJ74083.1
ATP/GTP-binding protein [Streptomyces misionensis]	22.7	22.7	100%	2425	100%	WP_074993556.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein CALCODRAFT_497008 [Calocera cornea HHB12733]	22.7	22.7	100%	2425	100%	KZT56831.1
endopeptidase La [Syntrophaceae bacterium CG2_30_58_14]	22.7	22.7	100%	2425	100%	OIP92341.1
endopeptidase La [Syntrophobacterales bacterium GWF2_56_9]	22.7	22.7	100%	2425	100%	OHE19364.1
endopeptidase La [Syntrophobacterales bacterium GWC2_56_13]	22.7	22.7	100%	2425	100%	OHE18652.1
endopeptidase La [Deltaproteobacteria bacterium RBG_16_58_17]	22.7	22.7	100%	2425	100%	OGP84478.1
Glutamate receptor 2.4 [Morus notabilis]	22.7	22.7	100%	2426	100%	EXB74933.1
glycoside hydrolase [Bifidobacterium asteroides]	22.7	22.7	100%	2426	100%	WP_045923871.1
hypothetical protein A1O7_07276 [Cladophialophora yegresii CBS 114405]	22.7	22.7	100%	2426	100%	EXJ56932.1
hypothetical protein CLCR_04624 [Cladophialophora carrionii]	22.7	22.7	100%	2426	100%	OCT49110.1
hypothetical protein G647_02815 [Cladophialophora carrionii CBS 160.54]	22.7	22.7	100%	2426	100%	ETI26038.1
Triacylglycerol lipase [Candidatus Amesbacteria bacterium GW2011_GWC2_45_19]	22.7	22.7	100%	2426	100%	KKU03285.1
hypothetical protein BVRB_007520 isoform B [Beta vulgaris subsp. vulgaris]	22.7	22.7	100%	2427	100%	KMS95512.1
FUSC family protein [Bacillus sp. Leaf406]	22.7	22.7	100%	2427	100%	WP_056541480.1
hypothetical protein BVRB_007520 isoform A [Beta vulgaris subsp. vulgaris]	22.7	22.7	100%	2427	100%	KMS95511.1
hypothetical protein [Bacillus aquimaris]	22.7	22.7	100%	2427	100%	WP_064091723.1
FUSC family protein [Bacillus aquimaris]	22.7	22.7	100%	2427	100%	WP_044340379.1
predicted protein [Laccaria bicolor S238N-H82]	22.7	22.7	100%	2427	100%	EDR10610.1
FUSC family protein [Bacillus marisflavi]	22.7	22.7	100%	2427	100%	WP_053427929.1
hypothetical protein [Bacillus sp. V-88]	22.7	22.7	100%	2427	100%	WP_079532983.1
FUSC family protein [Bacillus vietnamensis]	22.7	22.7	100%	2427	100%	WP_061811257.1
FUSC family protein [Bacillus vietnamensis]	22.7	22.7	100%	2427	100%	WP_051758544.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
glycosyl hydrolase 38 domain protein [Thermoanaerobacter ethanolicus]	22.7	22.7	100%	2427	100%	WP_003868712.1
molybdopterin oxidoreductase [Deltaproteobacteria bacterium RIFCSPLOWO2_02_FULL_53_8]	22.7	22.7	100%	2428	100%	OGQ51569.1
hypothetical protein SAMN05216222_1125 [Pseudomonas prosekii]	22.7	22.7	100%	2428	100%	SDS29286.1
Nuclear protein MDM1 [Struthio camelus australis]	22.7	22.7	100%	2428	100%	KFV79600.1
hypothetical protein K443DRAFT_680572 [Laccaria amethystina LaAM-08-1]	22.7	22.7	100%	2429	100%	KIJ98648.1
hypothetical protein A3A33_03350 [Candidatus Yanofskybacteria bacterium RIFCSPLOWO2_01_FULL_49_25]	22.7	22.7	100%	2429	100%	OGN28790.1
hypothetical protein [Bacillus sp. OK838]	22.7	22.7	100%	2429	100%	WP_089364139.1
ABC transporter permease [Bacillus simplex]	22.7	22.7	100%	2429	100%	WP_061462202.1
ABC transporter permease [Bacillus simplex]	22.7	22.7	100%	2429	100%	WP_061144479.1
hypothetical protein [Rhodobacter aestuarii]	22.7	22.7	100%	2429	100%	WP_076483836.1
Glutamate receptor 2.1 [Morus notabilis]	22.7	22.7	100%	2430	100%	EXC18797.1
hypothetical protein Z520_10332 [Fonsecaea multimorphosa CBS 102226]	22.7	22.7	100%	2430	100%	KIX93995.1
cell division protein FtsH [Bacillus andreraoultii]	22.7	22.7	100%	2430	100%	WP_033826442.1
hypothetical protein [Castellaniella defragrans]	22.7	22.7	100%	2431	100%	WP_052355505.1
hypothetical protein [Oribacterium sinus]	22.7	22.7	100%	2431	100%	WP_007157977.1
intramembrane protease 2 [Cordyceps brongniartii RCEF 3172]	22.7	22.7	100%	2431	100%	OAA43336.1
putative intramembrane protease [Beauveria bassiana D1-5]	22.7	22.7	100%	2431	100%	KGQ07297.1
signal peptide peptidase [Beauveria bassiana ARSEF 2860]	22.7	22.7	100%	2431	100%	EJP64410.1
spermidine synthase [Thalassomonas viridans]	22.7	22.7	100%	2432	100%	WP_044836875.1
spermidine synthase [Thalassomonas actiniarum]	22.7	22.7	100%	2432	100%	WP_044832282.1
cation acetate symporter [Lentzea kentuckyensis]	22.7	22.7	100%	2432	100%	WP_086661736.1
intramembrane protease 2 [Cordyceps confragosa RCEF 1005]	22.7	22.7	100%	2432	100%	OAA75388.1
hypothetical protein LLEC1_06773 [Cordyceps confragosa]	22.7	22.7	100%	2432	100%	OAR00651.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Equilibrative nucleoside transporter 2 [Aegilops tauschii]	22.7	22.7	100%	2432	100%	EMT16335.1
DNA repair protein RecN [Lactobacillus silagei]	22.7	22.7	100%	2432	100%	WP_089136592.1
hypothetical protein [Streptococcus suis]	22.7	22.7	100%	2433	100%	WP_024383290.1
intramembrane protease 2 [Cordyceps militaris CM01]	22.7	22.7	100%	2433	100%	EGX95053.1
major facilitator superfamily domain-containing protein [Syncephalastrum racemosum]	22.7	22.7	100%	2433	100%	ORY94015.1
hypothetical protein [Oribacterium asaccharolyticum]	22.7	22.7	100%	2433	100%	WP_009536731.1
hypothetical protein [Treponema denticola]	22.7	22.7	100%	2433	100%	WP_010694586.1
hypothetical protein A2014_12805 [Spirochaetes bacterium GWF1_49_6]	22.7	22.7	100%	2433	100%	OHD59413.1
hypothetical protein [Oribacterium sp. oral taxon 108]	22.7	22.7	100%	2434	100%	WP_009429425.1
hypothetical protein [Janthinobacterium sp. CG23_2]	22.7	22.7	100%	2434	100%	WP_054268368.1
methionine--tRNA ligase [Cephaloticoccus capnophilus]	22.7	22.7	100%	2434	100%	WP_068710929.1
alpha-N-arabinofuranosidase C [Capronia epimyces CBS 606.96]	22.7	22.7	100%	2435	100%	EXJ89390.1
hypothetical protein [Cellulophaga sp. Hel_I_12]	22.7	22.7	100%	2435	100%	WP_052188092.1
hypothetical protein [Aquimarina macrocephali]	22.7	22.7	100%	2435	100%	WP_084050122.1

Alignments

conserved hypothetical protein [Leishmania major strain Friedlin]
Sequence ID: **CAJ02748.1** Length: 2658 Number of Matches: 1
Range 1: 1242 to 1247

Score	Expect	Method	Identities	Positives	Gaps	Frame
22.7 bits(46)	2413()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  1     AFVFPK  6
             AFVFPK
Sbjct  1242  AFVFPK  1247
```

hypothetical protein PICMEDRAFT_74862 [Pichia membranifaciens NRRL Y-2026]

Sequence ID: **ODQ44257.1** Length: 2314 Number of Matches: 1
Range 1: 2075 to 2080

Score	Expect	Method	Identities	Positives	Gaps	Frame
22.7 bits(46)	2414()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  1     AFVFPK  6
             AFVFPK
Sbjct  2075  AFVFPK  2080
```

hypothetical protein AN3443.2 [Aspergillus nidulans FGSC A4]

Sequence ID: **EAA62983.1** Length: 2206 Number of Matches: 1
Range 1: 144 to 149

Score	Expect	Method	Identities	Positives	Gaps	Frame
22.7 bits(46)	2414()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  1    AFVFPK  6
            AFVFPK
Sbjct  144  AFVFPK  149
```

AMP deaminase, putative [Trypanosoma brucei gambiense DAL972]

Sequence ID: **CBH14311.1** Length: 1690 Number of Matches: 1
Range 1: 1644 to 1649

Score	Expect	Method	Identities	Positives	Gaps	Frame
22.7 bits(46)	2416()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  1     AFVFPK  6
             AFVFPK
Sbjct  1644  AFVFPK  1649
```

adenosine monophosphate deaminase, putative [Trypanosoma brucei brucei TREU927]

Sequence ID: **EAN76744.1** Length: 1690 Number of Matches: 1

See 1 more title(s)

Range 1: 1644 to 1649

Score	Expect	Method	Identities	Positives	Gaps	Frame
22.7 bits(46)	2416()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  1     AFVFPK  6
             AFVFPK
Sbjct  1644  AFVFPK  1649
```

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BLAST Results

Job title: NCBI BlastP_CRP_ESDTSYVSLK

RID S54UG73X015 (Expires on 08-04 11:06 am)

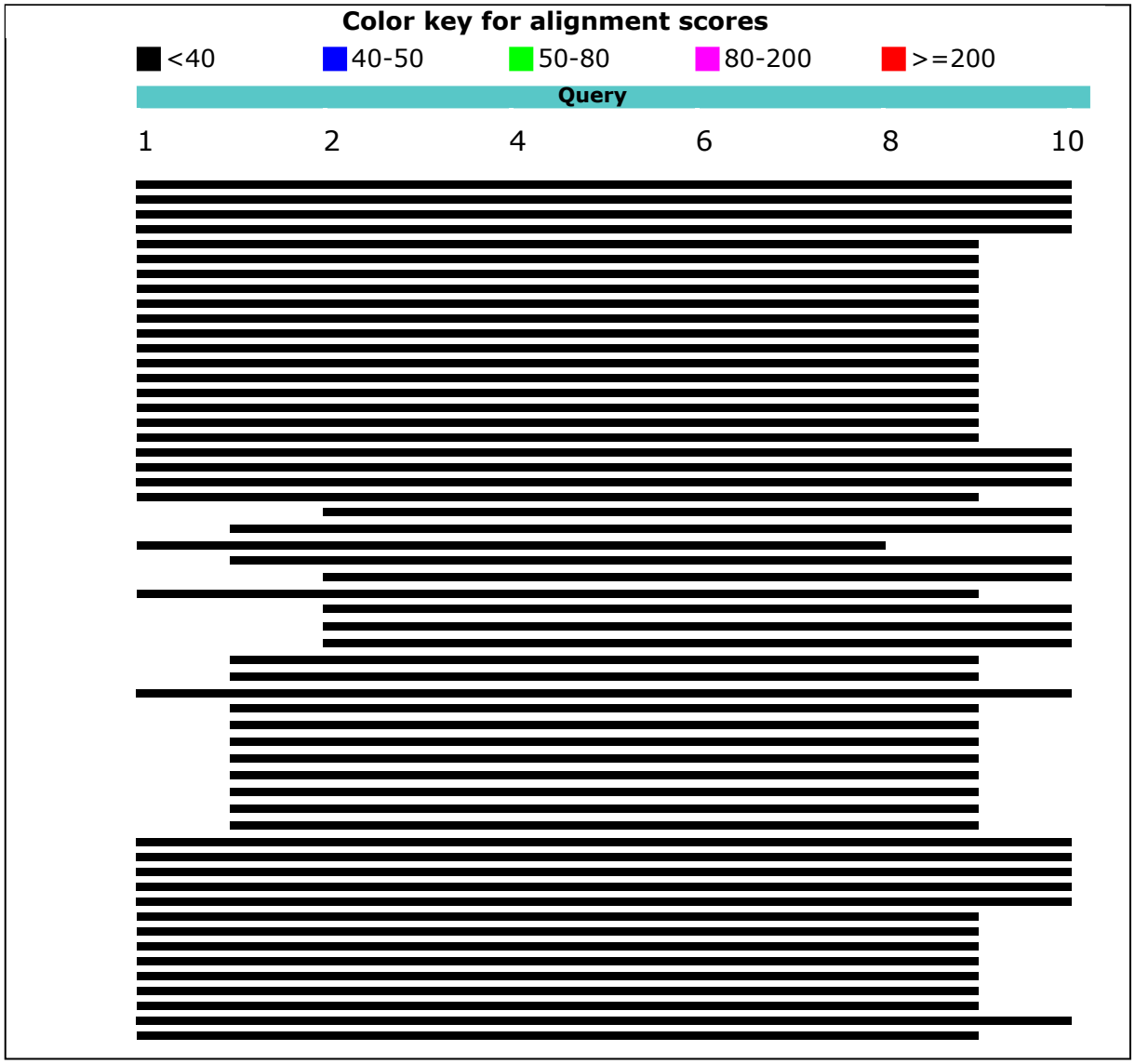
Query ID lcl|Query_256268
Description None
Molecule type amino acid
Query Length 10

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
C-reactive protein isoform 1 precursor [Homo sapiens]	33.7	33.7	100%	0.70	100%	NP_000558.2
C-reactive protein [Homo sapiens]	33.7	33.7	100%	0.70	100%	CAA39671.1
Chain A, Human C-Reactive Protein	33.7	33.7	100%	0.71	100%	1GNH_A
C-reactive protein isoform 2 precursor [Homo sapiens]	33.7	33.7	100%	0.73	100%	NP_001315987.1
C-reactive protein [Mus musculus]	30.8	30.8	90%	8.0	100%	CAA31928.1
precursor polypeptide (AA -19 to 206) [Mus musculus]	30.8	30.8	90%	8.0	100%	CAA35531.1
CRP [Niviventer cremoriventer]	30.8	30.8	90%	8.0	100%	AFA37883.1
CRP [Niviventer cremoriventer]	30.8	30.8	90%	8.0	100%	AFA37882.1
CRP [Niviventer cremoriventer]	30.8	30.8	90%	8.0	100%	AFA37880.1
CRP [Niviventer cremoriventer]	30.8	30.8	90%	8.0	100%	AFA37879.1
CRP [Mus caroli]	30.8	30.8	90%	8.0	100%	AFA37875.1
CRP [Mus caroli]	30.8	30.8	90%	8.0	100%	AFA37871.1
CRP [Mus caroli]	30.8	30.8	90%	8.0	100%	AFA37870.1
CRP [Apodemus agrarius]	30.8	30.8	90%	8.0	100%	AFA37837.1
CRP [Apodemus agrarius]	30.8	30.8	90%	8.0	100%	AFA37836.1
CRP [Apodemus agrarius]	30.8	30.8	90%	8.0	100%	AFA37831.1
CRP [Mus pahari]	30.8	30.8	90%	8.0	100%	AFA37826.1
C-reactive protein precursor [Mus musculus]	30.8	30.8	90%	8.0	100%	NP_031794.3
C-reactive protein [Fukomys damarensis]	29.9	29.9	100%	16	90%	KFO18163.1
C-reactive protein precursor [Camelus ferus]	29.9	29.9	100%	16	90%	EPY85699.1
hypothetical protein AUJ12_02400 [Alphaproteobacteria bacterium CG1_02_46_17]	28.6	28.6	100%	46	80%	OIN87330.1
hypothetical protein ASPGLDRAFT_163193 [Aspergillus glaucus CBS 516.65]	28.2	28.2	90%	65	89%	OJJ88642.1
putative reverse transcriptase domain-containing protein [Helianthus annuus]	27.8	27.8	80%	91	100%	OTG18875.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Heat-stable enterotoxin receptor [Columba livia]	27.8	27.8	90%	91	89%	EMC84809.1
Two-component sensor histidine kinase, contains HisKA and HATPase domains [Ulvibacter litoralis]	27.8	27.8	80%	91	100%	SDE50080.1
Heat-stable enterotoxin receptor, partial [Antrostomus carolinensis]	27.8	27.8	90%	91	89%	KFZ61734.1
dNA replication and repair protein RadC [Clostridium sp. CAG:58]	27.8	27.8	80%	92	100%	CDC50067.1
CRP [Apodemus draco]	27.8	27.8	90%	92	89%	AFA37827.1
putative aspartic peptidase domain-containing protein [Helianthus annuus]	27.8	27.8	80%	92	100%	OTG05771.1
hypothetical protein [Natronococcus jeotgali]	27.8	27.8	80%	94	100%	WP_008423224.1
hypothetical protein [Natronococcus jeotgali]	27.8	27.8	80%	94	100%	WP_008423505.1
peptidase M16 [Alteromonas australica]	27.4	27.4	80%	129	100%	WP_044446667.1
peptidase M16 [Alteromonas australica]	27.4	27.4	80%	129	100%	WP_044056557.1
RecName: Full=C-reactive protein; Flags: Precursor	27.4	27.4	100%	131	80%	P49254.1
CRP [Apodemus agrarius]	27.4	27.4	80%	131	100%	AFA37848.1
CRP [Apodemus agrarius]	27.4	27.4	80%	131	100%	AFA37847.1
CRP [Apodemus agrarius]	27.4	27.4	80%	131	100%	AFA37846.1
CRP [Apodemus agrarius]	27.4	27.4	80%	131	100%	AFA37845.1
CRP [Apodemus agrarius]	27.4	27.4	80%	131	100%	AFA37840.1
CRP [Apodemus agrarius]	27.4	27.4	80%	131	100%	AFA37838.1
CRP [Apodemus agrarius]	27.4	27.4	80%	131	100%	AFA37835.1
CRP [Apodemus agrarius]	27.4	27.4	80%	131	100%	AFA37832.1
C-reactive protein [Heterocephalus glaber]	27.4	27.4	100%	131	80%	EHB13682.1
C-reactive protein precursor [Macaca fascicularis]	27.4	27.4	100%	131	80%	NP_001306322.1
hypothetical protein EGK_01483 [Macaca mulatta]	27.4	27.4	100%	131	80%	EHH15399.1
hypothetical protein UY34_C0018G0010 [Parcubacteria group bacterium GW2011_GWA2_48_9]	26.9	26.9	100%	183	90%	KKW01096.1
hypothetical protein UY52_C0013G0024 [Parcubacteria group bacterium GW2011_GWC2_49_9]	26.9	26.9	100%	183	90%	KKW15868.1
C-reactive protein [Cricetulus griseus]	26.9	26.9	90%	185	89%	ERE72890.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
C-reactive protein precursor [Oryctolagus cuniculus]	26.9	26.9	90%	185	89%	NP_001075734.1
RecName: Full=C-reactive protein; Flags: Precursor	26.9	26.9	90%	185	89%	P02742.1
C-reactive protein [Oryctolagus cuniculus]	26.9	26.9	90%	185	89%	AAA75404.1
C-reactive protein [Cricetulus griseus]	26.9	26.9	90%	185	89%	EGV93413.1
hypothetical protein CLF_106201 [Clonorchis sinensis]	26.5	26.5	90%	259	89%	GAA51463.1
hypothetical protein IQ06DRAFT_258672 [Stagonospora sp. SRC1lsM3a]	26.5	26.5	90%	260	90%	OAK95510.1
thiol-activated cytolysin [Porphyromonadaceae bacterium KH3CP3RA]	26.5	26.5	100%	261	80%	SFL64226.1
phosphoribosyl-ATP diphosphatase [Sphingopyxis fribergensis]	26.5	26.5	90%	267	90%	WP_039577483.1
hypothetical protein SAMN05444375_11058 [Prevotella bryantii B14]	26.1	26.1	100%	370	80%	SEQ53831.1
hypothetical protein SAMN05216455_107207 [Prevotella bryantii]	26.1	26.1	100%	370	80%	SEA47310.1
hypothetical protein [Prevotella bryantii]	26.1	26.1	100%	370	80%	WP_050787956.1
hypothetical protein [Prevotella bryantii]	26.1	26.1	100%	370	80%	WP_083351018.1
hypothetical protein [Prevotella bryantii]	26.1	26.1	100%	370	80%	WP_081657164.1
hypothetical protein PBR_2778 [Prevotella bryantii B14]	26.1	26.1	100%	370	80%	EFI71307.1
hypothetical protein [Vibrio shilonii]	26.1	26.1	90%	370	78%	WP_088878529.1
CRISPR-associated protein Csy2 [Vibrio hangzhouensis]	26.1	26.1	90%	370	78%	SEF41368.1
hypothetical protein [Vibrio cidicii]	26.1	26.1	90%	370	78%	WP_061900693.1
hypothetical protein [Vibrio cholerae]	26.1	26.1	90%	370	78%	WP_001194012.1
Uncharacterised protein [uncultured Ruminococcus sp.]	26.1	26.1	90%	373	78%	SCH39969.1
hypothetical protein [Aquimarina spongiae]	26.1	26.1	90%	374	89%	WP_073319027.1
hypothetical protein DFA_11080 [Dictyostelium fasciculatum]	25.7	25.7	90%	524	78%	EGG13319.1
endoplasmic reticulum protein [Coprinopsis cinerea okayama7#130]	25.7	25.7	90%	524	78%	EFI28706.1
O-Glycosyl hydrolase [Streptomyces guanduensis]	25.7	25.7	100%	524	80%	SDN44809.1
galactosylceramidase [Streptomyces yeochonensis]	25.7	25.7	100%	524	80%	WP_051951856.1
galactosylceramidase [Streptacidiphilus carbonis]	25.7	25.7	100%	525	80%	WP_084719015.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
galactosylceramidase [Streptacidiphilus jeojiense]	25.7	25.7	100%	525	80%	WP_037597471.1
hypothetical protein AUK30_03325 [Nitrospirae bacterium CG2_30_70_394]	25.7	25.7	90%	525	78%	OIP66036.1
Glycosyl hydrolase family 59 [Streptomyces sp. DvalAA-14]	25.7	25.7	100%	525	80%	SCE41641.1
MFS transporter [Streptomyces aurantiacus]	25.7	25.7	90%	525	78%	WP_079103705.1
DUF3987 domain-containing protein [Stenotrophomonas maltophilia]	25.7	25.7	90%	526	89%	WP_046429186.1
hypothetical protein A2W95_03100 [Bacteroidetes bacterium GWA2_40_14]	25.7	25.7	90%	526	78%	OFX45959.1
hypothetical protein B6I25_03660 [Planctomycetales bacterium 4572_13]	25.7	25.7	100%	526	80%	OQY06572.1
NAD-reducing hydrogenase HoxS subunit beta [Phycisphaerae bacterium ST-NAGAB-D1]	25.7	25.7	100%	526	80%	AQT68294.1
cytochrome P450 [Nocardia brevicatena]	25.7	25.7	90%	527	78%	WP_040841650.1
mucosal pentraxin-like protein [Camelus ferus]	25.7	25.7	90%	528	78%	EPY85710.1
MULTISPECIES: LysR family transcriptional regulator [Rhizobium]	25.7	25.7	90%	528	78%	WP_062441805.1
hypothetical protein [Brochothrix thermosphacta]	25.7	25.7	90%	529	78%	WP_069129163.1
hypothetical protein SteCoe_34251 [Stentor coeruleus]	25.7	25.7	90%	529	78%	OMJ68332.1
hypothetical protein SteCoe_3749 [Stentor coeruleus]	25.7	25.7	90%	530	78%	OMJ93288.1
DUF2283 domain-containing protein [Streptomyces iakyrus]	25.7	25.7	90%	545	78%	WP_033311145.1
DUF2283 domain-containing protein [Streptomyces fradiae]	25.7	25.7	90%	545	78%	WP_043460142.1
DUF2283 domain-containing protein [Streptomyces sp. CNS615]	25.7	25.7	90%	545	78%	WP_017946688.1
MULTISPECIES: DUF2283 domain-containing protein [Streptomyces]	25.7	25.7	90%	545	78%	WP_031132526.1
DUF2283 domain-containing protein [Streptomyces sp. NRRL S-475]	25.7	25.7	90%	545	78%	WP_030842770.1
hypothetical protein IV43_GL000353 [Lactobacillus acidipiscis]	25.7	25.7	90%	552	89%	KRN79966.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Enterobacter cloacae complex sp. GN03164]	25.2	25.2	80%	743	88%	WP_047345336.1
filamentous hemagglutinin protein [Lyngbya aestuarii]	25.2	25.2	80%	743	88%	WP_023069171.1
hypothetical protein [Limnoraphis robusta]	25.2	25.2	80%	743	88%	WP_053221454.1
hypothetical protein [Lyngbya sp. PCC 8106]	25.2	25.2	80%	743	88%	WP_009786694.1
hypothetical protein WN50_10305 [Limnoraphis robusta CS-951]	25.2	25.2	80%	743	88%	KKD38175.1
hypothetical protein BHV77_03750 [Bacteroides sp. 43_108]	25.2	25.2	80%	744	88%	OKZ24880.1
hypothetical protein AYL99_09215 [Fonsecaea erecta]	25.2	25.2	70%	744	100%	OAP57102.1

Alignments

C-reactive protein isoform 1 precursor [Homo sapiens]
Sequence ID: **NP_000558.2** Length: 224 Number of Matches: 1

See 13 more title(s)
Range 1: 32 to 41

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.7 bits(72)	0.70()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   ESDTSYVSLK  10
           ESDTSYVSLK
Sbjct  32  ESDTSYVSLK  41
```

C-reactive protein [Homo sapiens]
Sequence ID: **CAA39671.1** Length: 224 Number of Matches: 1
Range 1: 32 to 41

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.7 bits(72)	0.70()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   ESDTSYVSLK  10
           ESDTSYVSLK
Sbjct  32  ESDTSYVSLK  41
```

Chain A, Human C-Reactive Protein

Sequence ID: **1GNH_A** Length: 206 Number of Matches: 1

See 84 more title(s)

Range 1: 14 to 23

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.7 bits(72)	0.71()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   ESDTSYVSLK  10
           ESDTSYVSLK
Sbjct  14  ESDTSYVSLK  23
```

C-reactive protein isoform 2 precursor [Homo sapiens]

Sequence ID: **NP_001315987.1** Length: 91 Number of Matches: 1

See 4 more title(s)

Range 1: 32 to 41

Score	Expect	Method	Identities	Positives	Gaps	Frame
33.7 bits(72)	0.73()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1   ESDTSYVSLK  10
           ESDTSYVSLK
Sbjct  32  ESDTSYVSLK  41
```

C-reactive protein [Mus musculus]

Sequence ID: **CAA31928.1** Length: 225 Number of Matches: 1

See 1 more title(s)

Range 1: 33 to 41

Score	Expect	Method	Identities	Positives	Gaps	Frame
30.8 bits(65)	8.0()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1   ESDTSYVSL  9
           ESDTSYVSL
Sbjct  33  ESDTSYVSL  41
```

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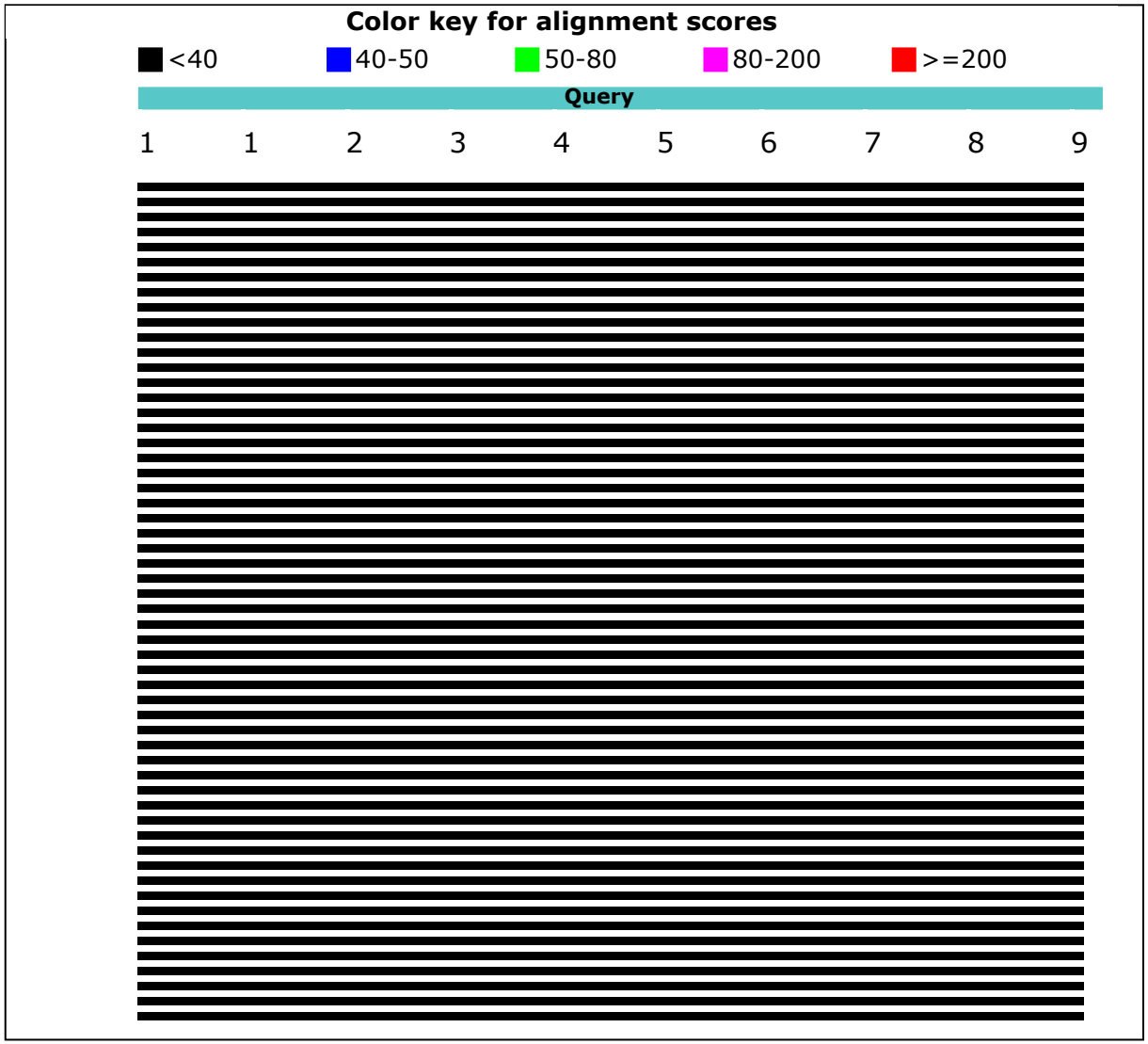
Job title: NCBI BlastP_F10_MLEVPYVDR

RID	S54FEYE7014 (Expires on 08-04 11:01 am)
Query ID	lcl|Query_153737
Description	None
Molecule type	amino acid
Query Length	9
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8
9

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Cullin-4A [Tupaia chinensis]	34.6	34.6	100%	0.32	100%	ELW47488.1
PREDICTED: coagulation factor X [Octodon degus]	34.6	34.6	100%	0.32	100%	XP_004631267.2
coagulation factor X-like [Meriones unguiculatus]	34.6	34.6	100%	0.32	100%	XP_021510988.1
PREDICTED: LOW QUALITY PROTEIN: coagulation factor X [Tupaia chinensis]	34.6	34.6	100%	0.32	100%	XP_006159749.1
F7 [Cervus elaphus hippelaphus]	34.6	34.6	100%	0.32	100%	OWK00910.1
PREDICTED: LOW QUALITY PROTEIN: coagulation factor X isoform X1 [Ovis aries]	34.6	34.6	100%	0.32	100%	XP_014953511.1
hypothetical protein A6R68_09737 [Neotoma lepida]	34.6	34.6	100%	0.32	100%	OBS59136.1
Coagulation factor X [Myotis brandtii]	34.6	34.6	100%	0.32	100%	EPQ19063.1
PREDICTED: coagulation factor X [Bubalus bubalis]	34.6	34.6	100%	0.32	100%	XP_006076685.1
PREDICTED: coagulation factor X [Manis javanica]	34.6	34.6	100%	0.32	100%	XP_017518363.1
PREDICTED: LOW QUALITY PROTEIN: coagulation factor X [Tursiops truncatus]	34.6	34.6	100%	0.32	100%	XP_019776391.1
PREDICTED: LOW QUALITY PROTEIN: coagulation factor X-like [Myotis lucifugus]	34.6	34.6	100%	0.32	100%	XP_014305644.1
PREDICTED: coagulation factor X [Elephantulus edwardii]	34.6	34.6	100%	0.32	100%	XP_006884018.1
PREDICTED: coagulation factor X [Lipotes vexillifer]	34.6	34.6	100%	0.32	100%	XP_007466434.1
PREDICTED: coagulation factor X [Equus asinus]	34.6	34.6	100%	0.32	100%	XP_014710400.1
PREDICTED: coagulation factor X-like [Myotis brandtii]	34.6	34.6	100%	0.32	100%	XP_005884491.1
PREDICTED: coagulation factor X-like isoform X2 [Myotis brandtii]	34.6	34.6	100%	0.32	100%	XP_014387436.1
PREDICTED: coagulation factor X-like isoform X1 [Myotis brandtii]	34.6	34.6	100%	0.32	100%	XP_005884493.1
PREDICTED: coagulation factor X [Dipodomys ordii]	34.6	34.6	100%	0.32	100%	XP_012878171.1
PREDICTED: coagulation factor X [Jaculus jaculus]	34.6	34.6	100%	0.32	100%	XP_004663431.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
coagulation factor X isoform X1 [Mus pahari]	34.6	34.6	100%	0.32	100%	XP_021075075.1
coagulation factor X [Odocoileus virginianus texanus]	34.6	34.6	100%	0.32	100%	XP_020752038.1
PREDICTED: coagulation factor X [Camelus ferus]	34.6	34.6	100%	0.32	100%	XP_014407846.1
coagulation factor X isoform 1 [Mus musculus]	34.6	34.6	100%	0.32	100%	NP_001229297.1
coagulation factor X precursor [Bos taurus]	34.6	34.6	100%	0.32	100%	NP_001073682.1
PREDICTED: coagulation factor X [Bos indicus]	34.6	34.6	100%	0.32	100%	XP_019827336.1
PREDICTED: coagulation factor X [Capra hircus]	34.6	34.6	100%	0.32	100%	XP_017900478.1
unnamed protein product [Mus musculus]	34.6	34.6	100%	0.32	100%	BAE41684.1
PREDICTED: coagulation factor X [Bison bison bison]	34.6	34.6	100%	0.32	100%	XP_010829751.1
coagulation factor X isoform X2 [Mus pahari]	34.6	34.6	100%	0.32	100%	XP_021075076.1
PREDICTED: coagulation factor X isoform X1 [Oryctolagus cuniculus]	34.6	34.6	100%	0.32	100%	XP_008251911.2
coagulation factor X precursor [Oryctolagus cuniculus]	34.6	34.6	100%	0.32	100%	NP_001075485.1
F10 [synthetic construct]	34.6	34.6	100%	0.32	100%	AKI71453.1
F10 [synthetic construct]	34.6	34.6	100%	0.32	100%	AKI71452.1
F10 [synthetic construct]	34.6	34.6	100%	0.32	100%	AKI71451.1
PREDICTED: coagulation factor X [Cercocebus atys]	34.6	34.6	100%	0.32	100%	XP_011913505.1
PREDICTED: coagulation factor X [Macaca nemestrina]	34.6	34.6	100%	0.32	100%	XP_011745816.1
PREDICTED: coagulation factor X [Mandrillus leucophaeus]	34.6	34.6	100%	0.32	100%	XP_011834825.1
PREDICTED: coagulation factor X [Colobus angolensis palliatus]	34.6	34.6	100%	0.32	100%	XP_011789309.1
PREDICTED: coagulation factor X [Rhinopithecus roxellana]	34.6	34.6	100%	0.32	100%	XP_010358374.1
PREDICTED: coagulation factor X [Chlorocebus sabaeus]	34.6	34.6	100%	0.32	100%	XP_007959163.1
PREDICTED: coagulation factor X [Macaca fascicularis]	34.6	34.6	100%	0.32	100%	XP_005586353.1
PREDICTED: coagulation factor X isoform X1 [Gorilla gorilla gorilla]	34.6	34.6	100%	0.32	100%	XP_004054811.1
coagulation factor X isoform 1 preproprotein [Homo sapiens]	34.6	34.6	100%	0.32	100%	NP_000495.1
Coagulation factor X [Macaca fascicularis]	34.6	34.6	100%	0.32	100%	EHH58718.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Coagulation factor X [Macaca mulatta]	34.6	34.6	100%	0.32	100%	EHH29132.1
PREDICTED: coagulation factor X isoform X1 [Nomascus leucogenys]	34.6	34.6	100%	0.32	100%	XP_003279806.1
PREDICTED: coagulation factor X [Pongo abelii]	34.6	34.6	100%	0.32	100%	XP_002824495.1
coagulation factor X precursor [Papio anubis]	34.6	34.6	100%	0.32	100%	NP_001162447.1
coagulation factor X precursor [Macaca mulatta]	34.6	34.6	100%	0.32	100%	NP_001098054.1
PREDICTED: coagulation factor X [Miniopterus natalensis]	34.6	34.6	100%	0.32	100%	XP_016068357.1
unnamed protein product [Bos taurus]	34.6	34.6	100%	0.32	100%	CAA25286.1
PREDICTED: coagulation factor X [Otolemur garnettii]	34.6	34.6	100%	0.32	100%	XP_003800050.1
PREDICTED: coagulation factor X [Rousettus aegyptiacus]	34.6	34.6	100%	0.32	100%	XP_016007406.1
PREDICTED: coagulation factor X [Pteropus alecto]	34.6	34.6	100%	0.32	100%	XP_006909460.1
PREDICTED: coagulation factor X [Eptesicus fuscus]	34.6	34.6	100%	0.32	100%	XP_008142141.1
PREDICTED: coagulation factor X isoform X2 [Ovis aries musimon]	34.6	34.6	100%	0.32	100%	XP_011974801.1
PREDICTED: coagulation factor X [Peromyscus maniculatus bairdii]	34.6	34.6	100%	0.32	100%	XP_006981368.1
PREDICTED: coagulation factor X [Equus caballus]	34.6	34.6	100%	0.32	100%	XP_005601408.1
PREDICTED: coagulation factor X [Marmota marmota marmota]	34.6	34.6	100%	0.32	100%	XP_015339545.1
F10 protein [Bos taurus]	34.6	34.6	100%	0.32	100%	AAI04608.1
PREDICTED: coagulation factor X [Hipposideros armiger]	34.6	34.6	100%	0.32	100%	XP_019500313.1
PREDICTED: coagulation factor X [Chinchilla lanigera]	34.6	34.6	100%	0.32	100%	XP_005374029.1
F10 protein [Mus musculus]	34.6	34.6	100%	0.32	100%	AAH03877.1
coagulation factor X [Mus musculus]	34.6	34.6	100%	0.32	100%	CAA10933.1
coagulation factor X isoform 2 preproprotein [Mus musculus]	34.6	34.6	100%	0.32	100%	NP_031998.3
PREDICTED: coagulation factor VII-like isoform X1 [Balaenoptera acutorostrata scammoni]	34.6	34.6	100%	0.32	100%	XP_007196820.1
PREDICTED: coagulation factor X [Microtus ochrogaster]	34.6	34.6	100%	0.32	100%	XP_005366330.1
PREDICTED: coagulation factor X [Orcinus orca]	34.6	34.6	100%	0.32	100%	XP_004273717.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: coagulation factor X-like [Propithecus coquereli]	34.6	34.6	100%	0.32	100%	XP_012518281.1
PREDICTED: coagulation factor X [Loxodonta africana]	34.6	34.6	100%	0.32	100%	XP_010592341.1
coagulation factor X precursor [Sus scrofa]	34.6	34.6	100%	0.32	100%	NP_001038057.1
PREDICTED: coagulation factor X [Chrysochloris asiatica]	34.6	34.6	100%	0.32	100%	XP_006851611.1
PREDICTED: coagulation factor X [Orycteropus afer afer]	34.6	34.6	100%	0.32	100%	XP_007940601.1
PREDICTED: coagulation factor X [Rhinolophus sinicus]	34.6	34.6	100%	0.32	100%	XP_019602161.1
PREDICTED: coagulation factor X [Panthera pardus]	34.6	34.6	100%	0.32	100%	XP_019299406.1
PREDICTED: coagulation factor X [Echinops telfairi]	34.6	34.6	100%	0.32	100%	XP_012860542.1
coagulation factor X [Microcebus murinus]	34.6	34.6	100%	0.32	100%	XP_012621013.1
PREDICTED: coagulation factor X [Panthera tigris altaica]	34.6	34.6	100%	0.32	100%	XP_007075386.1
PREDICTED: coagulation factor X [Felis catus]	34.6	34.6	100%	0.32	100%	XP_003980607.1
factor X prepeptide [Homo sapiens]	34.6	34.6	100%	0.32	100%	AAA52490.1
PREDICTED: coagulation factor X [Pantholops hodgsonii]	34.6	34.6	100%	0.32	100%	XP_005969107.1
PREDICTED: coagulation factor X [Camelus dromedarius]	34.6	34.6	100%	0.32	100%	XP_010981117.1
PREDICTED: LOW QUALITY PROTEIN: coagulation factor X [Vicugna pacos]	34.6	34.6	100%	0.32	100%	XP_006218256.1
coagulation factor X precursor [Camelus ferus]	34.6	34.6	100%	0.32	100%	EPY86933.1
coagulation factor X precursor [Homo sapiens]	34.6	34.6	100%	0.32	100%	AAA51984.1
coagulation factor X [Mus caroli]	34.6	34.6	100%	0.32	100%	XP_021025810.1
PREDICTED: coagulation factor X [Equus przewalskii]	34.6	34.6	100%	0.32	100%	XP_008516383.1
PREDICTED: LOW QUALITY PROTEIN: coagulation factor X [Bos mutus]	34.6	34.6	100%	0.32	100%	XP_014335770.1
coagulation factor X isoform 2 precursor [Homo sapiens]	34.6	34.6	100%	0.32	100%	NP_001299603.1
PREDICTED: coagulation factor X isoform X2 [Nomascus leucogenys]	34.6	34.6	100%	0.32	100%	XP_012362427.1
PREDICTED: coagulation factor VII-like isoform X2 [Balaenoptera acutorostrata scammoni]	34.6	34.6	100%	0.32	100%	XP_007196821.1
PREDICTED: coagulation factor VII [Physeter catodon]	34.6	34.6	100%	0.32	100%	XP_007117452.1
PREDICTED: coagulation factor X [Camelus bactrianus]	34.6	34.6	100%	0.33	100%	XP_010950658.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: coagulation factor X-like [Acinonyx jubatus]	34.6	34.6	100%	0.33	100%	XP_014940406.1
Coagulation factor X [Myotis brandtii]	34.6	34.6	100%	0.33	100%	EPQ19062.1
PREDICTED: coagulation factor X [Rhinopithecus bieti]	34.6	34.6	100%	0.33	100%	XP_017717257.1
factor X precursor peptide [Homo sapiens]	34.6	34.6	100%	0.33	100%	AAA52486.1
Coagulation factor X [Myotis davidii]	34.6	34.6	100%	0.33	100%	ELK25997.1
PREDICTED: coagulation factor X [Myotis davidii]	34.6	34.6	100%	0.33	100%	XP_015423048.1

Alignments

Cullin-4A [Tupaia chinensis]

Sequence ID: **ELW47488.1** Length: 1731 Number of Matches: 1
Range 1: 483 to 491

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.6 bits(74)	0.32()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    MLEVPYVDR  9
           MLEVPYVDR
Sbjct  483  MLEVPYVDR  491
```

PREDICTED: coagulation factor X [Octodon degus]

Sequence ID: **XP_004631267.2** Length: 957 Number of Matches: 1
Range 1: 852 to 860

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.6 bits(74)	0.32()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    MLEVPYVDR  9
           MLEVPYVDR
Sbjct  852  MLEVPYVDR  860
```

coagulation factor X-like [Meriones unguiculatus]

Sequence ID: **XP_021510988.1** Length: 954 Number of Matches: 1
Range 1: 849 to 857

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.6 bits(74)	0.32()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    MLEVPYVDR  9
           MLEVPYVDR
Sbjct  849  MLEVPYVDR  857
```

PREDICTED: LOW QUALITY PROTEIN: coagulation factor X [Tupaia chinensis]

Sequence ID: **XP_006159749.1** Length: 825 Number of Matches: 1
Range 1: 377 to 385

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.6 bits(74)	0.32()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    MLEVPYVDR  9
           MLEVPYVDR
Sbjct  377  MLEVPYVDR  385
```

F7 [Cervus elaphus hippelaphus]

Sequence ID: **OWK00910.1** Length: 813 Number of Matches: 1
Range 1: 695 to 703

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.6 bits(74)	0.32()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    MLEVPYVDR  9
           MLEVPYVDR
Sbjct  695  MLEVPYVDR  703
```

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Job title: NCBI BlastP_F10_SHAPEVITSSPLK

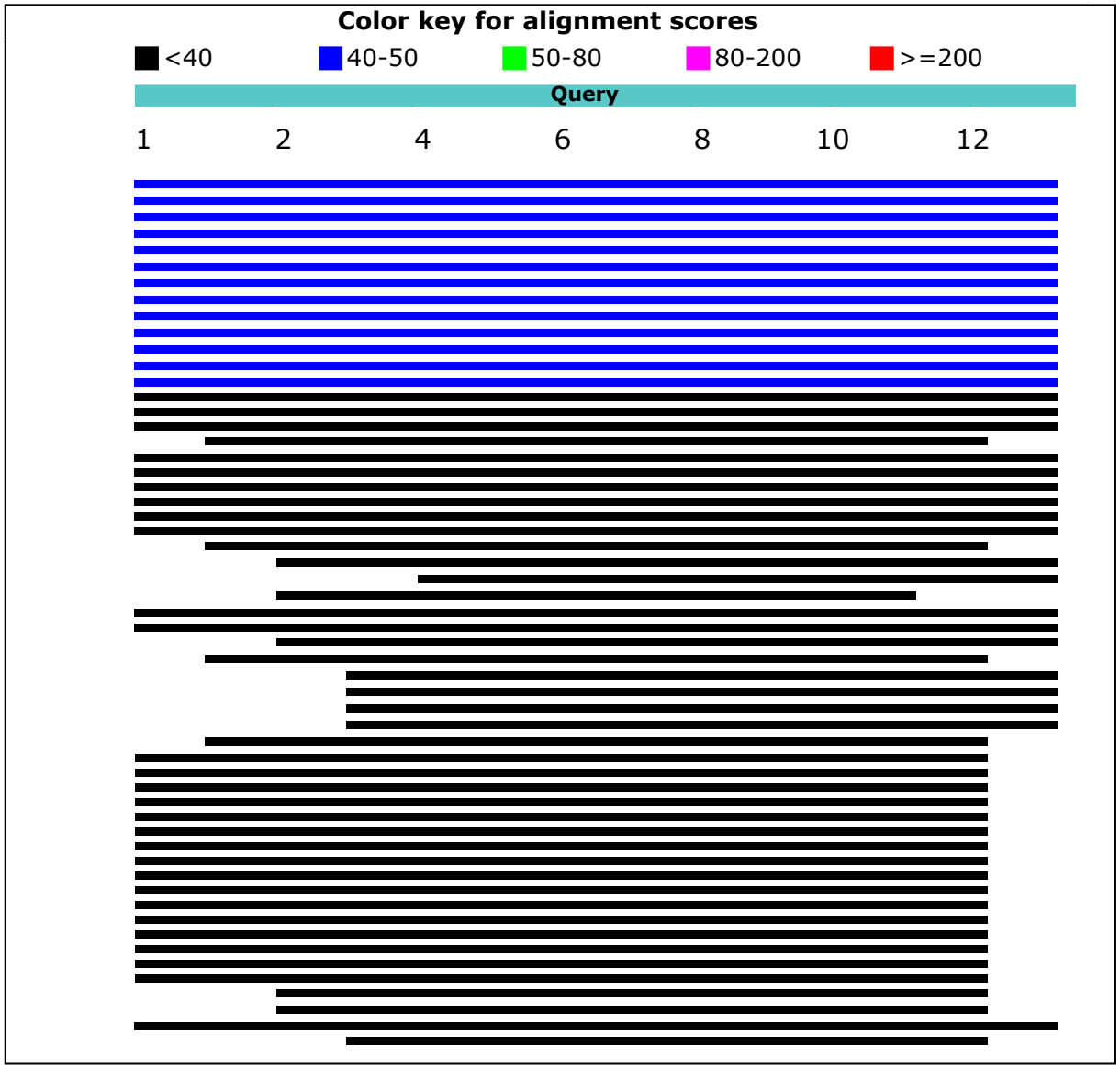
RID S54GT6V9015 (Expires on 08-04 11:01 am)

Query ID	lcl|Query_182306	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	13	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
F10 [synthetic construct]	42.6	42.6	100%	0.001	100%	AKI71454.1
F10 [synthetic construct]	42.6	42.6	100%	0.001	100%	AKI71453.1
F10 [synthetic construct]	42.6	42.6	100%	0.001	100%	AKI71452.1
F10 [synthetic construct]	42.6	42.6	100%	0.001	100%	AKI71451.1
coagulation factor X isoform 1 preproprotein [Homo sapiens]	42.6	42.6	100%	0.001	100%	NP_000495.1
PREDICTED: coagulation factor X [Pongo abelii]	42.6	42.6	100%	0.001	100%	XP_002824495.1
factor X prepeptide [Homo sapiens]	42.6	42.6	100%	0.001	100%	AAA52490.1
coagulation factor X precursor [Homo sapiens]	42.6	42.6	100%	0.001	100%	AAA51984.1
coagulation factor X isoform 2 precursor [Homo sapiens]	42.6	42.6	100%	0.001	100%	NP_001299603.1
factor X precursor peptide [Homo sapiens]	42.6	42.6	100%	0.001	100%	AAA52486.1
Chain A, Crystal Structure Of Human Coagulation Factor Xa Complexed With Rpr128515	42.6	42.6	100%	0.001	100%	1EZQ_A
Chain A, Coagulation Factor Xa Inhibitor Complex	42.6	42.6	100%	0.001	100%	1FAX_A
PREDICTED: coagulation factor X isoform X1 [Gorilla gorilla gorilla]	40.1	40.1	100%	0.008	92%	XP_004054811.1
PREDICTED: coagulation factor X isoform X1 [Nomascus leucogenys]	39.2	39.2	100%	0.016	92%	XP_003279806.1
PREDICTED: coagulation factor X isoform X2 [Nomascus leucogenys]	39.2	39.2	100%	0.016	92%	XP_012362427.1
Chain D, Structural Basis For Selectivity Of A Small Molecule, S1- Binding, Sub-Micromolar Inhibitor Of Urokinase Type Plasminogen Activator	38.4	38.4	100%	0.032	93%	1C5M_D
PREDICTED: uncharacterized protein LOC101901180 [Musca domestica]	32.9	32.9	84%	2.9	92%	XP_005179516.1
PREDICTED: coagulation factor X [Macaca nemestrina]	32.5	32.5	100%	4.1	85%	XP_011745816.1
PREDICTED: coagulation factor X [Cercocebus atys]	31.6	31.6	100%	8.3	85%	XP_011913505.1
PREDICTED: coagulation factor X [Colobus angolensis palliatus]	31.6	31.6	100%	8.3	85%	XP_011789309.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: coagulation factor X [Rhinopithecus roxellana]	31.6	31.6	100%	8.3	85%	XP_010358374.1
coagulation factor X precursor [Papio anubis]	31.6	31.6	100%	8.3	85%	NP_001162447.1
PREDICTED: coagulation factor X [Rhinopithecus bieti]	31.6	31.6	100%	8.3	85%	XP_017717257.1
Solute carrier family 2, facilitated glucose transporter member 3 [Smittium culicis]	31.2	31.2	84%	12	82%	OMJ26827.1
hypothetical protein ASPCAL02636 [Aspergillus calidoustus]	30.3	30.3	84%	23	82%	CEN60195.1
GDSL esterase/lipase [Zostera marina]	30.3	30.3	69%	24	100%	KMZ61096.1
Neither inactivation nor afterpotential protein C [Daphnia magna]	30.3	30.3	69%	24	100%	KZS18489.1
Acriflavin resistance periplasmic protein [Granulibacter bethesdensis]	29.9	29.9	100%	33	61%	APH54827.1
efflux RND transporter periplasmic adaptor subunit [Granulibacter bethesdensis]	29.9	29.9	100%	33	61%	WP_081368910.1
membrane protein [Collimonas fungivorans]	29.9	29.9	84%	34	82%	WP_014004987.1
hypothetical protein [Plantibacter flavus]	29.1	29.1	84%	67	82%	WP_085511332.1
toprim [Streptococcus iniae]	29.1	29.1	76%	67	90%	WP_071127929.1
nodulin homeobox isoform X1 [Arabidopsis lyrata subsp. lyrata]	29.1	29.1	76%	67	90%	XP_020876356.1
nodulin homeobox isoform X2 [Arabidopsis lyrata subsp. lyrata]	29.1	29.1	76%	67	90%	XP_020876357.1
nodulin homeobox isoform X3 [Arabidopsis lyrata subsp. lyrata]	29.1	29.1	76%	67	90%	XP_020876358.1
predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	29.1	29.1	84%	67	82%	XP_002185538.1
glycosyl transferase [Pseudomonas extremaustralis]	29.1	29.1	92%	67	75%	WP_010562726.1
glycosyl transferase [Pseudomonas extremaustralis]	29.1	29.1	92%	67	75%	WP_078833840.1
glycosyl transferase [Pseudomonas azotoformans]	29.1	29.1	92%	67	75%	WP_078048630.1
Glycosyltransferase like family 2 [Pseudomonas sp. NFACC42-2]	29.1	29.1	92%	67	75%	SFS24209.1
glycosyltransferase family 2 protein [Pseudomonas sp. 06C 126]	29.1	29.1	92%	67	75%	WP_070994832.1
glycosyl transferase [Pseudomonas marginalis]	29.1	29.1	92%	67	75%	WP_074846910.1
Glycosyl transferase family 2 [Pseudomonas proteolytica]	29.1	29.1	92%	67	75%	SEE34597.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Glycosyltransferase like family 2 [Pseudomonas grimontii]	29.1	29.1	92%	67	75%	SDR18423.1
glycosyl transferase [Pseudomonas sp. S3E12]	29.1	29.1	92%	67	75%	WP_065941700.1
MULTISPECIES: glycosyl transferase [Pseudomonas]	29.1	29.1	92%	67	75%	WP_065925217.1
glycosyl transferase [Pseudomonas fluorescens]	29.1	29.1	92%	67	75%	WP_057436603.1
glycosyl transferase [Pseudomonas paralactis]	29.1	29.1	92%	67	75%	WP_057703442.1
glycosyl transferase [Pseudomonas sp. MIACH]	29.1	29.1	92%	67	75%	WP_053129521.1
glycosyltransferase family 2 protein [Pseudomonas fluorescens]	29.1	29.1	92%	67	75%	WP_029291615.1
MULTISPECIES: glycosyl transferase [Pseudomonas]	29.1	29.1	92%	67	75%	WP_027606748.1
TRAP transporter small permease [Microbacterium sp. CH12i]	29.1	29.1	92%	67	75%	WP_036280041.1
hypothetical protein [Geoalkalibacter ferrihydriticus]	29.1	29.1	76%	67	90%	WP_040096361.1
PREDICTED: death-associated protein kinase 2-like [Notothenia coriiceps]	29.1	29.1	76%	68	90%	XP_010781630.1
coagulation factor X preproprotein (predicted) [Plecturocebus moloch]	28.6	28.6	100%	95	77%	ACA57945.1
MULTISPECIES: amino acid permease [Methanobacterium]	28.6	28.6	69%	95	89%	WP_048081228.1
hypothetical protein A9507_13660 [Methanobacterium sp. A39]	28.6	28.6	69%	95	89%	OEC85368.1
hypothetical protein A8B78_07620 [Jannaschia sp. EhC01]	28.2	28.2	76%	134	80%	OAN84321.1
hypothetical protein [Jannaschia sp. EhC01]	28.2	28.2	76%	134	80%	WP_068353895.1
hypothetical protein Hypma_01252 [Hypsizygus marmoreus]	28.2	28.2	76%	134	80%	KYQ44943.1
flagellar hook-length control protein FliK [Pleomorphobacterium xiamenense]	28.2	28.2	76%	134	80%	WP_072747392.1
PREDICTED: lon protease homolog, mitochondrial-like [Amphimedon queenslandica]	28.2	28.2	69%	134	89%	XP_019856651.1
hook-length control protein FliK [Pleomorphobacterium xiamenense]	28.2	28.2	76%	134	80%	SET54541.1
MFS transporter [Ruegeria halocynthiae]	28.2	28.2	69%	134	89%	WP_074736635.1
MFS transporter [Ruegeria sp. ANG-R]	28.2	28.2	69%	134	89%	WP_052265283.1
kinase-like protein [Sistotremastrum suecicum HHB10207 ss-3]	28.2	28.2	69%	134	89%	KZT41879.1
kinase-like protein [Sistotremastrum niveocremeum HHB9708]	28.2	28.2	69%	134	89%	KZS87749.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
MexE family multidrug efflux RND transporter periplasmic adaptor subunit [Erwinia tasmaniensis]	28.2	28.2	92%	134	69%	WP_012442192.1
polyprenyl synthetase family protein [Gordonia kroppenstedtii]	28.2	28.2	61%	135	100%	WP_018178597.1
1-acyl-sn-glycerol-3-phosphate acyltransferase [Sandaracinus amylolyticus]	28.2	28.2	69%	135	89%	WP_053234146.1
1-acyl-sn-glycerol-3-phosphate acyltransferase [Sandaracinus amylolyticus]	28.2	28.2	69%	135	89%	AKF06894.1
Hcp1 family type VI secretion system effector [Vibrio quintilis]	28.2	28.2	92%	135	65%	WP_073579573.1
Putative phage holin [Collimonas sp. OK607]	28.2	28.2	84%	136	73%	SFB12161.1
related to VPS41-required for the vacuolar assembly [Phialocephala subalpina]	27.8	27.8	61%	190	100%	CZR64445.1
hypothetical protein CARUB_v10000178mg [Capsella rubella]	27.8	27.8	92%	190	75%	XP_006287030.1
hypothetical protein ACD_63C00257G0002 [uncultured bacterium]	27.8	27.8	84%	190	73%	EKD49135.1
TonB-dependent copper receptor [Phaseolibacter flectens]	27.8	27.8	84%	190	75%	WP_084560694.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Taeniopygia guttata]	27.8	27.8	69%	190	89%	XP_002190492.1
serine/threonine-protein kinase PINK1, mitochondrial [Columba livia]	27.8	27.8	69%	190	89%	XP_021150887.1
serine/threonine-protein kinase PINK1, mitochondrial [Patagioenas fasciata monilis]	27.8	27.8	69%	190	89%	OPJ86221.1
PREDICTED: LOW QUALITY PROTEIN: serine/threonine-protein kinase PINK1, mitochondrial [Manacus vitellinus]	27.8	27.8	69%	191	89%	XP_017943347.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial-like [Manacus vitellinus]	27.8	27.8	69%	191	89%	XP_017934809.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Lepidothrix coronata]	27.8	27.8	69%	191	89%	XP_017687504.1
hypothetical protein ASPVEDRAFT_89278 [Aspergillus versicolor CBS 583.65]	27.8	27.8	84%	191	73%	OJJ08046.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Sturnus vulgaris]	27.8	27.8	69%	191	89%	XP_014737238.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Zonotrichia albicollis]	27.8	27.8	69%	191	89%	XP_005495912.1
hypothetical protein ASPSYDRAFT_94439 [Aspergillus sydowii CBS 593.65]	27.8	27.8	84%	191	73%	OJJ53950.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ABC transporter ATP-binding protein [Actinoplanes sp. TFC3]	27.8	27.8	76%	191	63%	WP_067497197.1
PREDICTED: LOW QUALITY PROTEIN: serine/threonine-protein kinase PAK 3-like [Ficedula albicollis]	27.8	27.8	69%	191	89%	XP_016160944.1
PREDICTED: LOW QUALITY PROTEIN: serine/threonine-protein kinase PAK 3-like [Taeniopygia guttata]	27.8	27.8	69%	191	89%	XP_012431508.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Pygoscelis adeliae]	27.8	27.8	69%	191	89%	XP_009323580.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Pseudopodoces humilis]	27.8	27.8	69%	191	89%	XP_014112659.1
PREDICTED: serine/threonine-protein kinase PAK 3-like [Ficedula albicollis]	27.8	27.8	69%	191	89%	XP_005062300.2
PREDICTED: serine/threonine-protein kinase PAK 3-like [Pseudopodoces humilis]	27.8	27.8	69%	191	89%	XP_005534549.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Ficedula albicollis]	27.8	27.8	69%	191	89%	XP_016158863.1
serine/threonine-protein kinase PINK1 [Amazona aestiva]	27.8	27.8	69%	191	89%	KQK79378.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Opisthocomus hoazin]	27.8	27.8	69%	191	89%	XP_009940843.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Corvus brachyrhynchos]	27.8	27.8	69%	191	89%	XP_017590567.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Charadrius vociferus]	27.8	27.8	69%	191	89%	XP_009888286.1
PREDICTED: serine/threonine-protein kinase PINK1, mitochondrial [Egretta garzetta]	27.8	27.8	69%	191	89%	XP_009644823.1

Alignments

F10, partial [synthetic construct]

Sequence ID: **AKI71454.1** Length: 488 Number of Matches: 1
Range 1: 476 to 488

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.6 bits(93)	0.001()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    SHAPEVITSSPLK  13
            SHAPEVITSSPLK
Sbjct  476  SHAPEVITSSPLK  488
```

F10, partial [synthetic construct]

Sequence ID: **AKI71453.1** Length: 488 Number of Matches: 1
Range 1: 476 to 488

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.6 bits(93)	0.001()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    SHAPEVITSSPLK  13
            SHAPEVITSSPLK
Sbjct  476  SHAPEVITSSPLK  488
```

F10, partial [synthetic construct]

Sequence ID: **AKI71452.1** Length: 488 Number of Matches: 1
Range 1: 476 to 488

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.6 bits(93)	0.001()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    SHAPEVITSSPLK  13
            SHAPEVITSSPLK
Sbjct  476  SHAPEVITSSPLK  488
```

F10, partial [synthetic construct]

Sequence ID: **AKI71451.1** Length: 488 Number of Matches: 1
Range 1: 476 to 488

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.6 bits(93)	0.001()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    SHAPEVITSSPLK  13
            SHAPEVITSSPLK
Sbjct  476  SHAPEVITSSPLK  488
```

coagulation factor X isoform 1 preproprotein [Homo sapiens]
Sequence ID: **NP_000495.1** Length: 488 Number of Matches: 1

See 13 more title(s)
Range 1: 476 to 488

Score	Expect	Method	Identities	Positives	Gaps	Frame
42.6 bits(93)	0.001()		13/13(100%)	13/13(100%)	0/13(0%)	

Features:

```
Query  1    SHAPEVITSSPLK  13
            SHAPEVITSSPLK
Sbjct  476  SHAPEVITSSPLK  488
```

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BLAST Results

Job title: NCBI BlastP_FLNA#_CSGPGLER

RID S54UXTFS014 (Expires on 08-04 11:07 am)

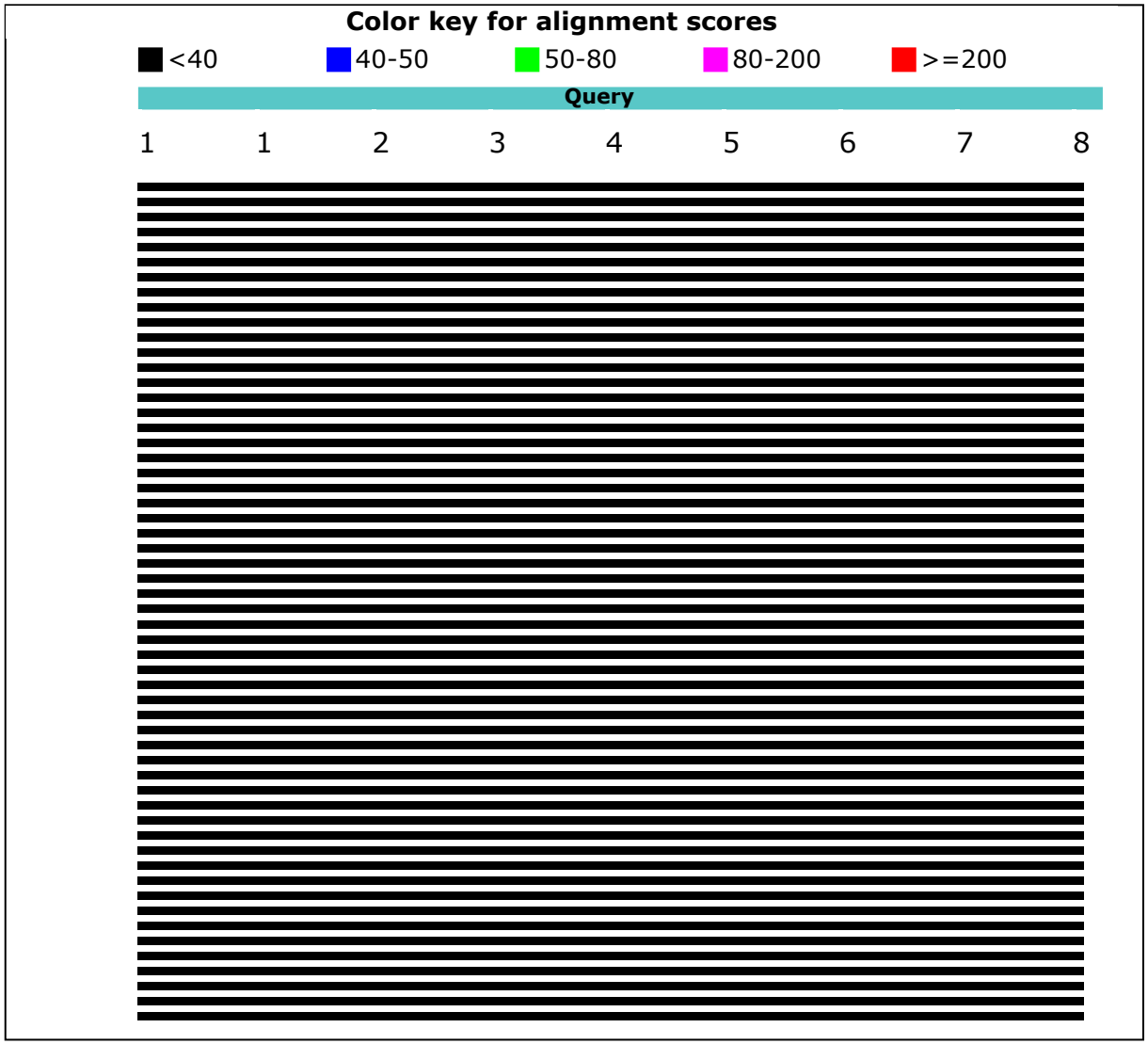
Query ID lcl|Query_120257
Description None
Molecule type amino acid
Query Length 8

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 380 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Filamin-A [Fukomys damarensis]	28.2	143	100%	41	100%	KFO35178.1
unnamed protein product [Tetraodon nigroviridis]	28.2	85.7	100%	41	100%	CAF93177.1
RecName: Full=Filamin-A; Short=FLN-A; AltName: Full=Actin-binding protein 280; Short=ABP-280; AltName: Full=Alpha-filamin; AltName: Full=Endothelial actin-binding protein; AltName: Full=Filamin-1; AltName: Full=Non-muscle filamin	28.2	125	100%	41	100%	Q8BTM8.5
filamin-A isoform 2 [Homo sapiens]	28.2	125	100%	41	100%	NP_001104026.1
unnamed protein product [Homo sapiens]	28.2	125	100%	41	100%	CAA37495.1
filamin A, alpha isoform 2 (predicted) [Otolemur garnettii]	28.2	125	100%	41	100%	ACH53071.1
Filamin-A [Pteropus alecto]	28.2	125	100%	41	100%	ELK09744.1
filamin-A [Bos taurus]	28.2	125	100%	41	100%	NP_001193443.1
filamin A, alpha isoform 2 (predicted) [Dasypus novemcinctus]	28.2	125	100%	41	100%	ACO95345.1
filamin A, alpha isoform 2 (predicted) [Callithrix jacchus]	28.2	125	100%	41	100%	ABZ10487.1
filamin-A [Oryctolagus cuniculus]	28.2	125	100%	41	100%	NP_001164842.1
Filamin-A [Bos mutus]	28.2	125	100%	41	100%	ELR49471.1
Flna [Castor fiber]	28.2	125	100%	41	100%	APD32923.1
filamin-A [Rattus norvegicus]	28.2	125	100%	41	100%	NP_001128071.1
mCG21234, isoform CRA_b [Mus musculus]	28.2	125	100%	41	100%	EDL29839.1
filamin A alpha [synthetic construct]	28.2	125	100%	41	100%	BAG72555.2
filamin-A [Papio anubis]	28.2	125	100%	41	100%	NP_001162272.1
filamin-A isoform 1 [Mus musculus]	28.2	125	100%	41	100%	NP_034357.2
filamin-A isoform 1 [Homo sapiens]	28.2	125	100%	41	100%	NP_001447.2
filamin A, alpha isoform 2 (predicted) [Rhinolophus ferrumequinum]	28.2	125	100%	41	100%	ACC68902.1
filamin-A [Cricetulus griseus]	28.2	125	100%	41	100%	ERE63086.1
filamin A [Homo sapiens]	28.2	125	100%	41	100%	BAD52436.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Filamin-A [Heterocephalus glaber]	28.2	125	100%	41	100%	EHB00999.1
filamin-A isoform X3 [Papio anubis]	28.2	125	100%	41	100%	XP_021788085.1
filamin-A [Cricetulus griseus]	28.2	125	100%	41	100%	ERE63085.1
filamin A [Homo sapiens]	28.2	125	100%	41	100%	BAD52435.1
hypothetical protein EGM_19347 [Macaca fascicularis]	28.2	125	100%	41	100%	EHH61351.1
filamin-A isoform X4 [Papio anubis]	28.2	125	100%	41	100%	XP_021788086.1
filamin, alpha (predicted), isoform CRA_b [Rattus norvegicus]	28.2	125	100%	41	100%	EDL84990.1
mCG21234, isoform CRA_c [Mus musculus]	28.2	125	100%	41	100%	EDL29840.1
hypothetical protein EGK_21101 [Macaca mulatta]	28.2	125	100%	41	100%	EHH31213.1
TPA: filamin A, alpha [Bos taurus]	28.2	125	100%	41	100%	DAA13210.1
Filamin-A [Myotis brandtii]	28.2	125	100%	41	100%	EPQ20180.1
Filamin-A [Tupaia chinensis]	28.2	125	100%	41	100%	ELV11387.1
filamin, alpha [Mus musculus]	28.2	125	100%	41	100%	CAT00729.1
filamin-A isoform X5 [Papio anubis]	28.2	125	100%	41	100%	XP_021788087.1
Filamin-A [Larimichthys crocea]	28.2	85.7	100%	41	100%	KKF31673.1
Filamin-A [Myotis davidii]	28.2	125	100%	41	100%	ELK27817.1
filamin-A-like [Scleropages formosus]	28.2	85.7	100%	41	100%	KPP74783.1
hypothetical protein A6R68_21406 [Neotoma lepida]	28.2	125	100%	41	100%	OBS80380.1
hypothetical protein PANDA_022175 [Ailuropoda melanoleuca]	28.2	125	100%	41	100%	EFB12904.1
Filamin-A [Cricetulus griseus]	28.2	125	100%	41	100%	EGW11368.1
filamin A, alpha (actin binding protein 280), isoform CRA_e [Homo sapiens]	28.2	125	100%	41	100%	EAW72748.1
hypothetical protein cypCar_00003514 [Cyprinus carpio]	28.2	85.7	100%	41	100%	KTG45199.1
filamin A, alpha (actin binding protein 280), isoform CRA_a [Homo sapiens]	28.2	125	100%	41	100%	EAW72744.1
filamin A [Homo sapiens]	28.2	103	100%	41	100%	BAG48306.1
filamin-A isoform 1 [Camelus ferus]	28.2	107	100%	41	100%	EPY72663.1
mCG21234, isoform CRA_a [Mus musculus]	28.2	107	100%	41	100%	EDL29838.1
filamin-A isoform 2 [Mus musculus]	28.2	89.1	100%	41	100%	NP_001277350.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
mFLJ00343 protein [Mus musculus]	28.2	71.1	100%	41	100%	BAD21429.1
filamin A, alpha isoform 2 (predicted) [Sorex araneus]	28.2	89.1	100%	41	100%	ACE79063.1
filamin-A-like [Scleropages formosus]	28.2	86.5	100%	41	100%	KPP63996.1
hypothetical protein cypCar_00000492 [Cyprinus carpio]	28.2	64.3	100%	41	100%	KTG42925.1
filamin A, alpha (actin binding protein 280), isoform CRA_d [Homo sapiens]	28.2	103	100%	41	100%	EAW72747.1
unnamed protein product [Mus musculus]	28.2	82.3	100%	41	100%	BAC40837.2
filamin, alpha [synthetic construct]	28.2	85.7	100%	42	100%	AAI72826.1
unnamed protein product [Oncorhynchus mykiss]	28.2	28.2	100%	42	100%	CDQ89129.1
methylamine utilization protein MauE [Salinisphaera shabanensis]	28.2	28.2	100%	43	100%	WP_006913761.1
Chain A, Structure Of Filamin A Immunoglobulin-Like Repeat 10 From Homo Sapiens	28.2	28.2	100%	44	100%	3RGH_A
AfsR family transcriptional regulator [Actinomadura meyerae]	25.7	25.7	100%	338	88%	WP_089325629.1
nitroreductase [Terasakiispira papahanaumokuakeensis]	25.7	25.7	100%	346	88%	WP_068998534.1
uracil phosphoribosyltransferase [Candidatus Synechococcus spongiarum 142]	25.2	25.2	100%	488	88%	KKZ15155.1
unnamed protein product [Tetraodon nigroviridis]	24.8	104	100%	679	100%	CAF95123.1
hypothetical protein XENTR_v90020032mg [Xenopus tropicalis]	24.8	137	100%	679	100%	OCA24533.1
hypothetical protein XELAEV_18041763mg [Xenopus laevis]	24.8	133	87%	679	100%	OCT65525.1
Filamin-A [Ophiophagus hannah]	24.8	139	100%	679	100%	ETE70682.1
hypothetical protein XELAEV_18002841mg [Xenopus laevis]	24.8	115	87%	679	100%	OCT57973.1
hypothetical protein CB1_000340017 [Camelus ferus]	24.8	24.8	87%	680	100%	EQB77354.1
hypothetical protein PFL1_04915 [Anthracocystis flocculosa PF-1]	24.8	24.8	87%	680	100%	EPQ27376.1
hypothetical protein [Sporisorium scitamineum]	24.8	24.8	87%	680	100%	CDW99383.1
rni-like protein [Melanopsichium pennsylvanicum 4]	24.8	24.8	87%	680	100%	CDI53815.1
uncharacterized protein UBRO_04679 [Ustilago bromivora]	24.8	24.8	87%	680	100%	SAM82328.1
filamin-C-like [Tropilaelaps mercedesae]	24.8	24.8	87%	680	100%	OQR80298.1
hypothetical protein PHSY_005150 [Pseudozyma hubeiensis SY62]	24.8	24.8	87%	680	100%	GAC97564.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ribonuclease inhibitor type leucine-rich repeat proteins [Moesziomyces antarcticus T-34]	24.8	24.8	87%	680	100%	GAC76035.1
RNI-like protein [Moesziomyces antarcticus]	24.8	24.8	87%	680	100%	GAK65769.1
hypothetical protein PaG_03655 [Moesziomyces aphidis DSM 70725]	24.8	24.8	87%	680	100%	ETS62095.1
uncharacterized protein SPSC_06497 [Sporisorium scitamineum]	24.8	24.8	87%	680	100%	CDU26303.1
Ribonuclease inhibitor type leucine-rich repeat proteins [Xanthophyllomyces dendrorhous]	24.8	24.8	87%	680	100%	CED83288.1
conserved hypothetical protein [Sporisorium reilianum SRZ2]	24.8	24.8	87%	680	100%	CBQ73376.1
hypothetical protein UMAG_02976 [Ustilago maydis 521]	24.8	24.8	87%	680	100%	KIS68997.1
uncharacterized protein UHOR_04679 [Ustilago hordei]	24.8	24.8	87%	680	100%	CCF52566.1
hypothetical protein AZE42_01541 [Rhizopogon vesiculosus]	24.8	24.8	87%	680	100%	OJA13747.1
predicted protein [Mycena chlorophos]	24.8	24.8	87%	681	100%	GAT60426.1
RNI-like protein [Peniophora sp. CONT]	24.8	24.8	87%	681	100%	KZV74163.1
hypothetical protein GALMADRAFT_243316 [Galerina marginata CBS 339.88]	24.8	24.8	87%	681	100%	KDR79326.1
epidermal growth factor receptor [Felis catus]	24.8	24.8	87%	681	100%	ALJ56200.1
hypothetical protein M413DRAFT_18150 [Hebeloma cylindrosporum h7]	24.8	24.8	87%	681	100%	KIM43835.1
hypothetical protein K443DRAFT_104334 [Laccaria amethystina LaAM-08-1]	24.8	24.8	87%	681	100%	KIJ98213.1
predicted protein [Laccaria bicolor S238N-H82]	24.8	24.8	87%	681	100%	EDR09862.1
hypothetical protein PLICRDRAFT_178724 [Plicaturopsis crispa FD-325 SS-3]	24.8	24.8	87%	681	100%	KII85687.1
hypothetical protein HYPSUDRAFT_40966 [Hypholoma sublateritium FD-334 SS-4]	24.8	24.8	87%	681	100%	KJA22574.1
hypothetical protein PAXRUDRAFT_833481 [Paxillus rubicundulus Ve08.2h10]	24.8	24.8	87%	681	100%	KIK80501.1
hypothetical protein CY34DRAFT_803805 [Suillus luteus UH-Slu-Lm8-n1]	24.8	24.8	87%	681	100%	KIK43461.1
RNI-like protein [Rhizopogon vinicolor AM-OR11-026]	24.8	24.8	87%	681	100%	OAX36792.1
RNI-like protein [Fistulina hepatica ATCC 64428]	24.8	24.8	87%	681	100%	KIY47737.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein PAXINDRAFT_113840 [Paxillus involutus ATCC 200175]	24.8	24.8	87%	681	100%	KIJ16074.1
Leucine-rich repeat-containing protein 68 [Termitomyces sp. J132]	24.8	24.8	87%	681	100%	KNZ78735.1
LuxR family transcriptional regulator [Actinomadura hibisca]	24.8	24.8	87%	682	100%	WP_067488361.1
hybrid sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus]	24.8	24.8	87%	682	100%	WP_041577507.1

Alignments

Filamin-A [Fukomys damarensis]

Sequence ID: **KFO35178.1** Length: 2676 Number of Matches: 7
Range 1: 1194 to 1201

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.2 bits(59)	41()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1     CSGPGLER  8
             CSGPGLER
Sbjct  1194  CSGPGLER  1201
```

Range 2: 1482 to 1487

Score	Expect	Method	Identities	Positives	Gaps	Frame
21.4 bits(43)	11329()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  1     CSGPGL  6
             CSGPGL
Sbjct  1482  CSGPGL  1487
```

Range 3: 2274 to 2279

Score	Expect	Method	Identities	Positives	Gaps	Frame
21.4 bits(43)	11329()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  3     GPGLER  8
             GPGLER
Sbjct  2274  GPGLER  2279
```

Range 4: 417 to 421

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194072()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  417  GPGLE  421
```

Range 5: 612 to 616

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194072()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  612  GPGLE  616
```

Range 6: 708 to 712

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194072()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  708  GPGLE  712
```

Range 7: 2465 to 2469

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194072()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3     GPGLE  7
             GPGLE
```

```
Sbjct  2465  GPGLE  2469
```

unnamed protein product, partial [Tetraodon nigroviridis]

Sequence ID: **CAF93177.1** Length: 2666 Number of Matches: 4
Range 1: 1108 to 1115

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.2 bits(59)	41()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1     CSGPGLER  8
             CSGPGLER
Sbjct  1108  CSGPGLER  1115
```

Range 2: 2233 to 2238

Score	Expect	Method	Identities	Positives	Gaps	Frame
21.4 bits(43)	11329()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  3     GPGLER  8
             GPGLER
Sbjct  2233  GPGLER  2238
```

Range 3: 422 to 426

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194072()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  422  GPGLE  426
```

Range 4: 618 to 622

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194072()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
```

```
Sbjct  618  GPGLE  622
```

RecName: Full=Filamin-A; Short=FLN-A; AltName: Full=Actin-binding protein 280; Short=ABP-280; AltName: Full=Alpha-filamin; AltName: Full=Endothelial actin-binding protein; AltName: Full=Filamin-1; AltName: Full=Non-muscle filamin
Sequence ID: **Q8BTM8.5** Length: 2647 Number of Matches: 6

See 1 more title(s)

Range 1: 1165 to 1172

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.2 bits(59)	41()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1     CSGPGLER  8
             CSGPGLER
Sbjct  1165  CSGPGLER  1172
```

Range 2: 1453 to 1458

Score	Expect	Method	Identities	Positives	Gaps	Frame
21.4 bits(43)	11329()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  1     CSGPGL  6
             CSGPGL
Sbjct  1453  CSGPGL  1458
```

Range 3: 2245 to 2250

Score	Expect	Method	Identities	Positives	Gaps	Frame
21.4 bits(43)	11329()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  3     GPGLER  8
             GPGLER
Sbjct  2245  GPGLER  2250
```

Range 4: 388 to 392

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  388  GPGLE  392
```

Range 5: 583 to 587

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  583  GPGLE  587
```

Range 6: 679 to 683

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  679  GPGLE  683
```

filamin-A isoform 2 [Homo sapiens]

Sequence ID: **NP_001104026.1** Length: 2647 Number of Matches: 6

See 5 more title(s)

Range 1: 1165 to 1172

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.2 bits(59)	41()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1     CSGPGLER  8
             CSGPGLER
Sbjct  1165  CSGPGLER  1172
```

Range 2: 1453 to 1458

Score	Expect	Method	Identities	Positives	Gaps	Frame

21.4 bits(43)	11329()	6/6(100%)	6/6(100%)	0/6(0%)

Features:

```
Query  1     CSGPGL  6
             CSGPGL
Sbjct  1453  CSGPGL  1458
```

Range 3: 2245 to 2250

Score	Expect	Method	Identities	Positives	Gaps	Frame
21.4 bits(43)	11329()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  3     GPGLER  8
             GPGLER
Sbjct  2245  GPGLER  2250
```

Range 4: 388 to 392

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  388  GPGLE  392
```

Range 5: 583 to 587

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  583  GPGLE  587
```

Range 6: 679 to 683

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  679  GPGLE  683
```

unnamed protein product [Homo sapiens]

Sequence ID: **CAA37495.1** Length: 2647 Number of Matches: 6
Range 1: 1165 to 1172

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.2 bits(59)	41()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1     CSGPGLER  8
             CSGPGLER
Sbjct  1165  CSGPGLER  1172
```

Range 2: 1453 to 1458

Score	Expect	Method	Identities	Positives	Gaps	Frame
21.4 bits(43)	11329()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  1     CSGPGL  6
             CSGPGL
Sbjct  1453  CSGPGL  1458
```

Range 3: 2245 to 2250

Score	Expect	Method	Identities	Positives	Gaps	Frame
21.4 bits(43)	11329()		6/6(100%)	6/6(100%)	0/6(0%)	

Features:

```
Query  3     GPGLER  8
             GPGLER
Sbjct  2245  GPGLER  2250
```

Range 4: 388 to 392

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  388  GPGLE  392
```

Range 5: 583 to 587

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  583  GPGLE  587
```

Range 6: 679 to 683

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194073()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  3    GPGLE  7
            GPGLE
Sbjct  679  GPGLE  683
```

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BLAST Results

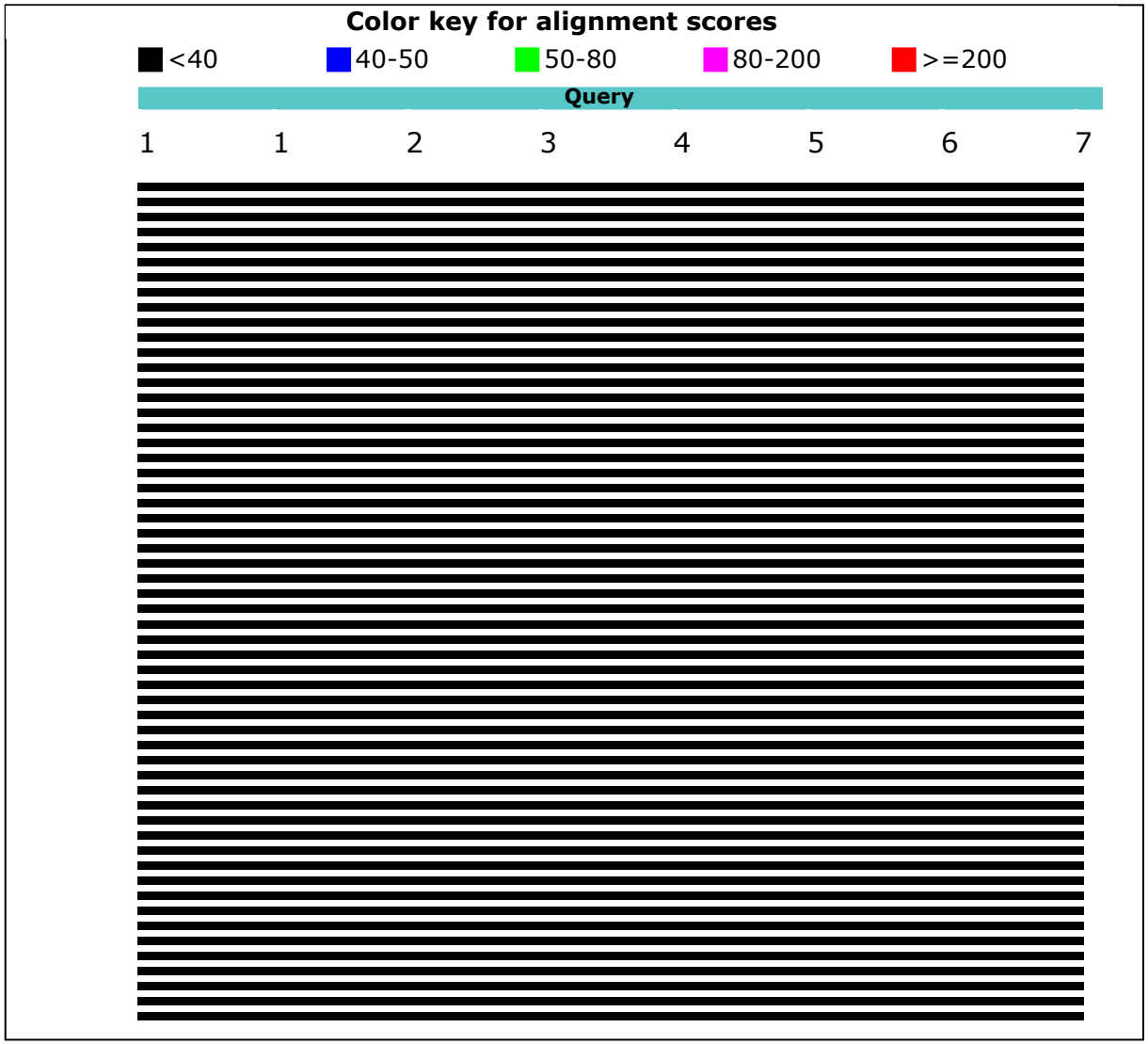
Job title: NCBI BlastP_APOE_WELALGR

RID	S54SV24C015 (Expires on 08-04 11:06 am)
Query ID	lcl|Query_221474
Description	None
Molecule type	amino acid
Query Length	7
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
TPR domain protein, putative component of TonB system [Labilithrix luteola]	26.5	26.5	100%	133	100%	AKV01095.1
hypothetical protein GPECTOR_1g82 [Gonium pectorale]	26.5	26.5	100%	133	100%	KXZ56909.1
hypothetical protein V500_00027 [Pseudogymnoascus sp. VKM F-4518 (FW-2643)]	26.5	44.5	100%	134	100%	KFZ02682.1
hypothetical protein PHLCEN_12390 [Phlebia centrifuga]	26.5	26.5	100%	134	100%	OKY67569.1
AfsR family transcriptional regulator [Thermocrispum agreste]	26.5	26.5	100%	134	100%	WP_051309768.1
AsmA family protein [Bosea thiooxidans]	26.5	26.5	100%	134	100%	WP_079591242.1
hypothetical protein ARD30_22425 [Bosea thiooxidans]	26.5	26.5	100%	134	100%	KQK28335.1
hypothetical protein [Haloarcula rubripromontorii]	26.5	26.5	100%	134	100%	WP_053966342.1
UDP-glucuronosyltransferase [Toxocara canis]	26.5	26.5	100%	134	100%	KHN87790.1
two-component sensor histidine kinase [Alcanivorax jadensis]	26.5	26.5	100%	134	100%	WP_035248937.1
hypothetical protein GGTG_04325 [Gaeumannomyces tritici R3-111a-1]	26.5	26.5	100%	134	100%	EJT79239.1
lipid-A-disaccharide synthase [Deinococcus wulumuqiensis]	26.5	26.5	100%	134	100%	WP_017870350.1
lipid-A-disaccharide synthase [Deinococcus radiodurans]	26.5	26.5	100%	134	100%	WP_010889249.1
conserved hypothetical protein [Deinococcus reticulitermitis]	26.5	26.5	100%	134	100%	SEJ59676.1
unnamed protein product [Chondrus crispus]	26.5	26.5	100%	134	100%	CDF36177.1
DUF2029 domain-containing protein [Verrucomicrobium sp. 3C]	26.5	26.5	100%	135	100%	WP_018290998.1
hypothetical protein PLEOSDRAFT_1098789 [Pleurotus ostreatus PC15]	26.5	26.5	100%	135	100%	KDQ32808.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
prenyltransferase [Streptomyces sp. CNH099]	26.5	26.5	100%	135	100%	WP_027755842.1
prenyltransferase [Mycobacterium sp. NE-TNMC-100812]	26.5	26.5	100%	135	100%	WP_071021972.1
prenyltransferase [Mycobacterium gordonae]	26.5	26.5	100%	135	100%	WP_069433854.1
prenyltransferase [Mycobacterium gordonae]	26.5	26.5	100%	135	100%	WP_065162528.1
prenyltransferase [Mycobacterium gordonae]	26.5	26.5	100%	135	100%	WP_065048660.1
prenyltransferase [Mycobacterium gordonae]	26.5	26.5	100%	135	100%	WP_055576657.1
prenyltransferase [Saccharomonospora marina]	26.5	26.5	100%	135	100%	WP_009157044.1
prenyltransferase [Mycobacterium pseudoshottsii]	26.5	26.5	100%	135	100%	WP_086085411.1
prenyltransferase [Mycobacterium vulneris]	26.5	26.5	100%	135	100%	WP_085289726.1
prenyltransferase [Mycobacterium szulgai]	26.5	26.5	100%	135	100%	WP_085671962.1
prenyltransferase [Mycobacterium sherrisii]	26.5	26.5	100%	135	100%	WP_085166177.1
prenyltransferase [Mycobacterium saskatchewanense]	26.5	26.5	100%	135	100%	WP_085257231.1
prenyltransferase [Mycobacterium parmense]	26.5	26.5	100%	135	100%	WP_085271258.1
prenyltransferase [Mycobacterium paraense]	26.5	26.5	100%	135	100%	WP_085173194.1
prenyltransferase [Mycobacterium paraense]	26.5	26.5	100%	135	100%	WP_085100214.1
prenyltransferase [Mycobacterium palustre]	26.5	26.5	100%	135	100%	WP_085078453.1
prenyltransferase [Mycobacterium interjectum]	26.5	26.5	100%	135	100%	WP_085203457.1
prenyltransferase [Mycobacterium europaeum]	26.5	26.5	100%	135	100%	WP_085238935.1
prenyltransferase [Mycobacterium florentinum]	26.5	26.5	100%	135	100%	WP_085220239.1
prenyltransferase [Mycobacterium scrofulaceum]	26.5	26.5	100%	135	100%	WP_083177173.1
prenyltransferase [Mycobacterium paraseoulense]	26.5	26.5	100%	135	100%	WP_083170670.1
prenyltransferase [Mycobacterium mantenii]	26.5	26.5	100%	135	100%	WP_083092518.1
prenyltransferase [Mycobacterium marseillense]	26.5	26.5	100%	135	100%	WP_083017201.1
prenyltransferase [Mycobacterium malmoense]	26.5	26.5	100%	135	100%	WP_083011106.1
prenyltransferase [Mycobacterium angelicum]	26.5	26.5	100%	135	100%	WP_083112734.1
prenyltransferase [Mycobacterium arosiense]	26.5	26.5	100%	135	100%	WP_083064565.1
prenyltransferase [Mycobacterium sp. AB308]	26.5	26.5	100%	135	100%	WP_077097028.1
prenyltransferase [Mycobacterium colombiense]	26.5	26.5	100%	135	100%	WP_077092144.1
prenyltransferase [Mycobacterium sp. IS-2888]	26.5	26.5	100%	135	100%	WP_076115257.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
prenyltransferase [Mycobacterium sp. IS-1264]	26.5	26.5	100%	135	100%	WP_076058697.1
MULTISPECIES: prenyltransferase [Mycobacterium]	26.5	26.5	100%	135	100%	WP_076128202.1
prenyltransferase [Mycobacterium paraffinicum]	26.5	26.5	100%	135	100%	WP_073873970.1
prenyltransferase [Mycobacterium malmoense]	26.5	26.5	100%	135	100%	WP_071510720.1
prenyltransferase [Mycobacterium sherrisii]	26.5	26.5	100%	135	100%	WP_069402543.1
prenyltransferase [Mycobacterium interjectum]	26.5	26.5	100%	135	100%	WP_066912851.1
prenyltransferase [Mycobacterium sp. 1245499.0]	26.5	26.5	100%	135	100%	WP_067020615.1
prenyltransferase [Mycobacterium sp. 1245111.1]	26.5	26.5	100%	135	100%	WP_067335427.1
prenyltransferase [Mycobacterium sp. 1165196.3]	26.5	26.5	100%	135	100%	WP_067183802.1
prenyltransferase [Mycobacterium sp. 1245852.3]	26.5	26.5	100%	135	100%	WP_067141627.1
prenyltransferase [Mycobacterium sp. 1165549.7]	26.5	26.5	100%	135	100%	WP_067169680.1
prenyltransferase [Mycobacterium sp. 1245801.1]	26.5	26.5	100%	135	100%	WP_066876743.1
prenyltransferase [Mycobacterium sp. 1482292.6]	26.5	26.5	100%	135	100%	WP_066863165.1
prenyltransferase [Mycobacterium sp. 1465703.0]	26.5	26.5	100%	135	100%	WP_066993767.1
prenyltransferase [Mycobacterium sp. 1245805.9]	26.5	26.5	100%	135	100%	WP_067147814.1
prenyltransferase [Mycobacterium sp. E787]	26.5	26.5	100%	135	100%	WP_068275936.1
prenyltransferase [Mycobacterium sp. E796]	26.5	26.5	100%	135	100%	WP_068139268.1
prenyltransferase [Mycobacterium sp. E2497]	26.5	26.5	100%	135	100%	WP_068092719.1
prenyltransferase [Mycobacterium sp. E2479]	26.5	26.5	100%	135	100%	WP_067934235.1
prenyltransferase [Mycobacterium sp. E342]	26.5	26.5	100%	135	100%	WP_068052378.1
prenyltransferase [Mycobacterium sp. E1715]	26.5	26.5	100%	135	100%	WP_068263460.1
prenyltransferase [Mycobacterium sp. E3247]	26.5	26.5	100%	135	100%	WP_067926713.1
prenyltransferase [Mycobacterium sp. E2699]	26.5	26.5	100%	135	100%	WP_067883313.1
MULTISPECIES: prenyltransferase [Mycobacterium]	26.5	26.5	100%	135	100%	WP_067950833.1
prenyltransferase [Mycobacterium sp. E3298]	26.5	26.5	100%	135	100%	WP_067781514.1
prenyltransferase [Mycobacterium sp. E3305]	26.5	26.5	100%	135	100%	WP_067750602.1
prenyltransferase [Mycobacterium sp. E3339]	26.5	26.5	100%	135	100%	WP_068217635.1
MULTISPECIES: prenyltransferase [Mycobacterium]	26.5	26.5	100%	135	100%	WP_067889657.1
hypothetical protein SHTP_2372 [Mycobacterium ulcerans subsp. shinshuense]	26.5	26.5	100%	135	100%	BAV41501.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
prenyltransferase [Mycobacterium malmoense]	26.5	26.5	100%	135	100%	WP_065497019.1
prenyltransferase [Mycobacterium malmoense]	26.5	26.5	100%	135	100%	WP_065471561.1
prenyltransferase [Mycobacterium malmoense]	26.5	26.5	100%	135	100%	WP_065446796.1
prenyltransferase [Mycobacterium asiaticum]	26.5	26.5	100%	135	100%	WP_065158777.1
prenyltransferase [Mycobacterium asiaticum]	26.5	26.5	100%	135	100%	WP_065156463.1
prenyltransferase [Mycobacterium asiaticum]	26.5	26.5	100%	135	100%	WP_065148932.1
prenyltransferase [Mycobacterium asiaticum]	26.5	26.5	100%	135	100%	WP_065131254.1
prenyltransferase [Mycobacterium asiaticum]	26.5	26.5	100%	135	100%	WP_065145367.1
prenyltransferase [Mycobacterium asiaticum]	26.5	26.5	100%	135	100%	WP_065140178.1
prenyltransferase [Mycobacterium asiaticum]	26.5	26.5	100%	135	100%	WP_065120663.1
prenyltransferase [Mycobacterium asiaticum]	26.5	26.5	100%	135	100%	WP_065038336.1
prenyltransferase [Mycobacterium colombiense]	26.5	26.5	100%	135	100%	WP_065074886.1
prenyltransferase [Mycobacterium colombiense]	26.5	26.5	100%	135	100%	WP_065028723.1
prenyltransferase [Mycobacterium sp. E2733]	26.5	26.5	100%	135	100%	WP_068048421.1
prenyltransferase [Mycobacterium sp. E2989]	26.5	26.5	100%	135	100%	WP_067818266.1
prenyltransferase [Mycobacterium scrofulaceum]	26.5	26.5	100%	135	100%	WP_067310195.1
prenyltransferase [Mycobacterium scrofulaceum]	26.5	26.5	100%	135	100%	WP_067278438.1
MULTISPECIES: prenyltransferase [Mycobacterium]	26.5	26.5	100%	135	100%	WP_067831685.1
MULTISPECIES: prenyltransferase [Mycobacterium]	26.5	26.5	100%	135	100%	WP_067909122.1
prenyltransferase [Mycobacterium sp. 852002-51057_SCH5723018]	26.5	26.5	100%	135	100%	WP_067119354.1
prenyltransferase [Mycobacterium sp. 852002-51971_SCH5477799-a]	26.5	26.5	100%	135	100%	WP_067132064.1
MULTISPECIES: prenyltransferase [Mycobacterium]	26.5	26.5	100%	135	100%	WP_066954521.1
prenyltransferase [Mycobacterium sp. 852002-50816_SCH5313054-b]	26.5	26.5	100%	135	100%	WP_066970725.1
prenyltransferase [Mycobacterium sp. ACS4054]	26.5	26.5	100%	135	100%	WP_067895061.1
prenyltransferase [Mycobacterium sp. 852002-10029_SCH5224772]	26.5	26.5	100%	135	100%	WP_067255789.1

Alignments

TPR domain protein, putative component of TonB system [Labilithrix luteola]

Sequence ID: **AKV01095.1** Length: 2017 Number of Matches: 1
Range 1: 379 to 385

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	133()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    WELALGR  7
            WELALGR
Sbjct  379  WELALGR  385
```

hypothetical protein GPECTOR_1g82 [Gonium pectorale]

Sequence ID: **KXZ56909.1** Length: 1072 Number of Matches: 1
Range 1: 985 to 991

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	133()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    WELALGR  7
            WELALGR
Sbjct  985  WELALGR  991
```

hypothetical protein V500_00027 [Pseudogymnoascus sp. VKM F-4518 (FW-2643)]

Sequence ID: **KFZ02682.1** Length: 643 Number of Matches: 2
Range 1: 511 to 517

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	134()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    WELALGR  7
            WELALGR
Sbjct  511  WELALGR  517
```

Range 2: 578 to 582

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	151181()		4/5(80%)	5/5(100%)	0/5(0%)	

Features:

```
Query  1    WELAL  5
           W+LAL
Sbjct  578  WDLAL  582
```

hypothetical protein PHLCEN_12390 [Phlebia centrifuga]

Sequence ID: **OKY67569.1** Length: 641 Number of Matches: 1
Range 1: 618 to 624

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	134()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    WELALGR  7
           WELALGR
Sbjct  618  WELALGR  624
```

AfsR family transcriptional regulator [Thermocrispum agreste]

Sequence ID: **WP_051309768.1** Length: 626 Number of Matches: 1
Range 1: 168 to 174

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	134()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    WELALGR  7
           WELALGR
Sbjct  168  WELALGR  174
```

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BLAST Results

Job title: NCBI Blast_ATRN_CINQSICEK

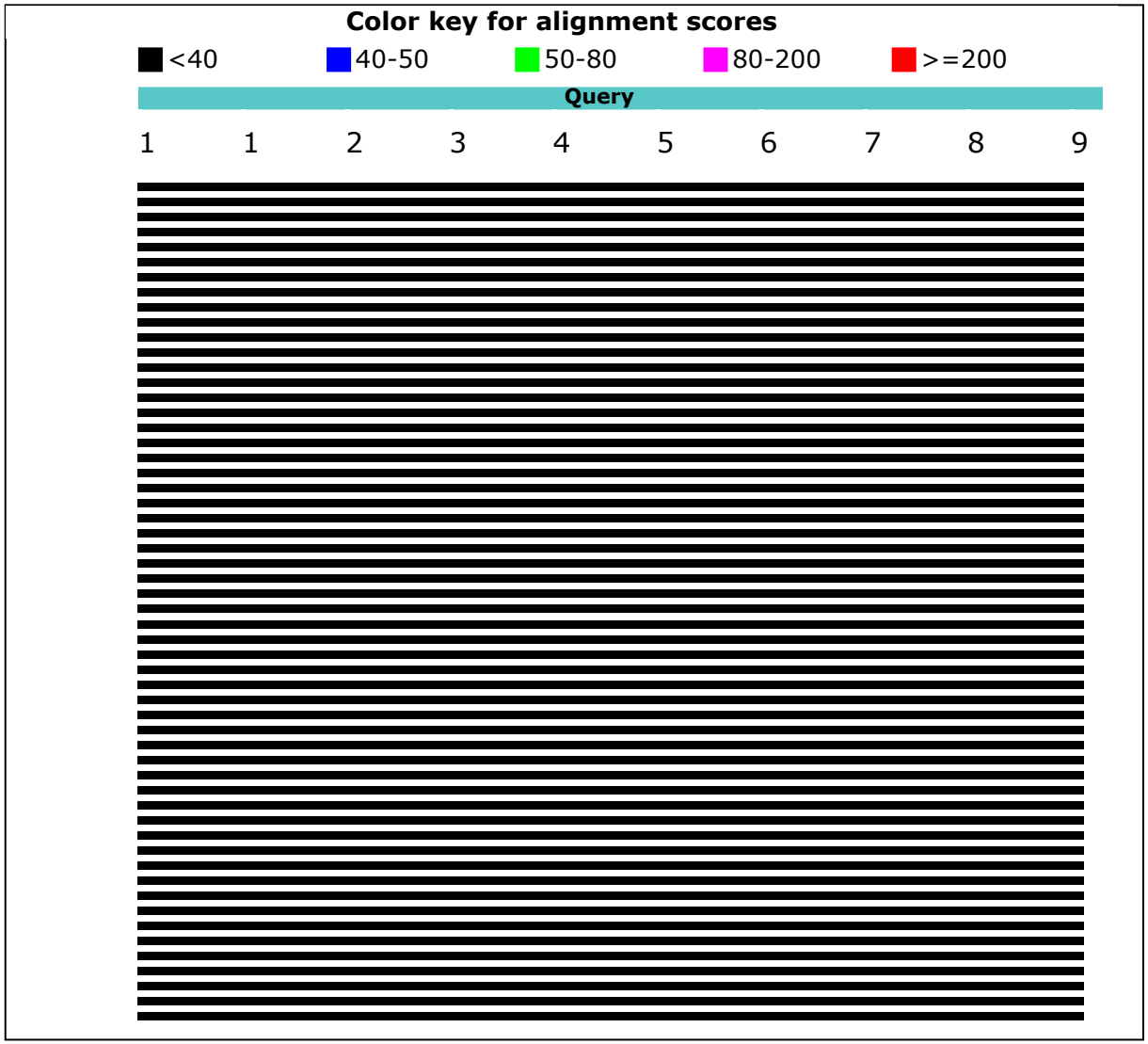
RID S54AMWZF014 (Expires on 08-04 10:58 am)

Query ID	lcl|Query_67391	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	9	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8
9

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin isoform X2 [Mus musculus]	34.1	34.1	100%	0.45	100%	XP_006498669.1
PREDICTED: attractin isoform X1 [Bubalus bubalis]	34.1	34.1	100%	0.45	100%	XP_006072963.1
PREDICTED: attractin isoform X3 [Panthera pardus]	34.1	34.1	100%	0.45	100%	XP_019318206.1
PREDICTED: attractin isoform X4 [Canis lupus familiaris]	34.1	34.1	100%	0.45	100%	XP_005634904.1
PREDICTED: attractin isoform X3 [Tursiops truncatus]	34.1	34.1	100%	0.45	100%	XP_019806237.1
PREDICTED: attractin isoform X5 [Rousettus aegyptiacus]	34.1	34.1	100%	0.45	100%	XP_015994583.1
PREDICTED: attractin isoform X4 [Felis catus]	34.1	34.1	100%	0.45	100%	XP_019682337.1
mahogany protein [Mus musculus]	34.1	34.1	100%	0.45	100%	AAD20947.1
attractin isoform X5 [Microcebus murinus]	34.1	34.1	100%	0.45	100%	XP_020137608.1
PREDICTED: attractin isoform X2 [Dipodomys ordii]	34.1	34.1	100%	0.45	100%	XP_012866494.1
PREDICTED: attractin [Bison bison bison]	34.1	34.1	100%	0.45	100%	XP_010834932.1
PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	34.1	34.1	100%	0.45	100%	XP_008017729.1
attractin, isoform CRA_b [Mus musculus]	34.1	34.1	100%	0.45	100%	EDL28293.1
PREDICTED: attractin isoform X1 [Chinchilla lanigera]	34.1	34.1	100%	0.45	100%	XP_005380851.1
PREDICTED: LOW QUALITY PROTEIN: attractin [Cavia porcellus]	34.1	34.1	100%	0.45	100%	XP_005008408.1
attractin precursor [Rattus norvegicus]	34.1	34.1	100%	0.45	100%	NP_112641.1
PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	34.1	34.1	100%	0.45	100%	XP_008017700.1
attractin [Aotus nancymaae]	34.1	34.1	100%	0.45	100%	XP_012310783.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin isoform X3 [Macaca nemestrina]	34.1	34.1	100%	0.45	100%	XP_011739578.1
PREDICTED: attractin isoform X1 [Cercocebus atys]	34.1	34.1	100%	0.45	100%	XP_011907600.1
PREDICTED: attractin isoform X1 [Macaca fascicularis]	34.1	34.1	100%	0.45	100%	XP_005568510.1
PREDICTED: attractin isoform X1 [Macaca mulatta]	34.1	34.1	100%	0.45	100%	XP_015004916.1
PREDICTED: attractin isoform X1 [Pan troglodytes]	34.1	34.1	100%	0.45	100%	XP_003316827.2
membrane attractin precursor [Homo sapiens]	34.1	34.1	100%	0.45	100%	AAF72881.1
attractin isoform 1 preproprotein [Homo sapiens]	34.1	34.1	100%	0.45	100%	NP_647537.1
PREDICTED: attractin [Jaculus jaculus]	34.1	34.1	100%	0.45	100%	XP_004661535.1
PREDICTED: attractin [Cebus capucinus imitator]	34.1	34.1	100%	0.45	100%	XP_017360299.1
attractin preproprotein [Mus musculus]	34.1	34.1	100%	0.45	100%	NP_033860.2
PREDICTED: attractin isoform X1 [Nomascus leucogenys]	34.1	34.1	100%	0.45	100%	XP_012367461.1
PREDICTED: attractin [Callithrix jacchus]	34.1	34.1	100%	0.45	100%	XP_002747358.1
attractin [Mesocricetus auratus]	34.1	34.1	100%	0.45	100%	NP_001268565.1
attractin isoform X1 [Castor canadensis]	34.1	34.1	100%	0.45	100%	XP_020032153.1
PREDICTED: attractin [Oryctolagus cuniculus]	34.1	34.1	100%	0.45	100%	XP_002710968.1
attractin [Ictidomys tridecemlineatus]	34.1	34.1	100%	0.45	100%	XP_005320577.1
PREDICTED: attractin [Ochotona princeps]	34.1	34.1	100%	0.45	100%	XP_004585711.1
PREDICTED: attractin isoform X1 [Loxodonta africana]	34.1	34.1	100%	0.45	100%	XP_003411658.1
attractin isoform X1 [Microcebus murinus]	34.1	34.1	100%	0.45	100%	XP_012610330.1
PREDICTED: attractin [Orycteropus afer afer]	34.1	34.1	100%	0.45	100%	XP_007958185.1
PREDICTED: attractin isoform X2 [Chinchilla lanigera]	34.1	34.1	100%	0.45	100%	XP_005380852.1
PREDICTED: attractin isoform X7 [Rhinolophus sinicus]	34.1	34.1	100%	0.45	100%	XP_019589316.1
attractin isoform X2 [Microcebus murinus]	34.1	34.1	100%	0.45	100%	XP_012610332.1
attractin isoform X1 [Heterocephalus glaber]	34.1	34.1	100%	0.45	100%	XP_004840782.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin [Chrysochloris asiatica]	34.1	34.1	100%	0.45	100%	XP_006874887.1
PREDICTED: attractin [Elephantulus edwardii]	34.1	34.1	100%	0.45	100%	XP_006894264.1
PREDICTED: attractin isoform X1 [Dipodomys ordii]	34.1	34.1	100%	0.45	100%	XP_012866493.1
attractin [Neomonachus schauinslandi]	34.1	34.1	100%	0.45	100%	XP_021544819.1
PREDICTED: attractin isoform X1 [Tursiops truncatus]	34.1	34.1	100%	0.45	100%	XP_019806235.1
PREDICTED: attractin [Odobenus rosmarus divergens]	34.1	34.1	100%	0.45	100%	XP_004398236.1
PREDICTED: attractin isoform X2 [Pan troglodytes]	34.1	34.1	100%	0.45	100%	XP_016792848.1
PREDICTED: attractin [Lipotes vexillifer]	34.1	34.1	100%	0.45	100%	XP_007465469.1
PREDICTED: attractin isoform X1 [Panthera pardus]	34.1	34.1	100%	0.45	100%	XP_019318201.1
PREDICTED: attractin [Orcinus orca]	34.1	34.1	100%	0.45	100%	XP_004285351.1
PREDICTED: attractin isoform X1 [Canis lupus familiaris]	34.1	34.1	100%	0.45	100%	XP_534360.2
attractin isoform X1 [Odocoileus virginianus texanus]	34.1	34.1	100%	0.45	100%	XP_020732718.1
PREDICTED: attractin isoform X1 [Rhinolophus sinicus]	34.1	34.1	100%	0.45	100%	XP_019589309.1
PREDICTED: attractin isoform X1 [Capra hircus]	34.1	34.1	100%	0.45	100%	XP_017912899.1
PREDICTED: attractin [Eptesicus fuscus]	34.1	34.1	100%	0.45	100%	XP_008139256.1
attractin [Bos taurus]	34.1	34.1	100%	0.45	100%	NP_776420.1
PREDICTED: attractin isoform X2 [Bubalus bubalis]	34.1	34.1	100%	0.45	100%	XP_006072964.1
PREDICTED: attractin isoform X1 [Rousettus aegyptiacus]	34.1	34.1	100%	0.45	100%	XP_015994231.1
PREDICTED: attractin [Pteropus alecto]	34.1	34.1	100%	0.45	100%	XP_006921705.1
PREDICTED: attractin isoform X1 [Felis catus]	34.1	34.1	100%	0.45	100%	XP_019682332.1
attractin [Bos taurus]	34.1	34.1	100%	0.45	100%	ACT32973.1
PREDICTED: attractin [Vicugna pacos]	34.1	34.1	100%	0.45	100%	XP_006207473.1
PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	34.1	34.1	100%	0.45	100%	XP_008017704.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin isoform X2 [Cercocebus atys]	34.1	34.1	100%	0.45	100%	XP_011907601.1
PREDICTED: attractin isoform X3 [Pan troglodytes]	34.1	34.1	100%	0.45	100%	XP_009435010.2
PREDICTED: attractin [Peromyscus maniculatus bairdii]	34.1	34.1	100%	0.45	100%	XP_006984624.1
PREDICTED: attractin [Fukomys damarensis]	34.1	34.1	100%	0.45	100%	XP_010609356.1
PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	34.1	34.1	100%	0.45	100%	XP_008017707.1
PREDICTED: attractin isoform X3 [Cercocebus atys]	34.1	34.1	100%	0.45	100%	XP_011907603.1
attractin isoform X2 [Heterocephalus glaber]	34.1	34.1	100%	0.45	100%	XP_021110653.1
PREDICTED: attractin [Marmota marmota marmota]	34.1	34.1	100%	0.45	100%	XP_015343524.1
attractin, isoform CRA_b [Homo sapiens]	34.1	34.1	100%	0.45	100%	EAX10531.1
PREDICTED: attractin [Propithecus coquereli]	34.1	34.1	100%	0.45	100%	XP_012494702.1
PREDICTED: attractin [Tupaia chinensis]	34.1	34.1	100%	0.45	100%	XP_014437769.1
PREDICTED: attractin isoform X2 [Rhinolophus sinicus]	34.1	34.1	100%	0.45	100%	XP_019589310.1
PREDICTED: attractin-like isoform X1 [Xenopus laevis]	34.1	54.3	100%	0.45	100%	XP_018098459.1
PREDICTED: attractin [Camelus bactrianus]	34.1	34.1	100%	0.45	100%	XP_010971103.1
PREDICTED: attractin [Ailuropoda melanoleuca]	34.1	34.1	100%	0.45	100%	XP_019654759.1
hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	34.1	34.1	100%	0.45	100%	EFB15456.1
PREDICTED: attractin [Ursus maritimus]	34.1	34.1	100%	0.45	100%	XP_008701660.1
PREDICTED: attractin [Pteropus vampyrus]	34.1	34.1	100%	0.45	100%	XP_011369298.1
PREDICTED: attractin [Bos mutus]	34.1	34.1	100%	0.45	100%	XP_005894036.1
PREDICTED: attractin [Camelus dromedarius]	34.1	34.1	100%	0.45	100%	XP_010986570.1
PREDICTED: attractin isoform X4 [Cercocebus atys]	34.1	34.1	100%	0.45	100%	XP_011907604.1
PREDICTED: attractin isoform X2 [Rousettus aegyptiacus]	34.1	34.1	100%	0.45	100%	XP_015994322.1
PREDICTED: attractin isoform X2 [Felis catus]	34.1	34.1	100%	0.45	100%	XP_019682335.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin [Sorex araneus]	34.1	34.1	100%	0.45	100%	XP_004611050.2
PREDICTED: attractin [Myotis lucifugus]	34.1	34.1	100%	0.45	100%	XP_006096513.1
PREDICTED: attractin isoform X1 [Mus musculus]	34.1	34.1	100%	0.45	100%	XP_011237561.1
PREDICTED: attractin isoform X1 [Otolemur garnettii]	34.1	34.1	100%	0.45	100%	XP_012659605.1
PREDICTED: attractin [Acinonyx jubatus]	34.1	34.1	100%	0.45	100%	XP_014933613.1
PREDICTED: attractin [Rhinopithecus roxellana]	34.1	34.1	100%	0.45	100%	XP_010377335.1
PREDICTED: attractin isoform X3 [Rhinolophus sinicus]	34.1	34.1	100%	0.45	100%	XP_019589312.1
PREDICTED: attractin isoform X1 [Ovis aries]	34.1	34.1	100%	0.45	100%	XP_012044119.1
Attractin [Heterocephalus glaber]	34.1	34.1	100%	0.45	100%	EHB04302.1
PREDICTED: attractin isoform X4 [Rhinolophus sinicus]	34.1	34.1	100%	0.45	100%	XP_019589313.1
PREDICTED: attractin-like [Galeopterus variegatus]	34.1	34.1	100%	0.45	100%	XP_008589101.1
PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	34.1	34.1	100%	0.45	100%	XP_008017712.1

Alignments

PREDICTED: attractin isoform X2 [Mus musculus]

Sequence ID: **XP_006498669.1** Length: 1510 Number of Matches: 1
Range 1: 1107 to 1115

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.1 bits(73)	0.45()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1     CINQSICEK  9
             CINQSICEK
Sbjct  1107  CINQSICEK  1115
```

PREDICTED: attractin isoform X1 [Bubalus bubalis]

Sequence ID: **XP_006072963.1** Length: 1495 Number of Matches: 1
Range 1: 1057 to 1065

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.1 bits(73)	0.45()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1     CINQSICEK  9
             CINQSICEK
Sbjct  1057  CINQSICEK  1065
```

PREDICTED: attractin isoform X3 [Panthera pardus]

Sequence ID: **XP_019318206.1** Length: 1491 Number of Matches: 1
Range 1: 1060 to 1068

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.1 bits(73)	0.45()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1     CINQSICEK  9
             CINQSICEK
Sbjct  1060  CINQSICEK  1068
```

PREDICTED: attractin isoform X4 [Canis lupus familiaris]

Sequence ID: **XP_005634904.1** Length: 1490 Number of Matches: 1
Range 1: 1059 to 1067

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.1 bits(73)	0.45()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1     CINQSICEK  9
             CINQSICEK
Sbjct  1059  CINQSICEK  1067
```

PREDICTED: attractin isoform X3 [Tursiops truncatus]

Sequence ID: **XP_019806237.1** Length: 1489 Number of Matches: 1
Range 1: 1062 to 1070

Score	Expect	Method	Identities	Positives	Gaps	Frame

34.1 bits(73)	0.45()	9/9(100%)	9/9(100%)	0/9(0%)

Features:

```
Query  1     CINQSICEK  9
            CINQSICEK
Sbjct  1062  CINQSICEK  1070
```

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BLAST Results

Job title: NCBI BlastP_ATRN_WSVLPRPDLHHDVNR

RID S54ERJNZ014 (Expires on 08-04 11:00 am)

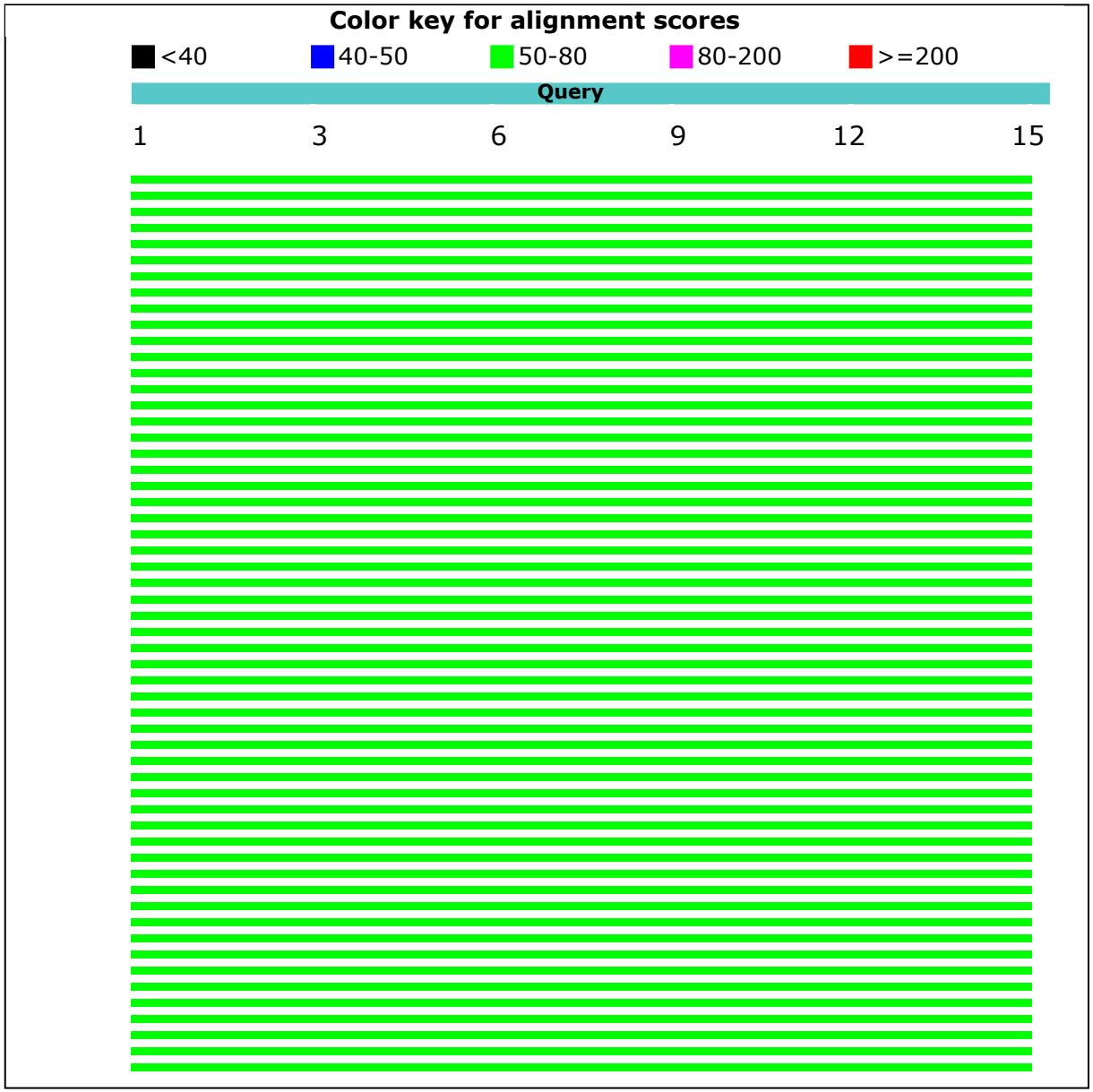
Query ID lcl|Query_142046
Description None
Molecule type amino acid
Query Length 15

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
3
6
9
12
15

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin isoform X3 [Mustela putorius furo]	54.5	54.5	100%	9e-08	100%	XP_012901500.1
PREDICTED: attractin isoform X1 [Bubalus bubalis]	54.5	54.5	100%	9e-08	100%	XP_006072963.1
PREDICTED: attractin isoform X3 [Panthera pardus]	54.5	54.5	100%	9e-08	100%	XP_019318206.1
PREDICTED: attractin isoform X4 [Canis lupus familiaris]	54.5	54.5	100%	9e-08	100%	XP_005634904.1
PREDICTED: attractin isoform X3 [Tursiops truncatus]	54.5	54.5	100%	9e-08	100%	XP_019806237.1
PREDICTED: attractin isoform X5 [Rousettus aegyptiacus]	54.5	54.5	100%	9e-08	100%	XP_015994583.1
PREDICTED: attractin isoform X4 [Ceratotherium simum simum]	54.5	54.5	100%	9e-08	100%	XP_014645597.1
PREDICTED: attractin isoform X4 [Felis catus]	54.5	54.5	100%	9e-08	100%	XP_019682337.1
attractin isoform X3 [Sus scrofa]	54.5	54.5	100%	9e-08	100%	XP_020933051.1
attractin isoform X5 [Microcebus murinus]	54.5	54.5	100%	9e-08	100%	XP_020137608.1
PREDICTED: attractin isoform X2 [Dipodomys ordii]	54.5	54.5	100%	9e-08	100%	XP_012866494.1
PREDICTED: attractin [Bison bison bison]	54.5	54.5	100%	9e-08	100%	XP_010834932.1
PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	54.5	54.5	100%	9e-08	100%	XP_008017729.1
PREDICTED: LOW QUALITY PROTEIN: attractin [Cavia porcellus]	54.5	54.5	100%	9e-08	100%	XP_005008408.1
PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	54.5	54.5	100%	9e-08	100%	XP_008017700.1
PREDICTED: attractin isoform X2 [Condylura cristata]	54.5	54.5	100%	9e-08	100%	XP_012583721.1
attractin [Aotus nancymaae]	54.5	54.5	100%	9e-08	100%	XP_012310783.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin isoform X3 [Macaca nemestrina]	54.5	54.5	100%	9e-08	100%	XP_011739578.1
PREDICTED: attractin isoform X1 [Cercocebus atys]	54.5	54.5	100%	9e-08	100%	XP_011907600.1
PREDICTED: attractin isoform X1 [Macaca fascicularis]	54.5	54.5	100%	9e-08	100%	XP_005568510.1
PREDICTED: attractin isoform X1 [Macaca mulatta]	54.5	54.5	100%	9e-08	100%	XP_015004916.1
PREDICTED: attractin isoform X1 [Pan troglodytes]	54.5	54.5	100%	9e-08	100%	XP_003316827.2
membrane attractin precursor [Homo sapiens]	54.5	54.5	100%	9e-08	100%	AAF72881.1
attractin isoform 1 preproprotein [Homo sapiens]	54.5	54.5	100%	9e-08	100%	NP_647537.1
PREDICTED: attractin [Cebus capucinus imitator]	54.5	54.5	100%	9e-08	100%	XP_017360299.1
PREDICTED: attractin isoform X1 [Nomascus leucogenys]	54.5	54.5	100%	9e-08	100%	XP_012367461.1
PREDICTED: attractin isoform X1 [Microtus ochrogaster]	54.5	54.5	100%	9e-08	100%	XP_005365652.1
attractin [Mesocricetus auratus]	54.5	54.5	100%	9e-08	100%	NP_001268565.1
attractin isoform X1 [Castor canadensis]	54.5	54.5	100%	9e-08	100%	XP_020032153.1
PREDICTED: attractin [Oryctolagus cuniculus]	54.5	54.5	100%	9e-08	100%	XP_002710968.1
PREDICTED: attractin isoform X1 [Loxodonta africana]	54.5	54.5	100%	9e-08	100%	XP_003411658.1
attractin isoform X1 [Microcebus murinus]	54.5	54.5	100%	9e-08	100%	XP_012610330.1
PREDICTED: attractin [Orycteropus afer afer]	54.5	54.5	100%	9e-08	100%	XP_007958185.1
PREDICTED: attractin isoform X7 [Rhinolophus sinicus]	54.5	54.5	100%	9e-08	100%	XP_019589316.1
attractin isoform X2 [Microcebus murinus]	54.5	54.5	100%	9e-08	100%	XP_012610332.1
attractin isoform X1 [Heterocephalus glaber]	54.5	54.5	100%	9e-08	100%	XP_004840782.1
PREDICTED: attractin isoform X1 [Dipodomys ordii]	54.5	54.5	100%	9e-08	100%	XP_012866493.1
attractin [Neomonachus schauinslandi]	54.5	54.5	100%	9e-08	100%	XP_021544819.1
PREDICTED: attractin isoform X1 [Mustela putorius furo]	54.5	54.5	100%	9e-08	100%	XP_004772932.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin isoform X1 [Tursiops truncatus]	54.5	54.5	100%	9e-08	100%	XP_019806235.1
PREDICTED: attractin [Odobenus rosmarus divergens]	54.5	54.5	100%	9e-08	100%	XP_004398236.1
PREDICTED: attractin isoform X2 [Pan troglodytes]	54.5	54.5	100%	9e-08	100%	XP_016792848.1
PREDICTED: attractin [Lipotes vexillifer]	54.5	54.5	100%	9e-08	100%	XP_007465469.1
PREDICTED: attractin isoform X1 [Condylura cristata]	54.5	54.5	100%	9e-08	100%	XP_004687417.1
PREDICTED: attractin isoform X1 [Panthera pardus]	54.5	54.5	100%	9e-08	100%	XP_019318201.1
PREDICTED: attractin [Orcinus orca]	54.5	54.5	100%	9e-08	100%	XP_004285351.1
PREDICTED: attractin isoform X1 [Canis lupus familiaris]	54.5	54.5	100%	9e-08	100%	XP_534360.2
PREDICTED: attractin isoform X1 [Ceratotherium simum simum]	54.5	54.5	100%	9e-08	100%	XP_004433859.1
attractin isoform X1 [Sus scrofa]	54.5	54.5	100%	9e-08	100%	XP_001927324.7
attractin isoform X1 [Odocoileus virginianus texanus]	54.5	54.5	100%	9e-08	100%	XP_020732718.1
PREDICTED: attractin isoform X1 [Rhinolophus sinicus]	54.5	54.5	100%	9e-08	100%	XP_019589309.1
PREDICTED: attractin isoform X1 [Capra hircus]	54.5	54.5	100%	9e-08	100%	XP_017912899.1
PREDICTED: attractin [Eptesicus fuscus]	54.5	54.5	100%	9e-08	100%	XP_008139256.1
attractin [Bos taurus]	54.5	54.5	100%	9e-08	100%	NP_776420.1
PREDICTED: attractin isoform X2 [Bubalus bubalis]	54.5	54.5	100%	9e-08	100%	XP_006072964.1
PREDICTED: attractin isoform X1 [Rousettus aegyptiacus]	54.5	54.5	100%	9e-08	100%	XP_015994231.1
PREDICTED: attractin isoform X1 [Felis catus]	54.5	54.5	100%	9e-08	100%	XP_019682332.1
attractin [Bos taurus]	54.5	54.5	100%	9e-08	100%	ACT32973.1
PREDICTED: attractin [Echinops telfairi]	54.5	54.5	100%	9e-08	100%	XP_004697922.1
PREDICTED: attractin [Vicugna pacos]	54.5	54.5	100%	9e-08	100%	XP_006207473.1
PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	54.5	54.5	100%	9e-08	100%	XP_008017704.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin isoform X2 [Cercocebus atys]	54.5	54.5	100%	9e-08	100%	XP_011907601.1
PREDICTED: attractin isoform X3 [Pan troglodytes]	54.5	54.5	100%	9e-08	100%	XP_009435010.2
PREDICTED: attractin [Peromyscus maniculatus bairdii]	54.5	54.5	100%	9e-08	100%	XP_006984624.1
PREDICTED: attractin isoform X1 [Lepisosteus oculatus]	54.5	54.5	100%	9e-08	100%	XP_006629173.1
PREDICTED: attractin [Fukomys damarensis]	54.5	54.5	100%	9e-08	100%	XP_010609356.1
PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	54.5	54.5	100%	9e-08	100%	XP_008017707.1
PREDICTED: attractin isoform X3 [Cercocebus atys]	54.5	54.5	100%	9e-08	100%	XP_011907603.1
attractin [Numida meleagris]	54.5	54.5	100%	9e-08	100%	XP_021251195.1
attractin isoform X2 [Heterocephalus glaber]	54.5	54.5	100%	9e-08	100%	XP_021110653.1
attractin, isoform CRA_b [Homo sapiens]	54.5	54.5	100%	9e-08	100%	EAX10531.1
PREDICTED: attractin [Tupaia chinensis]	54.5	54.5	100%	9e-08	100%	XP_014437769.1
PREDICTED: attractin isoform X2 [Rhinolophus sinicus]	54.5	54.5	100%	9e-08	100%	XP_019589310.1
PREDICTED: attractin [Camelus bactrianus]	54.5	54.5	100%	9e-08	100%	XP_010971103.1
PREDICTED: attractin [Ailuropoda melanoleuca]	54.5	54.5	100%	9e-08	100%	XP_019654759.1
hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	54.5	54.5	100%	9e-08	100%	EFB15456.1
PREDICTED: attractin [Chrysemys picta bellii]	54.5	54.5	100%	9e-08	100%	XP_008167842.1
PREDICTED: attractin [Ursus maritimus]	54.5	54.5	100%	9e-08	100%	XP_008701660.1
PREDICTED: attractin [Pelodiscus sinensis]	54.5	54.5	100%	9e-08	100%	XP_014437095.1
PREDICTED: attractin [Bos mutus]	54.5	54.5	100%	9e-08	100%	XP_005894036.1
PREDICTED: attractin [Camelus dromedarius]	54.5	54.5	100%	9e-08	100%	XP_010986570.1
PREDICTED: attractin isoform X4 [Cercocebus atys]	54.5	54.5	100%	9e-08	100%	XP_011907604.1
attractin [Cricetulus griseus]	54.5	54.5	100%	9e-08	100%	ERE69757.1
PREDICTED: attractin isoform X2 [Rousettus aegyptiacus]	54.5	54.5	100%	9e-08	100%	XP_015994322.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: attractin isoform X2 [Felis catus]	54.5	54.5	100%	9e-08	100%	XP_019682335.1
PREDICTED: attractin [Myotis lucifugus]	54.5	54.5	100%	9e-08	100%	XP_006096513.1
PREDICTED: attractin isoform X2 [Ceratotherium simum simum]	54.5	54.5	100%	9e-08	100%	XP_014645595.1
PREDICTED: attractin isoform X3 [Ceratotherium simum simum]	54.5	54.5	100%	9e-08	100%	XP_014645596.1
PREDICTED: attractin [Acinonyx jubatus]	54.5	54.5	100%	9e-08	100%	XP_014933613.1
PREDICTED: attractin isoform X1 [Cricetulus griseus]	54.5	54.5	100%	9e-08	100%	XP_003499099.1
PREDICTED: attractin isoform X3 [Rhinolophus sinicus]	54.5	54.5	100%	9e-08	100%	XP_019589312.1
PREDICTED: attractin isoform X1 [Ovis aries]	54.5	54.5	100%	9e-08	100%	XP_012044119.1
PREDICTED: attractin [Trichechus manatus latirostris]	54.5	54.5	100%	9e-08	100%	XP_004383126.1
Attractin [Heterocephalus glaber]	54.5	54.5	100%	9e-08	100%	EHB04302.1
PREDICTED: attractin isoform X4 [Rhinolophus sinicus]	54.5	54.5	100%	9e-08	100%	XP_019589313.1
PREDICTED: attractin-like [Galeopterus variegatus]	54.5	54.5	100%	9e-08	100%	XP_008589101.1
PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	54.5	54.5	100%	9e-08	100%	XP_008017712.1
PREDICTED: attractin isoform X2 [Macaca mulatta]	54.5	54.5	100%	9e-08	100%	XP_015004917.1
PREDICTED: attractin isoform X1 [Macaca nemestrina]	54.5	54.5	100%	9e-08	100%	XP_011739576.1
PREDICTED: attractin isoform X5 [Cercocebus atys]	54.5	54.5	100%	9e-08	100%	XP_011907605.1

Alignments

PREDICTED: attractin isoform X3 [Mustela putorius furo]
Sequence ID: **XP_012901500.1** Length: 1544 Number of Matches: 1
Range 1: 592 to 606

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	9e-08()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    WSVLPRPDLHHDVNR  15
            WSVLPRPDLHHDVNR
Sbjct  592  WSVLPRPDLHHDVNR  606
```

PREDICTED: attractin isoform X1 [Bubalus bubalis]

Sequence ID: **XP_006072963.1** Length: 1495 Number of Matches: 1
Range 1: 587 to 601

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	9e-08()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    WSVLPRPDLHHDVNR  15
            WSVLPRPDLHHDVNR
Sbjct  587  WSVLPRPDLHHDVNR  601
```

PREDICTED: attractin isoform X3 [Panthera pardus]

Sequence ID: **XP_019318206.1** Length: 1491 Number of Matches: 1
Range 1: 589 to 603

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	9e-08()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    WSVLPRPDLHHDVNR  15
            WSVLPRPDLHHDVNR
Sbjct  589  WSVLPRPDLHHDVNR  603
```

PREDICTED: attractin isoform X4 [Canis lupus familiaris]

Sequence ID: **XP_005634904.1** Length: 1490 Number of Matches: 1
Range 1: 588 to 602

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	9e-08()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    WSVLPRPDLHHDVNR  15
            WSVLPRPDLHHDVNR
Sbjct  588  WSVLPRPDLHHDVNR  602
```

PREDICTED: attractin isoform X3 [Tursiops truncatus]

Sequence ID: **XP_019806237.1** Length: 1489 Number of Matches: 1
Range 1: 591 to 605

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	9e-08()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    WSVLPRPDLHHDVNR  15
            WSVLPRPDLHHDVNR
Sbjct  591  WSVLPRPDLHHDVNR  605
```

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BLAST Results

Job title: NCBI BlastP_CPN2_LELLSLSK

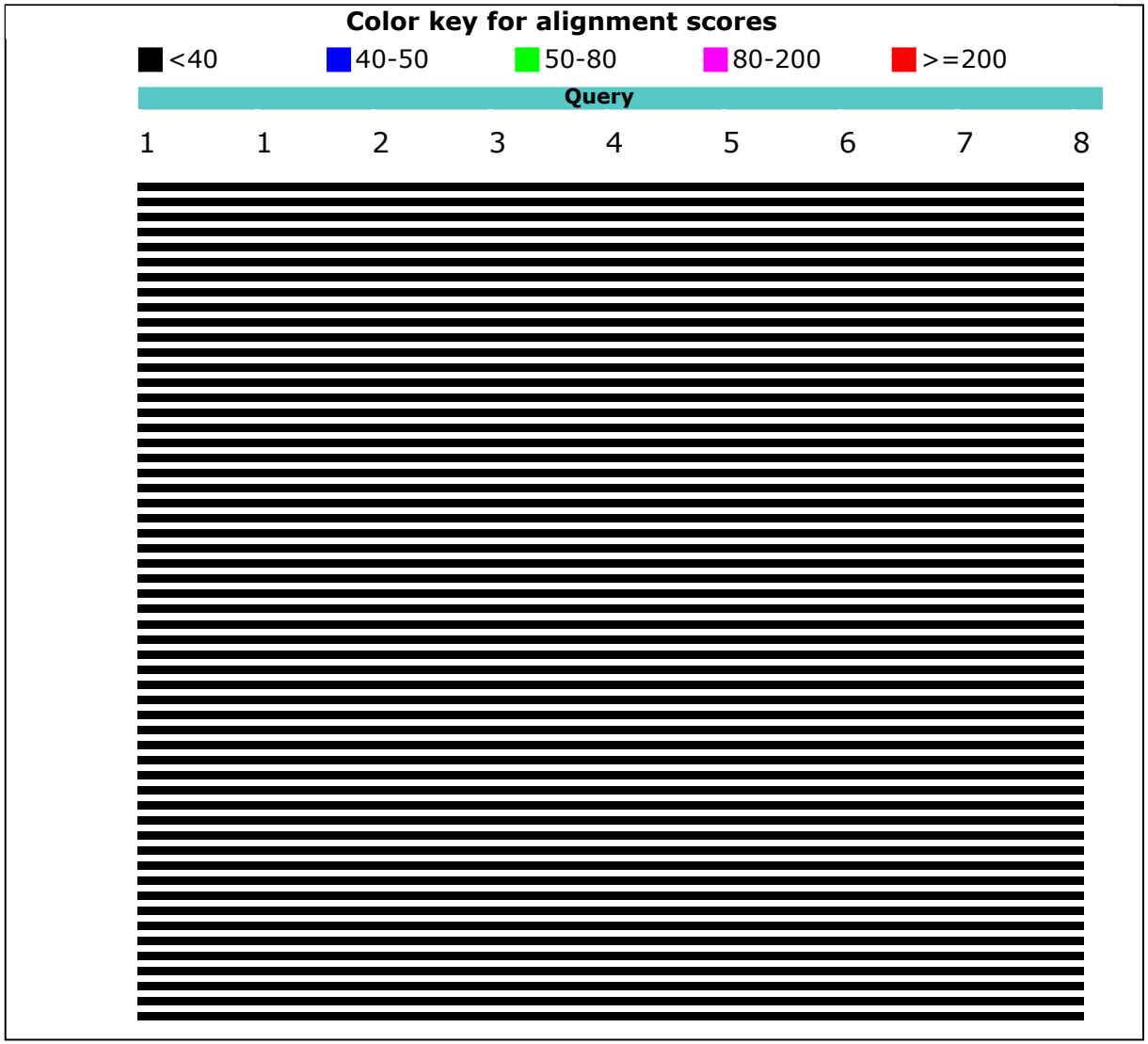
RID S54T775K014 (Expires on 08-04 11:06 am)

Query ID	lcl|Query_353882	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	8	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 104 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
leucine-rich transmembrane protein [Culex quinquefasciatus]	26.5	26.5	100%	168	100%	EDS27483.1
TIR-NBS-LRR disease resistance protein [Malus domestica]	26.5	44.5	100%	168	100%	CDK13059.1
AGAP007059-PA [Anopheles gambiae str. PEST]	26.5	26.5	100%	168	100%	EDO64711.1
hypothetical protein [Paraprevotella clara]	26.5	26.5	100%	168	100%	WP_008618188.1
hypothetical protein PPL_04819 [Polysphondylium pallidum PN500]	26.5	26.5	100%	168	100%	EFA82394.1
BTB domain-containing protein/DUF3420 domain-containing protein/NPR1_like_C domain-containing protein/Ank_2 domain-containing protein [Cephalotus follicularis]	26.5	26.5	100%	169	100%	GAV76236.1
hCG2040284 [Homo sapiens]	26.5	26.5	100%	169	100%	EAW78055.1
hypothetical protein X777_09600 [Ooceraea biroi]	26.5	26.5	100%	169	100%	EZA51592.1
Carboxypeptidase N, polypeptide 2 [Homo sapiens]	26.5	26.5	100%	169	100%	AAH42334.2
carboxypeptidase N subunit 2 precursor [Pongo abelii]	26.5	26.5	100%	169	100%	NP_001127634.1
Carboxypeptidase N, polypeptide 2 [Homo sapiens]	26.5	26.5	100%	169	100%	AAH31569.2
hypothetical protein EGM_11223 [Macaca fascicularis]	26.5	26.5	100%	169	100%	EHH51780.1
hypothetical protein EGK_12232 [Macaca mulatta]	26.5	26.5	100%	169	100%	EHH16865.1
carboxypeptidase N subunit 2 precursor [Homo sapiens]	26.5	26.5	100%	169	100%	NP_001073982.3
carboxypeptidase N precursor [Homo sapiens]	26.5	26.5	100%	169	100%	AAA51921.2
hypothetical protein [Flavobacterium antarcticum]	26.5	26.5	100%	170	100%	WP_022827797.1
electron transfer flavoprotein subunit alpha [candidate division Zixibacteria bacterium SM23_73_2]	26.5	26.5	100%	170	100%	KPL03122.1
DUF4367 domain-containing protein [Bacillus sp. FJAT-27264]	26.5	26.5	100%	170	100%	WP_066377724.1
alpha/beta hydrolase [Bacillus fastidiosus]	26.5	26.5	100%	171	100%	WP_066232760.1
ABC transporter ATP-binding protein [Nitrosococcus oceani]	26.5	26.5	100%	171	100%	WP_002809254.1
MULTISPECIES: hypothetical protein [Candidatus Arthromitus]	26.5	26.5	100%	176	100%	WP_005807222.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein SFB5_056G0 [Candidatus Arthromitus sp. SFB-5]	26.5	26.5	100%	184	100%	EIA29651.1
UNKNOWN [Stylonychia lemnae]	24.0	24.0	100%	1370	88%	CDW89768.1
hypothetical protein cubi_02354 [Cryptosporidium ubiquitum]	24.0	24.0	100%	1371	88%	OII73123.1
DNA ligase 4 [Atta colombica]	24.0	24.0	100%	1371	88%	KYM80800.1
DNA ligase 4 [Trachymyrmex zeteki]	24.0	24.0	100%	1371	88%	KYQ49262.1
hypothetical protein JL09_g3900 [Pichia kudriavzevii]	24.0	24.0	100%	1371	88%	KGK36949.1
MULTISPECIES: hypothetical protein [Pseudomonas]	24.0	24.0	100%	1371	88%	WP_085667922.1
hypothetical protein [Pseudomonas putida]	24.0	24.0	100%	1371	88%	WP_074688495.1
hypothetical protein [Pseudomonas fluorescens]	24.0	24.0	100%	1371	88%	WP_052266522.1
hypothetical protein QS95_04035 [Pseudomonas fluorescens]	24.0	24.0	100%	1371	88%	KIF63299.1
hypothetical protein CAS74_004211 [Pichia kudriavzevii]	24.0	24.0	100%	1372	88%	OUT20551.1
hypothetical protein VE03_00071 [Pseudogymnoascus sp. 23342-1-I1]	24.0	24.0	100%	1372	88%	OBT70486.1
nucleoporin Nup157/170 [Microdochium bolleyi]	24.0	24.0	100%	1372	88%	KXJ88307.1
DNA ligase 4 [Trachymyrmex septentrionalis]	24.0	24.0	100%	1372	88%	KYN45087.1
DNA ligase 4 [Trachymyrmex cornetzi]	24.0	24.0	100%	1372	88%	KYN22371.1
magnesium chelatase subunit H [Tolypothrix campylonemoides]	24.0	24.0	100%	1372	88%	WP_041033373.1
Putative disease resistance protein RGA1 [Aegilops tauschii]	24.0	24.0	100%	1372	88%	EMT15808.1
Putative disease resistance protein RGA1 [Triticum urartu]	24.0	24.0	100%	1372	88%	EMS49892.1
magnesium chelatase subunit H [Mastigocladopsis repens]	24.0	24.0	100%	1372	88%	WP_017318044.1
protoporphyrin IX magnesium chelatase [Scytonema sp. NIES-4073]	24.0	24.0	100%	1372	88%	BAZ22035.1
magnesium chelatase subunit H [Fischerella sp. PCC 9605]	24.0	24.0	100%	1372	88%	WP_026733216.1
magnesium chelatase subunit H [Scytonema sp. HK-05]	24.0	24.0	100%	1372	88%	WP_073630169.1
magnesium chelatase subunit H [Scytonema tolypothrichoides]	24.0	24.0	100%	1373	88%	WP_048870373.1
Putative disease resistance protein RGA3 [Aegilops tauschii]	24.0	24.0	100%	1373	88%	EMT25263.1
TMV resistance protein N-like [Prunus avium]	24.0	24.0	100%	1373	88%	XP_021805796.1
hypothetical protein PRUPE_2G060400 [Prunus persica]	24.0	24.0	100%	1373	88%	ONI21338.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
NBS2-RDG2A [Hordeum vulgare subsp. vulgare]	24.0	24.0	100%	1373	88%	ADK47522.1
unnamed protein product [Triticum aestivum]	24.0	42.4	100%	1373	88%	CDM86074.1
hypothetical protein PRUPE_2G060400 [Prunus persica]	24.0	24.0	100%	1373	88%	ONI21337.1
hybrid sensor histidine kinase/response regulator [Cupriavidus sp. UYPR2.512]	24.0	24.0	100%	1373	88%	WP_018308787.1
hypothetical protein FOMMEDRAFT_95786 [Fomitiporia mediterranea MF3/22]	24.0	24.0	100%	1373	88%	EJC98571.1
hypothetical protein PRUPE_2G060400 [Prunus persica]	24.0	24.0	100%	1373	88%	ONI21341.1
hypothetical protein PRUPE_2G060400 [Prunus persica]	24.0	24.0	100%	1373	88%	ONI21340.1
hypothetical protein [Mariprofundus ferrooxydans]	24.0	24.0	100%	1374	88%	WP_081610071.1
Disease resistance protein RGA2 [Triticum urartu]	24.0	24.0	100%	1374	88%	EMS51339.1
hypothetical protein Pmar_PMAR013111 [Perkinsus marinus ATCC 50983]	24.0	42.0	100%	1374	88%	EER08201.1
hypothetical protein, conserved [Leishmania guyanensis]	24.0	24.0	100%	1374	88%	CCM18051.1
conserved hypothetical protein [Leishmania braziliensis MHOM/BR/75/M2904]	24.0	24.0	100%	1374	88%	CAM42755.1
hypothetical protein LPMP_312850 [Leishmania panamensis]	24.0	24.0	100%	1374	88%	AIO00869.1
hypothetical protein POPTR_0001s43410g [Populus trichocarpa]	24.0	24.0	100%	1374	88%	EEE83755.2
unnamed protein product [Paramecium tetraurelia]	24.0	24.0	100%	1374	88%	CAK65954.1
hypothetical protein SOVF_066240 [Spinacia oleracea]	24.0	24.0	100%	1374	88%	KNA18926.1
DNA ligase 4 [Acromyrmex echinatior]	24.0	24.0	100%	1374	88%	EGI57410.1
kinase-like protein [Glonium stellatum]	24.0	24.0	100%	1375	88%	OCL05569.1
hypothetical protein BWI17_09555 [Betaproteobacteria bacterium GR16-43]	24.0	24.0	100%	1375	88%	APV49907.1
hypothetical protein UU87_C0004G0048 [Parcubacteria group bacterium GW2011_GWA2_42_11]	24.0	24.0	100%	1375	88%	KKS26064.1
nucleotidyl transferase [Chloroflexi bacterium 13_1_40CM_4_68_4]	24.0	24.0	100%	1375	88%	OLC54946.1
hybrid sensor histidine kinase/response regulator [Shewanella sp. Alg231_23]	24.0	24.0	100%	1375	88%	WP_065187600.1
mannose-1-phosphate guanyltransferase [Thermosulfidibacter takaii]	24.0	24.0	100%	1375	88%	WP_068549989.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
translation initiation factor IF-2 [bacterium TMED264]	24.0	24.0	100%	1375	88%	OUX30117.1
hybrid sensor histidine kinase/response regulator [Shewanella woodyi]	24.0	24.0	100%	1375	88%	WP_012323679.1
hypothetical protein PRUPE_2G060400 [Prunus persica]	24.0	24.0	100%	1375	88%	ONI21339.1
hypothetical protein Pmar_PMAR010262 [Perkinsus marinus ATCC 50983]	24.0	42.0	100%	1375	88%	EER20516.1
CRISPR-associated helicase/endonuclease Cas3 [Ruminococcus sp. YE71]	24.0	24.0	100%	1375	88%	WP_072419571.1
unnamed protein product [Vitrella brassicaformis CCMP3155]	24.0	24.0	100%	1375	88%	CEL93566.1
CRISPR-associated helicase/endonuclease Cas3 [Ruminococcus sp. YE71]	24.0	24.0	100%	1375	88%	WP_072416762.1
hypothetical protein QR46_3019 [Giardia intestinalis assemblage B]	24.0	24.0	100%	1375	88%	KWX12984.1
Glycosyl transferases group 1 [Devosia crocina]	24.0	24.0	100%	1376	88%	SFV38466.1
multi-sensor hybrid histidine kinase [Nitrosospira lacus]	24.0	24.0	100%	1376	88%	WP_004179312.1
hypothetical protein UV36_C0044G0004 [Parcubacteria group bacterium GW2011_GWC2_42_6]	24.0	24.0	100%	1376	88%	KKS65728.1
Putative disease resistance protein RGA1 [Aegilops tauschii]	24.0	24.0	100%	1376	88%	EMT15811.1
cell division protein FtsA [Pseudothermotoga thermarum]	24.0	24.0	100%	1376	88%	WP_013932518.1
hypothetical protein [Leisingera sp. ANG-Vp]	24.0	24.0	100%	1377	88%	WP_052249080.1
DNA ligase (NAD(+)) LigA [Pelagibacteraceae bacterium ETNP-OMZ-SAG-D9]	24.0	24.0	100%	1377	88%	WP_069282139.1
elongation factor G [Paeniclostridium sordellii]	24.0	24.0	100%	1377	88%	WP_057542680.1
hypothetical protein PRUPE_4G163400 [Prunus persica]	24.0	24.0	100%	1377	88%	ONI12413.1
diguanylate cyclase (GGDEF) domain-containing protein [Vibrio hangzhouensis]	24.0	24.0	100%	1378	88%	SEG43887.1
hypothetical protein RA20_19055 [Leisingera sp. ANG-Vp]	24.0	24.0	100%	1378	88%	KIC15152.1
hypothetical protein RF55_2653 [Lasius niger]	24.0	24.0	100%	1378	88%	KMQ97038.1
hypothetical protein PRUPE_4G163400 [Prunus persica]	24.0	24.0	100%	1379	88%	ONI12414.1
Carboxypeptidase N subunit 2 [Cricetulus griseus]	24.0	24.0	100%	1379	88%	EGW12890.1
acetyl-CoA synthetase-like protein [Laetiporus sulphureus 93-53]	24.0	24.0	100%	1379	88%	KZT05903.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
DegT/DnrJ/EryC1/StrS aminotransferase [Beggiatoa sp. PS]	24.0	24.0	100%	1380	88%	EDN67416.1
hypothetical protein PRUPE_3G095400 [Prunus persica]	24.0	24.0	100%	1380	88%	ONI16387.1
MULTISPECIES: DUF4010 domain-containing protein [Ferrovum]	24.0	24.0	100%	1380	88%	WP_082783096.1
FAD-binding oxidoreductase [Agrobacterium rhizogenes]	24.0	24.0	100%	1380	88%	WP_080761274.1
FAD-binding oxidoreductase [Marivita cryptomonadis]	24.0	24.0	100%	1380	88%	WP_085629055.1
FAD-binding oxidoreductase [Marivita geojedonensis]	24.0	24.0	100%	1380	88%	WP_085636005.1
FAD-binding oxidoreductase [Marivita hallyeonensis]	24.0	24.0	100%	1380	88%	WP_072779228.1

Alignments

leucine-rich transmembrane protein [Culex quinquefasciatus]
Sequence ID: **EDS27483.1** Length: 1512 Number of Matches: 1
Range 1: 865 to 872

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	168()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    LELLSLSK  8
            LELLSLSK
Sbjct  865  LELLSLSK  872
```

TIR-NBS-LRR disease resistance protein [Malus domestica]
Sequence ID: **CDK13059.1** Length: 1182 Number of Matches: 2
Range 1: 807 to 814

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	168()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    LELLSLSK  8
            LELLSLSK
Sbjct  807  LELLSLSK  814
```

Range 2: 432 to 436

Score	Expect	Method	Identities	Positives	Gaps	Frame
18.0 bits(35)	194200()		5/5(100%)	5/5(100%)	0/5(0%)	

Features:

```
Query  1    LELLS  5
            LELLS
Sbjct  432  LELLS  436
```

AGAP007059-PA [Anopheles gambiae str. PEST]

Sequence ID: **EDO64711.1** Length: 1098 Number of Matches: 1
Range 1: 77 to 84

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	168()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1   LELLSLSK  8
           LELLSLSK
Sbjct  77  LELLSLSK  84
```

hypothetical protein [Paraprevotella clara]

Sequence ID: **WP_008618188.1** Length: 1027 Number of Matches: 1

See 1 more title(s)

Range 1: 135 to 142

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	168()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    LELLSLSK  8
            LELLSLSK
Sbjct  135  LELLSLSK  142
```

hypothetical protein PPL_04819 [Polysphondylium pallidum PN500]

Sequence ID: **EFA82394.1** Length: 765 Number of Matches: 1

Range 1: 306 to 313

Score	Expect	Method	Identities	Positives	Gaps	Frame
26.5 bits(55)	168()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    LELLSLSK  8
            LELLSLSK
Sbjct  306  LELLSLSK  313
```

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BLAST Results

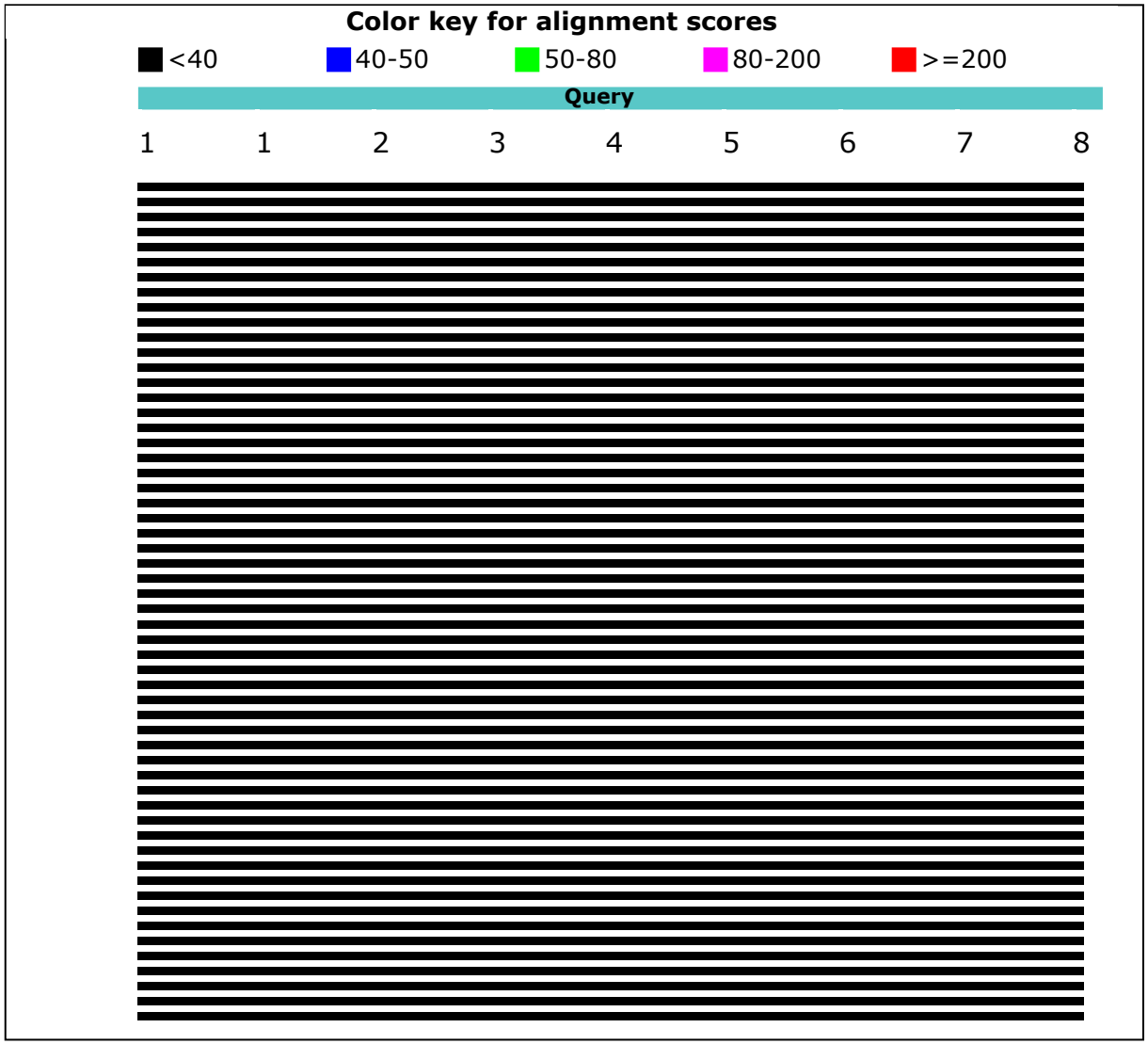
Job title: NCBI BlastP_CPN2_LTVSIEAR

RID	S54TM536015 (Expires on 08-04 11:06 am)
Query ID	lcl|Query_363692
Description	None
Molecule type	amino acid
Query Length	8
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
complement C3-H1-like precursor [Danio rerio]	27.4	27.4	100%	83	100%	NP_001008582.4
hCG2040284 [Homo sapiens]	27.4	27.4	100%	84	100%	EAW78055.1
Carboxypeptidase N, polypeptide 2 [Homo sapiens]	27.4	27.4	100%	84	100%	AAH42334.2
carboxypeptidase N subunit 2 precursor [Pongo abelii]	27.4	27.4	100%	84	100%	NP_001127634.1
Carboxypeptidase N, polypeptide 2 [Homo sapiens]	27.4	27.4	100%	84	100%	AAH31569.2
hypothetical protein EGM_11223 [Macaca fascicularis]	27.4	27.4	100%	84	100%	EHH51780.1
hypothetical protein EGK_12232 [Macaca mulatta]	27.4	27.4	100%	84	100%	EHH16865.1
carboxypeptidase N subunit 2 precursor [Homo sapiens]	27.4	27.4	100%	84	100%	NP_001073982.3
hypothetical protein AVO35_10290 [Candidatus Aegiribacteria bacterium MLS_C]	27.4	27.4	100%	84	100%	OPL19543.1
hypothetical protein GA0070620_4216 [Micromonospora krabiensis]	27.4	27.4	100%	84	100%	SBV28665.1
Zgc:103710 protein [Danio rerio]	27.4	27.4	100%	84	100%	AAI22312.1
hypothetical protein OSG_eHP6_00010 [Environmental Halophage eHP-6]	24.8	24.8	100%	681	88%	AFH21635.1
hypothetical protein OSG_eHP36_00015 [Environmental Halophage eHP-36]	24.8	24.8	100%	681	88%	AFH22830.1
hypothetical protein OSG_eHP12_00025 [Environmental Halophage eHP-12]	24.8	24.8	100%	681	88%	AFH21880.1
hypothetical protein OSG_eHP16_00175 [Environmental Halophage eHP-16]	24.8	24.8	100%	681	88%	AFH22127.1
Hypothetical protein A7982_06382 [Minicystis rosea]	24.8	24.8	100%	682	88%	APR81035.1
hypothetical protein SPPG_05260 [Spizellomyces punctatus DAOM BR117]	24.8	24.8	100%	683	88%	KNC99887.1
hypothetical protein [Acetobacterium wieringae]	24.8	24.8	100%	683	88%	WP_070370558.1
hypothetical protein [Leptolyngbya sp. 'hensonii']	24.8	24.8	100%	683	88%	WP_075599857.1
L-glutaminase [Corynebacterium cystitidis DSM 20524]	24.8	24.8	100%	684	88%	SES25182.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
glutaminase [Corynebacterium pilosum]	24.8	24.8	100%	684	88%	WP_018582449.1
accessory secretory protein Asp2 [Streptococcus oralis]	24.8	24.8	100%	684	88%	WP_049503153.1
hypothetical protein [Lacunisphaera limnophila]	24.8	24.8	100%	684	88%	WP_083270347.1
SAG-related sequence SRS38D [Hammondia hammondi]	24.8	24.8	100%	685	88%	KEP60473.1
Dicarboxylate transport [Lacunisphaera limnophila]	24.8	24.8	100%	685	88%	AOS45672.1
two-component sensor histidine kinase [Brevibacillus borstelensis]	24.8	24.8	100%	685	88%	WP_003390083.1
SAG-related sequence SRS38B [Toxoplasma gondii VAND]	24.8	24.8	100%	686	88%	KFH01761.1
SAG-related sequence SRS38B [Toxoplasma gondii ME49]	24.8	24.8	100%	686	88%	EPT27600.1
SAG-related sequence SRS38B [Toxoplasma gondii VEG]	24.8	24.8	100%	686	88%	ESS33465.1
SAG-related sequence SRS38B [Toxoplasma gondii GT1]	24.8	24.8	100%	686	88%	EPR57097.1
SAG-related sequence SRS54 [Toxoplasma gondii MAS]	24.8	24.8	100%	686	88%	KFH18277.1
SAG-related sequence SRS54 [Toxoplasma gondii VAND]	24.8	24.8	100%	686	88%	KFH02029.1
SAG-related sequence SRS54 [Toxoplasma gondii FOU]	24.8	24.8	100%	686	88%	KFG56380.1
SAG-related sequence SRS54 [Toxoplasma gondii p89]	24.8	24.8	100%	686	88%	KFG49383.1
SAG-related sequence SRS54 [Toxoplasma gondii ME49]	24.8	24.8	100%	686	88%	EPT25709.1
SAG-related sequence SRS38D [Toxoplasma gondii VEG]	24.8	24.8	100%	686	88%	ESS33467.1
SAG-related sequence SRS38D [Toxoplasma gondii ME49]	24.8	24.8	100%	686	88%	EPT27598.1
SAG-related sequence SRS54 [Toxoplasma gondii GT1]	24.8	24.8	100%	686	88%	EPR58797.1
SAG-related sequence SRS38D [Toxoplasma gondii VAND]	24.8	24.8	100%	686	88%	KFH01763.1
srs domain-containing protein [Neospora caninum Liverpool]	24.8	24.8	100%	686	88%	CBZ50818.1
SAG-related sequence SRS38D [Toxoplasma gondii GAB2-2007-GAL-DOM2]	24.8	24.8	100%	686	88%	KFG38843.1
hypothetical protein BVY02_01925 [bacterium J17]	24.8	24.8	100%	687	88%	OVE79905.1
SAG-related sequence SRS38B [Toxoplasma gondii GAB2-2007-GAL-DOM2]	24.8	24.8	100%	687	88%	KFG38845.1
SAG-related sequence SRS38D [Toxoplasma gondii GT1]	24.8	24.8	100%	687	88%	EPR57099.1
phenylalanyl-tRNA synthetase subunit alpha [Gluconobacter morbifer G707]	24.8	24.8	100%	687	88%	EHH67636.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
phenylalanine--tRNA ligase subunit alpha [Gluconobacter morbifer]	24.8	24.8	100%	687	88%	WP_040509129.1
SAG-related sequence SRS12D [Hammondia hammondi]	24.8	24.8	100%	687	88%	KEP60475.1
hypothetical protein STRATTON_76 [Erwinia phage vB_EamM_Stratton]	24.8	24.8	100%	687	88%	ANZ50501.1
hypothetical protein [Erwinia phage phiEaH2]	24.8	24.8	100%	687	88%	YP_007237894.1
phosphofructokinase [Frankia sp. NRRL B-16219]	24.8	24.8	100%	688	88%	OHV27871.1
cytochrome oxidase assembly protein [Leptospira alstonii]	24.8	24.8	100%	688	88%	WP_069608830.1
1-phosphofructokinase [Frankia sp. G2]	24.8	24.8	100%	688	88%	CUU59835.1
phosphofructokinase [Frankia sp. NRRL B-16219]	24.8	24.8	100%	688	88%	WP_083391057.1
phosphofructokinase [Frankia sp. Cc1.17]	24.8	24.8	100%	688	88%	WP_071083453.1
phosphofructokinase [Frankia sp. EUN1f]	24.8	24.8	100%	688	88%	WP_006540146.1
phosphofructokinase [Frankia elaeagni]	24.8	24.8	100%	688	88%	WP_018637687.1
SAG-related sequence SRS38B [Toxoplasma gondii TgCatPRC2]	24.8	24.8	100%	689	88%	KYK62299.1
hypothetical protein A3C45_00140 [Deltaproteobacteria bacterium RIFCSPHIGHO2_02_FULL_40_28]	24.8	24.8	100%	690	88%	OGQ07657.1
amino acid/amide ABC transporter ATP-binding protein 1, HAAT family [Rhizobiales bacterium GAS191]	24.8	24.8	100%	690	88%	SEF15503.1
amino acid/amide ABC transporter ATP-binding protein 1, HAAT family [Rhizobiales bacterium GAS113]	24.8	24.8	100%	690	88%	SDR57975.1
SAG-related sequence protein SRS38D [Toxoplasma gondii ARI]	24.8	24.8	100%	691	88%	KYF45576.1
SAG-related sequence SRS38D [Toxoplasma gondii RUB]	24.8	24.8	100%	691	88%	KFG58900.1
hypothetical protein AUK54_02340 [Helicobacteraceae bacterium CG2_30_36_10]	24.8	24.8	100%	692	88%	OIP56311.1
SAG-related sequence protein SRS38B [Toxoplasma gondii ARI]	24.8	24.8	100%	693	88%	KYF45575.1
SAG-related sequence protein SRS38B [Toxoplasma gondii MAS]	24.8	24.8	100%	693	88%	KFH13763.1
SAG-related sequence protein SRS38D [Toxoplasma gondii ARI]	24.8	24.8	100%	693	88%	KYF38502.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
SAG-related sequence protein SRS38D [Toxoplasma gondii GT1]	24.8	24.8	100%	693	88%	EPR57156.1
SRPBCC family protein [Oceaniovalibus guishaninsula]	24.8	24.8	100%	699	88%	WP_007426909.1
GM2 activator protein [Felis catus]	24.8	24.8	100%	699	88%	AAS64350.1
GM2 activator protein variant AB [Felis catus]	24.8	24.8	100%	700	88%	AAS64351.1
hypothetical protein AMJ64_00305 [Betaproteobacteria bacterium SG8_39]	24.8	24.8	100%	714	88%	KPK09328.1
hypothetical protein LOTGIDRAFT_232792 [Lottia gigantea]	24.4	24.4	87%	965	100%	ESO93399.1
hypothetical protein GUITHDRAFT_135976 [Guillardia theta CCMP2712]	24.4	24.4	100%	965	88%	EKX49278.1
hypothetical protein [Bacillus thuringiensis]	24.4	24.4	87%	965	100%	WP_062804305.1
hypothetical protein [Aureimonas altamirensis]	24.4	24.4	87%	965	100%	WP_039188836.1
hypothetical protein AMJ79_12610 [Phycisphaerae bacterium SM23_30]	24.4	24.4	87%	966	100%	KPK75060.1
hypothetical protein [Fibrobacter sp. UWB5]	24.4	24.4	100%	966	88%	WP_088628250.1
hypothetical protein B7988_06955 [Fibrobacter sp. UWB1]	24.4	24.4	100%	966	88%	OWV26051.1
hypothetical protein [Fibrobacter sp. UWOV1]	24.4	24.4	100%	966	88%	WP_073318055.1
hypothetical protein B7989_09470 [Fibrobacter sp. UWB5]	24.4	24.4	100%	966	88%	OWV11847.1
hypothetical protein [Fibrobacter sp. UWB1]	24.4	24.4	100%	966	88%	WP_088657360.1
hypothetical protein CBB61_02520 [Gammaproteobacteria bacterium TMED1]	24.4	24.4	87%	967	100%	OUT34801.1
hypothetical protein ASPSYDRAFT_95897 [Aspergillus sydowii CBS 593.65]	24.4	24.4	87%	967	100%	OJJ52204.1
AcrB/AcrD/AcrF family protein [Gayadomonas joobiniege]	24.4	24.4	87%	967	100%	WP_017445053.1
hypothetical protein [Agreia pratensis]	24.4	24.4	87%	968	100%	WP_085484016.1
Chitodextrinase [Agreia pratensis]	24.4	24.4	87%	968	100%	SMG24614.1
aminopeptidase N [Microbacterium sp. AISO3]	24.4	24.4	87%	968	100%	WP_088380321.1
aminopeptidase N [Microbacterium paludicola]	24.4	24.4	87%	968	100%	WP_071918249.1
aminopeptidase N [Microbacterium arborescens]	24.4	24.4	87%	968	100%	WP_064956737.1
aminopeptidase N [Microbacterium sp. TS-1]	24.4	24.4	87%	968	100%	WP_023951302.1
putative ABC transport system permease protein [Pedobacter suwonensis]	24.4	24.4	100%	968	88%	SFA45859.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
putative ABC transport system permease protein [Pedobacter terrae]	24.4	24.4	100%	968	88%	SDG52862.1
ABC transporter permease [Pedobacter sp. Leaf176]	24.4	24.4	100%	968	88%	WP_056091945.1
RNA-binding transcriptional accessory protein [Streptomyces sp. TAA040]	24.4	24.4	87%	968	100%	WP_037980569.1
ABC transporter permease [Pedobacter sp. Leaf41]	24.4	24.4	100%	968	88%	WP_056849703.1
hypothetical protein [Pedobacter agri]	24.4	24.4	100%	968	88%	WP_010601349.1
hypothetical protein [Sphingobacteriaceae bacterium GW460-11-11-14-LB5]	24.4	24.4	100%	968	88%	WP_086545380.1
putative ABC transport system permease protein [Pedobacter soli]	24.4	24.4	100%	968	88%	SDD53912.1
ABC transporter permease [Pedobacter kyungheensis]	24.4	24.4	100%	968	88%	WP_039476943.1
ABC transporter permease [Pedobacter sp. AJM]	24.4	24.4	100%	968	88%	WP_088302759.1

Alignments

complement C3-H1-like precursor [Danio rerio]

Sequence ID: **NP_001008582.4** Length: 1642 Number of Matches: 1
Range 1: 250 to 257

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	83()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    LTVSIEAR  8
            LTVSIEAR
Sbjct  250  LTVSIEAR  257
```

hCG2040284, partial [Homo sapiens]

Sequence ID: **EAW78055.1** Length: 564 Number of Matches: 1
Range 1: 553 to 560

Score	Expect	Method	Identities	Positives	Gaps	Frame

27.4 bits(57)	84()	8/8(100%)	8/8(100%)	0/8(0%)

Features:

```
Query  1    LTVSIEAR  8
            LTVSIEAR
Sbjct  553  LTVSIEAR  560
```

Carboxypeptidase N, polypeptide 2 [Homo sapiens]

Sequence ID: **AAH42334.2** Length: 545 Number of Matches: 1

Range 1: 534 to 541

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	84()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    LTVSIEAR  8
            LTVSIEAR
Sbjct  534  LTVSIEAR  541
```

carboxypeptidase N subunit 2 precursor [Pongo abelii]

Sequence ID: **NP_001127634.1** Length: 545 Number of Matches: 1

See 1 more title(s)

Range 1: 534 to 541

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	84()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    LTVSIEAR  8
            LTVSIEAR
Sbjct  534  LTVSIEAR  541
```

Carboxypeptidase N, polypeptide 2 [Homo sapiens]

Sequence ID: **AAH31569.2** Length: 545 Number of Matches: 1

See 2 more title(s)

Range 1: 534 to 541

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	84()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    LTVSIEAR  8
            LTVSIEAR
Sbjct  534  LTVSIEAR  541
```

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BLAST Results

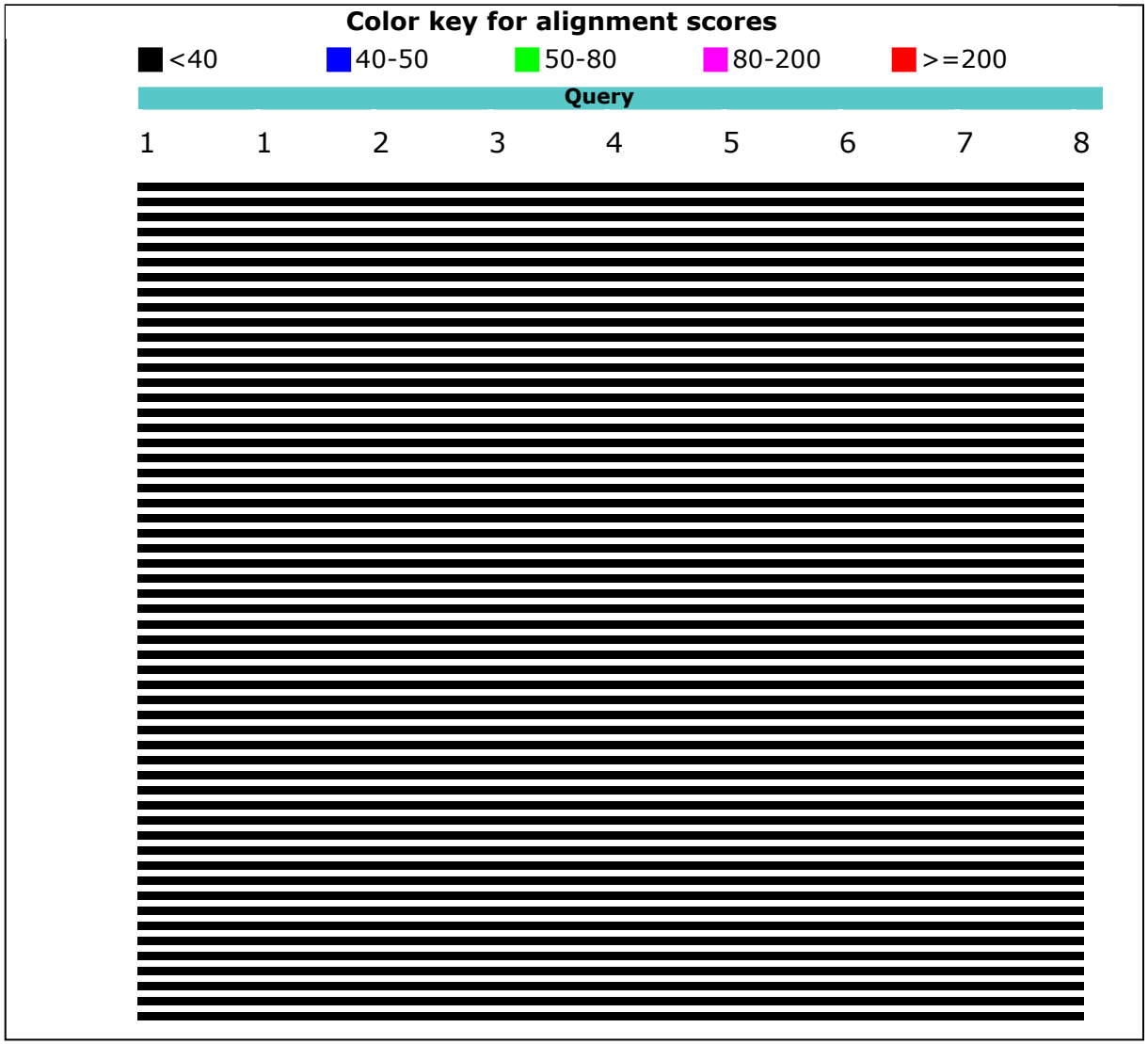
Job title: NCBI BlastP_AMBP_ETLLQDFR

RID	S54E2CG3014 (Expires on 08-04 11:00 am)
Query ID	lcl|Query_206114
Description	None
Molecule type	amino acid
Query Length	8
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein K443DRAFT_672800 [Laccaria amethystina LaAM-08-1]	29.5	29.5	100%	17	100%	KIK08316.1
predicted protein [Laccaria bicolor S238N-H82]	29.5	29.5	100%	17	100%	XP_001874875.1
LAME_0G13300g1_1 [Lachancea meyersii CBS 8951]	29.5	29.5	100%	17	100%	SCV00987.1
LAFA_0E21374g1_1 [Lachancea sp. CBS 6924]	29.5	29.5	100%	17	100%	SCU89846.1
hypothetical protein AUH13_06920 [Acidobacteria bacterium 13_2_20CM_58_27]	29.5	29.5	100%	17	100%	OLB31794.1
hypothetical protein OFPII_16010 [Osedax symbiont Rs1]	29.5	29.5	100%	17	100%	EPJ47028.1
signal transduction histidine kinase [Vibrio nigripulchritudo]	29.5	29.5	100%	17	100%	WP_022612979.1
signal transduction histidine kinase [Vibrio nigripulchritudo]	29.5	29.5	100%	17	100%	WP_022604450.1
sensor histidine kinase [Vibrio nigripulchritudo]	29.5	29.5	100%	17	100%	WP_004403083.1
PREDICTED: protein AMBP [Nomascus leucogenys]	29.5	29.5	100%	17	100%	XP_012364107.1
protein AMBP [Papio anubis]	29.5	29.5	100%	17	100%	XP_003911378.2
PREDICTED: protein AMBP [Gorilla gorilla gorilla]	29.5	29.5	100%	17	100%	XP_004048541.2
PREDICTED: protein AMBP [Pan troglodytes]	29.5	29.5	100%	17	100%	XP_016816990.1
PREDICTED: protein AMBP [Macaca mulatta]	29.5	29.5	100%	17	100%	XP_014972499.1
protein AMBP preproprotein [Homo sapiens]	29.5	29.5	100%	17	100%	NP_001624.1
PREDICTED: protein AMBP [Macaca nemestrina]	29.5	29.5	100%	17	100%	XP_011748670.1
PREDICTED: protein AMBP [Cercocebus atys]	29.5	29.5	100%	17	100%	XP_011947659.1
PREDICTED: protein AMBP [Colobus angolensis palliatus]	29.5	29.5	100%	17	100%	XP_011805484.1
PREDICTED: protein AMBP [Rhinopithecus roxellana]	29.5	29.5	100%	17	100%	XP_010368790.1
PREDICTED: protein AMBP [Chlorocebus sabaeus]	29.5	29.5	100%	17	100%	XP_007966514.1
PREDICTED: protein AMBP [Pan paniscus]	29.5	29.5	100%	17	100%	XP_003833120.1
PREDICTED: protein AMBP [Macaca fascicularis]	29.5	29.5	100%	17	100%	XP_005581045.1
protein AMBP precursor [Pongo abelii]	29.5	29.5	100%	17	100%	NP_001127069.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
polysaccharide deacetylase family protein [Marinobacter adhaerens]	29.5	29.5	100%	17	100%	WP_014577280.1
polysaccharide deacetylase [Marinobacter adhaerens]	29.5	29.5	100%	17	100%	ODM32257.1
lipoyl synthase [Elusimicrobia bacterium GWA2_66_18]	29.5	29.5	100%	17	100%	OGR47031.1
polysaccharide deacetylase [Marinobacter adhaerens]	29.5	29.5	100%	17	100%	WP_083231798.1
hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [Marinospirillum alkaliphilum]	29.5	29.5	100%	17	100%	WP_072325630.1
unnamed protein product [Homo sapiens]	29.5	29.5	100%	17	100%	BAH14052.1
DNA-binding response regulator [Ruminococcus flavefaciens]	29.5	29.5	100%	17	100%	WP_074742786.1
Chain A, Crystal Structure Of Protein Hc From Homo Sapiens At 2 Angstrom	29.5	29.5	100%	17	100%	4ES7_A
TetR/AcrR family transcriptional regulator [Enterococcus hermanniensis]	29.5	29.5	100%	17	100%	WP_071856672.1
Chain A, Crystal Structure Of Alpha-1-microglobulin At 2.3 A Resolution	29.5	29.5	100%	17	100%	3QKG_A
complex-forming glycoprotein HC	29.5	29.5	100%	17	100%	0801163A
alpha-1-microglobulin-bikunin [Macaca fascicularis]	29.5	29.5	100%	19	100%	AAK13302.1
alpha-1-microglobulin-bikunin [Colobus guereza]	29.5	29.5	100%	19	100%	AAK13303.1
hypothetical protein HHA_210345 [Hammondia hammondi]	26.9	26.9	100%	136	88%	XP_008888639.1
hypothetical protein [Chitinophaga jiangningensis]	26.9	26.9	100%	136	88%	WP_073079771.1
AAA domain-containing protein [Halobacillus alkaliphilus]	26.9	26.9	100%	136	88%	SFF64827.1
hypothetical protein BCR44DRAFT_1488001 [Catenaria anguillulae PL171]	26.9	26.9	100%	136	88%	ORZ31204.1
hypothetical protein PAXINDRAFT_14007 [Paxillus involutus ATCC 200175]	26.9	26.9	100%	136	88%	KIJ13249.1
hypothetical protein [Marinibacterium profundimaris]	26.9	26.9	100%	136	88%	WP_088649411.1
PREDICTED: aminopeptidase N [Plutella xylostella]	26.9	26.9	100%	137	88%	XP_011555477.1
RecName: Full=Aminopeptidase N; Short=AP-N; AltName: Full=Apn1; AltName: Full=Microsomal aminopeptidase; Flags: Precursor	26.9	26.9	100%	137	88%	P91887.1
aminopeptidase N precursor [Plutella xylostella]	26.9	26.9	100%	137	88%	NP_001296022.1
midgut target receptor [Plutella xylostella]	26.9	26.9	100%	137	88%	ADA59490.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
ABC transporter family protein [Tritrichomonas foetus]	26.9	26.9	100%	137	88%	OHS94973.1
hypothetical protein K443DRAFT_96970 [Laccaria amethystina LaAM-08-1]	26.9	26.9	100%	137	88%	KIK02422.1
hypothetical protein PAXINDRAFT_166730 [Paxillus involutus ATCC 200175]	26.9	26.9	100%	137	88%	KIJ19631.1
hypothetical protein PAXINDRAFT_170699 [Paxillus involutus ATCC 200175]	26.9	26.9	100%	137	88%	KIJ13247.1
DUF814 domain-containing protein [Desulfomicrobium orale]	26.9	26.9	100%	137	88%	WP_066606609.1
sensor histidine kinase [Vibrio ponticus]	26.9	26.9	100%	139	88%	GAK82729.1
ABC transporter ATP-binding protein [Fischerella sp. NIES-4106]	26.9	26.9	100%	139	88%	BAZ70160.1
MULTISPECIES: LPS export ABC transporter ATP-binding protein [Fischerella]	26.9	26.9	100%	139	88%	WP_062248721.1
ABC transporter ATP-binding protein [Mastigocladus laminosus]	26.9	26.9	100%	139	88%	WP_044452903.1
ABC transporter ATP-binding protein [Fischerella sp. PCC 9605]	26.9	26.9	100%	139	88%	WP_026731613.1
MULTISPECIES: ABC transporter ATP-binding protein [Hapalosiphonaceae]	26.9	26.9	100%	139	88%	WP_026721112.1
ABC transporter ATP-binding protein [Fischerella sp. PCC 9339]	26.9	26.9	100%	139	88%	WP_017312284.1
ABC transporter ATP-binding protein [Fischerella muscicola]	26.9	26.9	100%	139	88%	WP_016870127.1
ABC transporter ATP-binding protein [Fischerella muscicola]	26.9	26.9	100%	139	88%	WP_016858959.1
MULTISPECIES: ABC transporter ATP-binding protein [Fischerella]	26.9	26.9	100%	139	88%	WP_009756672.1
DUF484 domain-containing protein [Marichromatium gracile]	26.9	26.9	100%	139	88%	WP_082806140.1
DUF484 domain-containing protein [Marichromatium purpuratum]	26.9	26.9	100%	139	88%	WP_005221781.1
hypothetical protein AY586_14245 [Marichromatium gracile]	26.9	26.9	100%	139	88%	KXX64285.1
DNA-binding response regulator [Ruminococcus sp. HUN007]	26.9	26.9	100%	139	88%	WP_044975319.1
DNA-binding response regulator [Ruminococcus albus]	26.9	26.9	100%	139	88%	WP_074961169.1
DNA-binding response regulator [Ruminococcus albus]	26.9	26.9	100%	139	88%	WP_074833844.1
DNA-binding response regulator [Ruminococcus sp. YE71]	26.9	26.9	100%	139	88%	WP_072417979.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
DNA-binding response regulator [Ruminococcus albus]	26.9	26.9	100%	139	88%	WP_024856025.1
DNA-binding response regulator [Ruminococcus albus]	26.9	26.9	100%	139	88%	WP_037286940.1
prepilin-type cleavage/methylation domain-containing protein [Marinobacterium jannaschii]	26.9	26.9	100%	140	88%	WP_051560027.1
glutathione S-transferase [Leptospira borgpetersenii serovar Hardjo]	26.9	26.9	100%	141	88%	AMX71366.1
hypothetical protein PAXRUDRAFT_70757 [Paxillus rubicundulus Ve08.2h10]	26.9	26.9	100%	143	88%	KIK81404.1
hypothetical protein LEP1GSC137_1757 [Leptospira borgpetersenii str. Noumea 25]	26.9	26.9	100%	145	88%	EMO07835.1
hypothetical protein LEP1GSC055_1600 [Leptospira borgpetersenii str. Brem 307]	26.9	26.9	100%	145	88%	EMN12258.1
hypothetical protein LEP1GSC188_1189 [Leptospira weilii serovar Topaz str. LT2116]	26.9	26.9	100%	145	88%	EMF83726.1
hypothetical protein LEP1GSC179_1691 [Leptospira santarosai str. MOR084]	26.9	26.9	100%	145	88%	EKO34843.1
Hypothetical protein LBL_1856 [Leptospira borgpetersenii serovar Hardjo-bovis str. L550]	26.9	26.9	100%	145	88%	ABJ79294.1
hypothetical protein [Leptospira borgpetersenii]	26.9	26.9	100%	146	88%	WP_032851320.1
hypothetical protein [Leptospira borgpetersenii]	26.9	26.9	100%	146	88%	WP_002751919.1
hypothetical protein [Leptospira borgpetersenii]	26.9	26.9	100%	146	88%	WP_020780797.1
hypothetical protein [Leptospira mayottensis]	26.9	26.9	100%	146	88%	WP_002747816.1
MULTISPECIES: hypothetical protein [Leptospira]	26.9	26.9	100%	146	88%	WP_002731715.1
MULTISPECIES: hypothetical protein [Leptospira]	26.9	26.9	100%	146	88%	WP_004495872.1
MULTISPECIES: hypothetical protein [Leptospira]	26.9	26.9	100%	146	88%	WP_004458242.1
hypothetical protein LEP1GSC043_2679 [Leptospira weilii str. Ecochallenge]	26.9	26.9	100%	149	88%	EMY16292.1
MULTISPECIES: glycoside hydrolase family 2 [Bacteroidales]	26.5	26.5	100%	194	88%	WP_044230756.1
PREDICTED: kinesin-like protein KIN-5C isoform X1 [Musa acuminata subsp. malaccensis]	26.5	26.5	100%	194	88%	XP_018674804.1
PREDICTED: kinesin-like protein KIN-5C isoform X2 [Musa acuminata subsp. malaccensis]	26.5	26.5	100%	194	88%	XP_018674805.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein CBC62_03755 [Opitutae bacterium TMED102]	26.5	26.5	100%	194	88%	OUV41343.1
TonB-dependent receptor [Dyadobacter sp. 50-39]	26.5	26.5	100%	194	88%	OJV20614.1
phosphoglycerol transferase [Alistipes finegoldii]	26.5	26.5	100%	194	88%	WP_055211378.1
PREDICTED: Fanconi anemia group G protein [Eptesicus fuscus]	26.5	26.5	100%	194	88%	XP_008140163.1
PREDICTED: Fanconi anemia group G protein isoform X1 [Myotis lucifugus]	26.5	26.5	100%	194	88%	XP_006098782.1
PREDICTED: Fanconi anemia group G protein isoform X1 [Myotis brandtii]	26.5	26.5	100%	194	88%	XP_005884070.1
PREDICTED: Fanconi anemia group G protein [Myotis davidii]	26.5	26.5	100%	194	88%	XP_006758602.1
Fanconi anemia group G protein [Myotis brandtii]	26.5	26.5	100%	195	88%	EPQ18791.1
hypothetical protein PV08_05964 [Exophiala spinifera]	26.5	26.5	100%	195	88%	XP_016236130.1
phosphoenolpyruvate carboxykinase (ATP) [Salinarimonas rosea]	26.5	26.5	100%	195	88%	WP_029030185.1
hexokinase protein HXK6 [Physcomitrella patens]	26.5	26.5	100%	195	88%	XP_001762951.1

Alignments

hypothetical protein K443DRAFT_672800 [Laccaria amethystina LaAM-08-1]
Sequence ID: **KIK08316.1** Length: 1191 Number of Matches: 1
Range 1: 968 to 975

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	17()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    ETLLQDFR  8
            ETLLQDFR
Sbjct  968  ETLLQDFR  975
```

predicted protein [Laccaria bicolor S238N-H82]
Sequence ID: **XP_001874875.1** Length: 1191 Number of Matches: 1

See 1 more title(s)
Range 1: 968 to 975

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	17()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    ETLLQDFR  8
            ETLLQDFR
Sbjct  968  ETLLQDFR  975
```

LAME_0G13300g1_1 [Lachancea meyersii CBS 8951]
Sequence ID: **SCV00987.1** Length: 1048 Number of Matches: 1
Range 1: 700 to 707

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	17()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    ETLLQDFR  8
            ETLLQDFR
Sbjct  700  ETLLQDFR  707
```

LAFA_0E21374g1_1 [Lachancea sp. CBS 6924]
Sequence ID: **SCU89846.1** Length: 1007 Number of Matches: 1
Range 1: 640 to 647

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(62)	17()		8/8(100%)	8/8(100%)	0/8(0%)	

Features:

```
Query  1    ETLLQDFR  8
            ETLLQDFR
Sbjct  640  ETLLQDFR  647
```

hypothetical protein AUH13_06920 [Acidobacteria bacterium 13_2_20CM_58_27]
Sequence ID: **OLB31794.1** Length: 888 Number of Matches: 1
Range 1: 78 to 85

Score	Expect	Method	Identities	Positives	Gaps	Frame

29.5 bits(62)	17()	8/8(100%)	8/8(100%)	0/8(0%)

Features:

```
Query  1   ETLLQDFR  8
           ETLLQDFR
Sbjct  78  ETLLQDFR  85
```

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Job title: NCBI BlastP_APOA4_ISASAEELR

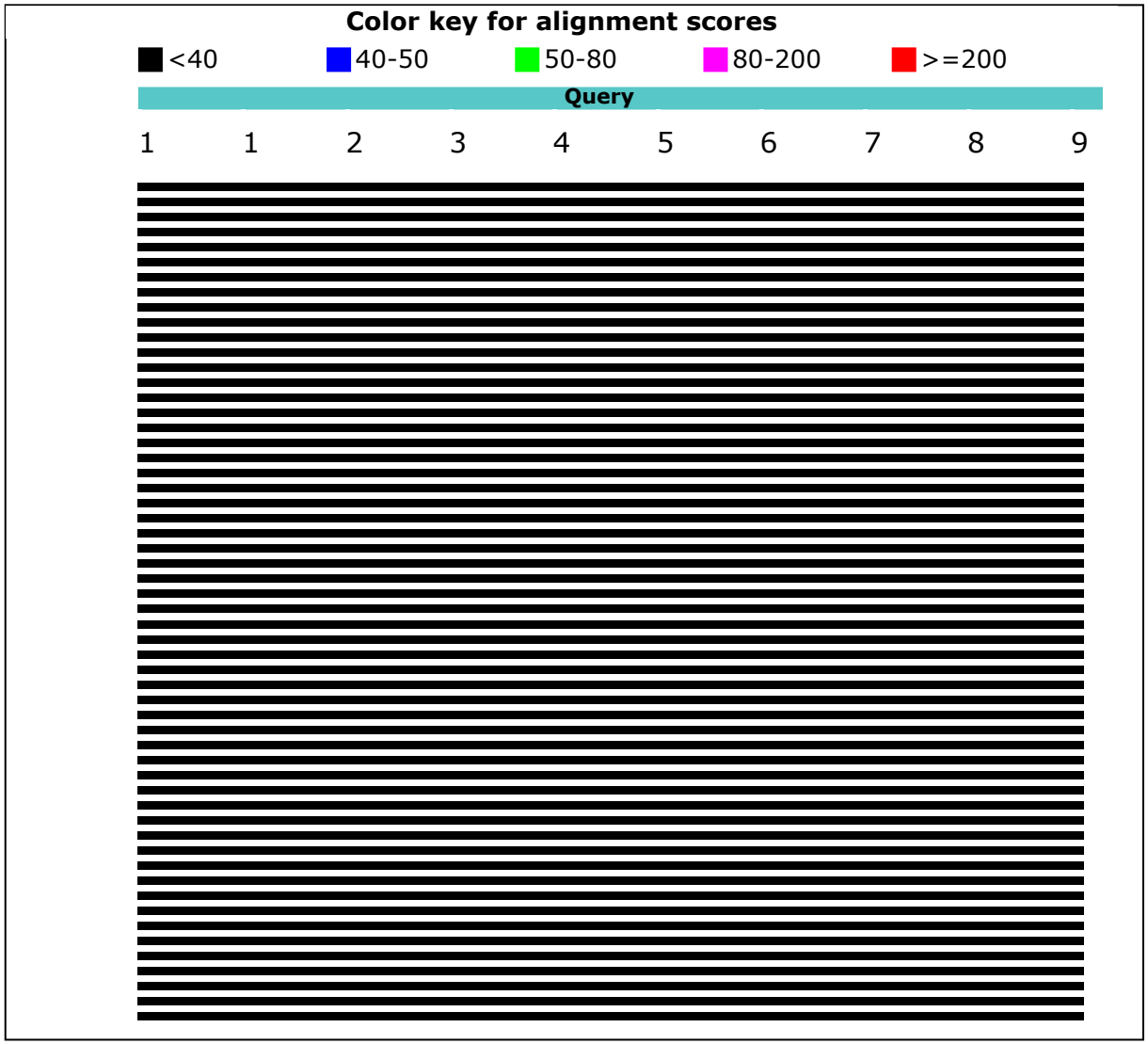
RID S54P2WPC015 (Expires on 08-04 11:04 am)

Query ID	lcl|Query_281249	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	9	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 115 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7
8
9

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein A-IV [Macaca mulatta]	29.9	29.9	100%	15	100%	XP_014971282.1
PREDICTED: apolipoprotein A-IV [Macaca fascicularis]	29.9	29.9	100%	15	100%	XP_005579784.1
PREDICTED: apolipoprotein A-IV [Macaca nemestrina]	29.9	29.9	100%	15	100%	XP_011730719.1
PREDICTED: apolipoprotein A-IV isoform X1 [Mandrillus leucophaeus]	29.9	29.9	100%	15	100%	XP_011837390.1
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	29.9	29.9	100%	15	100%	P33621.1
PREDICTED: apolipoprotein A-IV [Cercocebus atys]	29.9	29.9	100%	15	100%	XP_011908278.1
PREDICTED: apolipoprotein A-IV [Rhinopithecus bieti]	29.9	48.8	100%	15	100%	XP_017738599.1
PREDICTED: apolipoprotein A-IV [Chlorocebus sabaeus]	29.9	29.9	100%	15	100%	XP_008019167.1
apolipoprotein A-IV [Papio anubis]	29.9	29.9	100%	15	100%	XP_003910789.1
PREDICTED: apolipoprotein A-IV [Pongo abelii]	29.9	29.9	100%	15	100%	XP_009245367.1
PREDICTED: apolipoprotein A-IV isoform X1 [Colobus angolensis palliatus]	29.9	29.9	100%	15	100%	XP_011782210.1
PREDICTED: apolipoprotein A-IV [Rhinopithecus roxellana]	29.9	48.8	100%	15	100%	XP_010370007.1
hypothetical protein EGK_06926 [Macaca mulatta]	29.9	29.9	100%	15	100%	EHH23453.1
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	29.9	29.9	100%	15	100%	Q28758.1
apolipoprotein A-IV [Homo sapiens]	29.9	29.9	100%	15	100%	AAA51744.1
apolipoprotein A-IV precursor [Homo sapiens]	29.9	29.9	100%	15	100%	AAA96731.1
PREDICTED: apolipoprotein A-IV isoform X2 [Colobus angolensis palliatus]	29.9	29.9	100%	15	100%	XP_011782211.1
PREDICTED: apolipoprotein A-IV isoform X2 [Mandrillus leucophaeus]	29.9	29.9	100%	15	100%	XP_011837395.1
PREDICTED: apolipoprotein A-IV [Gorilla gorilla gorilla]	29.9	29.9	100%	15	100%	XP_004052227.1
PREDICTED: apolipoprotein A-IV [Pan paniscus]	29.9	29.9	100%	15	100%	XP_003820134.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein EGM_06258 [Macaca fascicularis]	29.9	29.9	100%	15	100%	EHH56782.1
PREDICTED: apolipoprotein A-IV [Pan troglodytes]	29.9	29.9	100%	15	100%	XP_522192.2
apolipoprotein A-IV precursor [Homo sapiens]	29.9	29.9	100%	15	100%	NP_000473.2
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	29.9	29.9	100%	15	100%	P06727.3
PREDICTED: apolipoprotein A-IV [Physeter catodon]	29.9	48.8	100%	15	100%	XP_007117219.1
apolipoprotein A-IV precursor [Homo sapiens]	29.9	29.9	100%	15	100%	AAA51748.1
Chain A, Dimeric Apoa-Iv	29.9	29.9	100%	15	100%	3S84_A
apolipoprotein A-IV [Cercopithecus mitis]	29.9	29.9	100%	15	100%	AEH95753.1
apolipoprotein A-IV [Lophocebus aterrimus]	29.9	29.9	100%	15	100%	AEH95752.1
apolipoprotein A-IV [Erythrocebus patas]	29.9	29.9	100%	15	100%	AEH95751.1
apolipoprotein A-IV [Macaca fascicularis]	29.9	29.9	100%	15	100%	AEH95750.1
apolipoprotein A-IV [Papio hamadryas]	29.9	29.9	100%	15	100%	AEH95749.1
apolipoprotein A-IV [Pygathrix nemaeus]	29.9	48.8	100%	15	100%	AEH95748.1
apolipoprotein A-IV [Semnopithecus entellus]	29.9	48.8	100%	15	100%	AEH95747.1
apolipoprotein A-IV [Gorilla gorilla]	29.9	29.9	100%	15	100%	AEX20371.1
apolipoprotein A-IV [Chlorocebus aethiops]	29.9	29.9	100%	15	100%	AEX20368.1
apolipoprotein A-IV [Nasalis larvatus]	29.9	48.8	100%	15	100%	AEX20367.1
apolipoprotein A-IV [Homo sapiens]	29.9	29.9	100%	15	100%	AAB59516.1
hypothetical protein TRFO_09413 [Tritrichomonas foetus]	27.4	27.4	100%	120	89%	OHS97425.1
conserved hypothetical protein [Trypanosoma vivax Y486]	27.4	27.4	100%	120	89%	CCC53784.1
TonB-dependent receptor [Novosphingobium panipatense]	27.4	27.4	100%	120	89%	WP_086494205.1
ATPase [Mycobacterium sherrisii]	27.4	27.4	100%	120	89%	WP_069400638.1
methyl-accepting chemotaxis protein [Dethiobacter alkaliphilus]	27.4	27.4	100%	121	89%	WP_008518434.1
methyl-accepting chemotaxis protein [Pseudomonas borbori]	27.4	66.4	100%	121	89%	SFP94344.1
histidine kinase [Pseudomonadales bacterium RIFCSPLOWO2_02_FULL_63_210]	27.4	66.4	100%	121	89%	OHC43459.1
methyl-accepting chemotaxis protein signaling domain protein [Clostridiales bacterium oral taxon 876 str. F0540]	27.4	27.4	100%	121	89%	ERI93394.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
methyl-accepting transducer [Clostridiales bacterium oral taxon 876]	27.4	27.4	100%	121	89%	WP_034569773.1
apolipoprotein A-IV precursor (predicted) [Plecturocebus moloch]	27.4	27.4	100%	121	89%	ACB21186.1
methyl-accepting chemotaxis protein [Paenibacillus amylolyticus]	27.4	27.4	100%	121	89%	GAS79974.1
methyl-accepting chemotaxis protein [Paenibacillus sp. VT-16-81]	27.4	27.4	100%	121	89%	WP_079349803.1
methyl-accepting chemotaxis protein [Paenibacillus sp. RU5A]	27.4	27.4	100%	121	89%	WP_079695143.1
methyl-accepting chemotaxis protein [Paenibacillus sp. FSL R5-0765]	27.4	27.4	100%	121	89%	WP_076214520.1
methyl-accepting chemotaxis protein [Paenibacillus pabuli]	27.4	27.4	100%	121	89%	WP_076290212.1
methyl-accepting chemotaxis protein [Paenibacillus xylanexedens]	27.4	27.4	100%	121	89%	WP_074093822.1
methyl-accepting chemotaxis protein [Paenibacillus sp. OK076]	27.4	27.4	100%	121	89%	SEM81760.1
methyl-accepting chemotaxis protein [Paenibacillus sp. OK003]	27.4	27.4	100%	121	89%	SEK87342.1
methyl-accepting chemotaxis protein [Paenibacillus sp. 276b]	27.4	27.4	100%	121	89%	SEB05171.1
methyl-accepting chemotaxis protein [Paenibacillus sp. CF095]	27.4	27.4	100%	121	89%	SDD04773.1
methyl-accepting chemotaxis protein [Paenibacillus sp. OK060]	27.4	27.4	100%	121	89%	SDL21188.1
methyl-accepting chemotaxis protein [Paenibacillus polysaccharolyticus]	27.4	27.4	100%	121	89%	SCY40484.1
methyl-accepting chemotaxis protein [Paenibacillus sp. AD87]	27.4	27.4	100%	121	89%	WP_064640271.1
MULTISPECIES: methyl-accepting chemotaxis protein [Paenibacillus]	27.4	27.4	100%	121	89%	WP_063564613.1
methyl-accepting chemotaxis protein [Paenibacillus amylolyticus]	27.4	27.4	100%	121	89%	WP_062832946.1
methyl-accepting chemotaxis protein [Paenibacillus pabuli]	27.4	27.4	100%	121	89%	WP_062324004.1
methyl-accepting chemotaxis protein [Paenibacillus sp. Root52]	27.4	27.4	100%	121	89%	WP_056693976.1
methyl-accepting chemotaxis protein [Paenibacillus sp. A59]	27.4	27.4	100%	121	89%	WP_053783349.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
MULTISPECIES: methyl-accepting chemotaxis protein [Paenibacillus]	27.4	27.4	100%	121	89%	WP_024632490.1
MULTISPECIES: methyl-accepting chemotaxis protein [Paenibacillus]	27.4	27.4	100%	121	89%	WP_036612082.1
MULTISPECIES: methyl-accepting chemotaxis protein [Paenibacillus]	27.4	27.4	100%	121	89%	WP_036672371.1
methyl-accepting chemotaxis protein [Paenibacillus sp. PAMC 26794]	27.4	27.4	100%	121	89%	WP_017690252.1
PREDICTED: apolipoprotein A-IV [Cebus capucinus imitator]	27.4	27.4	100%	121	89%	XP_017378828.1
PREDICTED: apolipoprotein A-IV [Otolemur garnettii]	27.4	27.4	100%	121	89%	XP_003794819.1
apolipoprotein A-IV precursor (predicted) [Otolemur garnettii]	27.4	27.4	100%	121	89%	ACH97051.1
PREDICTED: apolipoprotein A-IV [Callithrix jacchus]	27.4	27.4	100%	121	89%	XP_002754492.1
apolipoprotein A-IV [Aotus nancymaae]	27.4	27.4	100%	121	89%	XP_012325876.1
PREDICTED: apolipoprotein A-IV [Saimiri boliviensis boliviensis]	27.4	27.4	100%	121	89%	XP_003923712.1
PREDICTED: apolipoprotein A-IV [Nomascus leucogenys]	27.4	27.4	100%	121	89%	XP_003253231.1
apolipoprotein A-IV [Microcebus murinus]	27.4	47.1	100%	121	89%	XP_012629142.1
PREDICTED: apolipoprotein A-IV [Propithecus coquereli]	27.4	47.1	100%	121	89%	XP_012513783.1
PREDICTED: apolipoprotein A-IV [Canis lupus familiaris]	27.4	46.2	100%	121	89%	XP_546510.3
apolipoprotein A-IV (predicted) [Rhinolophus ferrumequinum]	27.4	27.4	100%	121	89%	ACC68865.1
PREDICTED: apolipoprotein A-IV [Rhinolophus sinicus]	27.4	27.4	100%	121	89%	XP_019569164.1
PREDICTED: apolipoprotein A-IV [Hipposideros armiger]	27.4	27.4	100%	121	89%	XP_019502926.1
PREDICTED: apolipoprotein A-IV [Ceratotherium simum simum]	27.4	27.4	100%	121	89%	XP_004427346.1
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	27.4	46.2	100%	121	89%	E2RE76.2
PREDICTED: apolipoprotein A-IV [Tupaia chinensis]	27.4	27.4	100%	121	89%	XP_014443865.1
beta-hexosaminidase [Oceanicola litoreus]	27.4	27.4	100%	121	89%	WP_084192966.1
hypothetical protein [Hyphomicrobium sp. CS1BSMeth3]	27.4	27.4	100%	122	89%	WP_072386518.1
apolipoprotein A-IV [Saimiri sciureus]	27.4	27.4	100%	122	89%	AEH95756.1
apolipoprotein A-IV [Callimico goeldii]	27.4	27.4	100%	122	89%	AEH95755.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
apolipoprotein A-IV [Saguinus fuscicollis]	27.4	27.4	100%	122	89%	AEH95754.1
apolipoprotein A-IV [Symphalangus syndactylus]	27.4	27.4	100%	122	89%	AEH95746.1
apolipoprotein A-IV [Hylobates lar]	27.4	27.4	100%	122	89%	AEH95745.1
apolipoprotein A-IV [Saguinus oedipus]	27.4	27.4	100%	122	89%	AEX20370.1
NAD(P)-dependent oxidoreductase [Nocardia jiangxiensis]	27.4	27.4	100%	122	89%	WP_040825251.1
MULTISPECIES: glycoside hydrolase [Streptomyces]	26.9	26.9	100%	171	89%	WP_079158440.1
ShlB/FhaC/HecB family hemolysin secretion/activation protein [Rhodanobacter spathiphylli]	26.9	26.9	100%	171	89%	WP_007807865.1
PREDICTED: apolipoprotein A-IV [Ochotona princeps]	26.9	26.9	100%	172	89%	XP_004585159.1
PREDICTED: apolipoprotein A-IV [Vicugna pacos]	26.9	45.8	100%	172	89%	XP_006207850.1
hypothetical protein M407DRAFT_21935 [Tulasnella calospora MUT 4182]	26.9	26.9	100%	172	89%	KIO28856.1

Alignments

PREDICTED: apolipoprotein A-IV [Macaca mulatta]

Sequence ID: **XP_014971282.1** Length: 505 Number of Matches: 1
Range 1: 320 to 328

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	15()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    ISASAEELR  9
           ISASAEELR
Sbjct  320  ISASAEELR  328
```

PREDICTED: apolipoprotein A-IV [Macaca fascicularis]

Sequence ID: **XP_005579784.1** Length: 441 Number of Matches: 1
Range 1: 256 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	15()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    ISASAEELR  9
            ISASAEELR
Sbjct  256  ISASAEELR  264
```

PREDICTED: apolipoprotein A-IV [Macaca nemestrina]

Sequence ID: **XP_011730719.1** Length: 435 Number of Matches: 1
Range 1: 256 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	15()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    ISASAEELR  9
            ISASAEELR
Sbjct  256  ISASAEELR  264
```

PREDICTED: apolipoprotein A-IV isoform X1 [Mandrillus leucophaeus]

Sequence ID: **XP_011837390.1** Length: 433 Number of Matches: 1
Range 1: 256 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	15()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    ISASAEELR  9
            ISASAEELR
Sbjct  256  ISASAEELR  264
```

RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor

Sequence ID: **P33621.1** Length: 429 Number of Matches: 1

See 1 more title(s)

Range 1: 256 to 264

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.9 bits(63)	15()		9/9(100%)	9/9(100%)	0/9(0%)	

Features:

```
Query  1    ISASAEELR  9
           ISASAEELR
Sbjct  256  ISASAEELR  264
```

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Job title: NCBI BlastP_APOA4_SELTQQLNALFQDK

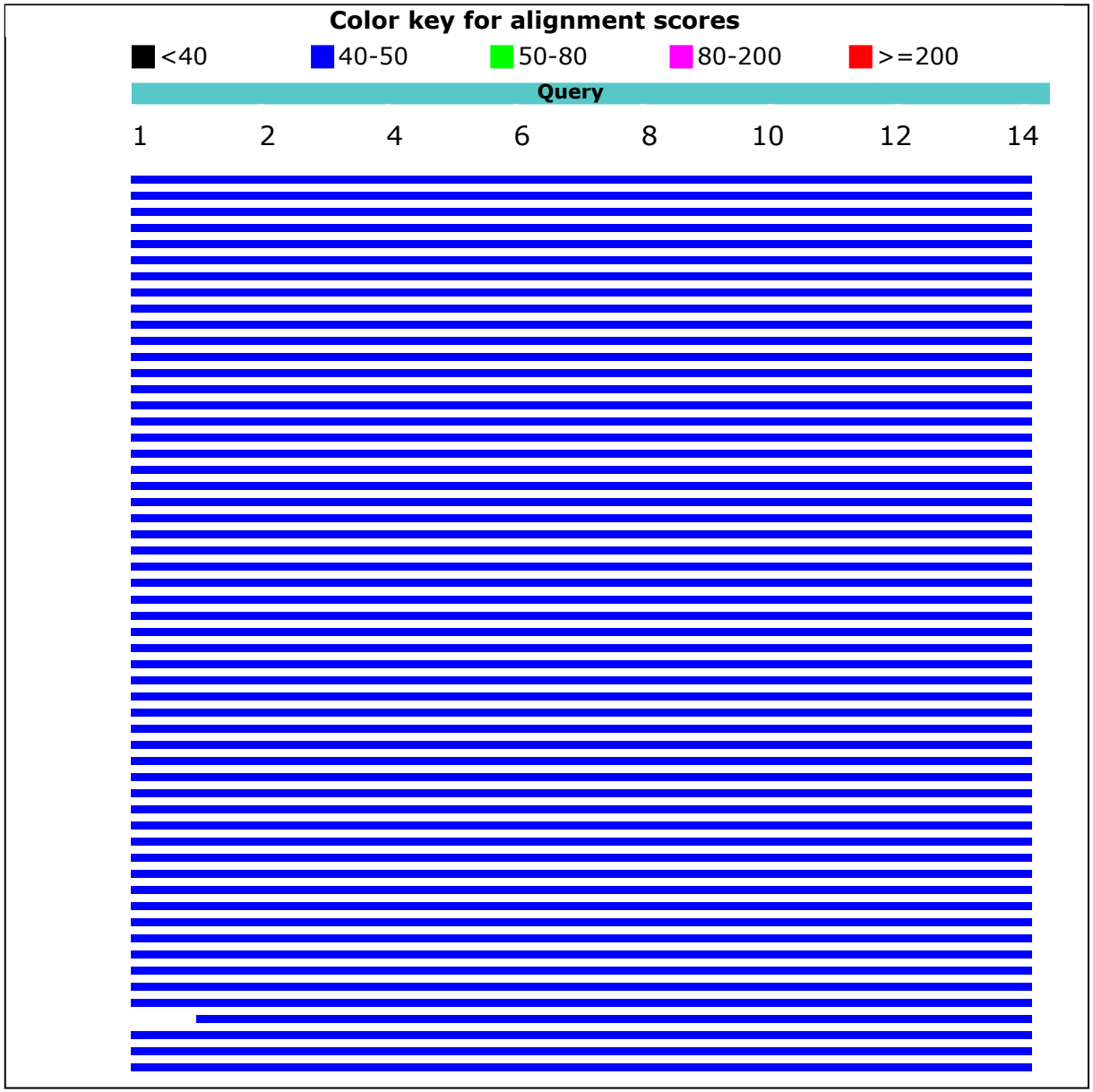
RID S54RB9XN015 (Expires on 08-04 11:05 am)

Query ID	lcl|Query_41762	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12
14

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein A-IV [Macaca fascicularis]	47.3	47.3	100%	3e-05	100%	XP_005579784.1
PREDICTED: apolipoprotein A-IV [Macaca nemestrina]	47.3	47.3	100%	3e-05	100%	XP_011730719.1
PREDICTED: apolipoprotein A-IV isoform X1 [Mandrillus leucophaeus]	47.3	47.3	100%	3e-05	100%	XP_011837390.1
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	47.3	47.3	100%	3e-05	100%	P33621.1
PREDICTED: apolipoprotein A-IV [Cercocebus atys]	47.3	47.3	100%	3e-05	100%	XP_011908278.1
PREDICTED: apolipoprotein A-IV [Rhinopithecus bieti]	47.3	47.3	100%	3e-05	100%	XP_017738599.1
PREDICTED: apolipoprotein A-IV [Chlorocebus sabaeus]	47.3	47.3	100%	3e-05	100%	XP_008019167.1
apolipoprotein A-IV [Papio anubis]	47.3	47.3	100%	3e-05	100%	XP_003910789.1
PREDICTED: apolipoprotein A-IV [Pongo abelii]	47.3	47.3	100%	3e-05	100%	XP_009245367.1
PREDICTED: apolipoprotein A-IV isoform X1 [Colobus angolensis palliatus]	47.3	47.3	100%	3e-05	100%	XP_011782210.1
PREDICTED: apolipoprotein A-IV [Rhinopithecus roxellana]	47.3	47.3	100%	3e-05	100%	XP_010370007.1
hypothetical protein EGK_06926 [Macaca mulatta]	47.3	47.3	100%	3e-05	100%	EHH23453.1
PREDICTED: apolipoprotein A-IV [Cebus capucinus imitator]	47.3	47.3	100%	3e-05	100%	XP_017378828.1
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	47.3	47.3	100%	3e-05	100%	Q28758.1
PREDICTED: apolipoprotein A-IV [Otolemur garnettii]	47.3	47.3	100%	3e-05	100%	XP_003794819.1
apolipoprotein A-IV precursor (predicted) [Otolemur garnettii]	47.3	47.3	100%	3e-05	100%	ACH97051.1
PREDICTED: apolipoprotein A-IV [Callithrix jacchus]	47.3	47.3	100%	3e-05	100%	XP_002754492.1
apolipoprotein A-IV [Homo sapiens]	47.3	47.3	100%	3e-05	100%	AAA51744.1
apolipoprotein A-IV precursor [Homo sapiens]	47.3	47.3	100%	3e-05	100%	AAA96731.1
PREDICTED: apolipoprotein A-IV isoform X2 [Colobus angolensis palliatus]	47.3	47.3	100%	3e-05	100%	XP_011782211.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein A-IV isoform X2 [Mandrillus leucophaeus]	47.3	47.3	100%	3e-05	100%	XP_011837395.1
PREDICTED: apolipoprotein A-IV [Gorilla gorilla gorilla]	47.3	47.3	100%	3e-05	100%	XP_004052227.1
PREDICTED: apolipoprotein A-IV [Pan paniscus]	47.3	47.3	100%	3e-05	100%	XP_003820134.1
hypothetical protein EGM_06258 [Macaca fascicularis]	47.3	47.3	100%	3e-05	100%	EHH56782.1
PREDICTED: apolipoprotein A-IV [Pan troglodytes]	47.3	47.3	100%	3e-05	100%	XP_522192.2
apolipoprotein A-IV precursor [Homo sapiens]	47.3	47.3	100%	3e-05	100%	NP_000473.2
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	47.3	47.3	100%	3e-05	100%	P06727.3
apolipoprotein A-IV [Aotus nancymaae]	47.3	47.3	100%	3e-05	100%	XP_012325876.1
PREDICTED: apolipoprotein A-IV [Saimiri boliviensis boliviensis]	47.3	47.3	100%	3e-05	100%	XP_003923712.1
PREDICTED: apolipoprotein A-IV [Nomascus leucogenys]	47.3	47.3	100%	3e-05	100%	XP_003253231.1
apolipoprotein A-IV [Carlito syrichta]	47.3	47.3	100%	3e-05	100%	XP_008054095.1
apolipoprotein A-IV [Microcebus murinus]	47.3	47.3	100%	3e-05	100%	XP_012629142.1
PREDICTED: apolipoprotein A-IV [Propithecus coquereli]	47.3	47.3	100%	3e-05	100%	XP_012513783.1
PREDICTED: apolipoprotein A-IV [Canis lupus familiaris]	47.3	47.3	100%	3e-05	100%	XP_546510.3
apolipoprotein A-IV [Neomonachus schauinslandi]	47.3	47.3	100%	3e-05	100%	XP_021552198.1
PREDICTED: apolipoprotein A-IV [Panthera pardus]	47.3	47.3	100%	3e-05	100%	XP_019324613.1
PREDICTED: apolipoprotein A-IV-like [Leptonychotes weddellii]	47.3	47.3	100%	3e-05	100%	XP_006747633.1
PREDICTED: apolipoprotein A-IV [Erinaceus europaeus]	47.3	47.3	100%	3e-05	100%	XP_007523056.1
PREDICTED: apolipoprotein A-IV [Ceratotherium simum simum]	47.3	47.3	100%	3e-05	100%	XP_004427346.1
PREDICTED: apolipoprotein A-IV [Odobenus rosmarus divergens]	47.3	47.3	100%	3e-05	100%	XP_004415535.1
PREDICTED: apolipoprotein A-IV [Felis catus]	47.3	47.3	100%	3e-05	100%	XP_011284667.1
PREDICTED: apolipoprotein A-IV [Loxodonta africana]	47.3	47.3	100%	3e-05	100%	XP_003418284.1
PREDICTED: apolipoprotein A-IV [Ailuropoda melanoleuca]	47.3	47.3	100%	3e-05	100%	XP_002919548.1
PREDICTED: apolipoprotein A-IV [Dasypus novemcinctus]	47.3	47.3	100%	3e-05	100%	XP_004466047.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
apolipoprotein A-IV precursor (predicted) [Dasypus novemcinctus]	47.3	47.3	100%	3e-05	100%	ACO95317.1
PREDICTED: LOW QUALITY PROTEIN: apolipoprotein A-IV [Panthera tigris altaica]	47.3	47.3	100%	3e-05	100%	XP_015392269.1
apolipoprotein A-IV precursor [Homo sapiens]	47.3	47.3	100%	3e-05	100%	AAA51748.1
hypothetical protein PANDA_008178 [Ailuropoda melanoleuca]	47.3	47.3	100%	3e-05	100%	EFB21765.1
PREDICTED: apolipoprotein A-IV [Manis javanica]	47.3	47.3	100%	3e-05	100%	XP_017509603.1
PREDICTED: apolipoprotein A-IV [Ursus maritimus]	47.3	47.3	100%	3e-05	100%	XP_008688424.1
PREDICTED: apolipoprotein A-IV [Acinonyx jubatus]	47.3	47.3	100%	3e-05	100%	XP_014918157.1
PREDICTED: apolipoprotein A-IV [Orycteropus afer afer]	44.8	44.8	100%	2e-04	93%	XP_007934790.1
PREDICTED: apolipoprotein A-IV [Mustela putorius furo]	44.8	44.8	92%	2e-04	100%	XP_004749954.1
PREDICTED: apolipoprotein A-IV [Miniopterus natalensis]	44.8	44.8	100%	2e-04	93%	XP_016060185.1
apolipoprotein A-IV precursor (predicted) [Plecturocebus moloch]	44.3	44.3	100%	3e-04	93%	ACB21186.1
PREDICTED: apolipoprotein A-IV isoform X1 [Bison bison bison]	44.3	44.3	100%	3e-04	93%	XP_010828681.1
PREDICTED: apolipoprotein A-IV [Bos mutus]	44.3	44.3	100%	3e-04	93%	XP_005896204.2
PREDICTED: apolipoprotein A-IV isoform X1 [Bubalus bubalis]	44.3	44.3	100%	3e-04	93%	XP_006056942.1
PREDICTED: apolipoprotein A-IV isoform X1 [Bos taurus]	44.3	44.3	100%	3e-04	93%	XP_005215909.1
PREDICTED: apolipoprotein A-IV isoform X2 [Bubalus bubalis]	44.3	44.3	100%	3e-04	93%	XP_006056943.1
PREDICTED: apolipoprotein A-IV [Ochotona princeps]	44.3	44.3	100%	3e-04	93%	XP_004585159.1
apolipoprotein A-IV (predicted) [Rhinolophus ferrumequinum]	44.3	44.3	100%	3e-04	93%	ACC68865.1
PREDICTED: apolipoprotein A-IV [Rhinolophus sinicus]	44.3	44.3	100%	3e-04	93%	XP_019569164.1
PREDICTED: apolipoprotein A-IV [Hipposideros armiger]	44.3	44.3	100%	3e-04	93%	XP_019502926.1
apolipoprotein A-IV precursor [Sus scrofa]	44.3	44.3	100%	3e-04	93%	NP_999553.1
apolipoprotein A-IV [Odocoileus virginianus texanus]	44.3	44.3	100%	3e-04	93%	XP_020758261.1
PREDICTED: apolipoprotein A-IV [Capra hircus]	44.3	44.3	100%	3e-04	93%	XP_005689539.3
apolipoprotein A-IV precursor [Bos taurus]	44.3	44.3	100%	3e-04	93%	NP_001032557.1
PREDICTED: apolipoprotein A-IV isoform X2 [Bison bison bison]	44.3	44.3	100%	3e-04	93%	XP_010828682.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein A-IV [Balaenoptera acutorostrata scammoni]	44.3	44.3	100%	3e-04	93%	XP_007196616.1
PREDICTED: apolipoprotein A-IV [Physeter catodon]	44.3	44.3	100%	3e-04	93%	XP_007117219.1
PREDICTED: apolipoprotein A-IV [Pantholops hodgsonii]	44.3	44.3	100%	3e-04	93%	XP_005980010.1
PREDICTED: apolipoprotein A-IV [Tursiops truncatus]	44.3	44.3	100%	3e-04	93%	XP_004316797.1
PREDICTED: apolipoprotein A-IV [Orcinus orca]	44.3	44.3	100%	3e-04	93%	XP_004273415.1
Apolipoprotein A-IV [Bos mutus]	44.3	44.3	100%	3e-04	93%	ELR56104.1
PREDICTED: apolipoprotein A-IV [Ovis aries]	44.3	44.3	100%	3e-04	93%	XP_004016096.1
PREDICTED: apolipoprotein A-IV isoform X2 [Bos taurus]	44.3	44.3	100%	3e-04	93%	XP_005215912.1
PREDICTED: apolipoprotein A-IV [Tupaia chinensis]	44.3	44.3	92%	3e-04	100%	XP_014443865.1
PREDICTED: apolipoprotein A-IV [Pteropus alecto]	43.1	43.1	100%	9e-04	93%	XP_006912896.1
PREDICTED: apolipoprotein A-IV [Pteropus vampyrus]	43.1	43.1	100%	9e-04	93%	XP_011381499.1
PREDICTED: apolipoprotein A-IV [Chrysochloris asiatica]	42.6	42.6	100%	0.001	93%	XP_006834042.1
PREDICTED: apolipoprotein A-IV [Eptesicus fuscus]	41.8	41.8	92%	0.002	92%	XP_008148441.1
PREDICTED: apolipoprotein A-IV [Fukomys damarensis]	40.9	40.9	100%	0.005	86%	XP_010627703.1
PREDICTED: apolipoprotein A-IV [Elephantulus edwardii]	40.9	40.9	100%	0.005	86%	XP_006890936.1
PREDICTED: apolipoprotein A-IV [Condylura cristata]	40.9	40.9	100%	0.005	86%	XP_004689289.1
PREDICTED: apolipoprotein A-IV [Marmota marmota marmota]	40.5	40.5	100%	0.007	86%	XP_015345330.1
apolipoprotein A-IV [Ictidomys tridecemlineatus]	40.5	40.5	100%	0.007	86%	XP_005328347.1
apolipoprotein A-IV [Castor canadensis]	40.1	40.1	100%	0.010	86%	XP_020039911.1
PREDICTED: apolipoprotein A-IV [Galeopterus variegatus]	40.1	40.1	92%	0.010	92%	XP_008589934.1
PREDICTED: apolipoprotein A-IV [Trichechus manatus latirostris]	40.1	40.1	100%	0.010	86%	XP_004385765.1
hypothetical protein CB1_000200068 [Camelus ferus]	39.7	39.7	100%	0.014	86%	EPY88082.1
PREDICTED: apolipoprotein A-IV [Camelus ferus]	39.7	39.7	100%	0.014	86%	XP_006175407.1
apolipoprotein A-IV (predicted) [Sorex araneus]	39.7	39.7	100%	0.014	86%	ACE77696.1
PREDICTED: apolipoprotein A-IV [Sorex araneus]	39.7	39.7	100%	0.014	86%	XP_004605119.1
PREDICTED: apolipoprotein A-IV [Equus caballus]	39.7	39.7	100%	0.014	86%	XP_001502503.1
PREDICTED: apolipoprotein A-IV [Equus asinus]	39.7	39.7	100%	0.014	86%	XP_014711020.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein A-IV [Camelus dromedarius]	39.7	39.7	100%	0.014	86%	XP_010979717.1
PREDICTED: apolipoprotein A-IV [Camelus bactrianus]	39.7	39.7	100%	0.014	86%	XP_010951808.1
PREDICTED: apolipoprotein A-IV [Vicugna pacos]	39.7	39.7	100%	0.014	86%	XP_006207850.1
PREDICTED: apolipoprotein A-IV [Equus przewalskii]	39.7	39.7	100%	0.014	86%	XP_008514965.1

Alignments

PREDICTED: apolipoprotein A-IV [Macaca fascicularis]
Sequence ID: **XP_005579784.1** Length: 441 Number of Matches: 1
Range 1: 52 to 65

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.3 bits(104)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SELTQQLNALFQDK  14
           SELTQQLNALFQDK
Sbjct  52  SELTQQLNALFQDK  65
```

PREDICTED: apolipoprotein A-IV [Macaca nemestrina]
Sequence ID: **XP_011730719.1** Length: 435 Number of Matches: 1
Range 1: 52 to 65

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.3 bits(104)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SELTQQLNALFQDK  14
           SELTQQLNALFQDK
Sbjct  52  SELTQQLNALFQDK  65
```

PREDICTED: apolipoprotein A-IV isoform X1 [Mandrillus leucophaeus]
Sequence ID: **XP_011837390.1** Length: 433 Number of Matches: 1
Range 1: 52 to 65

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.3 bits(104)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SELTQQLNALFQDK  14
           SELTQQLNALFQDK
Sbjct  52  SELTQQLNALFQDK  65
```

RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor
Sequence ID: **P33621.1** Length: 429 Number of Matches: 1

See 1 more title(s)
Range 1: 52 to 65

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.3 bits(104)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SELTQQLNALFQDK  14
           SELTQQLNALFQDK
Sbjct  52  SELTQQLNALFQDK  65
```

PREDICTED: apolipoprotein A-IV [Cercocebus atys]
Sequence ID: **XP_011908278.1** Length: 427 Number of Matches: 1

See 3 more title(s)
Range 1: 52 to 65

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.3 bits(104)	3e-05()		14/14(100%)	14/14(100%)	0/14(0%)	

Features:

```
Query  1   SELTQQLNALFQDK  14
           SELTQQLNALFQDK
Sbjct  52  SELTQQLNALFQDK  65
```

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BLAST ® » blastp suite » RID-S54S23B7014

BLAST Results

Job title: NCBI BlastP_APOA4_SLAELGGHLDQQVEEFR

RID S54S23B7014 (Expires on 08-04 11:05 am)

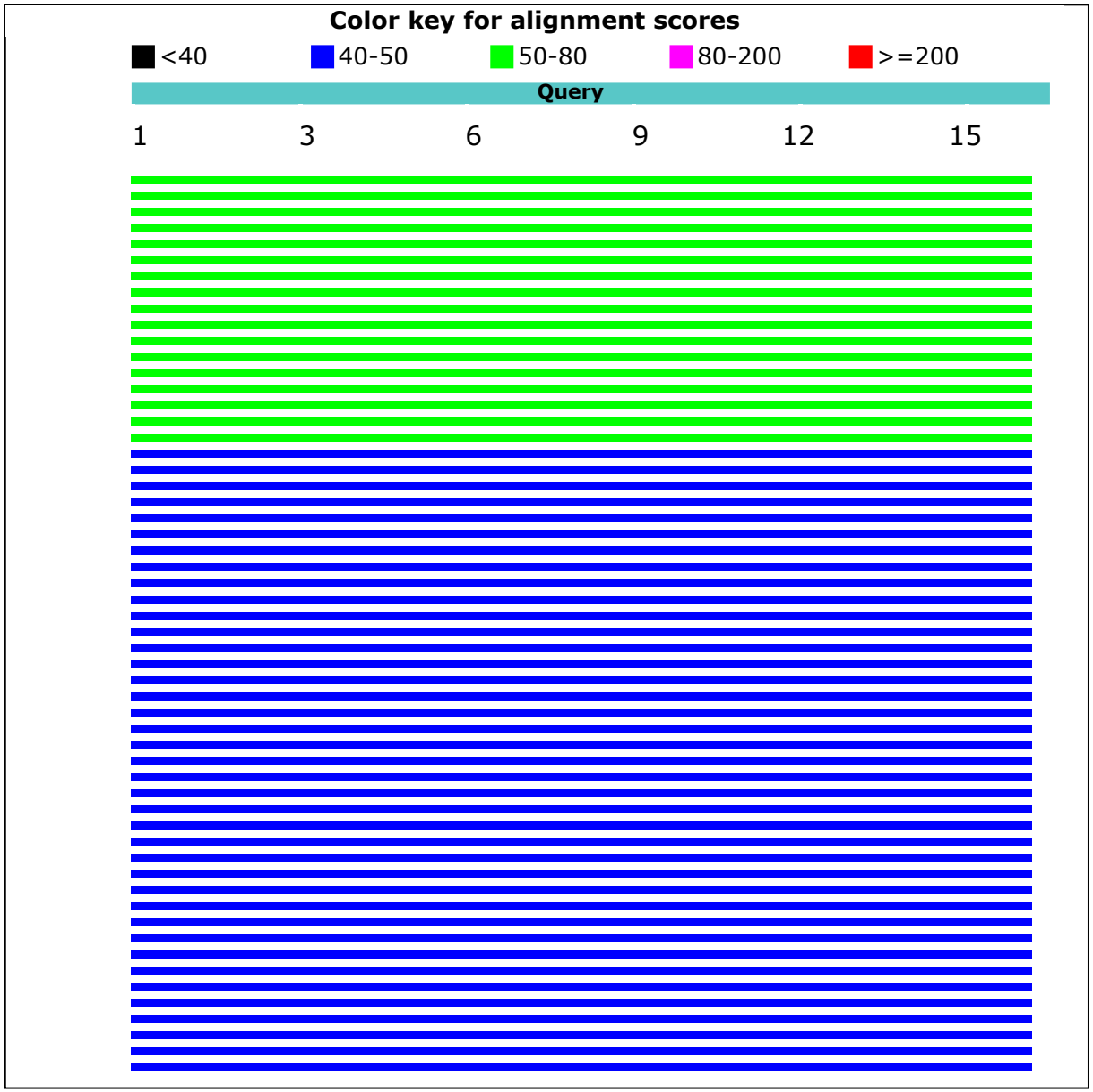
Query ID lcl|Query_326639
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 132 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
3
6
9
12
15

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein A-IV [Cebus capucinus imitator]	54.1	74.2	100%	2e-07	100%	XP_017378828.1
apolipoprotein A-IV [Homo sapiens]	54.1	54.1	100%	2e-07	100%	AAA51744.1
apolipoprotein A-IV precursor [Homo sapiens]	54.1	54.1	100%	2e-07	100%	AAA96731.1
PREDICTED: apolipoprotein A-IV [Gorilla gorilla gorilla]	54.1	54.1	100%	2e-07	100%	XP_004052227.1
PREDICTED: apolipoprotein A-IV [Pan paniscus]	54.1	54.1	100%	2e-07	100%	XP_003820134.1
PREDICTED: apolipoprotein A-IV [Pan troglodytes]	54.1	54.1	100%	2e-07	100%	XP_522192.2
apolipoprotein A-IV precursor [Homo sapiens]	54.1	54.1	100%	2e-07	100%	NP_000473.2
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	54.1	54.1	100%	2e-07	100%	P06727.3
apolipoprotein A-IV precursor [Homo sapiens]	54.1	54.1	100%	2e-07	100%	AAA51748.1
Chain A, Dimeric Apoa-Iv	54.1	54.1	100%	2e-07	100%	3S84_A
apolipoprotein A-IV [Gorilla gorilla]	54.1	54.1	100%	2e-07	100%	AEX20371.1
apolipoprotein A-IV [Homo sapiens]	54.1	54.1	100%	2e-07	100%	AAB59516.1
PREDICTED: apolipoprotein A-IV [Rhinopithecus bieti]	51.1	51.1	100%	2e-06	94%	XP_017738599.1
PREDICTED: apolipoprotein A-IV [Rhinopithecus roxellana]	51.1	51.1	100%	2e-06	94%	XP_010370007.1
apolipoprotein A-IV [Pygathrix nemaeus]	51.1	51.1	100%	2e-06	94%	AEH95748.1
apolipoprotein A-IV [Semnopithecus entellus]	51.1	51.1	100%	2e-06	94%	AEH95747.1
PREDICTED: apolipoprotein A-IV [Manis javanica]	50.7	92.3	100%	2e-06	94%	XP_017509603.1
PREDICTED: apolipoprotein A-IV [Pongo abelii]	49.8	49.8	100%	5e-06	94%	XP_009245367.1
PREDICTED: apolipoprotein A-IV [Callithrix jacchus]	49.8	49.8	100%	5e-06	94%	XP_002754492.1
apolipoprotein A-IV [Aotus nancymaae]	49.8	49.8	100%	5e-06	94%	XP_012325876.1
PREDICTED: apolipoprotein A-IV [Nomascus leucogenys]	49.8	49.8	100%	5e-06	94%	XP_003253231.1
PREDICTED: apolipoprotein A-IV [Ochotona princeps]	49.8	49.8	100%	5e-06	94%	XP_004585159.1
PREDICTED: apolipoprotein A-IV [Ceratotherium simum simum]	49.8	49.8	100%	5e-06	94%	XP_004427346.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
apolipoprotein A-IV [Callimico goeldii]	49.8	49.8	100%	5e-06	94%	AEH95755.1
apolipoprotein A-IV [Saguinus fuscicollis]	49.8	49.8	100%	5e-06	94%	AEH95754.1
apolipoprotein A-IV [Symphalangus syndactylus]	49.8	49.8	100%	5e-06	94%	AEH95746.1
apolipoprotein A-IV [Hylobates lar]	49.8	49.8	100%	5e-06	94%	AEH95745.1
apolipoprotein A-IV [Saguinus oedipus]	49.8	49.8	100%	5e-06	94%	AEX20370.1
PREDICTED: apolipoprotein A-IV [Odobenus rosmarus divergens]	47.3	47.3	100%	4e-05	88%	XP_004415535.1
PREDICTED: apolipoprotein A-IV [Ursus maritimus]	47.3	67.9	100%	4e-05	88%	XP_008688424.1
PREDICTED: apolipoprotein A-IV [Macaca mulatta]	46.9	46.9	100%	5e-05	88%	XP_014971282.1
PREDICTED: apolipoprotein A-IV [Macaca fascicularis]	46.9	46.9	100%	5e-05	88%	XP_005579784.1
PREDICTED: apolipoprotein A-IV [Macaca nemestrina]	46.9	46.9	100%	6e-05	88%	XP_011730719.1
PREDICTED: apolipoprotein A-IV isoform X1 [Mandrillus leucophaeus]	46.9	46.9	100%	6e-05	88%	XP_011837390.1
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	46.9	46.9	100%	6e-05	88%	P33621.1
PREDICTED: apolipoprotein A-IV [Cercocebus atys]	46.9	46.9	100%	6e-05	88%	XP_011908278.1
PREDICTED: apolipoprotein A-IV [Chlorocebus sabaeus]	46.9	46.9	100%	6e-05	88%	XP_008019167.1
apolipoprotein A-IV [Papio anubis]	46.9	46.9	100%	6e-05	88%	XP_003910789.1
PREDICTED: apolipoprotein A-IV isoform X1 [Colobus angolensis palliatus]	46.9	46.9	100%	6e-05	88%	XP_011782210.1
hypothetical protein EGK_06926 [Macaca mulatta]	46.9	46.9	100%	6e-05	88%	EHH23453.1
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	46.9	46.9	100%	6e-05	88%	Q28758.1
PREDICTED: apolipoprotein A-IV isoform X2 [Colobus angolensis palliatus]	46.9	46.9	100%	6e-05	88%	XP_011782211.1
PREDICTED: apolipoprotein A-IV isoform X2 [Mandrillus leucophaeus]	46.9	46.9	100%	6e-05	88%	XP_011837395.1
hypothetical protein EGM_06258 [Macaca fascicularis]	46.9	46.9	100%	6e-05	88%	EHH56782.1
apolipoprotein A-IV (predicted) [Rhinolophus ferrumequinum]	46.9	69.6	100%	6e-05	88%	ACC68865.1
PREDICTED: apolipoprotein A-IV [Rhinolophus sinicus]	46.9	71.7	100%	6e-05	88%	XP_019569164.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
apolipoprotein A-IV [Cercopithecus mitis]	46.9	46.9	100%	6e-05	88%	AEH95753.1
apolipoprotein A-IV [Lophocebus aterrimus]	46.9	46.9	100%	6e-05	88%	AEH95752.1
apolipoprotein A-IV [Erythrocebus patas]	46.9	46.9	100%	6e-05	88%	AEH95751.1
apolipoprotein A-IV [Macaca fascicularis]	46.9	46.9	100%	6e-05	88%	AEH95750.1
apolipoprotein A-IV [Papio hamadryas]	46.9	46.9	100%	6e-05	88%	AEH95749.1
apolipoprotein A-IV [Colobus guereza]	46.9	46.9	100%	6e-05	88%	AEX20369.1
apolipoprotein A-IV [Chlorocebus aethiops]	46.9	46.9	100%	6e-05	88%	AEX20368.1
PREDICTED: apolipoprotein A-IV [Galeopterus variegatus]	46.4	87.2	100%	8e-05	88%	XP_008589934.1
apolipoprotein A-IV [Microcebus murinus]	46.4	46.4	100%	8e-05	88%	XP_012629142.1
PREDICTED: apolipoprotein A-IV [Equus caballus]	46.4	46.4	100%	8e-05	88%	XP_001502503.1
PREDICTED: apolipoprotein A-IV [Equus asinus]	46.4	46.4	100%	8e-05	88%	XP_014711020.1
PREDICTED: apolipoprotein A-IV-like [Equus przewalskii]	46.4	46.4	100%	8e-05	88%	XP_008510513.1
apolipoprotein A-IV precursor (predicted) [Plecturocebus moloch]	46.0	66.2	100%	1e-04	88%	ACB21186.1
apolipoprotein A-IV [Nasalis larvatus]	44.8	44.8	100%	3e-04	88%	AEX20367.1
PREDICTED: apolipoprotein A-IV [Dipodomys ordii]	44.3	44.3	100%	4e-04	88%	XP_012865090.1
PREDICTED: apolipoprotein A-IV [Hipposideros armiger]	44.3	69.1	100%	4e-04	81%	XP_019502926.1
PREDICTED: apolipoprotein A-IV [Jaculus jaculus]	43.9	64.5	100%	6e-04	81%	XP_004666471.1
PREDICTED: apolipoprotein A-IV [Loxodonta africana]	43.9	64.5	100%	6e-04	81%	XP_003418284.1
PREDICTED: apolipoprotein A-IV [Otolemur garnettii]	43.5	64.1	100%	9e-04	81%	XP_003794819.1
apolipoprotein A-IV precursor (predicted) [Otolemur garnettii]	43.5	64.1	100%	9e-04	81%	ACH97051.1
Apolipoprotein A-IV [Pteropus alecto]	43.1	84.6	100%	0.001	81%	ELK11888.1
apolipoprotein A-IV [Castor canadensis]	43.1	63.6	100%	0.001	81%	XP_020039911.1
PREDICTED: apolipoprotein A-IV [Propithecus coquereli]	43.1	63.6	100%	0.001	81%	XP_012513783.1
apolipoprotein A-IV [Neomonachus schauinslandi]	43.1	43.1	100%	0.001	81%	XP_021552198.1
PREDICTED: apolipoprotein A-IV [Rousettus aegyptiacus]	43.1	63.6	100%	0.001	81%	XP_015990407.1
PREDICTED: apolipoprotein A-IV [Pteropus alecto]	43.1	84.6	100%	0.001	81%	XP_006912896.1
PREDICTED: apolipoprotein A-IV-like [Leptonychotes weddellii]	43.1	43.1	100%	0.001	81%	XP_006747633.1
PREDICTED: apolipoprotein A-IV [Pteropus vampyrus]	43.1	84.6	100%	0.001	81%	XP_011381499.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein A-IV [Ailuropoda melanoleuca]	43.1	63.6	100%	0.001	81%	XP_002919548.1
PREDICTED: apolipoprotein A-IV [Dasypus novemcinctus]	43.1	43.1	100%	0.001	81%	XP_004466047.1
apolipoprotein A-IV precursor (predicted) [Dasypus novemcinctus]	43.1	43.1	100%	0.001	81%	ACO95317.1
hypothetical protein PANDA_008178 [Ailuropoda melanoleuca]	43.1	63.6	100%	0.001	81%	EFB21765.1
PREDICTED: apolipoprotein A-IV [Canis lupus familiaris]	42.6	67.4	100%	0.002	81%	XP_546510.3
RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor	42.6	67.4	100%	0.002	81%	E2RE76.2
apolipoprotein A-IV [Odocoileus virginianus texanus]	42.2	42.2	100%	0.002	75%	XP_020758261.1
PREDICTED: apolipoprotein A-IV [Physeter catodon]	42.2	42.2	100%	0.002	81%	XP_007117219.1
PREDICTED: apolipoprotein A-IV [Tursiops truncatus]	42.2	62.8	100%	0.002	81%	XP_004316797.1
PREDICTED: apolipoprotein A-IV [Orcinus orca]	42.2	62.8	100%	0.002	81%	XP_004273415.1
APOA4 [Cervus elaphus hippelaphus]	42.2	42.2	100%	0.002	75%	OWK18067.1
PREDICTED: apolipoprotein A-IV [Saimiri boliviensis boliviensis]	41.8	41.8	100%	0.003	81%	XP_003923712.1
apolipoprotein A-IV [Ictidomys tridecemlineatus]	41.8	62.4	100%	0.003	81%	XP_005328347.1
apolipoprotein A-IV [Saimiri sciureus]	41.8	41.8	100%	0.003	81%	AEH95756.1
PREDICTED: apolipoprotein A-IV [Nannospalax galili]	41.4	61.9	100%	0.005	75%	XP_008849165.1
PREDICTED: apolipoprotein A-IV [Chinchilla lanigera]	40.9	40.9	93%	0.007	80%	XP_005378245.1
PREDICTED: apolipoprotein A-IV [Fukomys damarensis]	40.9	65.8	100%	0.007	80%	XP_010627703.1
PREDICTED: apolipoprotein A-IV [Octodon degus]	40.9	40.9	93%	0.007	80%	XP_004636539.1
PREDICTED: apolipoprotein A-IV isoform X1 [Bison bison bison]	40.1	40.1	100%	0.014	75%	XP_010828681.1
PREDICTED: apolipoprotein A-IV [Bos mutus]	40.1	40.1	100%	0.014	75%	XP_005896204.2
PREDICTED: apolipoprotein A-IV isoform X1 [Bubalus bubalis]	40.1	40.1	100%	0.014	75%	XP_006056942.1
PREDICTED: apolipoprotein A-IV isoform X1 [Bos taurus]	40.1	40.1	100%	0.014	75%	XP_005215909.1
PREDICTED: apolipoprotein A-IV isoform X2 [Bubalus bubalis]	40.1	40.1	100%	0.014	75%	XP_006056943.1
PREDICTED: apolipoprotein A-IV [Capra hircus]	40.1	40.1	100%	0.014	75%	XP_005689539.3
PREDICTED: apolipoprotein A-IV isoform X2 [Bison bison bison]	40.1	40.1	100%	0.014	75%	XP_010828682.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: apolipoprotein A-IV [Pantholops hodgsonii]	40.1	40.1	100%	0.014	75%	XP_005980010.1

Alignments

PREDICTED: apolipoprotein A-IV [Cebus capucinus imitator]
Sequence ID: **XP_017378828.1** Length: 406 Number of Matches: 2
Range 1: 289 to 304

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.1 bits(120)	2e-07()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1    LAELGGHLDQQVEEFR  16
            LAELGGHLDQQVEEFR
Sbjct  289  LAELGGHLDQQVEEFR  304
```

Range 2: 213 to 220

Score	Expect	Method	Identities	Positives	Gaps	Frame
20.2 bits(40)	171995()		6/8(75%)	6/8(75%)	0/8(0%)	

Features:

```
Query  9    DQQVEEFR  16
            DQ VEE R
Sbjct  213  DQAVEELR  220
```

apolipoprotein A-IV [Homo sapiens]
Sequence ID: **AAA51744.1** Length: 396 Number of Matches: 1

See 1 more title(s)
Range 1: 289 to 304

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.1 bits(120)	2e-07()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1    LAELGGHLDQQVEEFR  16
            LAELGGHLDQQVEEFR
Sbjct  289  LAELGGHLDQQVEEFR  304
```

apolipoprotein A-IV precursor [Homo sapiens]

Sequence ID: **AAA96731.1** Length: 396 Number of Matches: 1
Range 1: 289 to 304

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.1 bits(120)	2e-07()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1    LAELGGHLDQQVEEFR  16
            LAELGGHLDQQVEEFR
Sbjct  289  LAELGGHLDQQVEEFR  304
```

PREDICTED: apolipoprotein A-IV [Gorilla gorilla gorilla]

Sequence ID: **XP_004052227.1** Length: 396 Number of Matches: 1
Range 1: 289 to 304

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.1 bits(120)	2e-07()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1    LAELGGHLDQQVEEFR  16
            LAELGGHLDQQVEEFR
Sbjct  289  LAELGGHLDQQVEEFR  304
```

PREDICTED: apolipoprotein A-IV [Pan paniscus]

Sequence ID: **XP_003820134.1** Length: 396 Number of Matches: 1
Range 1: 289 to 304

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.1 bits(120)	2e-07()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1    LAELGGHLDQQVEEFR  16
            LAELGGHLDQQVEEFR
Sbjct  289  LAELGGHLDQQVEEFR  304
```

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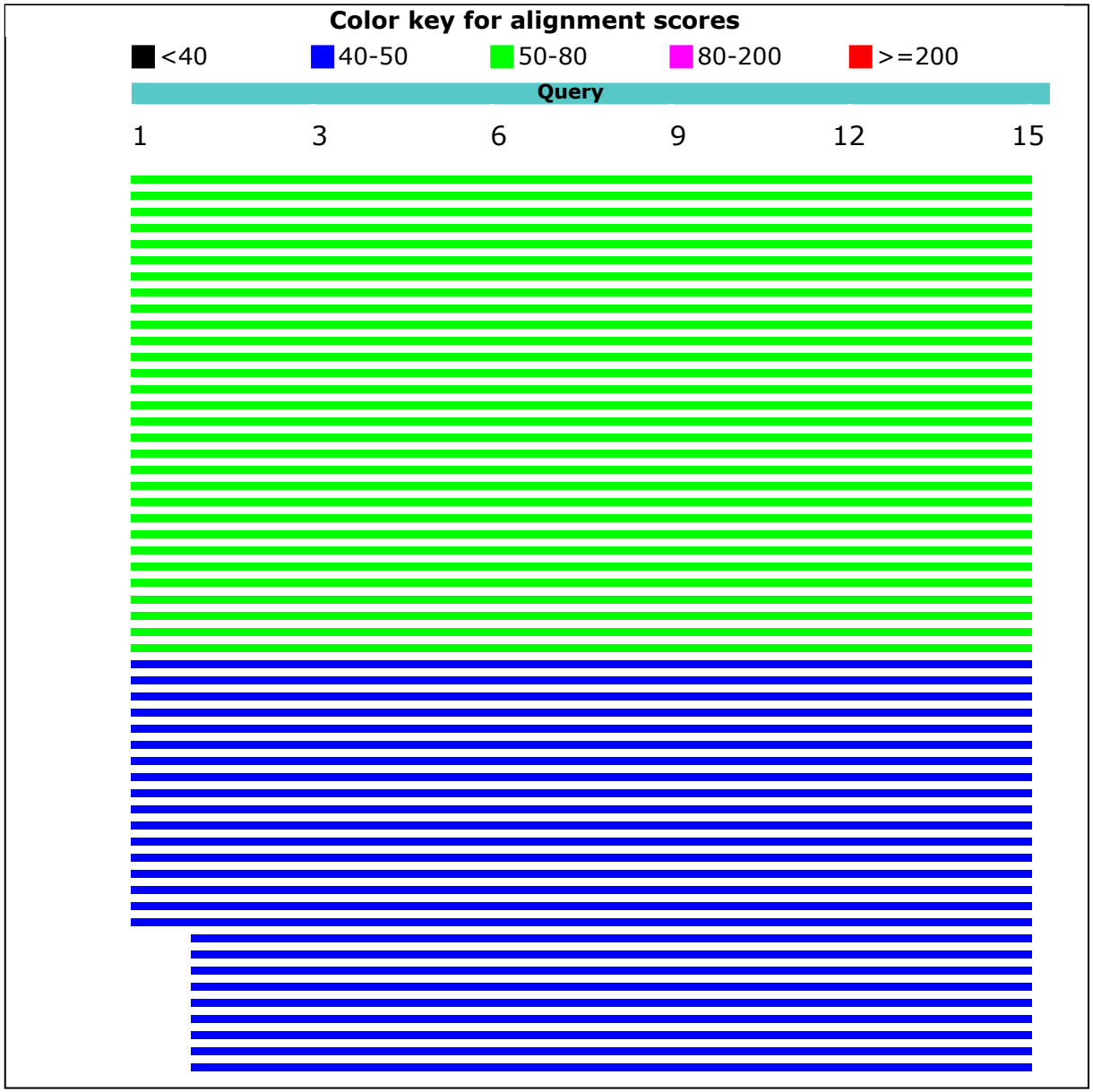
Job title: NCBI BlastP_APOE_SELEEQLTPVAEETR

RID	S54SEXCA015 (Expires on 08-04 11:05 am)
Query ID	lcl|Query_210239
Description	None
Molecule type	amino acid
Query Length	15
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 107 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
3
6
9
12
15

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
apolipoprotein E isoform a precursor [Homo sapiens]	50.3	50.3	100%	3e-06	100%	NP_001289617.1
ApoE1 [Cloning vector pcDNA3-ApoE1]	50.3	50.3	100%	3e-06	100%	ARQ79460.1
ApoE4A [Cloning vector pcDNA3-ApoE4A]	50.3	50.3	100%	3e-06	100%	ARQ79463.1
ApoE2 [Cloning vector pcDNA3-ApoE2]	50.3	50.3	100%	3e-06	100%	ARQ79459.1
apolipoprotein E [Homo sapiens]	50.3	50.3	100%	3e-06	100%	AAB59518.1
apolipoprotein E [Homo sapiens]	50.3	50.3	100%	3e-06	100%	AAB59397.1
apolipoprotein E precursor [Pan troglodytes]	50.3	50.3	100%	3e-06	100%	NP_001009007.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	50.3	50.3	100%	3e-06	100%	Q9GLM6.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	50.3	50.3	100%	3e-06	100%	Q9GLM8.1
apolipoprotein E isoform b precursor [Homo sapiens]	50.3	50.3	100%	3e-06	100%	NP_000032.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	50.3	50.3	100%	3e-06	100%	Q9GLM7.1
apolipoprotein E mutant E3K	50.3	50.3	100%	3e-06	100%	1506383A
Chain A, Nmr Structure Of Full Length Apoe3	50.3	50.3	100%	3e-06	100%	2L7B_A
apolipoprotein E [Pan troglodytes]	50.3	50.3	100%	3e-06	100%	AFS28580.1
apolipoprotein E [Homo sapiens]	50.3	50.3	100%	3e-06	100%	AFS60672.1
Chain A, Apolipoprotein E2 (Apoe2, D154a Mutation)	50.3	50.3	100%	3e-06	100%	1NFO_A
Chain A, Apolipoprotein E3 22kd Fragment Lys146gln Mutant	50.3	50.3	100%	3e-06	100%	1H7I_A
Chain A, Apolipoprotein E3 (Apoe3)	50.3	50.3	100%	3e-06	100%	1NFN_A
Chain A, Apolipoprotein E3 22kd Fragment Lys146glu Mutant	50.3	50.3	100%	3e-06	100%	1EA8_A
Chain A, Apolipoprotein E4 (Apoe4), 22k Fragment	50.3	50.3	100%	3e-06	100%	1B68_A
apolipoprotein E isoform 2 [Homo sapiens]	50.3	50.3	100%	3e-06	100%	ALQ33369.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Chain A, Nmr Solution Structure Of Complete Receptor Binding Domain Of Human Apolipoprotein E	50.3	50.3	100%	3e-06	100%	2KC3_A
unnamed protein product [Homo sapiens]	50.3	50.3	100%	3e-06	100%	CAA25017.1
Chain A, Apolipoprotein E4, 22k Domain	50.3	50.3	100%	3e-06	100%	1GS9_A
Chain A, Apolipoprotein E3 (Apoe3) Truncation Mutant 165	50.3	50.3	100%	3e-06	100%	1OR2_A
Chain A, Apolipoprotein E3 (Apoe3), Trigonal Truncation Mutant 165	50.3	50.3	100%	3e-06	100%	1OR3_A
Chain A, Structural Basis For Altered Function In The Common Mutants Of Human Apolipoprotein-E	50.3	50.3	100%	3e-06	100%	1LE2_A
Chain A, Structural Basis For Altered Function In The Common Mutants Of Human Apolipoprotein-E	50.3	50.3	100%	3e-06	100%	1LE4_A
Chain A, Apolipoprotein E3 (Apo-E3), Truncation Mutant 165	50.3	50.3	100%	3e-06	100%	1BZ4_A
Chain A, Three-Dimensional Structure Of The Ldl Receptor-Binding Domain Of Human Apolipoprotein E	50.3	50.3	100%	3e-06	100%	1LPE_A
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	P0DKW6.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	P0DOA3.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	P0DKW7.1
apolipoprotein E [Papio anubis]	47.3	47.3	100%	3e-05	93%	AAA35381.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	P0DO95.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	A0A0D9S1R0.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	P10517.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	P0DKY2.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	P0DO94.1
RecName: Full=Apolipoprotein E; Short=Apo-E	47.3	47.3	100%	3e-05	93%	P0DKW8.1
hypothetical protein EGK_10733 [Macaca mulatta]	47.3	47.3	100%	3e-05	93%	EHH30133.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
apolipoprotein E precursor [Chlorocebus aethiops]	47.3	47.3	100%	3e-05	93%	AAU25918.1
hypothetical protein [Macaca fascicularis]	47.3	47.3	100%	3e-05	93%	BAF47385.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	47.3	47.3	100%	3e-05	93%	P0DKW5.1
RecName: Full=Apolipoprotein E; Short=Apo-E	47.3	47.3	100%	3e-05	93%	Q28995.1
RecName: Full=Apolipoprotein E; Short=Apo-E	47.3	47.3	100%	3e-05	93%	Q28502.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	44.8	44.8	100%	2e-04	87%	P0DKU9.1
ORF2 [Rattus norvegicus]	42.2	42.2	93%	0.002	93%	AAA40756.1
apolipoprotein E precursor [Rattus norvegicus]	42.2	42.2	93%	0.002	93%	NP_620183.2
Apolipoprotein E [Rattus norvegicus]	42.2	42.2	93%	0.002	93%	AAH60313.1
apolipoprotein E [Rattus sp.]	42.2	42.2	93%	0.002	93%	AAC60703.1
unnamed protein product [Mus musculus]	42.2	42.2	93%	0.002	93%	BAE35071.1
unnamed protein product [Mus musculus]	42.2	42.2	93%	0.002	93%	BAE29894.1
unnamed protein product [Mus musculus]	42.2	42.2	93%	0.002	93%	BAE28964.1
Apoe [Mus musculus]	42.2	42.2	93%	0.002	93%	CAJ18420.1
apolipoprotein E precursor [Mus musculus]	42.2	42.2	93%	0.002	93%	AAA37251.1
apolipoprotein E precursor [Mus musculus]	42.2	42.2	93%	0.002	93%	NP_033826.2
apolipoprotein E [Rattus norvegicus]	42.2	42.2	93%	0.002	93%	CAA28650.1
apolipoprotein E [Mus musculus domesticus]	42.2	42.2	93%	0.002	93%	AAA37252.1
apolipoprotein E, isoform CRA_c [Rattus norvegicus]	42.2	42.2	93%	0.002	93%	EDM08152.1
apolipoprotein E, isoform CRA_f [Mus musculus]	42.2	42.2	93%	0.002	93%	EDL23181.1
apolipoprotein E, isoform CRA_a [Mus musculus]	42.2	42.2	93%	0.002	93%	EDL23176.1
Chain A, Crystal Structure Of The 22kda N-Terminal Fragment Of Mouse Apolipoprotein E	42.2	42.2	93%	0.002	93%	1YA9_A
unnamed protein product [Mus musculus]	42.2	42.2	93%	0.002	93%	BAE28740.1
apolipoprotein E, isoform CRA_e [Rattus norvegicus]	42.2	42.2	93%	0.002	93%	EDM08154.1
apolipoprotein E, isoform CRA_d [Rattus norvegicus]	42.2	42.2	93%	0.002	93%	EDM08153.1
apolipoprotein E, isoform CRA_d [Mus musculus]	42.2	42.2	93%	0.002	93%	EDL23179.1
apolipoprotein E, isoform CRA_g [Rattus norvegicus]	42.2	42.2	93%	0.002	93%	EDM08156.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
apolipoprotein E, isoform CRA_b [Mus musculus]	42.2	42.2	93%	0.002	93%	EDL23177.1
hypothetical protein [Acinetobacter baumannii]	42.2	42.2	93%	0.002	93%	WP_071211898.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	41.8	41.8	93%	0.003	86%	P0DOC3.1
apolipoprotein E precursor [Camelus ferus]	41.8	41.8	93%	0.003	86%	EPY87417.1
apolipoprotein E-like protein [Cricetulus griseus]	38.8	38.8	93%	0.028	86%	ERE59408.1
Apolipoprotein E [Cricetulus griseus]	38.8	38.8	93%	0.028	86%	EGW05330.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	35.8	35.8	86%	0.32	85%	P0DMM0.1
hypothetical protein [Ferrimonas balearica]	35.0	35.0	86%	0.64	77%	WP_013345597.1
hypothetical protein A6R68_11360 [Neotoma lepida]	35.0	35.0	93%	0.64	79%	OBS57523.1
apolipoprotein E precursor [Oryctolagus cuniculus]	35.0	35.0	100%	0.64	73%	NP_001076112.1
apolipoprotein E	35.0	35.0	100%	0.64	73%	1404236A
chromosome segregation protein SMC [Enterococcus massiliensis]	34.6	34.6	93%	0.90	71%	WP_048604535.1
apolipoprotein E [Meriones unguiculatus]	33.7	33.7	93%	1.8	79%	ADV16116.1
RecName: Full=Apolipoprotein E; Short=Apo-E; Flags: Precursor	33.7	33.7	86%	1.8	77%	P0DML7.1
apolipoprotein [Meriones unguiculatus]	33.7	33.7	93%	1.8	79%	ACF05250.1
peptide transporter [Pseudomonas cichorii]	33.3	33.3	80%	2.6	83%	WP_025262517.1
TIGR03086 family protein [Amycolatopsis rifamycinica]	33.3	33.3	80%	2.6	83%	WP_043775377.1
apolipoprotein E precursor [Heterocephalus glaber]	33.3	33.3	86%	2.6	77%	NP_001297225.1
3-oxoacyl-ACP reductase [Streptomyces sp. MUSC 14]	33.3	33.3	80%	2.6	83%	WP_071376047.1
Apolipoprotein A-I [Calypte anna]	33.3	33.3	86%	2.6	77%	KFP05502.1
Apolipoprotein A-I [Cuculus canorus]	33.3	33.3	86%	2.6	77%	KFO69473.1
Apolipoprotein A-I [Cuculus canorus]	33.3	33.3	86%	2.6	77%	KFO69475.1
TetR family transcriptional regulator [Rhodococcus koreensis]	33.3	33.3	93%	2.6	79%	WP_072943372.1
serine/threonine-protein kinase SIK3 [Patagioenas fasciata monilis]	32.9	32.9	93%	3.6	73%	OPJ68294.1
phosphatidylserine decarboxylase proenzyme, putative [Eimeria acervulina]	32.9	144	86%	3.6	85%	CDI80575.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
protein kinase domain-containing protein [Colletotrichum orbiculare MAFF 240422]	32.9	53.4	86%	3.6	65%	ENH80480.1
methionine adenosyltransferase [Actinomyces sp. ph3]	32.9	32.9	93%	3.6	63%	WP_034233675.1
methionine adenosyltransferase [Actinomyces sp. oral taxon 181]	32.9	32.9	93%	3.6	63%	WP_009409403.1
Apolipoprotein A-I [Charadrius vociferus]	32.9	32.9	93%	3.6	73%	KGL88706.1
TetR family transcriptional regulator [Streptomyces aureus]	32.9	32.9	80%	3.6	83%	WP_037616989.1
hemicentin-1 [Culex quinquefasciatus]	32.5	32.5	73%	5.1	91%	EDS27739.1
hypothetical protein cypCar_00024218 [Cyprinus carpio]	32.5	55.6	93%	5.1	83%	KTF89305.1

Alignments

apolipoprotein E isoform a precursor [Homo sapiens]

Sequence ID: **NP_001289617.1** Length: 343 Number of Matches: 1
Range 1: 120 to 134

Score	Expect	Method	Identities	Positives	Gaps	Frame
50.3 bits(111)	3e-06()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    SELEEQLTPVAEETR  15
           SELEEQLTPVAEETR
Sbjct  120  SELEEQLTPVAEETR  134
```

ApoE1 [Cloning vector pcDNA3-ApoE1]

Sequence ID: **ARQ79460.1** Length: 317 Number of Matches: 1
Range 1: 94 to 108

Score	Expect	Method	Identities	Positives	Gaps	Frame
50.3 bits(111)	3e-06()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    SELEEQLTPVAEETR  15
           SELEEQLTPVAEETR
Sbjct  94   SELEEQLTPVAEETR  108
```

ApoE4A [Cloning vector pcDNA3-ApoE4A]

Sequence ID: **ARQ79463.1** Length: 317 Number of Matches: 1
Range 1: 94 to 108

Score	Expect	Method	Identities	Positives	Gaps	Frame
50.3 bits(111)	3e-06()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    SELEEQLTPVAEETR  15
            SELEEQLTPVAEETR
Sbjct  94   SELEEQLTPVAEETR  108
```

ApoE2 [Cloning vector pcDNA3-ApoE2]

Sequence ID: **ARQ79459.1** Length: 317 Number of Matches: 1
Range 1: 94 to 108

Score	Expect	Method	Identities	Positives	Gaps	Frame
50.3 bits(111)	3e-06()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    SELEEQLTPVAEETR  15
            SELEEQLTPVAEETR
Sbjct  94   SELEEQLTPVAEETR  108
```

apolipoprotein E [Homo sapiens]

Sequence ID: **AAB59518.1** Length: 317 Number of Matches: 1
Range 1: 94 to 108

Score	Expect	Method	Identities	Positives	Gaps	Frame
50.3 bits(111)	3e-06()		15/15(100%)	15/15(100%)	0/15(0%)	

Features:

```
Query  1    SELEEQLTPVAEETR  15
            SELEEQLTPVAEETR
Sbjct  94   SELEEQLTPVAEETR  108
```

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Job title: NCBI BlastP_AMBP_AFIQLWAFDAVK

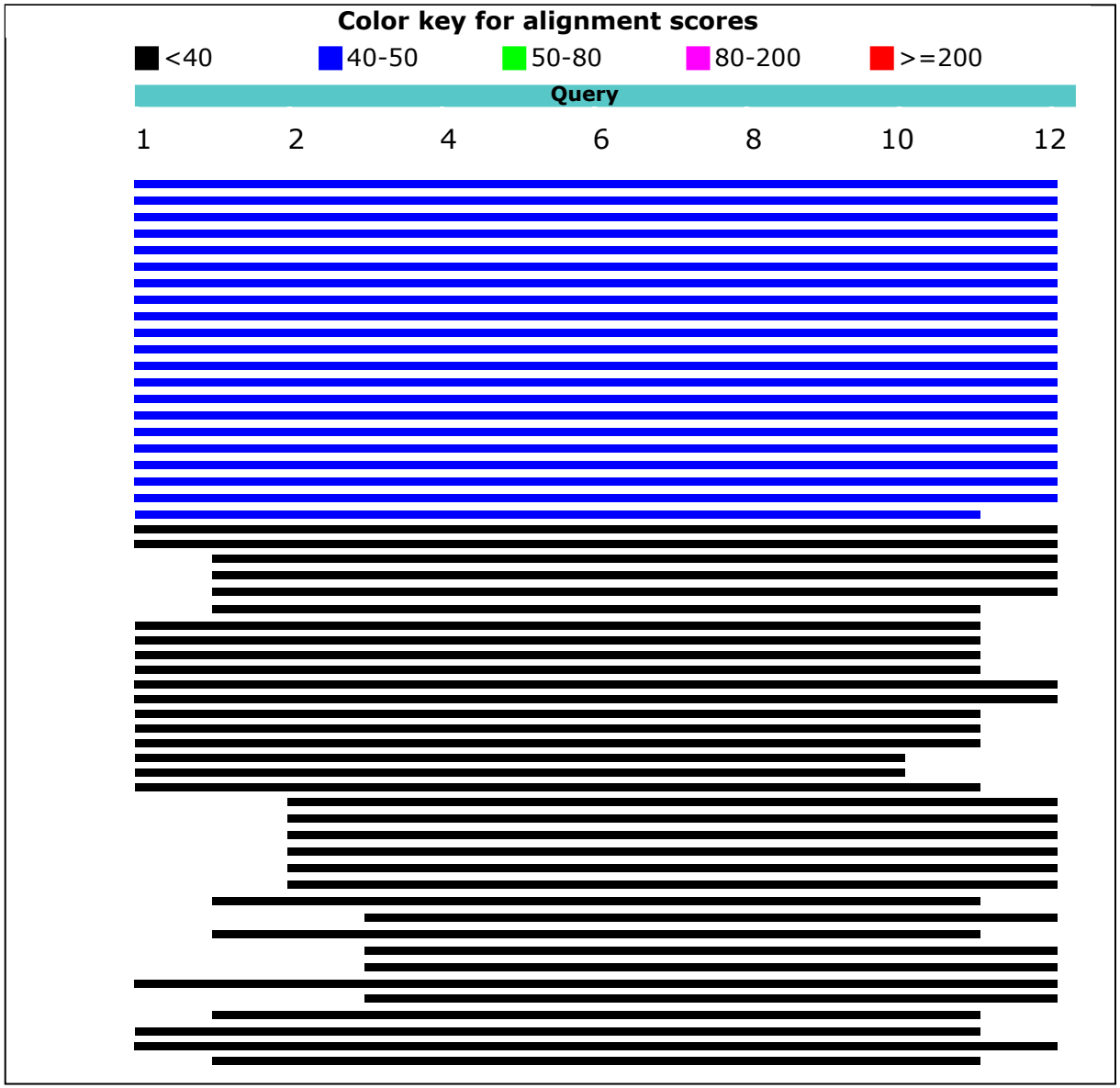
RID S548TCWC014 (Expires on 08-04 10:57 am)

Query ID	lcl|Query_33740	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	12	**Program**	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10
12

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: protein AMBP [Nomascus leucogenys]	43.1	43.1	100%	6e-04	100%	XP_012364107.1
protein AMBP [Papio anubis]	43.1	43.1	100%	6e-04	100%	XP_003911378.2
PREDICTED: protein AMBP [Pan troglodytes]	43.1	43.1	100%	6e-04	100%	XP_016816990.1
PREDICTED: protein AMBP [Macaca mulatta]	43.1	43.1	100%	6e-04	100%	XP_014972499.1
protein AMBP preproprotein [Homo sapiens]	43.1	43.1	100%	6e-04	100%	NP_001624.1
PREDICTED: protein AMBP [Macaca nemestrina]	43.1	43.1	100%	6e-04	100%	XP_011748670.1
PREDICTED: protein AMBP [Cercocebus atys]	43.1	43.1	100%	6e-04	100%	XP_011947659.1
PREDICTED: protein AMBP [Rhinopithecus roxellana]	43.1	43.1	100%	6e-04	100%	XP_010368790.1
PREDICTED: protein AMBP [Chlorocebus sabaeus]	43.1	43.1	100%	6e-04	100%	XP_007966514.1
PREDICTED: protein AMBP [Pan paniscus]	43.1	43.1	100%	6e-04	100%	XP_003833120.1
PREDICTED: protein AMBP [Macaca fascicularis]	43.1	43.1	100%	6e-04	100%	XP_005581045.1
protein AMBP precursor [Pongo abelii]	43.1	43.1	100%	6e-04	100%	NP_001127069.1
PREDICTED: protein AMBP [Mandrillus leucophaeus]	43.1	43.1	100%	6e-04	100%	XP_011853887.1
alpha-1-microglobulin [Homo sapiens]	43.1	43.1	100%	6e-04	100%	CAA38587.1
Chain A, X-Ray Structure Of Bikunin From The Human Inter-Alpha-Inhibitor Complex	43.1	43.1	100%	6e-04	100%	1BIK_A
bikunin	43.1	43.1	100%	6e-04	100%	2124279A
inhibitor HI30,trypsin	43.1	43.1	100%	6e-04	100%	0711211A
Chain X, Human Mesotrypsin Complexed With Bikunin Kunitz Domain 2	43.1	43.1	100%	6e-04	100%	4U30_X
inhibitor,Kunitz type proteinase	43.1	43.1	100%	6e-04	100%	0511271A
hypothetical protein [Pongo abelii]	43.1	43.1	100%	6e-04	100%	CAH89810.1
PREDICTED: protein AMBP [Myotis lucifugus]	40.1	40.1	91%	0.007	100%	XP_014302642.1
PREDICTED: protein AMBP [Gorilla gorilla gorilla]	39.2	39.2	100%	0.013	92%	XP_004048541.2
PREDICTED: protein AMBP [Colobus angolensis palliatus]	38.0	38.0	100%	0.037	92%	XP_011805484.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: protein AMBP isoform X1 [Bos indicus]	37.5	37.5	91%	0.053	91%	XP_019822347.1
protein AMBP precursor [Bos taurus]	37.5	37.5	91%	0.053	91%	NP_776414.1
TPA: protein AMBP precursor [Bos taurus]	37.5	37.5	91%	0.053	91%	DAA26456.1
PREDICTED: protein AMBP [Chrysochloris asiatica]	37.5	37.5	83%	0.053	100%	XP_006865791.1
Protein AMBP [Myotis davidii]	37.1	37.1	91%	0.075	91%	ELK26643.1
PREDICTED: protein AMBP [Myotis brandtii]	37.1	37.1	91%	0.075	91%	XP_005880981.1
PREDICTED: protein AMBP [Myotis davidii]	37.1	37.1	91%	0.075	91%	XP_006768680.1
protein AMBP [Ictidomys tridecemlineatus]	37.1	37.1	91%	0.075	91%	XP_005320935.1
AMBP [Cervus elaphus hippelaphus]	34.6	34.6	100%	0.60	75%	OWK07264.1
protein AMBP [Odocoileus virginianus texanus]	34.6	34.6	100%	0.60	75%	XP_020762338.1
protein AMBP [Aotus nancymaae]	34.6	34.6	91%	0.60	91%	XP_012317323.1
PREDICTED: protein AMBP [Callithrix jacchus]	34.6	34.6	91%	0.60	91%	XP_002743269.1
PREDICTED: protein AMBP [Octodon degus]	34.6	34.6	91%	0.60	91%	XP_004638530.1
hypothetical protein A6R68_04459 [Neotoma lepida]	34.1	34.1	83%	0.85	90%	OBS67002.1
protein AMBP [Mus pahari]	34.1	34.1	83%	0.85	90%	XP_021056650.1
PREDICTED: protein AMBP [Marmota marmota marmota]	34.1	34.1	91%	0.85	91%	XP_015347645.1
PREDICTED: protein AMBP isoform X1 [Capra hircus]	33.7	33.7	83%	1.2	90%	XP_013821748.1
PREDICTED: protein AMBP [Ovis aries musimon]	33.7	33.7	83%	1.2	90%	XP_012007629.1
PREDICTED: protein AMBP [Pantholops hodgsonii]	33.7	33.7	83%	1.2	90%	XP_005976114.1
PREDICTED: protein AMBP isoform X2 [Capra hircus]	33.7	33.7	83%	1.2	90%	XP_005684398.1
PREDICTED: protein AMBP [Ovis aries]	33.7	33.7	83%	1.2	90%	XP_004004032.1
RecName: Full=Inter-alpha-trypsin inhibitor; Short=ITI; AltName: Full=GIK-14; AltName: Full=Inhibitory fragment of ITI	33.7	33.7	83%	1.2	90%	P62756.1
alpha-1 microglobulin [Sus scrofa]	33.3	33.3	83%	1.5	90%	AAK57993.1
alpha-1-microglobulin/bikunin precursor [Tursiops truncatus]	33.3	33.3	75%	1.6	100%	AFH89705.1
protein AMBP precursor [Sus scrofa]	33.3	33.3	83%	1.7	90%	NP_001157478.1
PREDICTED: protein AMBP [Lipotes vexillifer]	33.3	33.3	75%	1.7	100%	XP_007449798.1
PREDICTED: protein AMBP [Balaenoptera acutorostrata scammoni]	33.3	33.3	75%	1.7	100%	XP_007178213.1
PREDICTED: protein AMBP [Bubalus bubalis]	33.3	33.3	100%	1.7	75%	XP_006061284.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: protein AMBP [Orcinus orca]	33.3	33.3	75%	1.7	100%	XP_004269353.1
protein AMBP isoform X1 [Sus scrofa]	33.3	33.3	83%	1.7	90%	XP_020938995.1
PREDICTED: protein AMBP [Eptesicus fuscus]	33.3	33.3	91%	1.7	82%	XP_008153478.1
PREDICTED: protein AMBP [Peromyscus maniculatus bairdii]	33.3	33.3	100%	1.7	75%	XP_006979613.1
RecName: Full=Protein AMBP; Contains: RecName: Full=Alpha-1-microglobulin; Contains: RecName: Full=Inter-alpha-trypsin inhibitor light chain; Short=ITI-LC; AltName: Full=Bikunin; AltName: Full=EI-14; AltName: Full=HI-30; Contains: RecName: Full=Trypstatin; Flags: Precursor	33.3	33.3	83%	1.7	90%	P04366.2
unnamed protein product [Sus scrofa]	33.3	33.3	83%	1.7	90%	CAA36306.1
PREDICTED: protein AMBP [Equus caballus]	32.9	32.9	83%	2.4	90%	XP_001488384.1
AMBP protein [Bos taurus]	32.9	32.9	91%	2.4	82%	AAI02638.1
PREDICTED: protein AMBP [Equus asinus]	32.9	32.9	83%	2.4	90%	XP_014704695.1
PREDICTED: protein AMBP [Dipodomys ordii]	32.9	32.9	83%	2.4	90%	XP_012885588.1
RecName: Full=Inter-alpha-trypsin inhibitor; Short=ITI; AltName: Full=EI-14; AltName: Full=HI-14; AltName: Full=Inhibitory fragment of ITI	32.9	32.9	83%	2.5	90%	P04365.2
protein AMBP [Mus caroli]	32.5	32.5	83%	3.4	90%	XP_021015755.1
protein AMBP preproprotein [Mus musculus]	32.5	32.5	83%	3.4	90%	NP_031469.1
alpha-1-microglobulin/bikunin precursor [Mus musculus]	32.5	32.5	83%	3.4	90%	CAA48640.1
unnamed protein product [Mus musculus]	32.5	32.5	83%	3.4	90%	BAB23659.1
alpha 1 microglobulin/bikunin, isoform CRA_f [Mus musculus]	32.5	32.5	83%	3.4	90%	EDL31127.1
alpha 1 microglobulin/bikunin, isoform CRA_b [Mus musculus]	32.5	32.5	83%	3.4	90%	EDL31123.1
alpha 1 microglobulin/bikunin, isoform CRA_d [Mus musculus]	32.5	32.5	83%	3.4	90%	EDL31125.1
alpha 1 microglobulin/bikunin, isoform CRA_a [Mus musculus]	32.5	32.5	83%	3.4	90%	EDL31122.1
alpha 1 microglobulin/bikunin, isoform CRA_c [Mus musculus]	32.5	32.5	83%	3.5	90%	EDL31124.1
PREDICTED: protein AMBP [Jaculus jaculus]	32.0	32.0	83%	4.8	90%	XP_004662786.1
PREDICTED: protein AMBP [Cebus capucinus imitator]	31.6	31.6	91%	6.8	82%	XP_017385777.1
PREDICTED: protein AMBP [Bison bison bison]	31.6	31.6	91%	6.8	73%	XP_010833447.1
PREDICTED: protein AMBP [Propithecus coquereli]	31.6	31.6	83%	6.8	90%	XP_012496649.1
PREDICTED: protein AMBP [Bos mutus]	31.6	31.6	91%	6.8	73%	XP_014335576.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Protein AMBP [Bos mutus]	31.6	31.6	91%	6.8	73%	ELR52128.1
PREDICTED: protein AMBP isoform X1 [Rhinolophus sinicus]	31.2	31.2	75%	9.7	89%	XP_019610145.1
protein AMBP [Castor canadensis]	31.2	31.2	75%	9.7	89%	XP_020015912.1
PREDICTED: protein AMBP isoform X2 [Rhinolophus sinicus]	31.2	31.2	75%	9.7	89%	XP_019610146.1
PREDICTED: protein AMBP [Miniopterus natalensis]	31.2	31.2	75%	9.7	89%	XP_016066571.1
protein AMBP precursor [Cavia porcellus]	31.2	31.2	75%	9.7	89%	NP_001166307.1
PREDICTED: protein AMBP isoform X1 [Cavia porcellus]	31.2	31.2	75%	9.7	89%	XP_012998119.1
hypothetical protein SNOG_08200 [Parastagonospora nodorum SN15]	30.8	30.8	66%	14	100%	XP_001798522.1
hypothetical protein [Bacillus sp. FJAT-25496]	30.8	30.8	75%	14	89%	WP_057771560.1
PREDICTED: protein AMBP [Hipposideros armiger]	30.8	30.8	66%	14	100%	XP_019491322.1
PREDICTED: protein AMBP [Manis javanica]	30.8	30.8	66%	14	100%	XP_017504235.1
PREDICTED: protein AMBP [Condylura cristata]	30.8	30.8	66%	14	100%	XP_004677464.1
glycoside hydrolase [Catenulispora acidiphila]	30.3	30.3	66%	19	100%	WP_015795433.1
PREDICTED: protein AMBP [Pteropus vampyrus]	30.3	30.3	66%	19	100%	XP_011359236.1
PREDICTED: protein AMBP [Pteropus alecto]	30.3	30.3	66%	19	100%	XP_006917168.1
PREDICTED: protein AMBP isoform X1 [Panthera pardus]	30.3	30.3	66%	19	100%	XP_019309628.1
protein AMBP [Carlito syrichta]	30.3	30.3	75%	19	89%	XP_008048352.1
PREDICTED: protein AMBP [Panthera tigris altaica]	30.3	30.3	66%	19	100%	XP_007094386.1
PREDICTED: protein AMBP [Chinchilla lanigera]	30.3	30.3	66%	19	100%	XP_005382713.1
protein AMBP [Heterocephalus glaber]	30.3	30.3	66%	19	100%	XP_004849569.1
Protein AMBP [Heterocephalus glaber]	30.3	30.3	66%	19	100%	EHB03304.1
protein AMBP precursor [Felis catus]	30.3	30.3	66%	19	100%	NP_001185483.1
PREDICTED: LOW QUALITY PROTEIN: protein AMBP [Acinonyx jubatus]	30.3	30.3	66%	19	100%	XP_014931634.1
PREDICTED: protein AMBP [Trichechus manatus latirostris]	30.3	30.3	66%	19	100%	XP_004372191.1

Alignments

PREDICTED: protein AMBP [Nomascus leucogenys]

Sequence ID: **XP_012364107.1** Length: 375 Number of Matches: 1
Range 1: 322 to 333

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	6e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    AFIQLWAFDAVK  12
            AFIQLWAFDAVK
Sbjct  322  AFIQLWAFDAVK  333
```

protein AMBP [Papio anubis]

Sequence ID: **XP_003911378.2** Length: 352 Number of Matches: 1
Range 1: 298 to 309

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	6e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    AFIQLWAFDAVK  12
            AFIQLWAFDAVK
Sbjct  298  AFIQLWAFDAVK  309
```

PREDICTED: protein AMBP [Pan troglodytes]

Sequence ID: **XP_016816990.1** Length: 352 Number of Matches: 1
Range 1: 298 to 309

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	6e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    AFIQLWAFDAVK  12
            AFIQLWAFDAVK
Sbjct  298  AFIQLWAFDAVK  309
```

PREDICTED: protein AMBP [Macaca mulatta]

Sequence ID: **XP_014972499.1** Length: 352 Number of Matches: 1
Range 1: 298 to 309

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	6e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    AFIQLWAFDAVK  12
           AFIQLWAFDAVK
Sbjct  298  AFIQLWAFDAVK  309
```

protein AMBP preproprotein [Homo sapiens]

Sequence ID: **NP_001624.1** Length: 352 Number of Matches: 1

See 13 more title(s)

Range 1: 298 to 309

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(94)	6e-04()		12/12(100%)	12/12(100%)	0/12(0%)	

Features:

```
Query  1    AFIQLWAFDAVK  12
           AFIQLWAFDAVK
Sbjct  298  AFIQLWAFDAVK  309
```

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Job title: NCBI BlastP_ACTG1_KDLYANTVLSGGTTMYPGIADR

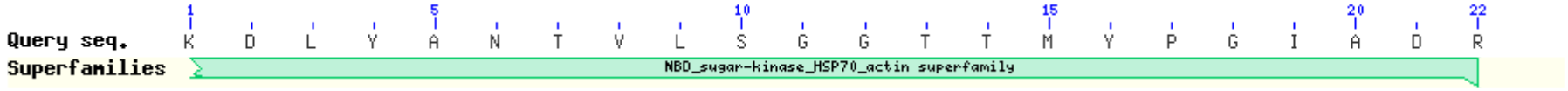
RID S54N1C09014 (Expires on 08-04 11:04 am)

Query ID	lcl|Query_355667	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	22	**Program**	BLASTP 2.6.1+

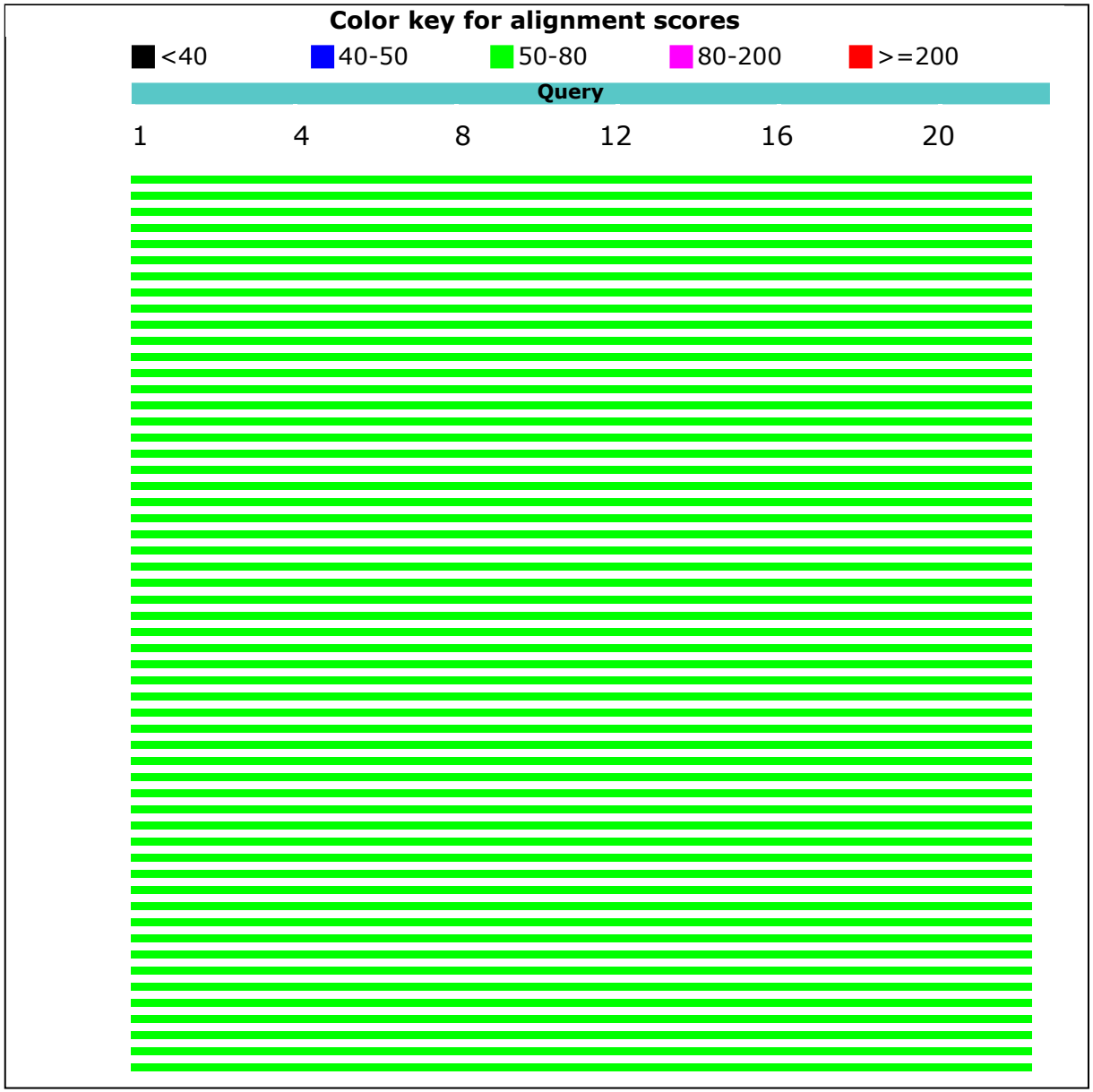
New Analyze your query with SmartBLAST

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 106 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
4
8
12
16
20

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
beta-actin [Folsomia candida]	72.7	72.7	100%	7e-15	100%	ACK77780.1
beta-actin [Folsomia candida]	72.7	72.7	100%	8e-15	100%	ABS85551.1
beta-actin [Folsomia candida]	72.7	72.7	100%	2e-14	100%	BAG75456.1
beta-actin [Centroptilum triangulifer]	72.7	72.7	100%	2e-14	100%	ADM21459.1
beta-actin [Ovis aries]	72.7	72.7	100%	2e-14	100%	ANK66213.1
beta-actin [Haliotis rufescens]	72.7	72.7	100%	2e-14	100%	AHW46516.1
beta-actin [Alligator sinensis]	72.7	72.7	100%	3e-14	100%	AER36707.1
beta-actin [Canis lupus familiaris]	72.7	72.7	100%	4e-14	100%	AAC48640.1
beta-actin [Apolygus lucorum]	72.7	72.7	100%	7e-14	100%	AEP31949.1
beta-actin [Orchesella cincta]	72.7	72.7	100%	7e-14	100%	AAV54528.1
beta-actin [Homo sapiens]	72.7	72.7	100%	7e-14	100%	AAB16906.1
beta-actin [Prionace glauca]	72.7	72.7	100%	8e-14	100%	AAS16921.1
actin [Diacamma sp. Okinawa-2006a]	72.7	72.7	100%	9e-14	100%	BAH80311.1
beta-actin [Atractosteus tropicus]	72.7	72.7	100%	9e-14	100%	ALV85598.1
actin [Truncattus flavus]	72.7	72.7	100%	9e-14	100%	AGJ82934.1
actin, cytoplasmic 2 [Ruegeria mobilis]	72.7	72.7	100%	9e-14	100%	KJZ21300.1
PREDICTED: actin, alpha skeletal muscle [Panthera pardus]	72.7	72.7	100%	9e-14	100%	XP_019295962.1
PREDICTED: actin, alpha skeletal muscle-like [Rhinopithecus bieti]	72.7	72.7	100%	9e-14	100%	XP_017722290.1
beta-actin [Squaliobarbus curriculus]	72.7	72.7	100%	9e-14	100%	ADV57163.1
PREDICTED: actin, alpha skeletal muscle-like [Xenopus laevis]	72.7	72.7	100%	1e-13	100%	XP_018098376.1
beta-actin [Lissorhoptrus oryzophilus]	72.7	72.7	100%	1e-13	100%	ADH95740.1
beta-actin [Megalobrama amblycephala]	72.7	72.7	100%	1e-13	100%	ADV57164.1
beta-actin [Hypophthalmichthys molitrix]	72.7	72.7	100%	1e-13	100%	ADV57162.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
beta-actin [Ctenopharyngodon idella]	72.7	72.7	100%	1e-13	100%	ADV57161.1
beta-actin [Mylopharyngodon piceus]	72.7	72.7	100%	1e-13	100%	ADV57160.1
beta actin precursor [Platichthys flesus]	72.7	72.7	100%	1e-13	100%	CAG29360.1
beta-actin [Anas platyrhynchos]	72.7	72.7	100%	1e-13	100%	ABG73406.1
PREDICTED: actin, alpha skeletal muscle [Rhinopithecus roxellana]	72.7	72.7	100%	1e-13	100%	XP_010381340.1
beta-actin [Miichthys miiuy]	72.7	72.7	100%	1e-13	100%	CBX36445.1
beta-actin [Pimephales promelas]	72.7	72.7	100%	1e-13	100%	ABX57722.1
PREDICTED: actin, alpha skeletal muscle [Xenopus laevis]	72.7	72.7	100%	1e-13	100%	XP_018098334.1
beta-actin [Tor putitora]	72.7	72.7	100%	1e-13	100%	AMJ39537.1
beta-actin [Anguilla australis]	72.7	72.7	100%	1e-13	100%	ADJ18353.1
beta-actin [Adelphocoris lineolatus]	72.7	72.7	100%	1e-13	100%	ACZ58018.1
beta-actin [Anguilla anguilla]	72.7	72.7	100%	1e-13	100%	ABF50546.1
beta-actin [Fundulus heteroclitus]	72.7	72.7	100%	1e-13	100%	AAL29465.1
beta-actin [Podarcis siculus]	72.7	72.7	100%	1e-13	100%	AAY34939.2
beta-actin [Phreatichthys andruzzii]	72.7	72.7	100%	1e-13	100%	ADL62678.1
beta-actin [Poeciliopsis lucida]	72.7	72.7	100%	1e-13	100%	ABW06848.1
hypothetical protein YQE_05577 [Dendroctonus ponderosae]	72.7	145	100%	1e-13	100%	ENN77900.1
muscle-like isoform 1 protein [Lasius niger]	72.7	72.7	100%	1e-13	100%	KMQ93592.1
actin, cytoplasmic 1 [Cricetulus griseus]	72.7	72.7	100%	1e-13	100%	ERE75950.1
cellular protein AbCp-71 [Androctonus bicolor]	72.7	72.7	100%	1e-13	100%	AIX87806.1
beta-actin [Clarias gariepinus]	72.7	72.7	100%	1e-13	100%	AIE58485.1
beta-actin [Anas platyrhynchos]	72.7	72.7	100%	1e-13	100%	ADD71533.1
beta-actin 2 [Squaliobarbus curriculus]	72.7	72.7	100%	1e-13	100%	ADV40648.1
beta-actin 2 [Mylopharyngodon piceus]	72.7	72.7	100%	1e-13	100%	ADV40645.1
hypothetical protein D910_05841 [Dendroctonus ponderosae]	72.7	177	100%	1e-13	100%	ERL88455.1
Actin, indirect flight muscle [Melipona quadrifasciata]	72.7	132	100%	1e-13	100%	KOX71963.1
Actin-2 [Mizuhopecten yessoensis]	72.7	104	100%	1e-13	100%	OWF48861.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Actin [Larimichthys crocea]	72.7	72.7	100%	1e-13	100%	KKF15719.1
Actin [Dictyocaulus viviparus]	72.7	72.7	100%	1e-13	100%	KJH45509.1
PREDICTED: actin, cytoplasmic 2-like [Rhinopithecus roxellana]	72.7	72.7	100%	1e-13	100%	XP_010355321.1
actin-2-like isoform X3 [Mizuhopecten yessoensis]	72.7	72.7	100%	1e-13	100%	XP_021356758.1
actin [Zabkattus brevis]	72.7	72.7	100%	1e-13	100%	AGJ82871.1
Actin [Drosophila melanogaster]	72.7	72.7	100%	1e-13	100%	CAA38618.1
PREDICTED: actin, cytoplasmic 1 isoform X1 [Pantholops hodgsonii]	72.7	72.7	100%	1e-13	100%	XP_005982177.1
PREDICTED: actin-2-like [Priapulus caudatus]	72.7	72.7	100%	1e-13	100%	XP_014662266.1
Actin, alpha cardiac muscle 1 [Strongyloides ratti]	72.7	72.7	100%	1e-13	100%	CEF67042.1
PREDICTED: actin-5C-like [Galendromus occidentalis]	72.7	145	100%	1e-13	100%	XP_003747695.2
PREDICTED: LOW QUALITY PROTEIN: actin, cytoplasmic 2-like [Stegastes partitus]	72.7	72.7	100%	1e-13	100%	XP_008290663.1
PREDICTED: actin, cytoplasmic-like [Larimichthys crocea]	72.7	72.7	100%	1e-13	100%	XP_019130606.1
PREDICTED: LOW QUALITY PROTEIN: actin, cytoplasmic 2-like [Neolamprologus brichardi]	72.7	72.7	100%	1e-13	100%	XP_006796239.1
actin [Echinococcus multilocularis]	72.7	72.7	100%	1e-13	100%	CDS39488.1
PREDICTED: actin, cytoplasmic A3a-like [Cimex lectularius]	72.7	72.7	100%	1e-13	100%	XP_014258398.1
PREDICTED: actin, cytoplasmic A3a isoform X1 [Bactrocera dorsalis]	72.7	72.7	100%	1e-13	100%	XP_011198527.1
actin, cytoplasmic 1 [Patagioenas fasciata monilis]	72.7	72.7	100%	1e-13	100%	OPJ87354.1
PREDICTED: actin, cytoplasmic 2 [Lepisosteus oculatus]	72.7	72.7	100%	1e-13	100%	XP_006635223.2
Actin, cytoplasmic 2 [Tupaia chinensis]	72.7	72.7	100%	1e-13	100%	ELW68212.1
PREDICTED: actin, cytoplasmic 2 isoform X1 [Nomascus leucogenys]	72.7	72.7	100%	1e-13	100%	XP_012367864.1
PREDICTED: actin, cytoplasmic 1 isoform X1 [Fulmarus glacialis]	72.7	72.7	100%	1e-13	100%	XP_009582089.1
PREDICTED: LOW QUALITY PROTEIN: actin, cytoplasmic 1-like [Mesitornis unicolor]	72.7	72.7	100%	1e-13	100%	XP_010181524.1
PREDICTED: LOW QUALITY PROTEIN: actin, cytoplasmic 1-like [Pelecanus crispus]	72.7	72.7	100%	1e-13	100%	XP_009476550.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: actin, cytoplasmic 2 isoform X1 [Colobus angolensis palliatus]	72.7	72.7	100%	1e-13	100%	XP_011815463.1
PREDICTED: LOW QUALITY PROTEIN: actin, cytoplasmic 1-like [Balearica regulorum gibbericeps]	72.7	72.7	100%	1e-13	100%	XP_010305896.1
PREDICTED: actin, cytoplasmic 1 isoform X1 [Egretta garzetta]	72.7	72.7	100%	1e-13	100%	XP_009644204.1
PREDICTED: actin, cytoplasmic 1 [Pygoscelis adeliae]	72.7	72.7	100%	1e-13	100%	XP_009318317.1
PREDICTED: actin, cytoplasmic 1 isoform X1 [Aptenodytes forsteri]	72.7	72.7	100%	1e-13	100%	XP_009284687.1
Actin, cytoplasmic 1 [Fukomys damarensis]	72.7	72.7	100%	1e-13	100%	KFO25358.1
actin, cytoplasmic 2 [Patagioenas fasciata monilis]	72.7	72.7	100%	1e-13	100%	OPJ88443.1
PREDICTED: actin, cytoplasmic 1 isoform X1 [Picoides pubescens]	72.7	72.7	100%	1e-13	100%	XP_009895225.1
PREDICTED: LOW QUALITY PROTEIN: actin, cytoplasmic 1-like [Pterocles gutturalis]	72.7	72.7	100%	1e-13	100%	XP_010082493.1
PREDICTED: POTE ankyrin domain family member F isoform X1 [Rattus norvegicus]	72.7	72.7	100%	1e-13	100%	XP_002728578.2
beta-actin [Callorhinchus milii]	72.7	72.7	100%	1e-13	100%	AFK11562.1
PREDICTED: LOW QUALITY PROTEIN: actin, gamma 1 [Leptonychotes weddellii]	72.7	72.7	100%	1e-13	100%	XP_006752408.1
PREDICTED: LOW QUALITY PROTEIN: actin, cytoplasmic 2 [Equus przewalskii]	72.7	72.7	100%	1e-13	100%	XP_008518606.1
hypothetical protein SINV_08795 [Solenopsis invicta]	72.7	72.7	100%	1e-13	100%	EFZ09249.1
PREDICTED: actin, cytoplasmic 1 [Camelus dromedarius]	72.7	72.7	100%	1e-13	100%	XP_010996228.1
Actin, cytoplasmic 1 [Myotis brandtii]	72.7	72.7	100%	1e-13	100%	EPQ10175.1
actin, cytoplasmic 1-like [Aotus nancymaae]	72.7	72.7	100%	1e-13	100%	XP_021533064.1
PREDICTED: POTE ankyrin domain family member F isoform X2 [Rattus norvegicus]	72.7	72.7	100%	1e-13	100%	XP_002725368.2
actin, cytoplasmic 2-like [Scleropages formosus]	72.7	72.7	100%	1e-13	100%	KPP71228.1
PREDICTED: actin, cytoplasmic 1 isoform X1 [Canis lupus familiaris]	72.7	72.7	100%	1e-13	100%	XP_005621076.1
cytoskeletal beta actin [Sus scrofa]	72.7	72.7	100%	1e-13	100%	AAS55927.1
Actin, cytoplasmic 2-like [Scleropages formosus]	72.7	72.7	100%	1e-13	100%	KPP63191.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein Y1Q_0007443 [Alligator mississippiensis]	72.7	72.7	100%	1e-13	100%	KYO39905.1
PREDICTED: LOW QUALITY PROTEIN: actin, cytoplasmic 2 [Ursus maritimus]	72.7	72.7	100%	1e-13	100%	XP_008692076.1
PREDICTED: actin, cytoplasmic 1 [Anser cygnoides domesticus]	72.7	72.7	100%	1e-13	100%	XP_013030340.1
hypothetical protein Y1Q_0001713 [Alligator mississippiensis]	72.7	72.7	100%	1e-13	100%	KYO21532.1
PREDICTED: actin, cytoplasmic 2 isoform X1 [Manis javanica]	72.7	72.7	100%	1e-13	100%	XP_017536124.1

Alignments

beta-actin, partial [Folsomia candida]

Sequence ID: **ACK77780.1** Length: 36 Number of Matches: 1
Range 1: 8 to 29

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.7 bits(164)	7e-15()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1   KDLYANTVLSGGTTMYPGIADR  22
           KDLYANTVLSGGTTMYPGIADR
Sbjct  8   KDLYANTVLSGGTTMYPGIADR  29
```

beta-actin, partial [Folsomia candida]

Sequence ID: **ABS85551.1** Length: 37 Number of Matches: 1
Range 1: 8 to 29

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.7 bits(164)	8e-15()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1   KDLYANTVLSGGTTMYPGIADR  22
           KDLYANTVLSGGTTMYPGIADR
Sbjct  8   KDLYANTVLSGGTTMYPGIADR  29
```

beta-actin, partial [Folsomia candida]

Sequence ID: **BAG75456.1** Length: 48 Number of Matches: 1
Range 1: 17 to 38

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.7 bits(164)	2e-14()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1   KDLYANTVLSGGTTMYPGIADR  22
           KDLYANTVLSGGTTMYPGIADR
Sbjct  17  KDLYANTVLSGGTTMYPGIADR  38
```

beta-actin, partial [Centroptilum triangulifer]

Sequence ID: **ADM21459.1** Length: 49 Number of Matches: 1
Range 1: 14 to 35

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.7 bits(164)	2e-14()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1   KDLYANTVLSGGTTMYPGIADR  22
           KDLYANTVLSGGTTMYPGIADR
Sbjct  14  KDLYANTVLSGGTTMYPGIADR  35
```

beta-actin, partial [Ovis aries]

Sequence ID: **ANK66213.1** Length: 50 Number of Matches: 1
Range 1: 12 to 33

Score	Expect	Method	Identities	Positives	Gaps	Frame
72.7 bits(164)	2e-14()		22/22(100%)	22/22(100%)	0/22(0%)	

Features:

```
Query  1   KDLYANTVLSGGTTMYPGIADR  22
           KDLYANTVLSGGTTMYPGIADR
Sbjct  12  KDLYANTVLSGGTTMYPGIADR  33
```

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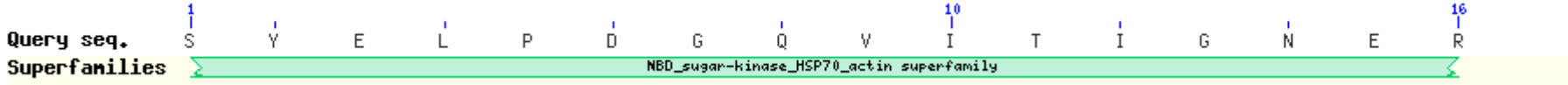
BLAST Results

Job title: NCBI BlastP_ACTG1_SYELPDGQVITIGNER

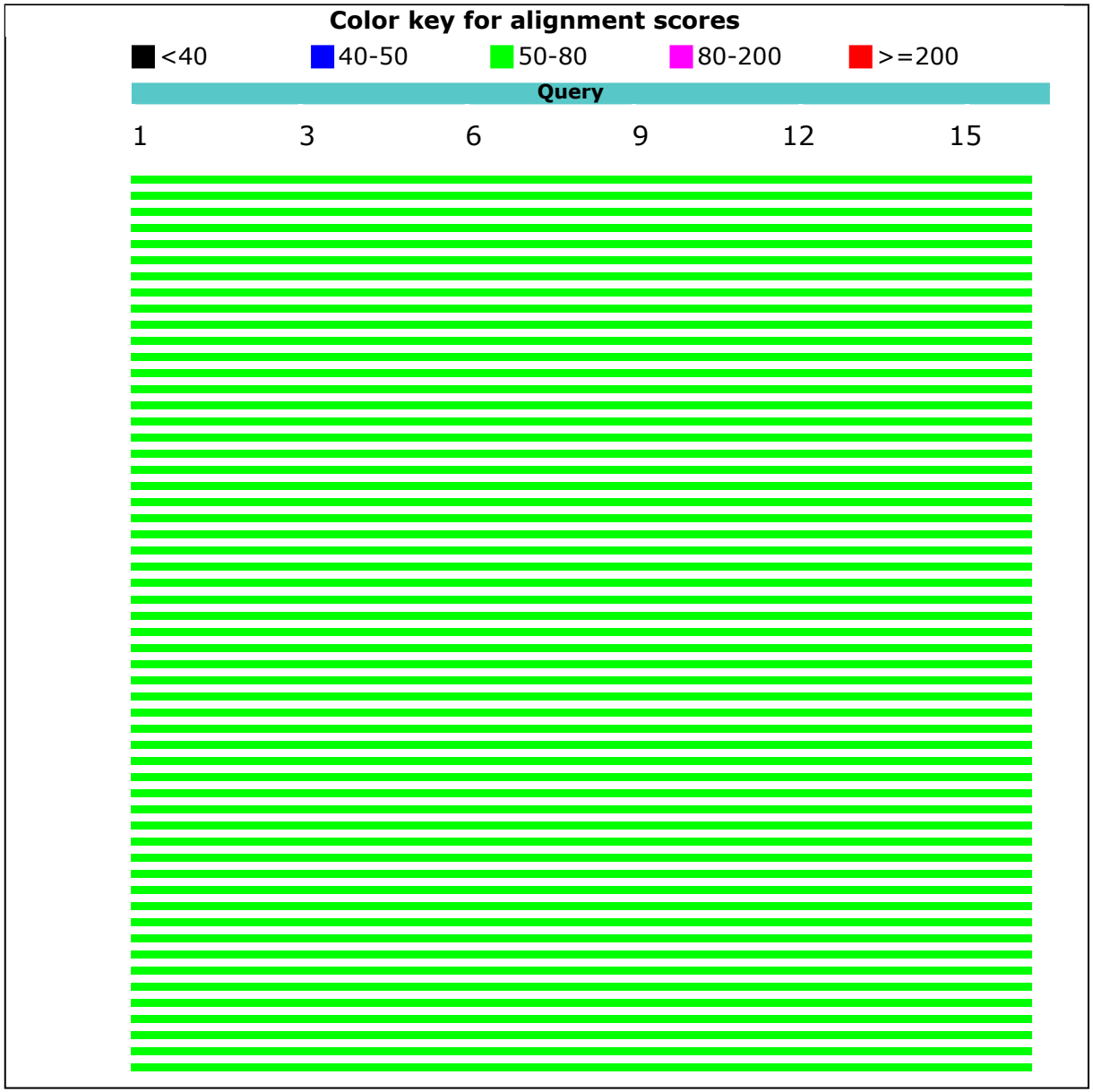
RID	S54NHTZ0014 (Expires on 08-04 11:04 am)
Query ID	lcl|Query_273350
Description	None
Molecule type	amino acid
Query Length	16
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 123 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
3
6
9
12
15

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
48 kda histamine receptor subunit peptide 4 {internal fragment} [human, peripheral blood mononuclear cells, Peptide Partial, 27 aa]	54.5	54.5	100%	1e-08	100%	AAB34251.1
hypothetical protein [Escherichia coli]	54.5	54.5	100%	3e-08	100%	WP_072775675.1
beta-actin [Coregonus lavaretus]	54.5	54.5	100%	4e-08	100%	ABB22794.1
beta-actin [Channa gachua]	54.5	54.5	100%	4e-08	100%	ACR25275.1
beta-actin [Chiloscyllium punctatum]	54.5	54.5	100%	5e-08	100%	AHA84099.1
actin [Bemisia tabaci]	54.5	54.5	100%	6e-08	100%	ACT78447.1
actin [Onnia tomentosa]	54.5	54.5	100%	6e-08	100%	AAW82382.1
actin [Pseudodiamesa branickii]	54.5	54.5	100%	7e-08	100%	ADQ43334.1
actin alpha cardiac muscle 1 precursor [Homo sapiens]	54.5	54.5	100%	1e-07	100%	ANH56391.1
cardiac actin [Canis lupus familiaris]	54.5	54.5	100%	1e-07	100%	AAG35634.1
hypothetical protein L969DRAFT_102075 [Mixia osmundae IAM 14324]	54.5	54.5	100%	1e-07	100%	XP_014569215.1
nuclear pore complex protein Nup133 [Patagioenas fasciata monilis]	54.5	54.5	100%	1e-07	100%	OPJ72754.1
hypothetical protein CB1_000252031 [Camelus ferus]	54.5	54.5	100%	1e-07	100%	EPY87376.1
PREDICTED: POTE ankyrin domain family member E isoform X2 [Pan troglodytes]	54.5	54.5	100%	1e-07	100%	XP_016804874.1
PREDICTED: POTE ankyrin domain family member F isoform X1 [Homo sapiens]	54.5	54.5	100%	1e-07	100%	XP_016860322.1
DUF1604 domain-containing protein [Rozella allomycis CSF55]	54.5	54.5	100%	1e-07	100%	EPZ34174.1
PREDICTED: POTE ankyrin domain family member I isoform X1 [Pongo abelii]	54.5	54.5	100%	1e-07	100%	XP_002812403.1
POTE-2 alpha-actin [Homo sapiens]	54.5	54.5	100%	1e-07	100%	ABP57734.1
POTE ankyrin domain family member E [Homo sapiens]	54.5	54.5	100%	1e-07	100%	NP_001077007.1
POTE ankyrin domain family member F [Homo sapiens]	54.5	54.5	100%	1e-07	100%	NP_001093241.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
actin [Moesziomyces antarcticus]	54.5	54.5	100%	1e-07	100%	XP_014654218.1
PREDICTED: POTE ankyrin domain family member E isoform X2 [Pongo abelii]	54.5	54.5	100%	1e-07	100%	XP_009235877.1
hypothetical protein ANOM_000787 [Aspergillus nomius NRRL 13137]	54.5	54.5	100%	1e-07	100%	XP_015411932.1
actin cytoplasmic type 5 [Hymenolepis microstoma]	54.5	54.5	100%	1e-07	100%	CDS26183.1
PREDICTED: POTE ankyrin domain family member E isoform X1 [Homo sapiens]	54.5	54.5	100%	1e-07	100%	XP_016859648.1
PREDICTED: POTE ankyrin domain family member E isoform X2 [Homo sapiens]	54.5	54.5	100%	1e-07	100%	XP_011509518.1
PREDICTED: activating signal cointegrator 1 complex subunit 3-like [Drosophila navojoa]	54.5	54.5	100%	1e-07	100%	XP_017967121.1
hypothetical protein YQE_05577 [Dendroctonus ponderosae]	54.5	130	100%	1e-07	100%	ENN77900.1
actin/actin family protein [Aspergillus oryzae]	54.5	54.5	100%	1e-07	100%	OOO05699.1
muscle-like isoform 1 protein [Lasius niger]	54.5	54.5	100%	1e-07	100%	KMQ93592.1
actin, cytoplasmic 1 [Cricetulus griseus]	54.5	54.5	100%	1e-07	100%	ERE75950.1
Actin-1 [Leucoagaricus sp. SymC.cos]	54.5	54.5	100%	1e-07	100%	KXN91167.1
PREDICTED: LOW QUALITY PROTEIN: POTE ankyrin domain family member E [Colobus angolensis palliatus]	54.5	54.5	100%	1e-07	100%	XP_011797114.1
actin [Stemphylium lycopersici]	54.5	54.5	100%	1e-07	100%	KNG50423.1
actin, gamma-enteric smooth muscle-like isoform 1 [Cricetulus griseus]	54.5	54.5	100%	1e-07	100%	ERE66270.1
hypothetical protein D910_05841 [Dendroctonus ponderosae]	54.5	130	100%	1e-07	100%	ERL88455.1
STAM-binding protein-like isoform 2 [Cricetulus griseus]	54.5	54.5	100%	1e-07	100%	ERE66271.1
Actin, indirect flight muscle [Melipona quadrifasciata]	54.5	109	100%	1e-07	100%	KOX71963.1
PREDICTED: uncharacterized protein LOC107346890 [Acropora digitifera]	54.5	86.1	100%	1e-07	100%	XP_015768232.1
PREDICTED: uncharacterized protein LOC109479655 [Branchiostoma belcheri]	54.5	109	100%	1e-07	100%	XP_019637201.1
actin actin-like protein [Coniophora puteana RWD-64-598 SS2]	54.5	109	100%	1e-07	100%	XP_007767488.1
PREDICTED: uncharacterized protein LOC109479654 [Branchiostoma belcheri]	54.5	109	100%	1e-07	100%	XP_019637200.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein BRAFLDRAFT_126063 [Branchiostoma floridae]	54.5	106	100%	1e-07	100%	XP_002590163.1
PREDICTED: uncharacterized protein LOC109482101 [Branchiostoma belcheri]	54.5	109	100%	1e-07	100%	XP_019640346.1
CLUMA_CG003286, isoform A [Clunio marinus]	54.5	109	100%	1e-07	100%	CRK89610.1
actin actin-like protein [Rhodotorula sp. JG-1b]	54.5	109	100%	1e-07	100%	KWU47311.1
Actin-2 [Mizuhopecten yessoensis]	54.5	84.0	100%	1e-07	100%	OWF48861.1
Actin [Larimichthys crocea]	54.5	54.5	100%	1e-07	100%	KKF15719.1
PREDICTED: LOW QUALITY PROTEIN: POTE ankyrin domain family member E [Pan paniscus]	54.5	54.5	100%	1e-07	100%	XP_014199441.1
Actin, gamma-enteric smooth muscle [Cricetulus griseus]	54.5	54.5	100%	1e-07	100%	EGW09955.1
actin-domain-containing protein [Hanseniaspora valbyensis NRRL Y-1626]	54.5	54.5	100%	1e-07	100%	OBA26716.1
actin [Pichia kudriavzevii]	54.5	54.5	100%	1e-07	100%	OUT23905.1
PREDICTED: LOW QUALITY PROTEIN: putative beta-actin-like protein 3 [Gorilla gorilla gorilla]	54.5	54.5	100%	1e-07	100%	XP_018877231.1
PREDICTED: POTE ankyrin domain family member F isoform X2 [Homo sapiens]	54.5	54.5	100%	1e-07	100%	XP_016860323.1
actin, alpha cardiac muscle 1-like protein [Cricetulus griseus]	54.5	54.5	100%	1e-07	100%	ERE72071.1
PREDICTED: actin, cytoplasmic 2-like [Rhinopithecus roxellana]	54.5	54.5	100%	1e-07	100%	XP_010355321.1
PREDICTED: POTE ankyrin domain family member F isoform X3 [Homo sapiens]	54.5	54.5	100%	1e-07	100%	XP_016860324.1
PREDICTED: POTE ankyrin domain family member E isoform X3 [Homo sapiens]	54.5	54.5	100%	1e-07	100%	XP_016859649.1
Actin, gamma [Metarhizium album ARSEF 1941]	54.5	54.5	100%	1e-07	100%	KHN95814.1
actin [Tropilaelaps mercedesae]	54.5	54.5	100%	1e-07	100%	OQR76811.1
actin [Rhizoctonia solani AG-1 IA]	54.5	54.5	100%	1e-07	100%	ELU37363.1
Actin [Trichuris suis]	54.5	54.5	100%	1e-07	100%	KHJ49510.1
hypothetical protein BN1723_005068 [Verticillium longisporum]	54.5	54.5	100%	1e-07	100%	CRK41133.1
PREDICTED: POTE ankyrin domain family member E isoform X1 [Pan troglodytes]	54.5	54.5	100%	1e-07	100%	XP_016804873.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
actin, cytoplasmic 1-like isoform X1 [Papio anubis]	54.5	54.5	100%	1e-07	100%	XP_003919284.3
hypothetical protein BRAFLDRAFT_86184 [Branchiostoma floridae]	54.5	54.5	100%	1e-07	100%	XP_002590512.1
PREDICTED: actin, cytoplasmic 1 [Taeniopygia guttata]	54.5	54.5	100%	1e-07	100%	XP_012425948.1
Actin1 [Acanthamoeba castellanii str. Neff]	54.5	54.5	100%	1e-07	100%	XP_004344919.1
PREDICTED: actin, cytoplasmic 1-like isoform X1 [Chlorocebus sabaeus]	54.5	54.5	100%	1e-07	100%	XP_008017958.1
PREDICTED: actin, gamma-enteric smooth muscle isoform X1 [Pseudopodoces humilis]	54.5	54.5	100%	1e-07	100%	XP_005533023.2
actin, cytoplasmic 1-like isoform X2 [Papio anubis]	54.5	54.5	100%	1e-07	100%	XP_009197935.2
PREDICTED: actin, cytoplasmic 1-like isoform X2 [Chlorocebus sabaeus]	54.5	54.5	100%	1e-07	100%	XP_008017959.1
PREDICTED: actin-1 [Crassostrea gigas]	54.5	109	100%	1e-07	100%	XP_011427615.2
hypothetical protein B2J93_2440 [Marssonina coronariae]	54.5	54.5	100%	1e-07	100%	OWP00223.1
PREDICTED: actin, cytoplasmic [Aplysia californica]	54.5	106	100%	1e-07	100%	XP_005101519.2
actin-2-like isoform X3 [Mizuhopecten yessoensis]	54.5	109	100%	1e-07	100%	XP_021356758.1
PREDICTED: actin, adductor muscle-like [Lingula anatina]	54.5	109	100%	1e-07	100%	XP_013410424.1
PREDICTED: actin, cytoplasmic-like [Biomphalaria glabrata]	54.5	109	100%	1e-07	100%	XP_013083901.1
PREDICTED: actin-2-like [Crassostrea gigas]	54.5	109	100%	1e-07	100%	XP_011448623.1
PREDICTED: actin [Crassostrea gigas]	54.5	109	100%	1e-07	100%	XP_011437202.1
PREDICTED: actin-1-like isoform X3 [Crassostrea gigas]	54.5	94.6	100%	1e-07	100%	XP_011448619.2
actin-domain-containing protein [Stagonospora sp. SRC1lsM3a]	54.5	54.5	100%	1e-07	100%	OAL06218.1
actin [Talaromyces cellulolyticus]	54.5	54.5	100%	1e-07	100%	GAM40862.1
actin beta/gamma 1 [Sporothrix schenckii 1099-18]	54.5	54.5	100%	1e-07	100%	XP_016586421.1
actin [Drechmeria coniospora]	54.5	54.5	100%	1e-07	100%	KYK58668.1
PREDICTED: actin, cytoplasmic 1 isoform X1 [Pantholops hodgsonii]	54.5	54.5	100%	1e-07	100%	XP_005982177.1
Actin [Opisthorchis viverrini]	54.5	54.5	100%	1e-07	100%	OON18391.1
PREDICTED: LOW QUALITY PROTEIN: actin, alpha skeletal muscle [Felis catus]	54.5	54.5	100%	1e-07	100%	XP_019669619.1
actin beta/gamma 1 [Blastomyces gilchristii SLH14081]	54.5	54.5	100%	1e-07	100%	OAT12422.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: actin, gamma-enteric smooth muscle isoform X1 [Saimiri boliviensis boliviensis]	54.5	54.5	100%	1e-07	100%	XP_010331747.1
PREDICTED: actin-2-like [Priapulus caudatus]	54.5	54.5	100%	1e-07	100%	XP_014662266.1
actin, aortic smooth muscle-like isoform 1 [Cricetulus griseus]	54.5	54.5	100%	1e-07	100%	ERE79103.1
PREDICTED: actin, aortic smooth muscle [Sarcophilus harrisii]	54.5	54.5	100%	1e-07	100%	XP_003759254.1
PREDICTED: actin, aortic smooth muscle [Bos indicus]	54.5	54.5	100%	1e-07	100%	XP_019844282.1
actin, alpha 1, skeletal muscle, isoform CRA_a [Rattus norvegicus]	54.5	54.5	100%	1e-07	100%	EDL96714.1
Actin, aortic smooth muscle [Tupaia chinensis]	54.5	54.5	100%	1e-07	100%	ELW66683.1
PREDICTED: actin-5C-like [Galendromus occidentalis]	54.5	109	100%	1e-07	100%	XP_003747695.2
actin, aortic smooth muscle-like isoform 1 [Cricetulus griseus]	54.5	54.5	100%	1e-07	100%	ERE79102.1
actin beta/gamma 1 [Clonorchis sinensis]	54.5	54.5	100%	1e-07	100%	GAA51173.1
actin, gamma [Fonsecaea multimorphosa]	54.5	54.5	100%	1e-07	100%	OAL19778.1

Alignments

48 kda histamine receptor subunit peptide 4 {internal fragment} [human, peripheral blood mononuclear cells, Peptide Partial, 27 aa]

Sequence ID: **AAB34251.1** Length: 27 Number of Matches: 1
Range 1: 1 to 16

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	1e-08()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1   SYELPDGQVITIGNER  16
           SYELPDGQVITIGNER
Sbjct  1   SYELPDGQVITIGNER  16
```

hypothetical protein [Escherichia coli]

Sequence ID: **WP_072775675.1** Length: 35 Number of Matches: 1
Range 1: 4 to 19

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	3e-08()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1   SYELPDGQVITIGNER  16
           SYELPDGQVITIGNER
Sbjct  4   SYELPDGQVITIGNER  19
```

beta-actin, partial [Coregonus lavaretus]

Sequence ID: **ABB22794.1** Length: 38 Number of Matches: 1
Range 1: 23 to 38

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	4e-08()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1   SYELPDGQVITIGNER  16
           SYELPDGQVITIGNER
Sbjct  23  SYELPDGQVITIGNER  38
```

beta-actin, partial [Channa gachua]

Sequence ID: **ACR25275.1** Length: 41 Number of Matches: 1
Range 1: 22 to 37

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	4e-08()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1   SYELPDGQVITIGNER  16
           SYELPDGQVITIGNER
Sbjct  22  SYELPDGQVITIGNER  37
```

beta-actin, partial [Chiloscyllium punctatum]

Sequence ID: **AHA84099.1** Length: 44 Number of Matches: 1
Range 1: 2 to 17

Score	Expect	Method	Identities	Positives	Gaps	Frame
54.5 bits(121)	5e-08()		16/16(100%)	16/16(100%)	0/16(0%)	

Features:

```
Query  1   SYELPDGQVITIGNER  16
           SYELPDGQVITIGNER
Sbjct  2   SYELPDGQVITIGNER  17
```

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BLAST Results

Job title: NCBI BlastP_AFM_DADPDTFFAK

RID S547WUSU015 (Expires on 08-04 10:57 am)

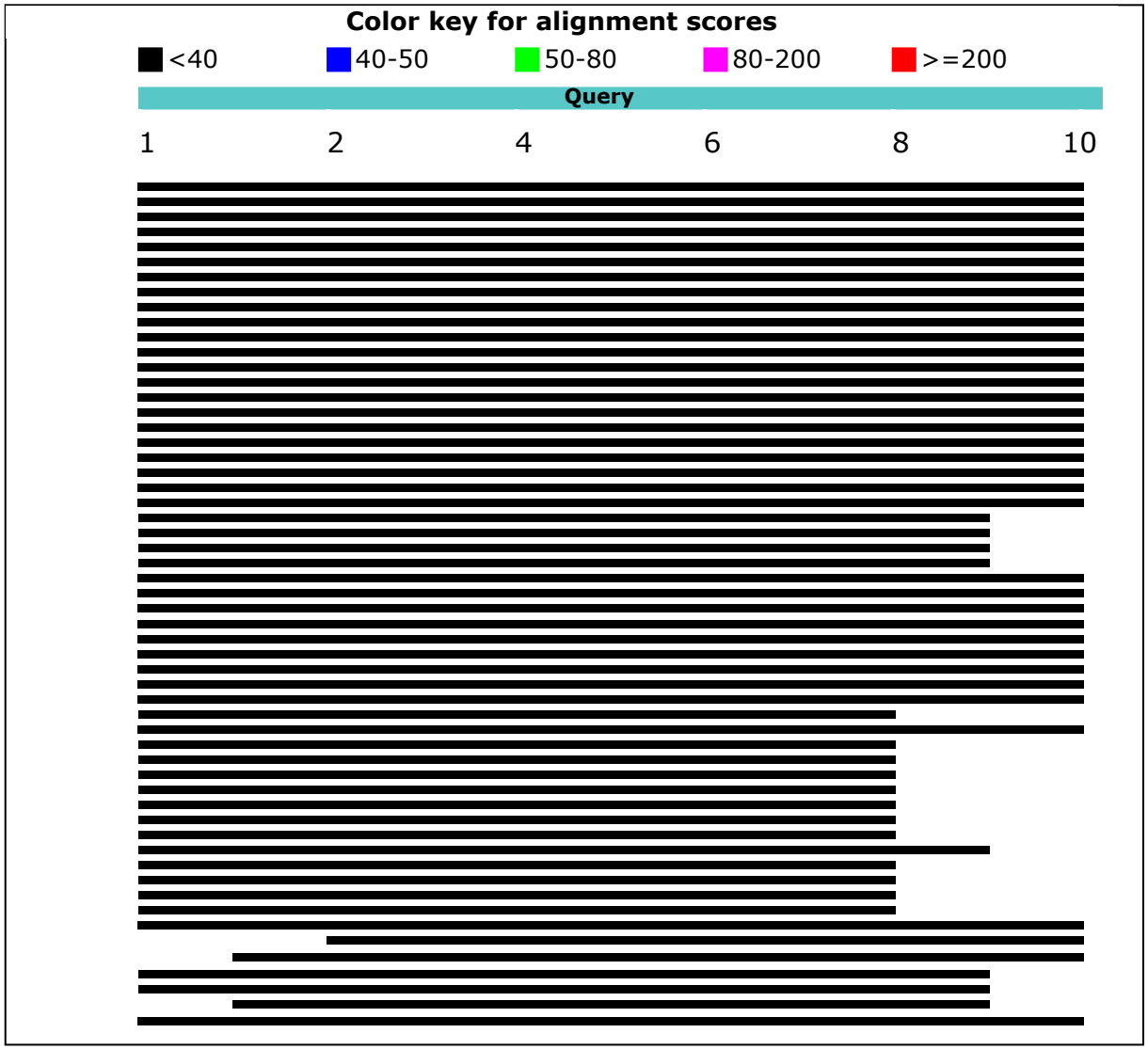
Query ID lcl|Query_10436
Description None
Molecule type amino acid
Query Length 10

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 100 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
2
4
6
8
10

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: afamin [Nomascus leucogenys]	35.4	35.4	100%	0.20	100%	XP_003265781.2
PREDICTED: afamin isoform X1 [Rhinopithecus bieti]	35.4	35.4	100%	0.20	100%	XP_017719559.1
afamin precursor [Homo sapiens]	35.4	35.4	100%	0.20	100%	NP_001124.1
PREDICTED: afamin isoform X1 [Cercocebus atys]	35.4	35.4	100%	0.20	100%	XP_011938375.1
PREDICTED: afamin [Colobus angolensis palliatus]	35.4	35.4	100%	0.20	100%	XP_011782536.1
PREDICTED: afamin [Rhinopithecus roxellana]	35.4	35.4	100%	0.20	100%	XP_010357302.1
PREDICTED: afamin isoform X1 [Chlorocebus sabaeus]	35.4	35.4	100%	0.20	100%	XP_007997055.1
PREDICTED: afamin isoform X1 [Gorilla gorilla gorilla]	35.4	35.4	100%	0.20	100%	XP_004038853.1
PREDICTED: afamin isoform X1 [Pan paniscus]	35.4	35.4	100%	0.20	100%	XP_003832388.1
PREDICTED: afamin [Pongo abelii]	35.4	35.4	100%	0.20	100%	XP_002814901.1
PREDICTED: afamin isoform X1 [Pan troglodytes]	35.4	35.4	100%	0.20	100%	XP_517229.2
PREDICTED: afamin isoform X2 [Chlorocebus sabaeus]	35.4	35.4	100%	0.20	100%	XP_007997056.1
afamin [Papio anubis]	35.4	35.4	100%	0.20	100%	XP_017814009.1
PREDICTED: afamin isoform X2 [Gorilla gorilla gorilla]	35.4	35.4	100%	0.20	100%	XP_018881585.1
PREDICTED: afamin isoform X2 [Rhinopithecus bieti]	35.4	35.4	100%	0.20	100%	XP_017719560.1
PREDICTED: afamin isoform X1 [Homo sapiens]	35.4	35.4	100%	0.20	100%	XP_016863331.1
PREDICTED: afamin isoform X2 [Cercocebus atys]	35.4	35.4	100%	0.20	100%	XP_011938376.1
PREDICTED: afamin isoform X2 [Pan troglodytes]	35.4	35.4	100%	0.20	100%	XP_009446018.1
PREDICTED: afamin isoform X2 [Pan paniscus]	35.4	35.4	100%	0.20	100%	XP_008955979.1
PREDICTED: afamin isoform X3 [Chlorocebus sabaeus]	35.4	35.4	100%	0.20	100%	XP_007997057.1
PREDICTED: afamin isoform X2 [Homo sapiens]	35.4	35.4	100%	0.20	100%	XP_016863332.1
PREDICTED: afamin isoform X3 [Homo sapiens]	35.4	35.4	100%	0.20	100%	XP_016863333.1
PREDICTED: afamin [Saimiri boliviensis boliviensis]	32.5	32.5	90%	2.3	100%	XP_010340893.1
PREDICTED: afamin [Callithrix jacchus]	32.5	32.5	90%	2.3	100%	XP_002745806.2
PREDICTED: afamin [Cebus capucinus imitator]	32.5	32.5	90%	2.3	100%	XP_017368428.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
afamin [Aotus nancymaae]	32.5	32.5	90%	2.3	100%	XP_012319828.1
PREDICTED: afamin [Mandrillus leucophaeus]	32.0	32.0	100%	3.2	90%	XP_011824362.1
PREDICTED: LOW QUALITY PROTEIN: afamin [Macaca fascicularis]	31.6	31.6	100%	4.6	90%	XP_005555149.1
PREDICTED: afamin isoform X1 [Macaca mulatta]	31.6	31.6	100%	4.6	90%	XP_014994020.1
PREDICTED: afamin isoform X2 [Macaca mulatta]	31.6	31.6	100%	4.6	90%	XP_014994021.1
PREDICTED: afamin isoform X1 [Macaca nemestrina]	31.6	31.6	100%	4.6	90%	XP_011732065.1
Alpha-albumin [Macaca fascicularis]	31.6	31.6	100%	4.6	90%	EHH53733.1
Alpha-albumin [Macaca mulatta]	31.6	31.6	100%	4.6	90%	EHH25934.1
PREDICTED: afamin isoform X3 [Macaca mulatta]	31.6	31.6	100%	4.6	90%	XP_014994022.1
PREDICTED: afamin isoform X2 [Macaca nemestrina]	31.6	31.6	100%	4.6	90%	XP_011732066.1
PREDICTED: arginine-glutamic acid dipeptide repeats protein-like [Saccoglossus kowalevskii]	29.9	29.9	80%	18	100%	XP_006823033.1
transglutaminase [Flavobacterium hercynium]	29.9	29.9	100%	18	90%	WP_089049688.1
amino acid ABC transporter ATP-binding protein [Micrococcus luteus]	29.9	29.9	80%	19	100%	WP_073117075.1
amino acid ABC transporter ATP-binding protein [Micrococcus sp. MS-ASIII-49]	29.9	29.9	80%	19	100%	WP_044659403.1
amino acid ABC transporter ATP-binding protein [Micrococcus luteus]	29.9	29.9	80%	19	100%	WP_010080547.1
putative glutamate uptake system ATP-binding protein [Micrococcus luteus Mu201]	29.9	29.9	80%	19	100%	SJN38718.1
putative glutamate uptake system ATP-binding protein [Brachybacterium faecium]	29.9	29.9	80%	19	100%	SLN05385.1
amino acid ABC transporter ATP-binding protein [Brachybacterium faecium]	29.9	29.9	80%	19	100%	WP_015776277.1
amino acid ABC transporter ATP-binding protein [Micrococcus luteus]	29.9	29.9	80%	19	100%	WP_087114922.1
Arginine transport ATP-binding protein ArtM [uncultured Ruminococcus sp.]	29.9	29.9	90%	19	89%	SCH03014.1
amino acid ABC transporter ATP-binding protein [Sporosarcina ureae]	29.9	29.9	80%	19	100%	WP_085426161.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
amino acid ABC transporter ATP-binding protein [Sporosarcina koreensis]	29.9	29.9	80%	19	100%	WP_040285418.1
amino acid ABC transporter ATP-binding protein [Sporosarcina sp. ZBG7A]	29.9	29.9	80%	19	100%	WP_039041491.1
amino acid ABC transporter ATP-binding protein [Sporosarcina sp. D27]	29.9	29.9	80%	19	100%	WP_025782896.1
amino acid ABC transporter ATP-binding protein [Rhodococcus sp. CUA-806]	29.5	29.5	100%	26	80%	WP_075840059.1
hypothetical protein A2215_03675 [Candidatus Berkelbacteria bacterium RIFOXYA2_FULL_43_10]	29.5	29.5	80%	26	100%	OGD62306.1
predicted protein [Naegleria gruberi]	29.1	29.1	90%	37	89%	XP_002673762.1
MULTISPECIES: aspartate aminotransferase family protein [Virgibacillus]	29.1	29.1	90%	37	89%	WP_021291935.1
NAD(P)-dependent oxidoreductase [Streptomyces paucisporeus]	29.1	29.1	90%	37	89%	WP_073494209.1
alpha/beta hydrolase [Herbidospora mongoliensis]	29.1	29.1	80%	37	100%	WP_066367203.1
hypothetical protein AWB81_01153 [Burkholderia arationis]	29.1	29.1	100%	38	63%	SAK53658.1
CLUMA_CG017475, isoform A [Clunio marinus]	28.6	28.6	90%	52	89%	CRL04384.1
PREDICTED: afamin [Cavia porcellus]	28.6	28.6	100%	52	80%	XP_003467576.2
PREDICTED: afamin [Otolemur garnettii]	28.6	28.6	90%	52	89%	XP_012660776.1
hypothetical protein CHLNCDRAFT_145120 [Chlorella variabilis]	28.6	28.6	90%	52	89%	XP_005848368.1
hypothetical protein [Sphingomonas sp. Leaf198]	28.6	28.6	90%	53	89%	WP_056050118.1
non-ribosomal peptide synthetase [Catenuloplanes japonicus]	28.2	28.2	90%	74	90%	WP_033338808.1
arylsulfatase [Microbacterium yannicii]	28.2	28.2	90%	74	90%	WP_026059665.1
alkene reductase [Paenibacillus pabuli]	28.2	28.2	90%	75	89%	WP_062323405.1
NAD(P)-binding protein [Pycnoporus coccineus BRFM310]	28.2	28.2	100%	75	90%	OSC96390.1
hypothetical protein [Streptomyces sp. NBRC 110468]	28.2	28.2	90%	75	89%	WP_062643641.1
predicted protein [Mycena chlorophos]	28.2	28.2	90%	75	90%	GAT51062.1
mitogen-activated protein kinase kinase kinase 15 [Sus scrofa]	27.8	27.8	100%	105	80%	XP_020936466.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: mitogen-activated protein kinase kinase kinase 15 [Tupaia chinensis]	27.8	27.8	100%	105	80%	XP_014446857.1
PREDICTED: mitogen-activated protein kinase kinase kinase 15 [Pantholops hodgsonii]	27.8	27.8	100%	105	80%	XP_005972968.1
LOW QUALITY PROTEIN: mitogen-activated protein kinase kinase kinase 15-like [Castor canadensis]	27.8	27.8	100%	105	80%	XP_020007976.1
PREDICTED: mitogen-activated protein kinase kinase kinase 15-like [Capra hircus]	27.8	27.8	100%	105	80%	XP_017899975.1
glycosidase [Enterobacter mori]	27.8	27.8	90%	105	89%	OXL38259.1
glycosidase [Enterobacter cloacae complex sp. GN06232]	27.8	27.8	90%	105	89%	WP_063451968.1
glycosidase [Enterobacter mori]	27.8	27.8	90%	105	89%	WP_010435243.1
tRNA nucleotidyltransferase [Algoriphagus marinus]	27.8	27.8	90%	105	89%	WP_075349559.1
tRNA nucleotidyltransferase [Algoriphagus vanfongensis]	27.8	27.8	90%	105	89%	WP_026955550.1
hypothetical protein [Zea mays]	27.8	27.8	90%	107	89%	ACG24053.1
tubulin monoglycylase TTLL3-like [Labrus bergylta]	27.4	27.4	80%	149	88%	XP_020485011.1
hypothetical protein PILCRDRAFT_824683 [Piloderma croceum F 1598]	27.4	27.4	80%	149	88%	KIM78205.1
LOW QUALITY PROTEIN: tubulin monoglycylase TTLL3 [Columba livia]	27.4	27.4	80%	149	88%	XP_021150272.1
class I poly(R)-hydroxyalkanoic acid synthase [Herbaspirillum chlorophenolicum]	27.4	27.4	100%	149	80%	WP_050468298.1
hypothetical protein [Chryseobacterium sp. OV705]	27.4	27.4	80%	149	88%	WP_047488451.1
tubulin monoglycylase TTLL3 [Patagioenas fasciata monilis]	27.4	27.4	80%	149	88%	OPJ71982.1
hypothetical protein AV530_009311 [Patagioenas fasciata monilis]	27.4	27.4	80%	149	88%	OPJ71983.1
hypothetical protein TRSC58_03460 [Trypanosoma rangeli SC58]	27.4	27.4	90%	150	78%	ESL08831.1
DUF2213 domain-containing protein [Serratia fonticola]	27.4	27.4	90%	150	75%	WP_059200668.1
reverse transcriptase [Pseudomonas fluorescens]	27.4	27.4	90%	150	78%	WP_065261854.1
reverse transcriptase [Burkholderia pseudomallei]	27.4	27.4	80%	150	88%	OMW09755.1
reverse transcriptase [Burkholderia pseudomallei]	27.4	27.4	80%	150	88%	OMV27728.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
phage-related reverse transcriptase/maturase family protein [Burkholderia pseudomallei]	27.4	27.4	80%	150	88%	CFL44741.1
hypothetical protein BP354E_5695 [Burkholderia pseudomallei 354e]	27.4	27.4	80%	150	88%	EIF69525.1
hypothetical protein ACJ73_01056 [Blastomyces percursus]	27.4	27.4	90%	150	78%	OJD27556.1
MULTISPECIES: reverse transcriptase [Haematobacter]	27.4	27.4	80%	150	88%	WP_088216108.1
reverse transcriptase [Burkholderia pseudomallei]	27.4	27.4	80%	150	88%	WP_076907424.1
reverse transcriptase [Burkholderia pseudomallei]	27.4	27.4	80%	150	88%	WP_076840054.1
reverse transcriptase [Burkholderia pseudomallei]	27.4	27.4	80%	150	88%	WP_076802723.1
Maltose-binding periplasmic proteins/domains [uncultured Ruminococcus sp.]	27.4	27.4	90%	150	78%	SCH89158.1
hypothetical protein [Burkholderia pseudomallei]	27.4	27.4	80%	150	88%	WP_011204832.1
FAD-dependent oxidoreductase [Mesorhizobium sp. ORS3428]	27.4	27.4	100%	150	80%	WP_071099424.1

Alignments

PREDICTED: afamin [Nomascus leucogenys]

Sequence ID: **XP_003265781.2** Length: 665 Number of Matches: 1
Range 1: 344 to 353

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.20()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DADPDTFFAK  10
           DADPDTFFAK
Sbjct  344  DADPDTFFAK  353
```

PREDICTED: afamin isoform X1 [Rhinopithecus bieti]

Sequence ID: **XP_017719559.1** Length: 599 Number of Matches: 1
Range 1: 344 to 353

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.20()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DADPDTFFAK  10
            DADPDTFFAK
Sbjct  344  DADPDTFFAK  353
```

afamin precursor [Homo sapiens]

Sequence ID: **NP_001124.1** Length: 599 Number of Matches: 1

See 9 more title(s)

Range 1: 344 to 353

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.20()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DADPDTFFAK  10
            DADPDTFFAK
Sbjct  344  DADPDTFFAK  353
```

PREDICTED: afamin isoform X1 [Cercocebus atys]

Sequence ID: **XP_011938375.1** Length: 599 Number of Matches: 1

Range 1: 344 to 353

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.20()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DADPDTFFAK  10
            DADPDTFFAK
Sbjct  344  DADPDTFFAK  353
```

PREDICTED: afamin [Colobus angolensis palliatus]

Sequence ID: **XP_011782536.1** Length: 599 Number of Matches: 1

Range 1: 344 to 353

Score	Expect	Method	Identities	Positives	Gaps	Frame
35.4 bits(76)	0.20()		10/10(100%)	10/10(100%)	0/10(0%)	

Features:

```
Query  1    DADPDTFFAK  10
            DADPDTFFAK
Sbjct  344  DADPDTFFAK  353
```

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BLAST Results

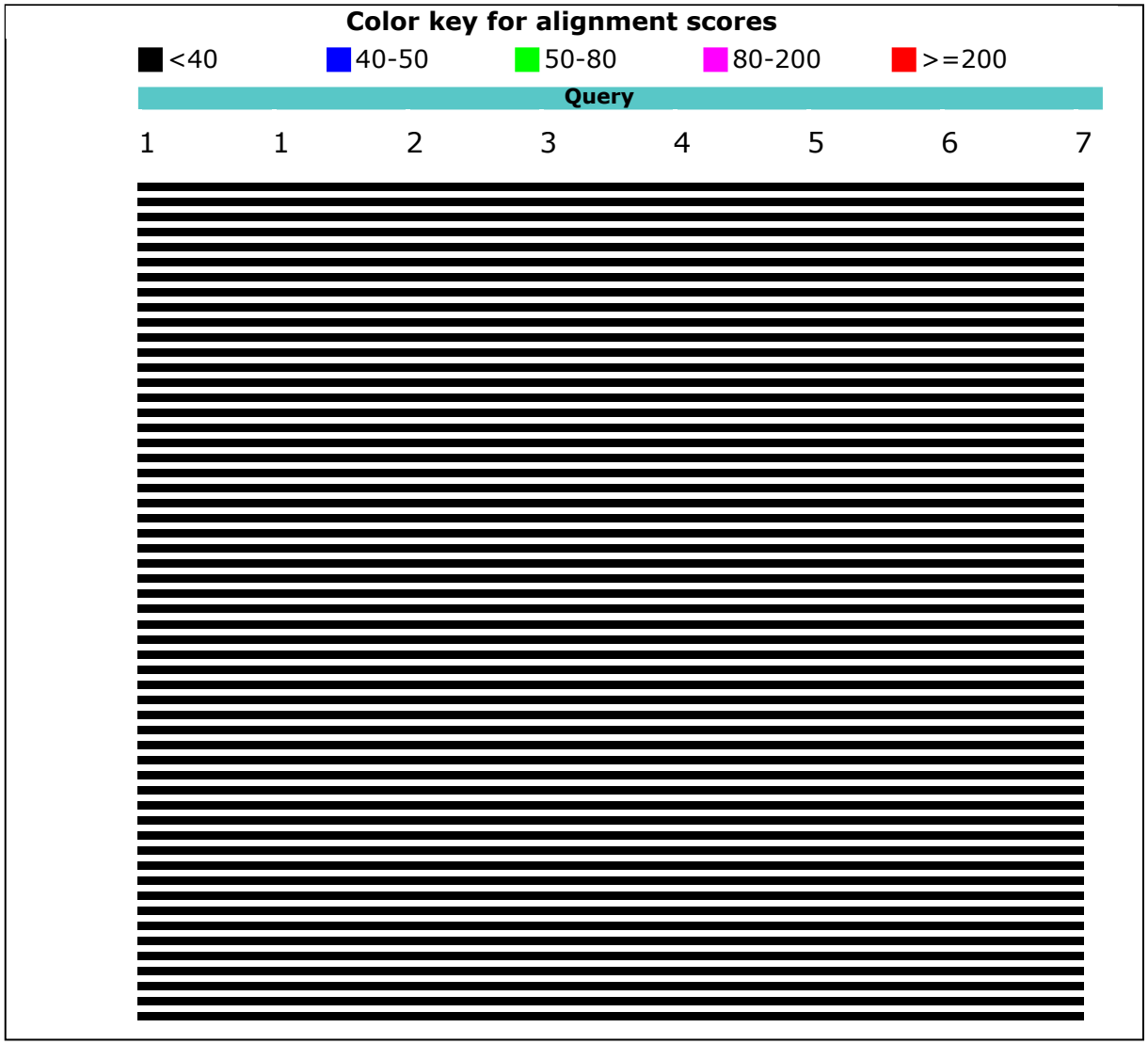
Job title: NCBI BlastP_AFM_FTFEYSR

RID	S54877R2014 (Expires on 08-04 10:57 am)
Query ID	lcl|Query_20348
Description	None
Molecule type	amino acid
Query Length	7
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.6.1+

Graphic Summary

No putative conserved domains have been detected

Distribution of the top 101 Blast Hits on 100 subject sequences


Color key for alignment scores
<40
40-50
50-80
80-200
>=200
Query
1
1
2
3
4
5
6
7

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein [Mesorhizobium sp. L48C026A00]	27.4	27.4	100%	77	100%	WP_023802817.1
hypothetical protein ER33_12930 [Cyanobium sp. CACIAM 14]	27.4	27.4	100%	77	100%	KEF41135.1
PREDICTED: afamin [Nomascus leucogenys]	27.4	27.4	100%	77	100%	XP_003265781.2
hypothetical protein [Salinarchaeum sp. Harcht-Bsk1]	27.4	27.4	100%	77	100%	WP_020446497.1
hypothetical protein EMIHUDRAFT_231710 [Emiliania huxleyi CCMP1516]	27.4	27.4	100%	77	100%	XP_005783973.1
PREDICTED: LOW QUALITY PROTEIN: afamin [Macaca fascicularis]	27.4	27.4	100%	77	100%	XP_005555149.1
PREDICTED: afamin isoform X1 [Macaca mulatta]	27.4	27.4	100%	77	100%	XP_014994020.1
PREDICTED: afamin isoform X1 [Rhinopithecus bieti]	27.4	27.4	100%	77	100%	XP_017719559.1
PREDICTED: afamin isoform X2 [Macaca mulatta]	27.4	27.4	100%	77	100%	XP_014994021.1
afamin precursor [Homo sapiens]	27.4	27.4	100%	77	100%	NP_001124.1
PREDICTED: afamin isoform X1 [Macaca nemestrina]	27.4	27.4	100%	77	100%	XP_011732065.1
PREDICTED: afamin isoform X1 [Cercocebus atys]	27.4	27.4	100%	77	100%	XP_011938375.1
PREDICTED: afamin [Colobus angolensis palliatus]	27.4	27.4	100%	77	100%	XP_011782536.1
PREDICTED: afamin [Mandrillus leucophaeus]	27.4	27.4	100%	77	100%	XP_011824362.1
PREDICTED: afamin [Rhinopithecus roxellana]	27.4	27.4	100%	77	100%	XP_010357302.1
PREDICTED: afamin isoform X1 [Chlorocebus sabaeus]	27.4	27.4	100%	77	100%	XP_007997055.1
PREDICTED: afamin isoform X1 [Gorilla gorilla gorilla]	27.4	27.4	100%	77	100%	XP_004038853.1
PREDICTED: afamin isoform X1 [Pan paniscus]	27.4	27.4	100%	77	100%	XP_003832388.1
Alpha-albumin [Macaca fascicularis]	27.4	27.4	100%	77	100%	EHH53733.1
PREDICTED: afamin [Pongo abelii]	27.4	27.4	100%	77	100%	XP_002814901.1
PREDICTED: afamin isoform X1 [Pan troglodytes]	27.4	27.4	100%	77	100%	XP_517229.2
Alpha-albumin [Macaca mulatta]	27.4	27.4	100%	77	100%	EHH25934.1
PREDICTED: afamin isoform X3 [Macaca mulatta]	27.4	27.4	100%	77	100%	XP_014994022.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein EMIHUDRAFT_237375 [Emiliania huxleyi CCMP1516]	27.4	27.4	100%	77	100%	XP_005778384.1
PREDICTED: afamin isoform X2 [Chlorocebus sabaeus]	27.4	27.4	100%	77	100%	XP_007997056.1
afamin [Papio anubis]	27.4	27.4	100%	77	100%	XP_017814009.1
PREDICTED: afamin isoform X2 [Gorilla gorilla gorilla]	27.4	27.4	100%	77	100%	XP_018881585.1
PREDICTED: afamin isoform X2 [Rhinopithecus bieti]	27.4	27.4	100%	77	100%	XP_017719560.1
PREDICTED: afamin isoform X1 [Homo sapiens]	27.4	27.4	100%	77	100%	XP_016863331.1
PREDICTED: afamin isoform X2 [Macaca nemestrina]	27.4	27.4	100%	77	100%	XP_011732066.1
PREDICTED: afamin isoform X2 [Cercocebus atys]	27.4	27.4	100%	77	100%	XP_011938376.1
PREDICTED: afamin isoform X2 [Pan troglodytes]	27.4	27.4	100%	77	100%	XP_009446018.1
PREDICTED: afamin isoform X2 [Pan paniscus]	27.4	27.4	100%	77	100%	XP_008955979.1
PREDICTED: afamin isoform X3 [Chlorocebus sabaeus]	27.4	27.4	100%	77	100%	XP_007997057.1
PREDICTED: afamin isoform X2 [Homo sapiens]	27.4	27.4	100%	77	100%	XP_016863332.1
PREDICTED: afamin isoform X3 [Homo sapiens]	27.4	27.4	100%	77	100%	XP_016863333.1
hypothetical protein [Methylocystis parvus]	27.4	27.4	100%	80	100%	WP_016921707.1
non-ribosomal peptide synthetase [Vibrio tritonius]	24.8	24.8	100%	620	86%	WP_068716452.1
predicted protein putative [Albugo laibachii Nc14]	24.8	24.8	100%	620	86%	CCA20897.1
1,4-alpha-glucan branching enzyme GlgB [Chlamydia pneumoniae]	24.8	24.8	100%	623	86%	CRI42588.1
glycogen-branching enzyme [Chlamydia pneumoniae]	24.8	24.8	100%	623	86%	WP_014517672.1
glycogen-branching enzyme [Chlamydia pneumoniae]	24.8	24.8	100%	623	86%	WP_010883113.1
MULTISPECIES: TonB-dependent receptor [Pseudohongiella]	24.8	24.8	100%	623	86%	WP_082866560.1
DNA polymerase III subunit [Pseudomonas putida DOT-T1E]	24.8	24.8	100%	623	86%	AFO48738.1
hypothetical protein HMPREF1544_08604 [Mucor circinelloides f. circinelloides 1006PhL]	24.8	24.8	100%	624	86%	EPB84661.1
hypothetical protein MUCCIDRAFT_51105 [Mucor circinelloides f. lusitanicus CBS 277.49]	24.8	24.8	100%	624	86%	OAC98670.1
hypothetical protein [Marinilabilia salmonicolor]	24.8	24.8	100%	625	86%	WP_010665086.1
endosomal membrane protein EMP70 [Mucor ambiguus]	24.8	24.8	100%	625	86%	GAN11044.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
alpha/beta hydrolase [Actinokineospora enzanensis]	24.8	24.8	100%	625	86%	WP_018682734.1
hypothetical protein BGO87_09020 [Flavobacteriia bacterium 40-80]	24.8	24.8	100%	625	86%	OJX34874.1
1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type [Chlamydia pneumoniae B21]	24.8	24.8	100%	625	86%	ETR80373.1
hypothetical protein [Hymenobacter sp. CRA2]	24.8	24.8	100%	626	86%	WP_078010319.1
histidine phosphatase family (branch 2) protein [Tetrahymena thermophila SB210]	24.8	24.8	100%	626	86%	XP_001019210.2
hypothetical protein B0919_00965 [Hymenobacter sp. CRA2]	24.8	24.8	100%	626	86%	OON71152.1
HipA-like protein [Polaromonas sp. CF318]	24.8	24.8	100%	627	86%	EJL77555.1
phosphatidylinositol kinase [Polaromonas sp. CF318]	24.8	24.8	100%	627	86%	WP_036840794.1
acyl-CoA dehydrogenase [Nocardia salmonicida]	24.8	24.8	100%	628	86%	WP_062983409.1
flavin-dependent oxidoreductase [Mycobacterium sp. PH-06]	24.8	24.8	100%	628	86%	WP_087076335.1
3-isopropylmalate dehydrogenase [Aneurinibacillus sp. XH2]	24.8	24.8	100%	628	86%	WP_057897776.1
hypothetical protein FOMPIDRAFT_1056818 [Fomitopsis pinicola FP-58527 SS1]	24.8	24.8	100%	630	86%	EPS92494.1
class I SAM-dependent methyltransferase [Ottowia thiooxydans]	24.8	24.8	100%	630	86%	WP_084652160.1
hypothetical protein A2317_02725 [Candidatus Uhrbacteria bacterium RIFOXYB2_FULL_41_10]	24.8	24.8	100%	631	86%	OGL97031.1
hypothetical protein UT52_C0008G0029 [Candidatus Uhrbacteria bacterium GW2011_GWE1_39_46]	24.8	24.8	100%	631	86%	KKR22729.1
PREDICTED: lens fiber major intrinsic protein [Crassostrea gigas]	24.8	24.8	100%	631	86%	XP_011428741.1
Sugar phosphate isomerase/epimerase [Haloferax larsenii]	24.8	24.8	100%	632	86%	SEL70877.1
sugar phosphate isomerase/epimerase [Haloferax larsenii]	24.8	24.8	100%	632	86%	WP_074795605.1
sugar phosphate isomerase/epimerase [Haloferax larsenii]	24.8	24.8	100%	632	86%	WP_007540560.1
Zinc carboxypeptidase family protein [Oxytricha trifallax]	24.4	24.4	100%	881	86%	EJY70473.1
putative pol protein [Zea mays]	24.4	24.4	100%	881	86%	AAL75483.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein SAMN02927937_01894 [Flavobacterium marinum]	24.4	24.4	100%	882	86%	SEH87700.1
Alpha-fetoprotein [Myotis brandtii]	24.4	43.3	100%	882	86%	EPQ13062.1
Zinc carboxypeptidase family protein [Oxytricha trifallax]	24.4	24.4	100%	882	86%	EJY82797.1
PA domain protein [Dictyocaulus viviparus]	24.4	24.4	100%	882	86%	KJH40883.1
beta-galactosidase [[Eubacterium] hallii]	24.4	24.4	100%	883	86%	WP_055183184.1
PREDICTED: alpha-protein kinase 1 [Clupea harengus]	24.4	24.4	100%	883	86%	XP_012686251.1
zinc carboxypeptidase family protein [Stylonychia lemnae]	24.4	24.4	100%	883	86%	CDW90020.1
AbrB family transcriptional regulator [Halorubrum sp. T3]	24.4	24.4	100%	885	86%	WP_017341799.1
SpoVR family protein [Halorubrum saccharovorum]	24.4	24.4	100%	885	86%	WP_004048061.1
SpoVR family protein [Halorubrum californiense]	24.4	24.4	100%	885	86%	WP_008444181.1
AbrB family transcriptional regulator [Halorubrum lacusprofundi]	24.4	24.4	100%	885	86%	WP_088901658.1
AbrB family transcriptional regulator [Halorubrum lacusprofundi]	24.4	24.4	100%	885	86%	WP_012659281.1
SpoVR family protein [Halorubrum lipolyticum]	24.4	24.4	100%	885	86%	WP_008005624.1
SpoVR family protein [Halorubrum aidingense]	24.4	24.4	100%	885	86%	WP_008002004.1
SpoVR family protein [Halorubrum coriense]	24.4	24.4	100%	885	86%	WP_006111421.1
stage V sporulation protein R [Halorubrum sodomense]	24.4	24.4	100%	885	86%	SFR32113.1
SpoVR family protein [Halorubrum hochstenium]	24.4	24.4	100%	885	86%	WP_008582959.1
SpoVR family protein [Halorubrum tebenquichense]	24.4	24.4	100%	885	86%	WP_006629207.1
AbrB family transcriptional regulator [Halorubrum chaoviator]	24.4	24.4	100%	885	86%	WP_089308715.1
AbrB family transcriptional regulator [Halorubrum sp. SD683]	24.4	24.4	100%	885	86%	WP_086216948.1
AbrB family transcriptional regulator [Halorubrum ezzemoulense]	24.4	24.4	100%	885	86%	WP_049932875.1
SpoVR family protein [Halorubrum arcis]	24.4	24.4	100%	885	86%	WP_007995466.1
SpoVR family protein [Halorubrum kocurii]	24.4	24.4	100%	885	86%	WP_008848618.1
SpoVR family protein [Halorubrum litoreum]	24.4	24.4	100%	885	86%	WP_008366652.1
MULTISPECIES: SpoVR family protein [Halorubrum]	24.4	24.4	100%	885	86%	WP_004599186.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
AbrB family transcriptional regulator [Halorubrum vacuolatum]	24.4	24.4	100%	885	86%	WP_089383937.1
AbrB family transcriptional regulator [Halorubrum tropicale]	24.4	24.4	100%	885	86%	WP_053770239.1
stage V sporulation protein R [Candidatus Halobonum tyrrellensis]	24.4	24.4	100%	885	86%	WP_023393987.1
hypothetical protein SteCoe_25800 [Stentor coeruleus]	24.4	24.4	100%	885	86%	OMJ75141.1
alpha-fetoprotein [Neomonachus schauinslandi]	24.4	24.4	100%	885	86%	XP_021558086.1
PREDICTED: afamin [Propithecus coquereli]	24.4	24.4	100%	886	86%	XP_012515294.1

Alignments

hypothetical protein [Mesorhizobium sp. L48C026A00]
Sequence ID: **WP_023802817.1** Length: 931 Number of Matches: 1

See 1 more title(s)
Range 1: 28 to 34

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	77()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1   FTFEYSR  7
           FTFEYSR
Sbjct  28  FTFEYSR  34
```

hypothetical protein ER33_12930 [Cyanobium sp. CACIAM 14]
Sequence ID: **KEF41135.1** Length: 710 Number of Matches: 1
Range 1: 400 to 406

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	77()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    FTFEYSR  7
            FTFEYSR
Sbjct  400  FTFEYSR  406
```

PREDICTED: afamin [Nomascus leucogenys]

Sequence ID: **XP_003265781.2** Length: 665 Number of Matches: 1
Range 1: 354 to 360

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	77()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    FTFEYSR  7
            FTFEYSR
Sbjct  354  FTFEYSR  360
```

hypothetical protein [Salinarchaeum sp. Harcht-Bsk1]

Sequence ID: **WP_020446497.1** Length: 663 Number of Matches: 1

See 1 more title(s)

Range 1: 513 to 519

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	77()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    FTFEYSR  7
            FTFEYSR
Sbjct  513  FTFEYSR  519
```

hypothetical protein EMIHUDRAFT_231710 [Emiliania huxleyi CCMP1516]

Sequence ID: **XP_005783973.1** Length: 639 Number of Matches: 1

See 1 more title(s)

Range 1: 245 to 251

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.4 bits(57)	77()		7/7(100%)	7/7(100%)	0/7(0%)	

Features:

```
Query  1    FTFEYSR  7
            FTFEYSR
Sbjct  245  FTFEYSR  251
```

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