

Supporting Information:

Biosynthesis of the Novel Macrolide Antibiotic Anthracimycin

Silke Alt and Barrie Wilkinson^{*}

Department of Molecular Microbiology, John Innes Centre, Norwich Research Park,
Norwich, Norfolk NR4 7UH, United Kingdom

Corresponding Author:

^{*}E-mail: barrie.wilkinson@jic.ac.uk

TABLE OF CONTENTS

Table S1.

List of strains and plasmids used in this study.

Table S2.

List of PCR primers used in this study.

Figure S1.

HPLC chromatograms of anthracimycin production in the heterologous host strains *Streptomyces coelicolor* M1146, M1152, and M1154.

Table S3.

Incorporation of isotopically labelled acetates into anthracimycin.

Figure S2.

^{13}C NMR spectrum of [1,2- $^{13}\text{C}_2$] sodium acetate labelled anthracimycin in CDCl_3 .

Figure S3.

Domain sequences and phylogenetic trees of AT (A) and KS (B) domains from various *trans*-AT PKS pathways.

Table S1.

List of strains, plasmids and PCR primers used in this study.

Bacterial strains	Description	Reference
<i>E. coli</i> DH5 α	cloning strain; F ⁻ <i>endA1 glnV44 thi-1 recA1 relA1 gyrA96 deoR nupG</i> Φ 80 <i>dlac</i> Δ (<i>lacZ</i>)M15 Δ (<i>lacI</i> ZYA- <i>argF</i>)U169 <i>hsdR17</i> (r _K ⁻ m _K ⁺) λ -	1
<i>E. coli</i> DH10B	cloning strain; F ⁻ <i>endA1 recA1 galE15 galK16 nupG rpsL</i> Δ <i>lacX74</i> Φ 80 <i>dlac</i> Δ (<i>lacZ</i>)M15 <i>araD139</i> Δ (<i>ara-leu</i>)7697 <i>mcrA</i> Δ (<i>mrr-hsdRMS-mcrBC</i>) λ ⁻	1
<i>E. coli</i> Top10	cloning strain; F ⁻ <i>mcrA</i> Δ (<i>mrr-hsdRMS-mcrBC</i>) Φ 80 <i>dlac</i> Δ (<i>lacZ</i>)M15 Δ <i>lacX74 nupG recA1 araD139</i> Δ (<i>ara-leu</i>)7697 <i>galE15 galK16 rpsL</i> (Str ^R) <i>endA1</i> λ ⁻	1
<i>E. coli</i> ET 12567	methylation deficient strain used for conjugation with <i>Streptomyces</i> ; <i>dam dcm hsdM hsdS hsdR cat tet</i>	2
<i>Streptomyces</i> sp. T676	wild type producer strain of anthracimycin	MerLion Pharma, Singapore
<i>S. coelicolor</i> M1146	heterologous host strain; Δ <i>act</i> Δ <i>red</i> Δ <i>cpk</i> Δ <i>cda</i>	3
<i>S. coelicolor</i> M1152	heterologous host strain; Δ <i>act</i> Δ <i>red</i> Δ <i>cpk</i> Δ <i>cda rpoB</i> [C1298T]	3
<i>S. coelicolor</i> M1154	heterologous host strain; Δ <i>act</i> Δ <i>red</i> Δ <i>cpk</i> Δ <i>cda rpoB</i> [C1298T] <i>rpsL</i> [A262G]	3
<i>S. coelicolor</i> M1146/PAC-14M	M1146 containing PAC-14M	This work
<i>S. coelicolor</i> M1152/PAC-14M	M1152 containing PAC-14M	This work
<i>S. coelicolor</i> M1154/PAC-14M	M1154 containing PAC-14M	This work
<i>S. coelicolor</i> M1146/pESAC13	M1146 containing pESAC13	This work
<i>S. coelicolor</i> M1152/pESAC13	M1152 containing pESAC13	This work
<i>S. coelicolor</i> M1146/pESAC13 Δ pUC	M1146 containing pESAC13 Δ pUC	This work
<i>S. coelicolor</i> M1152/pESAC13 Δ pUC	M1152 containing pESAC13 Δ pUC	This work
Plasmids/ P1 artificial chromosomes (PAC)	Description	Reference
pESAC13	PAC vector (P1-phage replicon) for genomic library construction; RP conjugative, Φ C31 integrative <i>tsr</i> , <i>neo</i> , <i>oriT</i> , <i>attP</i> and <i>int</i> from Φ C31, <i>P1 rep</i> , <i>sacB</i>	5 GenBank No.: LM999999.1
pESAC13 Δ pUC	<i>Bam</i> HI digested pESAC13 to remove pUC backbone; <i>Bam</i> HI religation	This work
PAC-14M	P1 artificial chromosom; pESAC13 with 100 kb insert in <i>Bam</i> HI site	This work
PAC-18J	P1 artificial chromosom; pESAC13 with 155 kb insert in <i>Bam</i> HI site	This work
pR9406	driver plasmid for conjugation	David Figurski; unpublished

Table S2.

List of PCR primers used in this study.

Primer	Sequence (5'-3')	Description
P1	CTCACGCTTCGTAGTGTTAGTTTC	<i>atc</i> cluster upstream screening primer forward (f)
P2	GACGTTGATCCAGAAGACCGATC	<i>atc</i> cluster upstream screening primer reverse (r)
P3	GTCTACGTCGGCGTCATGTAC	<i>atc</i> cluster centre screening primer (f)
P4	GTGGCCGATGTTGACTTCAC	<i>atc</i> cluster centre screening primer (r)
P5	CTTCTGTGTGATCGTCGGCATG	<i>atc</i> cluster downstream screening primer (f)
P6	CTGTCCTGCACCATGCTCATG	<i>atc</i> cluster downstream screening primer (r)
P7	CCGTCGACATTTAGGTGACAC	pESAC13 sequencing primer (f)
P8	CGGCCGCTAATACGACTC	pESAC13 sequencing primer (r)
P9	GGACCGAAGCCCAGCTC	sequencing primer for frameshift in <i>atcE</i> (f)
P10	CCACAGCTCGTCCAGGTC	sequencing primer for frameshift in <i>atcE</i> (r)
P11	CTCCTCGCCGAACCTCCTC	sequencing primer for 15 bps omission in <i>atcE</i> (f)
P12	GTCGGGTAGTTGAAGAAGTCG	sequencing primer for 15 bps omission in <i>atcE</i> (r)
P13	CAGGGGGAGGACACGGTGAA	sequencing primer for 186 bps insertion <i>atcD</i> (f)
P14	CTGCTGCGGGTCCATCAGTT	sequencing primer for 186 bps insertion in <i>atcD</i> (r)

Figure S1.

HPLC chromatograms of **1** production in the heterologous host strains *Streptomyces coelicolor* M1146, M1152, and M1154. **(A)** anthracimycin standard (1 mM, 5 μ l injection); **(B)** *S. coelicolor* M1146/pSAC13 Δ pUC (control); **(C)** *S. coelicolor* M1146/PAC-14M; **(D)** *S. coelicolor* M1152/PAC-14M; **(E)** *S. coelicolor* M1154/PAC-14M. PAC-14M contains a 100 kb insert including the full **1** gene cluster.

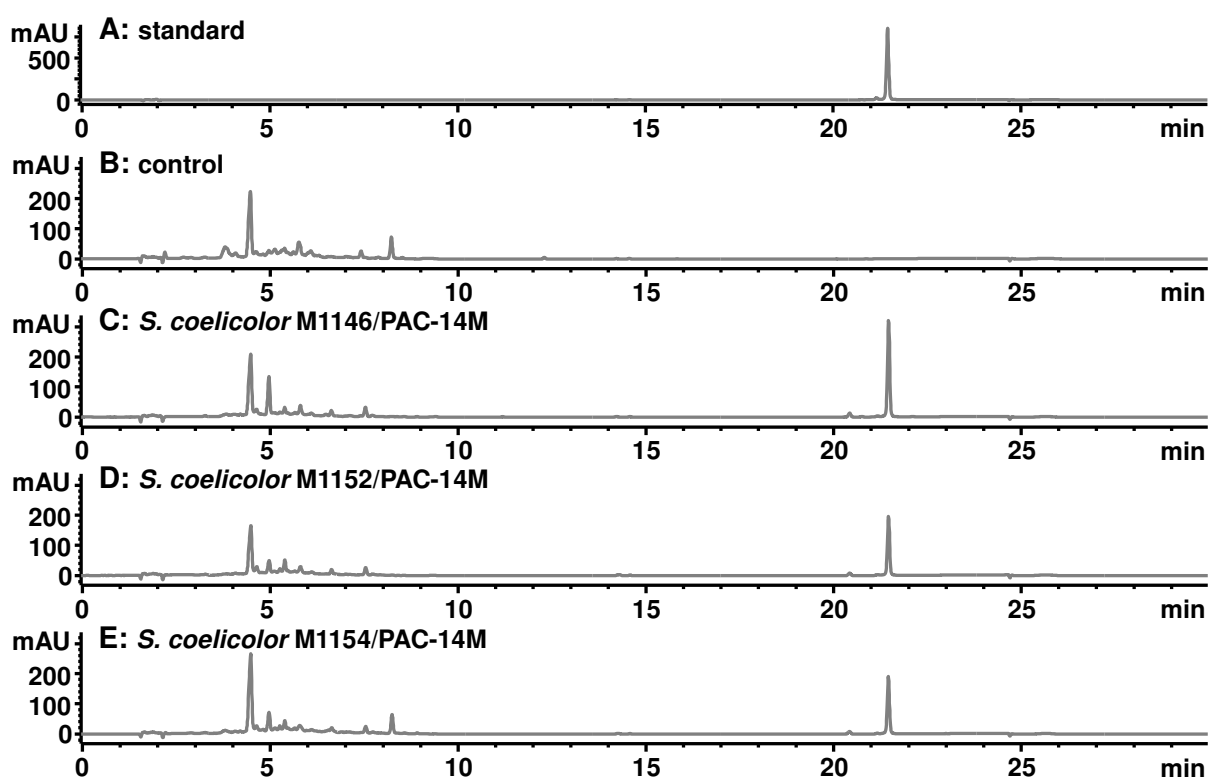
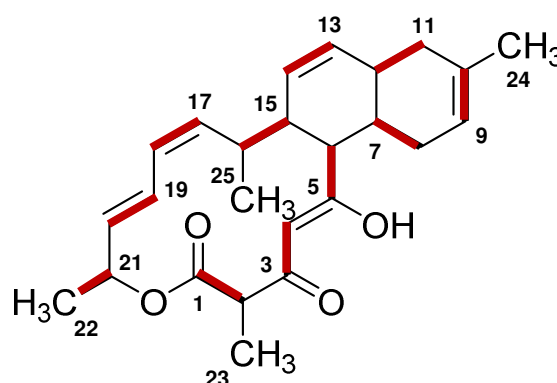


Table S3.

Incorporation of [1,2- $^{13}\text{C}_2$] sodium acetate into **1**. Data were recorded on a Bruker Avance III 500 MHz instrument equipped with a DUL cryoprobe at 25 °C in CDCl_3 .

Carbon	δ_c / ppm	J(CC)/Hz
1	168.93	54.36
2	49.25	54.33
3	190.87	61.83
4	103.04	61.81
5	194.20	45.62
6	52.71	45.63
7	37.57	*
8	31.41	34.38
9	121.08	72.39
10	134.01	72.36
11	37.47	*
12	33.06	34.31
13	133.07	69.30
14	124.95	69.30
15	46.09	32.71
16	32.82	32.70
17	139.12	68.84
18	126.11	68.86
19	123.80	73.08
20	131.71	73.08
21	70.01	38.88
22	21.00	38.88
23	11.85	-
24	23.57	-
25	16.47	-



* The coupling constant could not be measured because of overlapping signals.

Figure S2. ^{13}C NMR spectrum of $[1,2-^{13}\text{C}_2]$ sodium acetate labelled anthracimycin in CDCl_3 .

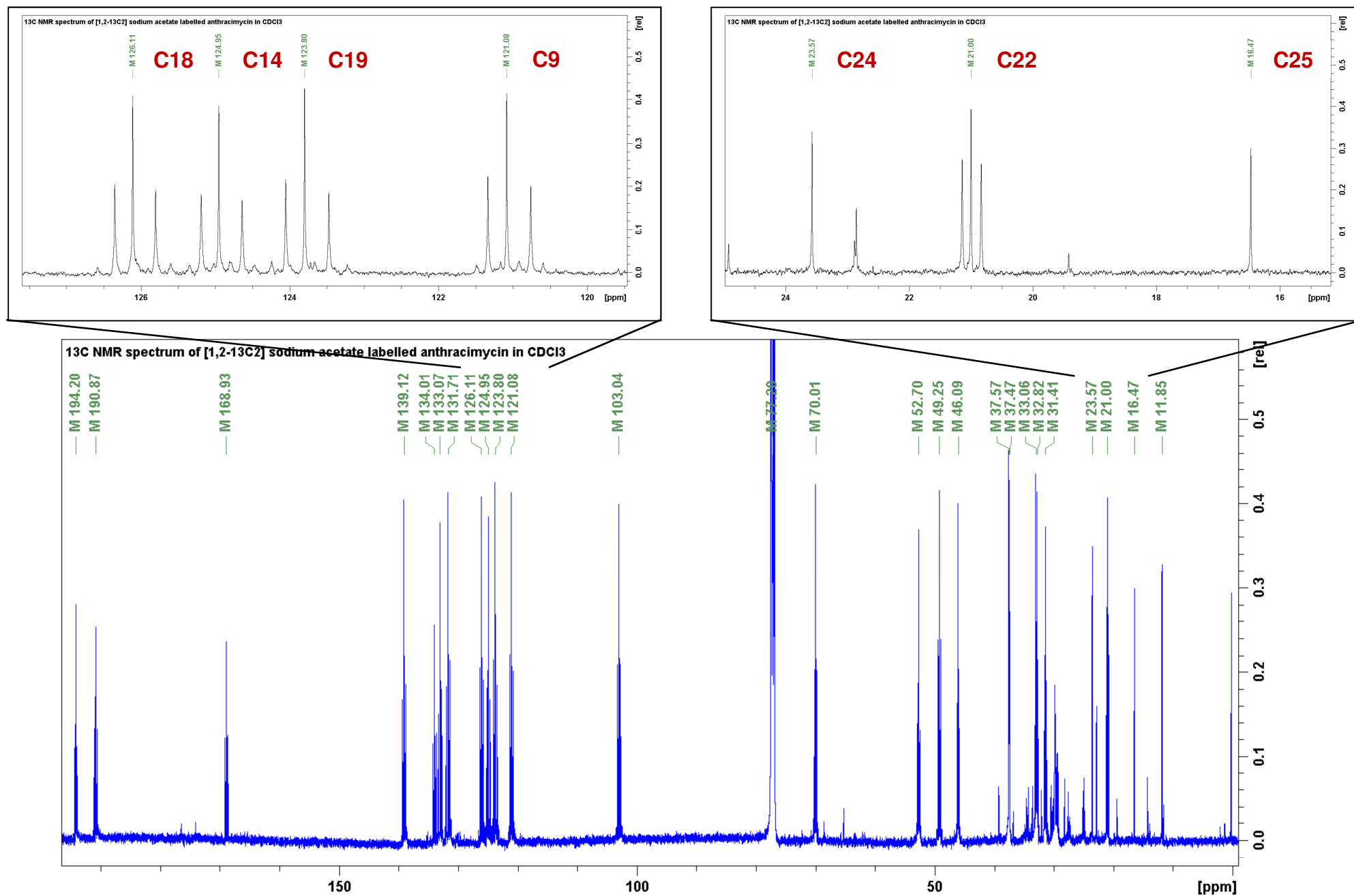


Figure S3.

Domain sequences and phylogenetic trees of AT **(A)** and KS **(B)** domains from various *trans*-AT PKS pathways. The enterobacteriaceae malonyl CoA-ACP transacylase FabD (WP_000191372) was used as outgroup for (A); KS4 of the erythromycin biosynthetic gene cluster (*cis*-AT PKS) (W63677) was used as outgroup for (B). KS numbering refers to the position within the gene cluster starting from the upstream end. Clade types according to Nguyen *et al.* 2008 are shown in roman numerals.⁵ Sequences from the following pathways were used; the accession numbers are given in parentheses: Atc, anthracimycin (this study); Bae, bacillaene (AJ634060); Bry, bryostatins (DQ889942); Chi, chivosazol (DQ065771); Cor, corallopironin A (HM071004); Dif, difficidin (AJ634062); Dis, disorazol (AJ874112); Els, elansolid (CP001699); Kir, kirromycin (AM746336); Lkc, Lankacidin (GQ925917); Lnm, leinamycin (AF484556); Mln, Macrolactin (NC009725); Mmp, mupirocin (AF318063); Ooc, oocydin (JX315604); Ozm, oxazolomycin (EF552687); Ped, peridin (AY328023); Rhi, rhizoxin (AM411073); Sor, Sorangicin (HM584908); Ta, mycovirescin (NC008095); Tai, Thailandamide (NC007650); Vir, virginiamycin (AB283030). Sequence alignments were performed using ClustalX2. For the generation of the phylogenetic trees the software FigTree v1.4.2 was used.

>AtcC_AT1

EIYREDRTAAHPFDTLAYTHPAILMVELALVETLRAEGVRPDHVLGASLGEFAAAAAAGVLDVEELARSLAEQVRL
VDRHCPPGGMIAVLDDIRTYRARGEDGPLDQRLTGGLLEAAVNFDHRFVLTGEPDEVARFEARLRADGRLCQRLPV
TYAFHSRLMDVAAEPYRRALAGLRVRPPDVPFVSCAAGTALDDVRVDHFWRMVREPIDFRRAVGHLENQGRASLYL
DLGPSATMANFATRNFAPGS

>AtcC_AT2-ER

IFPGQGSQSRGMGAALFPRFPELVAGADEVLGYSVAECLREDPDRRLDSTEFTQPALYTVCALSHLDRAGGGWHGA
HFFAGHSLGEYTALFAAGAFDFLTGLRLVRERGRMLGKIRDGGMAAVIGLDDEKVRTVLTENGLTDVDIANHNSPG
QLILSGPRERVHGARDAFLRAGARNFLPLKVSGAFHSRAMEFVRGEFEAFLAATAFAPPAPVPIANVTGRPHTPEG
LRHALAEQLVRPVRWEQSVRHLLAQGVTDFEETGPGTVLTRLVDRIRRSPPAPRPA

>BaeC_AT

LFPQGGSQKQGMGSSLFDEFKDLTEQADETLGYSMKRLCLENPYSNLHKTQFTQPALYVVNVLSYLKKIQDNDIKP
DYVAGHSLGEYNALFAAGAFDFITGLQLVRKRGEELMSMATDGKMAAVMGLTAAQVSDALQTHGLHTIDIANMNSPH
QVVISGRKEDIERAKSVFEGLKDVTFHPLNVSGAFHSRYMSEAKQEFKFLQSFHFSAISIPVISNVHARPYEQD
GIHSLVADQIDHSVRWNDSIRYLLDKGRMEFEFEEVGPGHVLTGLIHRIRKNETEA

>BaeD_AH

MFSGQGSQYYQMKGELFAHNAAFRQKMLDLDDFAVSRFGYSVLKEMYHTGNRLSDPFDRLLFSHPAIFMAEYALAY
ALEQRGIRPDYVIGASLGEYAAAASVSVLSAEDALDCVLEQARIVTETCRNGSMLAILGDPALYQDDPLLGEHSEL
ASVNYHSHFVISGEREHIKKIMDDLREKQIPHQLLPVSYGFHSALVDQAEQPYKRFLAQKSIRTPFIPYISSATGE
AETDIQADFFWDIVRKPIRFREALQFADSRQKGLYIDAGPSGTAAFAKQILPAGSAE

>BaeE_AT-ER

VFPQGGSQRIGMGEDLFGRYPELTAKADHILGYSIQELCRDGERLNQTQFTQPALYVVNALSYLKKTEETGLKPDF
TAGHSLGEYNALYASGAFDFEEGLQLVKKRGELMSRAKGGGMAAVIGLTHEQVTDVLRNHLDMIDIANMNTQQI
VISGYKEDIEKAASVFNAVNGKVMVHRLNVSGAFHSRYMLEAKEEFSRFIESFHFKPLSIPVISNVTARPYEQREL
KETLTGQITGSVNWTDSSIRFLMGRKNMSFEEIGPGKVLTLGLIQRITAEAE

>BryP_AH

IFMYSGQGSQYYQMKGELYDNNSLFRHHMNYCSNQLKDRLGVSLIDIIYDKSKKSEEFDNIIYTNPALYIFGYSLT
QVLIDKGIKPDAFLGHSLGEYIAATVAGIIPLEDGLNLILTQAQLEKHCNTGKILNVFSPPDFYYKNKNLFFNTP
LACVNFSSNFSVSGYRYEIDLVKKELDKRKIFSSYLPVSHGFHSHAIDPIENDFKKYVSQIKYSDNKLPIYSCYYT
SEITQDNIDNMKNYLWEVIRNTINFENLISSSFQNTSNNIFIDTSPNAALSNSLK

>BryP_AT

TIYLFPGQGSQHKKMGKYLFDKYPELIHQADQQLHYSIKELCLEDPDQLLNKTQFTQPALYIINALSFLDKIELES
HKPSYVAGHSLGEYNALFAAGAFDFLTGLKLQVQKRGLLMEEAPKGAMAAIIGITHNQVKCILEDIPQKNIDIANIN
SEKQFIISGLYDEIIACENSFTKMGANFIPLNVSAAFHSRYMKDIEIKFEQYLQKFQLNPLRTPVISNYSARPYPK
ENYRDYMVVKQISHPVKWYESISWLIQQDHFEFEFEEVGPGRVLTN

>ChiA_AT-ER

VFPQGGAQRKGMGADLFDPRFRRVIGAADAILGYSIKELCLENPDQRLNQTQYTQPALFTINALSYQRLEDQGVPR
AYLAGHSLGEYSALLAAGAFDFETGLLLVKKRGELMSKADKGGMAAVFGLREDDILEALQRHGLRRLHIANHNTPS
QIVISGAAEEIQRAKPVFDGIAGARYVPLNVSGAFHSPLMAEAREEFAAYIARFDLRNPGIPVVSNTARPYVDGR
ASQLLTEQITSSVQWTDSSIRYLMGLGETDFKEIGPGNVLTCLVQQIKQEA

>CorA_AT-ER

GAALFDQYPRQVQQADEILGYSIRSLCLEDPDRRLLEETSQYTPALYVVSALSYLKSQEAGVTPSYAAGHSLGEYNA
LFAAGVDFDQTGLRLVQKRGQLMGRAKGGGMAAVIGLGEEAIQQTAAESLSGVSANFNTPSQLVISGPRDEVAR
AEAPLLAKGARHFVMLRVSAAFHSRYMIEAEQEFSAFLSGFRLAPPRFPVFSNVHALPYEPERLHETLAAQISRPV
RWAEIMRRLLSLEDVRFEEVGPGNVLTGMLRKIRAES

>Difa_AT-ER

VFPQGGSQFKGMGAGLDEFQDLTRQADDILGYSIEELCLEDPNHQLGKTQFTQPALYTVSALSYLKKMKESGREP
DYAAGHSLGEYNALFAAGCFDFETGLQLVKKRGELMSKAAPGGMAAVLGFTAQVKEVLSYHLTGIDIANHNPSQ
QIVIAGTKQDIEKAGPVFEKAGVRMYLPLNVSGAFHSRYMKDAEKEFADYLEETAFLPLRFPVISNLHAAPYKNDK
IKTNLTLQMTNQVKWTDITIRRLMGLENNEIAEVGPGEVLTKLTRQIKKD

>DisD_AT-ER

MFPQGGSQAKGMGRALFDAPALTARADGVLGYSIRALCQDDPDQRLSQTQFTQPALYVVNALSYLKRREEEAPPD
FLAGHSLGEFSALFAAGVDFDFETGLALVKKRGELMGDARGGGMAAVIGLDEERVRELLDQNGATAVDIANLNPSQ
VVISGAKDEIARLQVPFEAAGAKKYTVLRVSAAFHSRMRPAMVEFGFRFLEGYDFAPPKIPVISNVTARPCKADGI
RAALSEQIASPVRWCESIRYLMGRGVVEEFVECGHGIVLTGLYAQIRRDAQ

>ElsB_AH

LFAGQGSQYYNMGRALFDTNPTFRNTMLGLDEVAVRLTGLSVIEYLYDGNKRYPLDRLLYSHPAIFMVQYALARTV
SELLPAAPAYVLGSSSLGETVAAAVSGAIPAEDMLEIVIRQAALVERSCAEGGMITLLHDQTFENEPALYMNNAVIA
AYNYDAHFTLSAAKTALSGISSFLHTREIMYSVLPVKYAFHSSEMEKIGALFLDGNRDKHFSLPVIPFYSSVYARE
WYDISITYFWQVIRRRIRFKEAIESLEKSGPYYYIDCSPSGTLKNLTAKIAPAS

>ElsA_AT-ER

LFPQGGSQKRGMGKELFDKYTSLTEEASEILGYNIRELCVTDEHRLNQTQYTQPALYVVNALSYLDRLDTMPKPD
FVLGHSLGEYVALFAAGAFSFTETGLKLVKQRAEIMGRVKNGGMAALLGLKMDTVRKILVESSYTSIDIANYNsAEQ
IVISGLRDDIISAQKVFEANGAKLYYPLNVSGAFHSRYMKEAQDAFALCVSSVHFSPQLIPVISNVLARPYEDGRI
GELLTTQITSQVKWYESISFLLHNGVATFQEVGPGDVLTKMQGFIA

>FabD

MTQFAFVFPGQGSQTVGMLADMAASYPIVEETFAEASAALGYDLWALTQQGPAAEELNKTWQTQPALLTASVALYRV
WQQQGGKAPAMMAGHSLGEYSALVCAGVIDFADAVRLVEMRGKFMQEAVPEGTGAMAAIIGLDDASIAKACEEAAE
GQVVSPVNFNSPGQVVIAGHKEAVERAGAACKAAGAKRALPLPVSVPSHCALMKPAADKLAVELAKITFNAPTVPV
VNNVDVKCETNGDAIRDALVRQLYNPVQWTKSVEYMAAQGVHELYEVGPGKVLTKLTKRIVDTLTASALNEPSAMA
AALEL

>KirCI_AH

LFAGQGSQYHGMGRWLYGADPFFRDALDSLDAVVREINGDSVIDAIHGDGRGAELAMTRLSLTQPAIFMVEYALAR
MLRAHGFEPELVLGASLGEVVAAAVAGIFDPEECLRSLLQVALFEAECPRGGMLAVLADAGLVDRPALAGAHLA
AINGPDNDFVLAGTAGRLDAIERHLAASGVLCQRLPVLPFFHSPLIDGVRDAFTKLVGGLTPRAASIPLISGTTGAE
VRHPGPDHFWQVLRFPDLSRALEPLLARDLLFLDLGPSGSMANLVRARLPEGSRSRVLPLL

>KirCI_AT

VFPQGGAQVKGMGRDLFDRFPELVERADAVLGYSIRELCLEDPGRNLRDTRYTQPALYVVGALSWLATVQEGGRLP
DYLLGHSLGEFAALFAAGVYDFETGLRLVAERGRMQVTTGGTMAAVSAVDSSSLVREVLRDDDELSGLDIANYNAPT
QTVVAGPADAVNRALAVFKDKGARCAPLNVSAPFHSRYMAQAAEEFGRLLDATAFAAPKIPVISNVDARPYEPDAV
AATLRRQIVSPVRWTDISIRLLMGRGDFRVRELGPQVLTCLIARIRDEAT

>KirCII_AT

VFAGQGAQWDGMGLELLDTEPVFGAALRRCDERVRELAFSVIQQLRAGPAMSRLGEIDVLQPTMVSLQIALVALW
RSWRVEPDAVTGHSMGEISAGYAAGALTDDALLIACRRSALLRRIAGRGALATTELSPEAAHALAASSGGRICVA
GENSPRSTVLAGDTATLTALVEDLDRRGVYCRMVRGTVASHSHYVDELRDDLAGALRPLSPVPSRVVPFYSTVTAAP
VPGTDLGPAYWMRNLREPVRLAAATGRLAEDGHEIFVEVSTHPVLLSSLRQTLESAGRPGEVLP SGRR

>LkcD_AT

MFPQGGSQRIGMGKEVFDAYPQLCDRADEIVGHSLRELCLKDPDGRNETSRTQEAVYFVSCLMYLAYAEHGAEQ
VRCLTGHSGLGLPALFAAGVFDLFEGLEIVSRRGALMQEARDGAMVAVLGPRASEIDHHLARLEFFDQDVANYNPS
EQVVL SALKPRLEELVPRLEETGHRVCWLPVSGAFHSRHMEPARLRFQAQFLDRDTFTPTPKPVSTTSGRTL GARH
LLEEMVFQLVKPVRWWQTVTHLSRTGHKTFDEVGPGRVLTKL SAEILGDEP

>LnmG_AT-ER

VFPQGGSQQRKGMGADLFARFPDLTRQADTVLGHSVEELCRSSGDGRDLRTEYAQPALFVVSALSYLARDPGLPQPT
LLAGHSLGEYALFAAGCFDFATGVRLVRERGAALMGRAQGGGMLAVLGVDGDEVQALLAGTGARQVDVANYNTPTQ
TVLSGPLDELRMVSAALGQRPGVRCVPVRVSAAAFHSRHRMPAAQEFATFLTGFSEFADPHRTVISSVTARPYGAGQV
AELLSRQIESPVRWSETMAYLRERGTTELEEMGPGKVLTLGLWKQGRADGAKA

>MlnA_AT-ER

VFPQGGAQFKGMGRDLFDEFSELIKKADHILGYSIKDLCLSDKERLTDTKYTQPAIYTVSALQYLKGLKEGHTRP
DAVAGHSLGEYTALFAAGVFNFETGLRLVAKRGELMSEASEGGMAAVIGLDEHHIKKILQKYDLGQIDIANYNSTSS
QIVIAGAAEEIKRAASFFEKEGAKAYIVLQVGGAFHSRFMESAQRKFAEFIEEFHFSELNFPVISNYTARPYKQED
IKRNLIEQITNSVKWTESIRYLMGQGVTLFEEIGPGNLTCLKLIQTIQRDE

>MmpC_AH

MFSGQGSQYRHMGRALYERHAGFGRHMRALDEVVRQTGGYSVLDGLYGDQPQAAALDDILVTHPAIFMVEYALAQS
LIEHGVYPDHVLGSSSLGEVAAAAVSGALDAEQALGFVVRQARLFHEHCPAGGMTAVLADIAVFEQLQADGIEVELA
AINYPQHLVISGTVSALAAAQMQQLARRNVVFQRLDVNRPFHSSHMDPLRDAFIQTSQALQLRTPRMGYVSSTLGGP
VSQFAPEHLWHVVRSTLQLAPAIYEYLEGLGPHEYLDAGPSGSMANFAKRCRSHASAS

>MmpC_AT-ER

MFPQGGSQFRGMGEGLFERFAELTACADRVLGYSIRELCENDPRNELGQTRFTQPALYVNVNLSYLAQAGDAAPPD
YVLGHSLSGEFCALFAAGAYDFETGLRLVKRRGELMSEATGGGMSAVLNLDLATIKQVLRQAGSTQLDFANFNAPQQ
TVLAGPLDALESVRTQIEDASGICVALNVSAFPFHSRYMRGAQEAFAAELARVTFKPLTLPVIANVDARPYEQEAIA
SQLARQMTSSVQWVESIEYLLQAGITQFKEIGPGNVLTNLQAKIEKNRSPA

>OocV_AT

FPGQGSQYRTMGYGLFEQFPELAAQASQALGYDIAELCIKDPQRVLNQTQYTQPALYTVNALSYLERKARGAAPPD
ILAGHSLGEYNALFAAGAFDFITGLKLVQKRGQLMSLAPKGMAAVLEINVADIERILAESGFQHVDIANINSLQQ
CIISGAYDEVLALEPRFLEAGARFVQLNVSAAFHSRLMSDIEREFADYLTQFTFQPLSTPVLNVNTARAYPRTDYQ
TLLTRQISSPVRWYESISWLLAQGCDDFAEVGPGDVLTKLHQRITEA

>OocV_AH

MFAGQGSQYYQMGRAFYHSDGHFRQTMDRDLCHKVYMLSGVNLLQLYSERDAAAEFDDIRHHPALFCFGYSLAQM
LIARGIQPAAVVGHSLSGEYIAAVVAGMLRLDDALRLVVEQAHLLEQHAPAGRLAVVLAAPDIFHRATEVFSRCTLA
GVNFGNNFFISGEQSAVTSIQKLTERDILSLSLPVRYAFHSASIDAIPSYQKLLDKTPCFAPTMPVYSSVLGRA
VGEMQQADAQGYLWQVIRDKVDFSTLVDSVFTMSDHHFFIDASATGSLSNFLK

>OocW_AT

MFPQGGSQQPGMGRELFSQFPDLTRIADDILGYSIERLCLDDPDGELNKTQYTQPAIYVNVNALSYYKKRQETGIQP
DFVLGHSLSGEFNALLAAECFDFATGLKLVKKRGELMAQAAGGGMAAVLGLSEAKLRAFLTEKKLDTIDLANFNTPS
QIVISGQRDDVTKAVTEFEQSGMRCVPLNTSGAFHSRLMRGSMDFESYLNQNFQFSALKIPVIANTTARPYEDDTL
LTCLAQQIASPVRWTASIQYLMSLGTPEFTTELGHSEVVSGLVEKIKAEETED

>OzmM_AH

MGSALYETEPVFRRVMDRLDAAASGELGESVLAALYAPGRGRAEPFDDIAFTHPAIVMVELAAAETLIASGIRPDL
LLGASLGEFTASVLAGVLDADACLRLVLRQAAAVRDAPRGMLAVLDDVALHARLPLLRERTEIAARNYPGHFVLA
GAHEDLVAAEEELRARKVVCHRVPVPYAFHSRLMDSGEPLFRSAMAGTELRPRLPVISCATGGQVERVTVDHLLWR
ATRLPIEYAGTLAALERRGPFQYVDLGPSTLHNFARNGLPASSRSRSLPL

>OzmM_AT-ER

FPGQGSQAKGMGKDLFEFFPEETALADSVLGHSIRELCVEDPRRELKLTRFTQPALYVVSALAWLRERRENVPVPPD
FLVGHSLSGEYVALFAAGSDFDFETGLRLVARRGELMSRADGGRMAAVLKCDLETVEGALAGHGLTGLDIANHNAPGQ
FVIAGPTEQITAAPKPVFEGLGAHYVQLNVSAFPFHSRYLRDTAEFFGRYLEGFTLRDPAPVPIANVDARPYRPGEVA
RQLARQIASPVRWTDITIRYLMGLGDFEFVELGPGRVLGKLVAKIRAEAE

>PedC_AH

MFSGQGSQYFQMGRQLYEQDETFHAWMKSLDDNVRDYIGQSLDDIIYDTGHERSLPFDRLIHTHPALFMVQYALAK
SLLARGLPAPDFLIGASLGEFIAISLAGDTHVENILFNLIKQARLFDEYCNAGAMLLVIDHIDTFSTTPAFSKDCE
LAGINFDCVSVSGPRTGILQTRKSLTKQNIACQLLPVSI AFHSSWMDDEVHEIFIQQFPEQICRRLHTPVISICALP
VPEQLTRFSSTYWWHVIRQPIAFHLAINTFHQSSPNAVYLDLGPAGNMAAATKYNLPSSIHYRILP

>PedD_AT

IEEAANDILGYSIKTLCLEDPQRQLRLTQYTQVALYVVNALTIRQHLQQGGGLPDPFVAGHSLGEYNALESAGVFSF
EDGLRLVQKRGDLMSQAPRGAMAAAILGISADSVAGILAEQGLTRIDIANYNAPTQTIISGLEADIRDAQAVFESCQ
AMYVPLNTSGAFHSRYMQSARDEFAQFLEAFEFRRDPQIPVVANVTAKPYVGTEVVRTLADQLTGSVRWLDSMRFL
DQGVTEFRELGP GDVLSKLIVESIRSSAMSK

>RhiG_AH

MFPGGQGCQFYQMGRELYQNNVSHRWMNELDALIRVELGHSLIAEIIDANNARSKTFDDLRI SHPAIFMVEYALGK
TLIEQQIQPDYLLGTSLGELAAAAAETLPLSDAIRFVTRQGQLFHRRQSPATEGTM LAILCDESLYQQTPLLHDH
CDIAAYNAQSLI VIAGQSARIAEAERYLSSRDIVFQRLPVKQAFHSRHIDFLKPEVDVLASELRLRRAQIPVISCH
NTETLNQLTTDHFWRITIREPIRFSQTLARIEREAAERGESMIYLDLGP SGTLANLIKQNI RDRQAPQTFAVL

>RhiG_AT

VFPGGQSQRVGMGAELFEQFPDHVAQADEILGYSLRTLCLLEDPDRQLSHTQYTQPALYTVNALAF LNKQQQDRRQP
DYL AGHSLGEYCALFAAGAFSFETGLKLVKKRGELMARATGGSMAAVIGRSAD EIKSLLSQHGLNALDVANYNSPS
QTVLAGPVEALSQAKEIFQALEITVIPLSVSAPFHSRYMQSAMEEFGEY LKQFSYSPLQIPVISNIH AVPYRDNEL
IDNLTRQICG SVRWVETVQYLIRQGECEFEELGPGNVLT KLINSIRAA

>SorO_AH

MFSGQGSQSHYFQMGOELYERQATFRRWMDRLDVVTRDLSGASVVEALYKRGHGKGD LFDRTLLSHPALFMVEYALAR
ALLEAGVEPGMVLGASLGTF TAATIAGCLDVEDGLKAAIQHAKALESTCEPGAMIAVLAPLRLCEDASLHRYGELA
AVNFDGNFVLSVRTHDVS AVQEILRGRGVTFRRLPVSFAFHSRWMDPAETSFKRHMRSVITRRGD LPLVCCARSQP
LDALSDERLWRATRDP IRFQDTLRRLEASGPHQYVMDPAGTLATFVKYNLAQTPSA

>SorO_AT-ER

MFPGGQSQKRGMGAGLFD SVPQYRAVEKDVDALLGYSLRALCLEDPKNVLSDSQFTQPALYMVNALHY YQLLAEGA
RPDYIAGHSLGEYNALHAAGAFD LLTG LRLVKRRGELMSQAKKGGMAAVIDMDERGIRK VLEENDLGTIDIANFNS
PGQIVISG PLDDISRAKSIFERSGARSFIPLPVGA AFHSRYVADAARAFA DFLAPMTFAPLQLPVISNVTARPYEA
GNPSVAIKSLLVEQITRPVRW MQSVEYLIDKGVRDFREVGP GNVLTRLVN KIHK

>TaiC_AH

MFSGQGSQYVGMGRALYSEPTFRHHVDRFDEVTRDKTGTSLVARLYGRDARAGEPFDDTHVTHPALFAVQYALAR
TLQARGAQPDIVLGSSLGDFVAAAALAQVAPAEIVAWLIDQAASMARACEPGFMLAVLGPASIYRGS DTLREFSDL
VGVNYAEHFVIGGNRADLVRVEAALAREGVVFHRLPVRF GFHSRN VAPVVPWLHAREANLS CRAPTIPWASCTAGG
IVEAPTARFLTRIAIDPLRFQEAARAIEQTGSPDTLHWVDLGP SGTLANFARR

>TaiC_AT-ER

LFPGGQSQVKMGMAALFARFPDRMLANEILGYDLAALCIENPDNRLGQTQFTQ PAMYVVNALAYLARREDDAGAP
AFVAGHSLGEYSALFAAGAFSFEDGLRLVKRRGELMSAARDGGMAAVLGLDEARVAEILALS DLRGIDIANLNAPT
QIVIAGPADEIRRAQQWF EQGCCYAYVVL PVSGAFHSRMMRDAQREFERFIAPFDIGAPGIPVIANVTGRPYRGDE
VRRGLVEQIASPVRWVD TIRYLSEQGVVERFAEIGTGTVLTDL LRKILPQKAGA

>TaV_AH

LFSGQGTQSYFMAKELFDTQTGFKRQLLELDEQFKQRLGHSILERIYDARAARLDPLDDVLVSFPAIFMIEHALAR
LLIDRGIQPD AVVGASMGEVAAAAIAGAI SVDA AVALVAAQAQLFARTAPRGMLAVLHELEACRGFTSVARDGEV
AAINYP SNFVLAAD EAGLGRIQQE LSQRSVAFHRLPVRYPFHSSHLDPLREEYRSRVRADSLTWPRIPMYSCTTAN
RVHDLRSDHFWNVVRAP IQLYD TVLQLEGQGGCDFIDVGPAA SFATIIKRILARDSTSRLFP LL

>TaV_AT
LFPQGGSQERGMGAALFDEFDPDLTDIADAILGYSIKRLCLEDPGKELAQTQFTQPALYVVNALSYLKRLREGAEQP
AFVAGHSLGEYNALLVAGAFDFETGLRLVKRRGELMSGASGGTMAAVVGCDAAVEQVLRDRQLTSLDIANINSPD
QIVVSGPAQDIERARQCFVDRGARYVPLNVRAPFHSRYMQPAASEFERFLSQFYAPLRCVVISNVTGRPYAHDNV
VQGLALQLRSPVQWTATVRYLLEQGVEDFEELGPGRVLTRLITANK

>VirI_AT
MFPQGGAQRVGMGRITLLDRFPDLEREASDTLGYSLRRLCLEDPGRLGNTRYTQPAMFAVNALAHRAAVEDGARPD
IAIGHSLGEYNALAAAGVFGFTDGLRLVAARAAAMAEEVGGGMSAVVGLTETKLRFLLLRAGFATLDLANLNTASQ
TVLAGPLEDLEEAGQVLEDAGARMVRRLDVSGPFHSRYMAPAAAALVPLVRSARLRPPAFPVIANRTAQPYRAELA
ADLLLQQIDHPVRWHETVRTLLDEPDVAFTEIGESTVLTSMVRQIKRDAE

>Atc_KS1
IAVVGIGCRLPGARDHRAWANLDAGLCSVREITADRWD TARHYS PDPSSPDTSVSKWCGLLDHPYAFDHAF FRLS
PRDAALMDPQQRLVLEETWHCVEDAAIP LAELSRARTAVYVGMARDHLQEAGRDGAPVEGHSGLGGYDGLLANRV
SHTLGLRGASVSVDAAACASSLVALHAGMRALLDGEADYVLAGGVSLNLHPWKYLTFSKARMLSPEGLCKTF SHDAD
GYVPGDGVAMVLLRPLADAVRDGNHVYGVLAGSAVNHVGRGGTITAPSVDAQREVVSAAALARAGWDPRVTYVEAH
GTGTSLGDP IEVEALHRVYAPASPDGTGWCRI GSVKPNIGHLEAAAGVAGLVKVLMMMRARTVPPSLHIRDLNPLIR
WADGPF EVTRRSVPWRPHREGRPLRAGVSSFGMGGVNAHVVEEY

>Atc_KS2
VAVIGMAGRYPLAPDLDAFWRNLAAGRDCVTAIPPDRRRDWGLPATGDLPGDSGIYCPSGGFLDGVD RFDPLFFHV
SPREAEVMDPQERIFLEVAWSAFEDAGYPPHRLGDPDDPAQRRVG VFAGVTTQTYLLWGPGRWNADDPVIPTSTPW
SVANRVSHRLDLHGFSMPVDTACASSLHAVHLARVSLARGECDMALVGGVNLYLHPAKYRWLCQMRMLSPTGRCHA
FGEAADGFVPGEGAGALLKPLRRALADGDRVLGLIRGTSVNHGGR TSGFTVPNPRAQAE LVRAALRDAGVAPDAV
GYVEAHGTGTALGDPVEIAGLAQAFQDVP AHGAAEGDGCALG SVKTNIGHLESAAGIAGLTKVLLQLRHGTLVPSL
HAERENPRLDLAGTPFRLQREVSPWHRKTGADGRELP RRAGISSFGAGGANAHVIVEEY

>Atc_KS3
VAIVGMHAEMPGCPDLDAYWRHIEAGDELISEIPADRWDWRDHYDPTGRREGTTVSKWGGFLPEVDTFDARFFGV S
PREAELMDPQQRLFLQTAHRAVEEAGYRPCDLAAGRTGLFVGVA THEYYDLLREAGVPTEAYTTTGLFHAILANRV
SYLMNLSG PSLPIDTACSSSLVALRTAVESLRAGSCDAALVGGVNLLLSPTIYVSFSRAGMLSPDGRCKTFDAAAD
GYVRGEGVAALLKPLSAAERDGDHVVHAVIRGSAVNHGGRVNTLTTPNPNAQSSLIVDAFEEAGVDPETVGYVEMH
GTGTALGDP IEINGLKKA FRELRDRAGRSRLTQPCTAIGSVKPVIGHLEAAAGMAGVVKAILAMKHGKLP GSPHIR
EPNPHIQLRGGPLRIPRTTEPWP RRTGPDGRELP RRAAVSSFGFGGTNGHV LLEE

>Atc_KS4
IAVIGMSGRYPGAATLAELWDNLARGVCAAGEVPPSRWPAERYHDPDPARLDTTYCSRGAFLDDVD AFDAPFFAMS
GKEAAQTDPQQRLFLEEAWRALEDAGYPSGALEGRPCGVFVGVPSEYLTRMNRAGVLKEAQSFWGNEASVLAARI
SYFLNLKGPSLAVNTACSSSLVAVHLACRSLLSGECETALAGGVFLTLAPDYFVVASNGTMLAPDG VCKTFDADSAD
GFGPGEGVGALVLKPLRAALRDGDHVHG VVKGSAINQDGR TNGITAPSGAAQTAVELAAWERAGISPETLGYVEAH
GTGTRLGDPVEIEALANAF AHHTDRKAFCPIGSVKANIGHTAAAAGIAGI IKVLLAFRHDR LPPSANYRTPNRLID
FPDTPFRVVT ELSWPWGRDGAP RRAAVSSFGFSGTNAHLVLEEP

>Atc_KS5
IAVVGISARFPQAENLDVFWENLRDGRDSVTEIPPDRWDHARHFDPRPGVPGKSYTKWGGFLDGVDTFDAGFFHLS
PREAERMDPQERLLLQEVWHALEDGGLTRDRLAGTAVGVYVGMYSQYQLLQAEQAVRG NPLHLGSSYASLANRLS
YFFDLRGPSMAVD TMCSSSLTAIHLACEALARGDLQA AVAGGVNLT LHPAKHIDLSQGRYASSDGRCRSFGEGGDG
YVPGEVGAVVLKRLDDALADGDRVHAVIRGSALAHGGR TNGYTVPNPAEQARLVAEACRRAGIAPRDLGYVEAHG
TGTS LGDP IEIRALARALGPRPEDRPPCAIGSVKSNIGHLEGAAGIAGLAKVILQFRHRR LVP SLHAEPVNP HIDE
DAAGLRLQRTLEDWPALLDDTGAPLPRLAGISSFGAGGANAHVVEEP

>Atc_KS6

AIVGVSGRYPMAGTLDEFWHNLREGDCVTEVPRSRWDHGRYFAPDADRPGTTYAKWGGFLDDVDRFDPLFFAIPP
REARMMDPQERLFLQAAWHALEDAGHARSAPGGRRIGVYVGVMYAQYQLYGADPALQSRGFVPGSLSASVANRVSH
ALGLTGPSVALDTMCSASLTALHLACAGIRLGDCDAALVGGVNAILHPNRYLQLAQSRFASSDGRCRSFGEGGDGY
VPGEVGVGALLVKPLSRAEADGDHVVHAVIRGTAVNHGGRSNGFTVPTPAAQAEVIGEALRRSGVAPGDIGYVEAHGT
GTALGDP I E I A G L G R A F R S A A P D G T D T E P I P I G S V K S N I G H L E S A A G I A A L T K V L L Q F R H R A L V P S L H A D P P N P H V
D F G A G P F R V Q R V H A P W P A R R T G G R D L P R L A A V S S F G A G G S N A H V V L Q E Y

>Atc_KS7

VAVIGMSGRFADAADLDELWANLAAGRDSVREIPP HRWDVGAHWDPDPAAPGKTYGKWGSVLDGIDRFDPDFFGIS
PREARLMDPQQRLFLMEAWRAIEDAGYGERTLDGLECPVFVGTSMGDYHHLLRQRGVPEGYTFMGTHPAVLSSRL
SYHLNLKGASLAVDTSCSSSLMAVHLACEAIREGRGELALAGGVAALVTPELHVLASKAGMLSPRGRCRPFDDGAD
GFVPGEGVGVVLLKRLDSALRDGDHVGVIATGANQDGRITAPSAQAQSALLTSVYERFGIDPDRIGYVECH
GTGTRLGDP I E I E A L T E A F R A F T A R R G F C A V G S V K S N L G H T L T A S G V A G L L K A L L S V K H G G L A P T A H F R T P N R H I P
F E E S P F Y V S D A L R D W P A E P G S P R Y A A V S S F G F S G T N V H V V V R E A P

>Atc_KS8

I A V I G L S A R Y A D A P S A E A L W R L L A A G E C A V R E V P P D R W P A G R Y Y D P D P R A P G K T P S R W G A F I E D A A A F D P L F F H L S
G H E A E R M D P Q Q R L F L E G C W T A L E N A G H A G D S L A G T R C G V F A G T P A S D Y P R E E Q R S G P E A D A Q V L L G N D T S L L A A R I
S Y L L D L R G P S V A L N T A C S S S L V A I D L A C E A I R A G R C D T A L A G G V C L F V G P G F Y L S A G K G G M L S P R G R C S A F D R D A D
G F V P G E G C G V V L L K A L D A A L R D G D H I H G V I L G S A V N Q D G K S N G I T A P R A R A Q T D V Q L Q A Y A R A G V S P R T L S L V E A H
G T G T A L G D P I E I E A L T R S F A R Y T D E R Q F C A I G S V K T N L G H T G Q A A G V A G L I K C L L A F A H E E I P P T L H Y S V P N D R I D
F A A T P F R P V T A P S P W P R R A G V P R R A A V S S F G Y S G T N A H L V V E E P

>Atc_KS9

I A V I G L A G R Y P G A G D L E E F W R N L V G G R D C V T T I P E D R W P L D G F Y D P E G G P G R S Y G K W G G F L D G I D R F D P L F F G I A P
R D A D M M D P Q E R V F L E T V W H A L E D S G R T R A D L R R G T T G V F V G V M Y G D Y Q R Y G P A P D G R M G V S S Y A S I A N R V S Y F F D F
R G P S M A L D T M C S S S L T A L H L A C E S L R R G E C D T A V A G G V N L S T H P D K Y R Q L S L A R F L S T D G R C R S F G A G G D G Y V P G E
G A G A L L L K P L A A A R A D G D T V H A V I R G S A V N H G G R T N G Y T V P G T R A Q S A A I R E A L R R A R V R P G D V G Y V E A H G T G T A L
G D P I E V A A L T E V F G T P E A T P G A A P E A T P D A A P G A V P G A V P A E P P A G P D D P S R I P I G S V K S G I G H L E S A A G V A A V T K
V I L Q M R H R T L V P S L H A E D L N P H A A L D S S P F R V Q R G P A A W A P R G T D R P R L I A G V S S F G A G G S N A H V I L E A

>Atc_KS10

VAVIGMSGRFPGRDLDRYWDNLYHRRDLITEVPADRWDWRALDSEELPPERRTPYRWGGFVEGADTFDPLFFGIS
PAEAEMMDPQQRMLLQTVWSAVEDAGYRPSALAGRVPVGLFSGIQFSDYQHLMEAGVMSAQSGLGNEHSISVNRI
YLLDLRGPSEPVNTACSSSLVAVHRAVRSLRQGECELA VAGGISLNLSPHSTVAAGMMGLLSPDGRCKTL DAAANG
YVKGEVGMVLVKPLDRALADGDQVHAVIRGTAVNHGGRAASLTAPNAEAQAALLCAAAREADAGPETIGYLELHG
TGTELGDPEVNGIKLAFRRLARERGTELPAAPYCGIGSVKTNIGHLEPASGIAGLMKVILALRHRALPGMAHLDE
VNPYVDLAGSPFRIVDGTVPWEPLTGPDGGRLPLRAGVSSFGFGGVNSHVLVEEP

>Bae_KS1

AVIGISCEFPGAKDHYEFWNNIKEGKESITFFSKEELRRSGISEELADHPGFVPAKSVLEGKEMFDPGFFGFSPKD
AEYMDPQLRMLLLHSWKAIEDAGYISKEIPETSVYMSASTNSYRSLLPEETTAQLETPDGYVSWVLAQSGTIPTMI
SHKLGLKGPSYFVHANCSSSLIGLHSAFQSLQSGEAKYALVGGATLHTESSAGYVHQPLNFSSDGHIAFDADAD
GMIGGEGAGAVLLKKASDAVKDGDHIYALLRGIGVNNDGADKVGFYAPSVKGQAEVIQKVIDQTGIHPETIAYVEA
HGTGTLGDP I E L S A L Q S V Y G R Y T D K K Q Y C G I G S V K T N L G H L D T A A G M A G C I K V M S L Y H Q E I A P S I N Y K E P N P N L
H L E D S P F F V A E E K K E L T R E N R A H R M A L S S F G L G G T N T H A I F E Q Y P

>Bae_KS2

V A I V G I S G R F P G A K D I E E F W R N L K E G K D S I T T I P K E R W D W Q A F D G D P N L E G N K T N I K W G G F I D G I A E F D P L F F G I S
P R E A Q Y L D P Q Q R L L L T Y A W R A I E D A G C K P E S L S G T N T G V F I G T G N T G Y K D L F T R A G L A P E G H A A T G S M I P S I G P N R
L S Y L L N L H G P S E P I E T A C S S S L V A I H R A V S A I E N G E C D M A I A G G I N T I L T E E A H I S Y S K A G M L S K D G K C K T F S K D A
N G Y V R G E G A G I L M L K K L S D A E R D G N P I Y G V I R G T A E N H G G R A N T L T S P N P K L Q A D L L V K A Y R K A G V D P S T V T Y I E A
H G T G T E L G D P I E I N G L K A A F H E L A K T N Q E P E V S G H R C G I G S V K S N I G H L E L A A G V S G V M K V L L Q M K H K T L V K S L H C
E T I N P Y I Q L D D S P F Y I V R E N Q E W T A A K D R N G N A I P R R A G V S S F G I G G V N A H I V I E E Y

>Bae_KS3

IADVGMSCRFPGAASLEAYWSLLAEGRSAIRPVPAERWGLKTPYYAGMLDGIHQFDPDFFLLAEEDVKAMDPQALA
ALEECLNLWYHAGYTPDEIKGEAIGVYLGGRSRHRPGEDKLLDAKNP IVALGQNYLAANLSQYFDMRGPSVVLDTA
CSSALVGMNMAVQALVSGEIKAAVVGVSLEFESEETHKLFEQRGILSKAQSFHVFDERADGVVLGEGVGMVLLKTV
SQAIEDGDSIYAVVKAASVNNDGRTAGPATPSLEAQKSVMKTALEKSGKQPEDITHIEANGSGTVVTDLLELKAIQ
SVYRSKDAGPLGIGSVKPNIGHPLCAEGIASFIKVVLMLEKESFIPFLSGEHENTHFDREKANIQFSRTLADWPSP
IPAAGINCFADGGTNAHVIVEA

>Bae_KS4

IAIIGMAGRYPQAENIHEFWENLKEGKNCVTEIPESRWDWRRFENVKSPSGKSISKWGGFIDDPDCFDPQFFRITP
REAETMDPQERLFLQTCWETIEDAGYTPKSLAEARGNRKRQRVGVFAGVMHKDYTLVGAEASSEDHVFPVLSLNYAQ
IANRVSYFCNFHGSPMAVDTVCSSSLTAVHLAAESIRRGECESAVAGGVNLSLHPNKYLTLYGLWDMFSTDGVCHTF
GKDGDGYVPAEGIGAVLLKPLREAVKDGDRIYAVIKGSAVNHVGTVSGISVSPVAQADLIEECLDKAGIDPRTVS
YIEAHGTGTSLGDP IEVQGLVKAFRQYTQDKQFCSIGSVKSNIGHAESAGISGLSKVALQLHHKTLVPSLHSEEL
NPYLDFEQSPFFYVQHHTAEWQQPSVTENGNETVYPRRAGISSFGATGSNVHLILEEF

>Bae_KS5

IAIIGISGRYPQAENLQEFWKNLSEGTDCITEIPNDRWDHSLYYDADKDKKEGKTYGKWGGFLKDVDKFDPPQFFSIS
PRDAKLMDPQERLFLQCVYETMEDAGYTRKKLTEKSGDLLGANVG VYVGVMYEYQLYGAEEQARGKSLALTGNPS
SIANRASVVFNGFNGPSMALDTMCSSSLTAIHLACQSLRNGECEAAAFAGGVNVSVHPNKYLMGQNRFLSSSKGRCES
FGEAGDGYVPGEGVGAVLLKPLSKAKADGDHIYGLIKGTAVNHDGKTNGYSVPNPNAQAAVIKQALKDAGTDPRAV
SYIEAHGTGTSLGDP IETITGLTKAFSEQTQDKQFCAIGSAKSNIGHCESAAGIAGLTKVLLQMKHKQLAPSLHSRT
LNPNIIDFLATPFKVQQTLEEWKRPVINENGVNKELPRTAGLSSFGAGGVNAHIVIEEY

>Bae_KS6

IAIVGMSGKYPDAPELKYWDNLARAKNAIRD IPLSRWDVNKYYDPALNKKGKVYCRSIGMLDDIEEFDPLFFNIS
PSEAELMDPQHRIFLQEGFKAFEDAGYSSKELNGKNCGVYLGIMNNEYGMMLNKHQTGGSATGNSFSIAAARLPYY
LNLKGPAIPIDTACSSSLVGAHLARQALLNHEIDMALVGGVTLYLTPEYSYISMCEAGMLSPDGQCKAFDNSANGFV
PGEAGALVLKRLKDAEADQDHIYGVIIIGSGINQDGKTNGITAPSAKSQMDLERQVYEAHNHHPESITYAEMHGTG
TKQGDPIELEALSSVFKEKTDKQFCAIGSVKSNIGHTSAAAGVASVQKVLLSMKHQQVPTLHFSTPNEHFDFFD
SPLFVNTELKPWETGGAPRRACVSSFGYSGTNAHLVIEEY

>Bae_KS7

IADVGMSCRFPGAESLEQYWDLLRSGRSAIGSVPAERFGYANQYVAGLIDNMDHFDSEFFFIPENDAKAMDPQALA
VLEESLKLWCHAGYSREEIKGIEAGVYIGGRSQHQPDPEILANTRNP IVAGGQNYLAANVSQFFDLRGPSIVLDTA
CSSALTGMNMAVQALRSGDIKAAVVGVSLLNTDAAHRMFQERGLLNEKPAFHVFDKRSGGVVLGEGVGMVLLKTV
SQAQKDGDTIHAVIKAAAMNNDGRTAGPSAPNMQAQKDVMSALFKSGKKPEDISYIEANGSGSAVTDLLELKAIQ
SVYRSQHVPLGIGSIKPNIGHPLCAEGIASFIKVVLMLEKHKQTVPFVLSGDEPMPHFDITKTDFHFHKTAGEWDAA
RPSAAINCFADGGTNAHVILEA

>Bae_KS8

IAIIGMAGRYPKAKSVAEFWENLKAGTDCITEVPKSRWDWKTYKNVTSPSGKTVSKWGGFIDDACCFDPQFFRISP
REAETMDPQERLFLFETCETIEDAGYTPETLGNKGEKQHP IGVFAGVMHKDYSLIGAEQLSETDPFPVSLNYAQIA
NRVSYCYDFHGPSIAVDTVCSSSLTAVHLAIESIRRGECEAALAGGVNLSLHPAKYLSYGSVGMHSSDGRCRTFGE
GGDGYVSGEGVGAVLLKPLEKAEQDGDRIYAVIKGSAINHVGVKVSGITVPSPAQAEVIKACLKAGISPRTVSYV
EAHGTGTSLGDP IETIEGLSKAFSQGTQDQQFCSIGSVKSNIGHAESAGISGLTKAALQLHHKTLVKSLSHSAELNP
YLKFEESPFYVQQQTAPWKQPSAEENGKVTHYPRRAGLSSFGASGSNAHIILEEY

>Bae_KS9

VAIIGVSGRYPQAKTAAELWANIKKGKNCIEEIPRERWNWQDYDEEKGKEGSIYTKWGGFIEDMDKFDPLFFQIS
PLEAERMDPQERLFLFETAYASIEDAGYTPDNLCQSRKIGVFAGAMNKNYPTGYGYWSIANRVSYLDFDQGPSIAVD
TACSSSLTAIHLALESIYSGSSECAIAGGVNIVTDP IHYMNLSVMNMLSAGDTCKSFGDRADGFVDGEGVGAVVLK
PLDRAIADNDHIYGVIKGSTINSGGKTNGYTVPNPNAQAALIKEAFERANVPARTVSYIEAHGTGTALGDP IETIAG
LTKAFEEDTTDKQFCAIGSAKSNIGHCESAAGIAGLTKILFQLKDRQIAPSLHADQLNPNIIDFAYTPFAVQQELGE
WKRFPVIGGKELPRRAGLSSFGAGGANAHVIEEY

>Bae_KS10

VAIVGISQCPFGAKNHHEFWKQLREGKESVRFYSEEELREAGVPEDLIENPDYVPALSTIEGKDLFDPEFFHISP
DAEFMDPQRLRLLLLSHWKAVEDAGYVSKEIPKTSVYMSASNNSYRSLLEPKTTEGHESPDGYVSWVLAQSGTIPTM
VSHKLGLKGPSYFVHSNCSSSLVGLYSAYKSITSGESEYALVGGATLHAATSIGYVHQNLNFSDDGHVKAFDASA
DGMAGGEGAAVILLKKASQAVQDGDHIYAMLRGIGLNNNDGADKVGIFYAPSVKGQTDVIQHVLDSTNIHPETISYIE
AHGTGTTLGDPiemsalQQVYKRYTDREQYCGIGSVKTNIGHLDTAAGLAGCIKVAMSLYHRELAPTINYTSPNPN
IKFSGSPFFYVADKRKTLPERETPHRAALSSFGGLGGTNAHAIFEQY

>Bae_KS11

IAIVGISGIFPMAEDIEAYWQNLKEGKDCMTEIPKDRWDWRDYYGDPakeANKTNVNQGGFIDGIAEFDPLFFGIS
PREAEQMDPQQRLLLTyAWKAIEDAGYASKSLSGTKTGvfIGTGNTGYGSLLANADAEIEGSSAANTSPSVGNRV
SYTLNLHGPSEPIDTACSSSLVAIHHAHVSSIEEGTCMALAGGINTIVLPDVYISFDKAGALSKEGRCKTFSDQAD
GFAHGEGAGLFFLKKLKAAEADGDHIYGVIKGSavNHGGRASLTTPNPKQQAevIKAAYKKAGIDPKTVSYIEAH
GTGTelGDPVEINGLkQAFSSFADGKEKAAGYCGLGsvKTNIGHLSLAAGAAGIikILLQMKHRTLvKSLHCETVN
PYIQLEDSPFFYLVRETMEWKTRTDERGNEQPRRAGISSFGIGGVNAHVVIEEY

>Bae_KS12

IAIVGMSGVFPKAANIDEYWRNLEEGKDCITEVPADRWDWREYYGDPLNEANKTNVKWGGFIDGVADFDPLFFGIS
PLEAEQMDPQQRLLMMYAWKAIEDAGYSAKSLSGTKTGLYIGTGNTGYGSLFSDLDIGGASANMSPSAGPNRVSY
MLNLHGPSEPIDTACSSSLVAIHHAHVCAIENGNCMAIAGGVNTVVTpQGHIAyDKAGALSKEGKCKTFSDRADGF
AVSEGAGILFLKKLSEAekAGDHIYGVIKGSavNHGGRANSLTPNPKQAevVRTAYDKAGIDPRVTYIEAHGT
GTelGDPVEINGLkSAFQKLYEKTGDPavYASHCGLGSAKTNIGHLSLAAGVAGVIKVLQMkHKTlAKSLHSEVI
NPYIKLDSPFFYIVQEKREWTALKDENGHLPRRAGISSFGIGGVNAHVVIEEY

>Bae_KS13

IAIIGISGRYPESETLDELWEHLKAGDSCITEAPENRWKSGLLKTMaketrKEERKTRYGGFLQHIDAFDHHLFDI
REDHVMEMTPELRLSLETVWETfENGgYSLERVTEWQESDSGIGVFMGSMYNQYFWNIPsLEKAALSSNGGDWHIA
NRISHFFNLTGpSMGVTTACSSSLSAIHLACESLKLNSCSMAIAGGVNLTLEPSKYDALERANLLEQGSesKSFGT
GTGLMPGEGVGAVLLKPLSKALADKDHIYGVIKSSALCHSGGRQMYTAPDPKQQAkLMAASIDKAGINPETISYVE
SAANGSVLGDPiEVIALtNAFAQYTDKKRFcALGSVKSnlGHLEAASGMSQLAKVLLQMERETLVPTINAKPQNPn
INLEQTAFYLQEKTEYWERMRAETGDIIPRRSMINSFGAGGAYANLIVEEY

>Bae_KS14

IAIIGMSAQFPQSPDIQSFWEHIVNGDHCITEIPADRWDWRRYAGDENDTSLRWGGFIDGVGEFDPLFFGISPKEA
SQMGPEQFLLLMHTWKAMEDAGLTNKALSSRPTGVFVAAGNSDPNNGTAIPSIIPNRISYALNLQGPSEYEEAACT
STLVALHRAVQSIRHNECEQAVVGAANILQSPKGFIGFDSMgYLSKNGRAKSFQKDADGFVRSEGAGVIIKPLEA
AIEDGDHIHMVIKGTGVSHGGKGMSLHAPNPAGMKAAmKKAYEDTDVDPQTVTYIEAHGIASEMADALEFNAIKAG
YGESANQEEsAPCYISTVKPCIGHGELASGLAALIKVAMAMKHHTIPGIPRFTAANEQMAIQSRFRFTEDNQEWt
QLTDHTGRPIPRAAINSYFGFGGMNAHVVLEQY

>Chi_KS1

IAIIGMSCRFPGADDIDAFWSALCRGESAIRSVPPDRWETAPGGGEEGAAPDRTSASRWGGFLDRVDGFDPLFFGI
SPREAADMDPQQRLTLELCWEAIEDAGVVPATLkESRTGVYFGVLFgDYAALQSRRGIEAVTAYSSGTSHCIVAN
RVSYFLELNGPSMTVETACSSSLVA AHLACQAIRAGECDLALIGGVNLMLAPDAAIGMHKLGVMSPTGRCWTFDAR
ADGYVRGEGGGVLLKPLSRAQRDGDRIYGVIRGSavNNDGFSNGLTAPNPRAQEAVLREACARAGVAPRSVQYVE
AHGTGTelGDPVEAAALGAVYGAGRPAEDGLRIGSVKTNIGHLEAAAGVAGLIKTVLCLHHRTLVPSCNYETPNPH
IDFGALRLGVVTGLAPWPESGEGPPRAGVSSFGYGGTNAHmVLEG

>Chi_KS2

IAVIGMSGVFPASDSVDELWSHLEAGRDVIEVIPRDRWNWEEHWASSEELDKTAVRWGGFMKHVDRFDAAFFGISP
REAALMDPQQRILLEITWKAIEHAGYRPSSLSGSRTGVYVGIGNADYREVMARRLVPAAHLATGALSHAIAPNRI
SYLLNLHGPSEVVDSACSSSLVAVCRAVDALLAGECDTALAGGVNVIVSPTLYISLSKAGMLSPDGRCKTFDKDAD
GYVRSEGAGMLLLKRLSRALEDGDPiHGILRGHAVNHGGRVNTLTTPNPSAQaALVAEAWRRAGVDPATVSYIETH
GTGTKLGDPiEIEALKKAFEALFAQQGAAAPDAPFCALGSIKTNIGHLETAAGIAGLIKILLAMKHKKLPGNLHFR
ELNPYIRLEGSPPFFVLDRTPWDPiEGAPRRAGISSFGFGGVNAHVVVEDF

>Chi_KS3

IAIIGMSGRFPGANGLDAYWQNLAAAGVCSVTEVPRDRWDPAVFYDPDRDVKTYSKWGGFLEDIDSFDASFFNIS
GKEADLSDPQQRLFLQEAFAHALEDAGYADASVSETRCGVFVGADRGEYLSLLRDEGARREGQCVWGNDSVSLASRI
SYFLDLKGPALAVHTACSSSLVAVHLACRALMDGDCDMALAGGIFVNLTADWFIWSSGSMSPAGECRAFDNRAD
GFVPGEGVGVVVLKPLHAALRDGDRILGIIKSGSVNQDGRITNGISAPSTLSQTELEVSVYERSGVSPATVGVEAH
GTGTLGDP IEVEALTRAFRRFTDERQYCAIGSVKTNIGHAATAAGMAGLLKILLAMQHGEIPPSLHFREANEHID
FASSPFFVSTARTAWRP IGGAPRRAAISAFGIGGTNAHLVLEEF

>Chi_KS4

VAVVGMAATFAGAADVDAFWRNLVEGRSSIREIPEPRRSHAGFRDPDPFDASGRRRRRAGFIDDVGGFDPLFFNIS
LEAEFMEPQQRLFLQAAWHALEDAGCSSERLRGRRCGVFVGCSADSGYLHLVEQSSANAYQLMGIATSI LASRLAY
FLDWKGPAAVADTACSSSLTALHMAFRSIREGESELA VVGVAAFSTAVIYDLLGKAGMLSPDRQCKAFDRRADGF
VPGEGVGVVVLKPLEAALADGNPVYGVIKGIGVNDGKTNGITAPSAASQAE LIRRVYTEFRIDPEAIGYVEAHGT
GTKLGDP IECDALTDAFRSFTAKRSYCALGSKVKNIGHTLAAAGIASLIKVLRLCLDRKQLVPSLHVEAINPHIALD
ESPFYISTEHRDWDAPPGRPRMAALSSFGFSGTNVHAVIAE

>Chi_KS5

IAVIGMACNFPGAADLDITYWRNLAAGKSGIAEVPPSRWPVERFY SATLEPGKSTGKWGGFIEGIELFDPEHFGFKP
EDAPSVDP LIRQALQVATQAFRHAGYERRELGGRAIGVFVGGRGVDYGERIHMGTKSVMASTGQNFIAAHISHVFD
LAGPSLLVDTACSSSLVAIHLACHSLLSGEVEMALAGGV D LLLDEKPYLRLESQALSPDGVCRADFDEKASGLVPG
EGAGAVLLKPLAQALADGDRI LAVIEATAVNNDGRTMGITTPNPDAQARVVS AALRRAGISARAITYVETHGTGMT
IGDPIELKALTRVFREDTDARGYCAVGSIKTNIGHLLS AAGMAGFIKVVL SLQNRQIPPTLNCETPNPRFRFADSP
FFPNLRLREWEQGGDLGRHAGISAFGFGGTNAHVIVGE

>Chi_KS6

VAIVGVSGRYPMAPDLDRFWENLEAGRDCITEIPAERWNHSAFFAEGSPGKAYTRWGGFLDDVD RFDPMFFHINPR
DAATLDPQERLFLEIAWQALEDAGYTRAQLGGKRVGVFAGVMWQYQLHGVPPSDLGHP IALSSSFSSIANRVSYF
FDLSGSPMAVDTMCSSSLTAIHLACQSLVSGESELALAGGVNLT LHPNKHFLSLSQGHLASPDGRCRAFGESANGYV
PGEVGAVLLKPLDRAIADGDRIHAVIKAI AINHGGR TSGYTVSPAAQ GALIEDALRQAGWPPRTVTYVEAHGTG
TALGDP IEIAGLSRAFGPAAVEPGRCAIGSVKSNIGHLESAAGIAGLTKVLLQMKHRQVAPSLHAARLNPRALDG
SPFRVAQELAPWRPATDAEGRALPLRAGVSSFGAGGANIHV LLESH

>Chi_KS7

IAVIGASGRYPGAPDLRRLWSNLEKGISSIREIPPDRWDFRPHFDPAEGKGGRSYSRWGGFLDEVRCFDGLLFNIS
PKEAEGMDPQERLFLEVWVSLFEDAGYAH DALLRAAPKTGVFVGMNRDYEWLGGYACARGKLYAHSSFWSIANR
VSYFFNLRGPSMAVDTACSSSLTALHLACESLRAGSCTSAVVGGVNL LLSPIHYARLTLVDMLSRDDCKSFGADA
DGFVVGEGVGAVLLKPLSLALADGDRI LAVLKGS AVNAGGKTGGYTVPNPNAQAE LITRALEEAQIDPATIGYVEA
HGTGTVLGDP IEIAGLSRAFQSGTGAHGRCAVGSVKPNIGHLESAAGIAGLTKVLLQLEHRTLAPSLHAEPNPRI
DWASSPFSLQTRREPWTP IARDGEGTAWPRRASVSSFGAGGANAHVIVEEH

>Chi_KS8

IAIIGASGIFPRSRDLRAF WENLRDGVDLITEVPPERWDFRAYDGDPT EP GKTRSRWGGFIPDHDAFDPRFFNLSP
AEAELMDPQHRLLLQAAWHAIEDAGYRASDLGGQPVGVFAGIQYDDYSRILQQSGAWGAQAATGNNLAMLANRVSF
LLNLHGPSEVVTTACSSSLVAVHRAVHSLRLGESTLALAGGV TLMCSPEGVIGADQLGILSPDGRCKTFDRRADGF
VKGEGVGVVLLKPLERAVLDGDRI LAVIRATAVNHGGRASLTAPNAQAQADLLVDAYARAGVSPETVT LIETHGT
GTELGDVPVEVDGLKLA FRRLAERQGLALPARPYCALGAVKTQIGHLEPAAGIAGLLKLVLSMQHRTLPGNLHLREP
NPYLHLEGSPFYLTETRPWSP LLDHGDVPVRRAGVSSFGFGGTNAHVVLEEYP

>Chi_KS9

IAIALDGRYPQARSPEELWENLRAGRECTREVPADRWDVSAYYDADPRRAAAGRM YCKWGGFLDDIGRFDALFFQ
ISPTEAASLDPSERLFLEIAWSTLERAGYARRRPQSR SVGVFVG VNVGDYHLLALEEQARGRWVFSNP SFSAIANR
VSYFFDFQGPSLAIDTQCSSSLTAIHLACESLLRGECEMALAGGVNLYPHPSRYVNLCQVKALSSTGQTRSF GAGG
DGFVPGEGVGAVLLKPLRQALLDRDPI LAVIKGSALNHAGKTS GFMAPSPAAQADLLERALARANVDPGSVSYIEA
QGMGSTLVDAELA AAFTRVLRRGRRQGPCLLGS IKPNIGHLEGAAGISQLTKVVHQLRSRQIAPSLHADPVNPEVG
FDASLFRIPGALEPWMPVVDGHAEPSTRRACISSFGAGGSGVYLIVEEL

>Chi_KS10

IAIVGQSGRYPGAPDAAALWERLRRGERSIRPAPADRWDPAPLQATGPDKGGIYCSSGGFLDDVDRFDCLLFRMSP
AEARSIDPQERLFLLEAAWACLEAAGTTAERLNAQAGKVGVFVGMWVNDQNEGVVEGFREDHVARAVALHSSIANRV
SHTFDFKGPSVAVDTSCSSAMTALHLACESIQRGECRAAIVGGVNLMTHPYHQGLLCSLGMVSESGFGNALGEDAT
GWIPGEGVGAVLIRPADDAERSGDHIHALIKATAINHTGATPRYGMPSAEQAASIRDVLRRLAGLGEAVSYVEAA
ATGAATADASEIAALIEVFGERQGSAPRVALGSIKPNIGHLESASAMSQLAKVLLQIQHKTLPAPHLVLSGALNPMIP
WDRAPFWVPEQPAAWQPRSGPRRALVNAFGATGSLGHAVIEEY

>Chi_KS11

IAIIGVAGRYPGADDLREFWQNLREGKDCITEIPADRWDAAWYDPDRSKLGRIHNKWGGFLRGIDLFDPMFFRIS
PREAEFMDPQERLFLLEVAWSTFEDAGYTRELLQRRHGGCVGVFAGVMYSEYPFYGVEATLRGRPVAVGLGYGSIAN
RVSFVMDLNGPSLSVDTLCSSTLCLHLAVESLRRGECAMALAGGVNLSLHPNKYLQHSLFKMTAPDGRCSRFGEG
GDGFTPGEGVGCVLLKPLSHALRDGDP IHGVIRGVAVNHGGRSSGYTVP SAKAQAAVKA AVARAGIPARSIGYIE
AHGTGTPLGDP IELEGLNQAFQGA AEPGFSCP IGSLKSNMGHLEAAAGVAGLTKVLLQMKHGELAPSLHAEALNPN
IDWTATPFFVQRRPAPWERATVEVDGRSQVLP RRAGISSFGAGGANAHVIVEEAP

>Chi_KS12

IAVIGLACRFPGAPSPA AFWENLAAGVCSIREVPLSRWDWRRLYSPALQEGKSISRWGGFVDDIEGFDPGYFNLPE
SDAVMLDPLVRLFLLEAGVTAFLDAGYDRKALGGRKVGVFVGARSANFAERSRHASKASIVSGGQNFIAAHLSHALN
LKGPSLVVDTACSSALVGISLACQSLASDACEMAVAGGVVDVLLDEKPYLVLSAGRALSPDGKCHVFDEKANGFVPG
EGAGAVILKRLDRALADGDRIEAVIEGIAVNNDGRTMGISTPNPEAQSAVIEEALSRAGAAAETLGYVEAHGTGTL
IGDPIELRGLTQVFRRSTEERGFCVGVSVKTNIGHLLSAAGIASFIKVVLLALRHRQIPPTLHCETPNPRFAFADSP
FYPATRLAPWRPRRGVRRAGISSFGFGGTNAHAIVAEL

>Chi_KS13

IAIVGLAGFY PQSEDLHAFWRHLAEAHDLVIEIPGERWDYRSHFDPEERRQGTSPCKWGSFLERFDQFDPLFFNIS
PREAEILD P QERLFLQAAHYAIEDAGHGGDRLAAERVAVFAGVMWQYQLFSAGVGPGQPGPTLGSLYASVANRVS
YFFNFAGPSVSLDTMCSSSLTAIHLACQAIRAGDCTAAIAGGVNLSLHPNKYTFLSQGNLLSDEGRCTRFGEGGTG
YVPGEGVGAVVLKPLARAVADEDWIYAVIKGTAVNHGGRASGFTVPSPKAQGDCIEEALRKAGVAARSISYIEAHG
TGTALGDP IEIAGLSRAYRKGTADRQYCAIGSAKSNLGHLEAAAAIAGVTKVLLQMHYRQLAPSLHADPPNPNIDF
EGSPFRVQARLAPWQRPVLEEKGARRTVPRRAGVSSFGAGGSNAHVILEEH

>Chi_KS14

IAVIGLSGRFPGSPDLDAFWDNLAAGRDCITEVPKDRWDPDRIGGSAAQFRWGGFLDDIDKFDPLFFKISGREAE
SDPQQRLFLLEEA WKALEGAGYTPEALDRARCGVYAGALDGN YQAFMSPKDLDEPQTLWANDTSVIAARIAYFLNLK
GPAITINGACSSSLIAIHMACQALWSGEVDLMLAGGVCLMTSHHFHEVAGKAGMLSPSGRCRTFDDGADGFVPGEG
VGVVLLKRLDDALRDGDP IRAVIAGSGVNQDGRNTGITAP SALSQAELEARIYRDFDVHPESITLVEAHGTGTRLG
DPIEVNALTDAFRTLTSKTYCAIGSVKTNIGHTALASGVAGFIKAVLAMERGQIPPSLHFRGANEHIDFANSPPF
VNTELRPWRPSGPRRAA ISSFGMSGTNAHVILEEP

>Chi_KS15

IAVIGLSGRYPRSP TLEVFWDNLNRHGRSCIDEIPRDRWRWEDHYDPDPGVGGKHYTRWGGFIEDVDKFDPLFFRV
AKDAENMDPQERLFLLET SWACLEDGGYTTESLARHAFKVGVFVGMNCNYEWLSAASCARGRMTGAQSAYWSIANR
VSFFLNLQGPSLAVDTACSASMTAIHLACESLRRGECEAAVAGGVNLI LHPMHYLR LTHMRMLSPDEKCKSFGAGA
NGFVDGEGVGAVLLKPLVRALTDGDRIYGVIKGSSINAGGRNTGYTVPNPNAQADLILAALASTGIDPRTIGYVEA
HGTGTSLGDP IEIAGLTSAYRRYTDGNGYCAIGSVKSNIGHLEAAAGIAGLTKVLLQLQNKQLVPSLHSERLNEKI
GFADSPFYVQRELSPWPEG TSLGAGDPPLRRAGVSSFGAGGANAHVILEEF

>Chi_KS16

IAVIGVACHFPQSPDKETFWRNLESGADLISEVPPSRWDSERYDATRSPGRTISKWGGFIDGIELFDPEYFRMTP
ESAPFVDPLIRKALEVGVTC LRDAGYEQREL AGQQVGVMGARTANFTDKITMPAKNGIPGVAQN FVAALLAHFLD
LKGPNLVVDTACSSSLVGIHLACQSLLCGESTMALAGGV DILLDEKPFVSLSEAGALSPDGRC HVFDERANGFVPG
EGCGAVLLKALDRALADGDRIYAVIEGSAVNNDGRTMGVTTPNPD AQGQVIEQALARAGAGADTVSYVEAHGTGTM
IGDPIELRALTRVFRKSSQDRGFCVGVSVKSNMGHLLSAAGIASFIKVVLSLWHRIPPTLHCSAPNPRFEFASSP
FYPNTALQDWLPRSGVRRAGISSFGFGGTNAHVIVGEL

>Chi_KS17

IAVIGVSGRYPMADDLDAFWENLAAGRDCITEVPADRFPVDAYYDPEVGKLGKTYTRWGGFLSDVDRFDPLVFNIA
PREAELMDPQERLFLQTAWATLENAGYARGALAKRRVGVFAGVMWGQYQLLGAERAGRSTVLPASIFASIANRVSY
CFDWRGPSLAVDTMCSSSLTAIHLACESIRRGECMALAGGVNVTVHPMKYLYLSQGRMVSTDGRCRGFGQGGDGY
VPGEGVGAVLLKPLSRALEDGDHIAVIKGTAINHGGRSSGYTVPNPEAHGALIRDALSAAGFEPESVSUYVEAHGT
GTSLGDP IEMTGLAAAFPGLPARSRALGTVKSNIGHLEAAAGIAALTKVLLQLEHRQLAPSLHADPPNPNIIDFDAS
PFHVQRELAAWQPPEVPGQQGRARYPRRAGISSFGAGGNVHVHLLLEEH

>Chi_KS18

AIIGIGGRYPEAADVREFWENLKAGRSCIGEVPPHRWDGDAYYRPDGGGASRSKWGGFLEDVDRFDPLLFNISP
AERLDPQLRLFLQTAWETFEDAGYPRRRLRVVQQGATSGVGVFVGS MYQHYPFVAPDGATAAQLSSFPGSAIANRV
SHYFDLKGPSMLVDTACSSSLTAIYMACE SLARGE CAMALAGGVNLSLHPQKYVIFSQMGLLGSKERSSSLGEGDG
ITVGEVGALLKPLALALRDGDRVYAVIKGGFVNHHGGRTHGATVPNP SAQADLIVEAFRRAGVRPDVSYIEVAA
NGSPLGDSIEIAGLKQAFRRFTVERGFCALGSVKSSIGHLEAAASGVSVQTKVAYQLHHRTLVP TLNSEPLNPNI
DDSPFYVQRE RAPWRPAVEGEPLRAAVASFGAGGANAYLILESF

>Dif_KS1

IAVIGMSGMFPKAENQHDFWNNLMENKDCVSEIPEDRWDSSYYSEEKTA EYASYSKWGGFIDHPDQFDPLFFSVSP
WEADLMDPQQKLYVTCCWEAMEDAGYGNPAARPTDQIGVFAGVTWNEYSLIAHEEGFLKDQYKGP GSYWGIPNRV
SYFLDLHGPSIAVDTACSSSLVAVHQACQAIMSGDCMALAGGVNLSLHPQKYMFLSQSHFLSSEGKCRSFGE GGD
GYVPGEGAGAVLLKPLKKA IADKDHIYGVIKGSATNHGGKTTGYTVPNPEAHRDLILSALNRAAVSPADISYIEAH
GTGTALGDP I EIRGLSMAFDKQTEKNYCGIGSVKSNIGHLEAAAGIAGLIKVLLSMKYETLPASLHSEELNRKIS
FSDSPFYVVRNNRPWPAEGDKPRIAAISSFGAGGSNAHLIVGA

>Dif_KS2

IAVIGLSGRYPGADHVDELWENVKAGRHSITEVPKDRWDWKTIFYNEERGKWGS IYSKWGGFLEDIDKFDPLFFRIS
PAEAERMDPQERVFLQTA YSSIEDAGYTPATLCDSRKIGVFVGV MNSNYPTVPSDWSIANRVSF LNFQGPSMAVD
TACSSSLTAVHLAAESLRSGMSETAIAGGVNLIVDPAHYERLSAFSMLSPGEKCKSF GDSADGFVDGEGVGAIVLK
PLAQAEKGDGDIYGVIKGSMLNAAGR TNAYMVPNPKAQFDLIAETLKRTDIHPRTVSYLEAHGTGTALGDP I EIDG
LTKAFRLTTEDRQFC SIGSIKSNIGHLESAAGIAGITKLLQLKHKRIAPSLHAAELNPNI EFEHTPFVQQKETE
WKR PVLNITGEMKEYPRIAGISSFGAGGSNAHVIIQ EY

>Dif_KS3

VAIIGISCAFPMAENPEMFWENLAGEKDCISEIPPERWDWRQYYGDPQKDKNASNVKWGGFIDETAQFDPLFFGIS
PHEAEMMDPQQRLLMHVWKAIEDAGCSAKSLSGTNTGIFAGTTNSGYAQEASKFHIEIEGSSAAGTVPSIGPNRM
SYFLNIHG PSEPIETACSSSLVAVHRAVRAIQAGDCGIAIAGGVNAIVSPDMHISFNKAGMLSEDGRCKTFSDQAD
GYVRAEGAGMIVLKTLSDAERDGDRIYAVIRGTAENHGGRAASLTSPNPKAQTEVMIKAYQQANIDPRTVSYIEAH
GTGTALGDP I EINGLKAFAALYQKAGVTAPDQPHCGIGSVKTNIGHTELAAGMAGLLKIILQM QHKT LVKSLHCE
TVNSYISLDGSPFYFVRDTPQWKAATDDSGNELPRRAGVSSFGFGGVNAHVVLEEY

>Dif_KS4

IAIIGVSGRYPQAETLEEYWDNLAAGKDCVTEIPEERWEKDKYYNPDP EAAVKEGKSYSKRGGFLKDAAFFDPLFF
QISPRDALNMDPQERLFIEMCWQVLEDAGYTKEQLENLYNGRVGVFAGITKNGYGMWKNGGTLQPKTSFSSAANR
VSYFLNLKGPSMPVDTMCSSSLTAIHEACENILRGECDMAIAGGVNVYTHPSAYAE LSAYRMLSKDGTCKSFGE GGD
DGFVPGEGVGAVLLKPLSKAMADKDHIYGVIRGTHINHGGRTNGYTVPSPSAQADVISGALEKSGIHPRMISCIEA
HGTGTALGDP I EIDGLTRAFQTKTSDKGFC AISSVKS NIGHLEAAAGIAGVT KLLLQLQKRKLAPSLHCRKLNPNI
VFDRTPFV VQRELADWKRPVIEENGAQKEIPRIAGISSFGAGGANAHILIEEY

>Dif_KS5

IAVVGMSCRFPGAESIEAYWKLLSEGTS AIQRVPKERWKTEKADYAGLLQNVTHFDPEFFLIPEEDIKAMDIQSFL
ILEEALHLFRDSGYSLQEMKGRSAGVYLGGRGGSMPDENRLKHAKNP IVAAGPNYLAANLSQFFDLKGPSLVLDTA
CSSALVGMNMAIQALSCGEIDS AVVGGVSLLESQQTHRMFELRNLLSEEP AFHIFDRRTGGIVLGEGVGMVYLKTA
AQAVKGDGRIHIAVIKGISVNNDGRTAGPATPN IQAQKEVMAKALAKSGRKAEDISYIEANGSGSEVTDLLELRAIE
AVYRMQNSAPCELGSMKPNIGHPLCAEGIAGFIKTVLMLSRMRVPFLSGKEPMTHYDLSASPFYF SHALREWTD S
PRIAAVSSFADGGTNAHVIVEA

>Dif_KS6

IAIVGMAGRYPGAKNLREFWTNLKNGENSVTEVPRSRWDTRTYEHLRSPSGKPI SKWGGFIDDPDCFDAKFFRISP
REAEAKDPQERLFLETWCWETIEDAGYTPETIVQPKGNKRMNVGVFAGVMHMDYSLAGAEAAAKGLVFPYPLNYAP
IANRVSYFCNFHGPSMAVDTVCSSSLTAVHMAAESLRRGECEAALAGGVNLSLHPTKYITYGLMDMHSSDGLCRTF
GEGGTGYVSADGIGAVLLKPLHKA EEDKDHIYAVIKGS AVNHVGT VSGITVPSPVAQGD MIAE CLEKTGIDPRTIS
YVEAHGTGTS LGDPIEIQGLVKAYRTFTEDRQFCAIGSVKSNIGHAES AAGISGLHKT V LQLFHKT L VPSLHSETI
NPYLRL EDS PFYVQQKTESWKRPAYTENGREHACPRRAGISSFGATGSNVHLILEEY

>Dif_KS7

VAIVGLAGRYPGAENVNEFWERLKTGEHGITEIPKDRWDWRDYYDETKGKEGRMYTKWGGFLTDIDKFDPLFFKIS
PKEAERMDPQERLFLETAYAALEDAGYTPDSL CAGKKVGVFAGVMNGNYPTGAHYHFIPNRVSYVDFHGPSIAVD
TACSSSLTAIHLAAESIRTGASECAIAGGVNLTDPVHYIGLSSMRMLSPSNACKAFGDKADGFVDGEGVGCIVLK
PLKKA VEDHDHIYGVIKGSALNAGGKTNGFTVPNPNAQGEVIADAMERAGIDPRAISYLEAHGTGTS LGDPIE IAG
LTKAFFRYTDANQFCSIGSVKSNIGHLESAAGIAAVTKILLQMKHGYLVPSLH SKQLNPEIDFETSPFIVQQETAE
WRRPVIESEGV TREY PRIA GTSSFGAGGANAHLLIEEY

>Dif_KS8

IAIIGMSGRFPQARTADELWDILFQEKDVVAPVAKKGFTSSKWKLGAVPGADEFDPLFFEISPREAETMDPKQRLL
LQEA WRALEDAGYGASHIRQQTIGMFVGAEEGDYHLLTRDKGNVTSHHNGILAA RLAYHLNLSGPVMAINTACSSG
LVS VHQAVLSLQNECTTAVAAGVNIMNTPDFFETIDKAGMLSENGKCFADF KRADGMVPG EAAA AV LKPLREAE
KGDPIYGVIRASGINYD GKTNGITAPSGVAQTRLLTSVYDRGRINPEDIEYIVTHGTGTKLGD PVEINALYDAFS
AYTNEEAFCALTSIKTNIGHTFAASGIVSLISLLQAFSREMIPASLHCSGENRYINWEKSPFYVNKTGKPWPSLPG
KNRMGAVSAFGMSGTNAHVVMESY

>Dif_KS9

IAIIGISGIFPQAKDIDEFWTRLQKGEHCITEIPRDRWDWREYYGDPAADANKTSIKWGGFIDGIAEFDPLFFGIS
PKEAEMMDPQQRLLMMYVWKAIEDAGYS AKRIAGTKTGIFTGTLGSGYQTLINKAGLPVEGYTMTGIVPSVGP NRM
SYFLDIHG PSEP VETACSSSLVAIHRAVKAIETGDCDMAVAGGVNTIVTPEGHIGFQKAGMLSE DGRCKTFSDQAD
GYVRGEGAGMIVLKKLSEAERDRDHIYGLIRGTAENHGGRSASLTAPNPQAQTDVLKSAYQKAGIHPSTITYIEAH
GTGTALGDPIEINALKKAFTD GAPGGYCGIGSVKTNIGHLELAAGIAGVIKVLMLQKHRTLAKSLHCENINPHIK
LKDSPFIYIVTETKEWEALCDENGRVLP RRAGVSSFGFGGVNAHIVIEEY

>Dif_KS10

VAIIGMACHFPKAGDIKEFWKNLRSGTDAVTEVPPDRWNAGEHYQPGEYQEGKSISKWGGFIHDIDQFDPEYFNIS
ETLAPMIDPLQRQWLEVSAEALADAGYQKEDLWGRRIGVFAGARAGAFHHKFQYLKKDAIIGAGQNFITAHMAHIY
NFTGPNLVVDTACSSSLTAIHLAVQAIQNGEAEAAFAGGVDILLDEKPFLTMSAARILSPNGRSKSF DADADGTGI
GEGCGVLM LKPLEKAIEDEDKIYGVIDGSAINNDGSTMGVTPNPRAQQDLIEQAVQSAEIEPDTMTYVETHGTGT
LIGDPIELKGLTNVLSAYSDEKQFCGVGSVKSNIGHLLSAAGAAGI IKVLLAIANEELPPTLHCHKPNPRFQFNDS
PLYPVLELKRWDGKKEILRAGVSAFGLGGNNAHIIVS

>Dif_KS11

IAVIGLAGRYPQAGSIDEFYQNLRS GKDCITTMPKDRWKGYPFPSY EADQFYRYGGFLDRIDSFDPLFFNLTPRQAE
MMDPQARLFLETAW EACEDAGFYQDR TARGPSSQKRKR VGVFAGVFW SHYELFGAEITQRGTPLSMGVTPASVPNI
VSHCLNFTGPSMAVD TMCSSSLTSIHLACESIKRGECEFAIAGGVNAVTHPHKYAFLANAGFLSSEGVCKSFADGG
DGYVPGEGVGAVLLTTVQEAERMGCPIYGVIKGSALNHVGKTSGLTVDPASQAEVITDSFQSAGIDPETLSYIEA
HGTGTS LGDPIEIEGLSRAFRKWTNKKRFCAIGSAKSNIGHLEGAAGIAGLTKVLLQLKHGEIFPSLHADTLNPHI
FPDP TPFYVADRLEEWERP SHPDQPRRAGLSSFGASGSNAHFVIEEY

>Dif_KS12

IAVVGMSCRFPGAGGTDAFWELLMKGNTAIRPVPATRW HATANAKDYAGWIDDIDMFDAGFFGISEKDAAIMDPQA
RIILEEAVHSVYDAGYGQKDL SGRKVGVIYIGGRAQPSAGMEHILQAPNPILGAGQNYLAANISRFLNVTGPSLVVD
TACSSGLIGLSFAKDALLAGRIDAAALVGSVSLLLSPSAHRLFGARHILNENGVFHIFDRESAGEVLGEGAGAVFIK
RLSDAVRDGDRIYGVIKAVSVNNDGRTLGP GSPNIRAQRDAIQ TALDMAEKSPEDIGYIEVNGGGSPIVDSVEIKA
LSDVYQLNRKTTLLPCRIGSVKPNVGHLLSSGLAGFIRCVLSVYHKRIPPFLSAREPF EHYDFEASRIHFNREPVD
WHSEKKPRVAAQSSFPDGGTNAHILVEEY

>Dif_KS13

IAIVGISGKYPQADDINAFWENLKQKDCITEIPKDRWKWEHYFSEDRTAPGAIYSKWGGFIDGIADFDPPEFFKIS
PREAEHLDPQERLFLMHAWMAMEDAGYTRTSPQLGRQVGVYAGVMYQEYPLFAAEAGVKGRHIGLPGGISSIANRV
SYFCDFQGPSISVDTMCSGSLTSLYMACRDLRDHRIIRAALAGGVNLTVHPNKYFMLSQGGFISSEKGCSSFGAGGD
GYIPAEGVGVLLKRLDAVQDGDRIYGVKIGAAINHGGRASGYTVPNPKAQSEVISQALQEAGVSPGQISYVEAH
GTGTLGDPIEIRALTDAFGDVPETCLIGSVKSNIGHGESAAAGIAAVTKVLLQMKHKQIAPSLHADVLNPNIQFDE
GPFVSCRELTDWKRIAADGAEQPLRAGISSFGAGGSNAHIIIEEY

>Dif_KS14

IAIIGMSGRFAESENLEHFWHEHLAAGRDLIKKADRWDVSDSQCYGSFIEDIECFDPVFFHISGREATYMDPQQRL
FLEESWKALEDAGYAGDSVRGRECGVYAGSCGGDYQAIQKQGPAPAFWGNHNSVTPARIAYHLNLQGPATVDTA
CSSSLTAIHLACQGLWTKETEMAVAGGVFIQSTPAFYQSSNKANMLSPTGRCHTFDQSDAGFVPGEGVAVVLKRL
SDAVSDGDHVGVIKGSAMNQDGATNGITAPSALSQERLERHVDYTFHIDPETIQMVEAHGTGTALGDPIEFGALT
RAFRRYTDDKKGCAIGSVKTNLGHAAAAAGMAGLFKILLSLKHRQIPASLHFHQANQHIQFADSPFFVNEKLIPWE
RNPDAARRAAISSFGSGTNAHLVIEEAP

>Dis_KS1

IAIIGVACRFPGSPDYGRYWQLLERGEHAILEIPPGRWDPRAHYSPDFNKPCKSISKWCGLIDDIASFDHRFFNVS
EREAKSMDPQQRLLEEAWRCEIDSGVPLEQLRARKTSIYVGFMATDYHQESAAPGRPVDSYAALGSYGSILANRV
SYTLGLRGASIAIDAACASSLVALHEARRALQRGESEFALAAGVSLNFHPWKYVSFSKSRMLSPDGLCKTFDADAN
GYVPGDGVGVLLHPLAKAIAAGCHVYGVVAGSAVNHTGTARSITAPRVAAQRDVILEAYEDAGWNPETVTVYEAH
GTGTSGLDPIEVEALTQAFRRYTARQRCAGSVKSNIGHLEAAAAGVAGVIKVLMLLKHVRIPRTLHVQTLNPLIR
FEETPFVVATRAMEWRAEGGEPLRAGVSSFGFGGANAHVLISE

>Dis_KS2

IAIIGMSARFPKSPDLDAFWQNLLSGRDCVDEIPAERWDHRRYFAEAAQPHKTYGRWGGFIEDVDRFDPMPFFNIS
REAEQMDPQQRLFLECAWATMEHAGYGDPRAYGDRAVGLFVGVMWNEYSRIGSQTTLQTARYAGPGSLYWAIANRV
SYWMNLTGPSLAIDTACSSSLVAVHQACMSIRNGECDMAMAGGINLSIHPDKYLYLAQSKFLSLDGRCSRFGQGGT
GYVPGEGVGAVLLKPLEQALRDGDHVGIVIRGSAINHGGRATGFTVPDPEAQARLVFDALRRARVSPDQLSYIECH
GTGTALGDPIEIALTDAFAAFTDKKGFVPGSVKTGIGHTLAASGAASLIKVLCLQHRTLVP SLHYDRPNRHIHFE
FEEVPFEVVNETRSWQGDGGAPRFAGVSSFGAGGSNAHVILESY

>Dis_KS3

IAVVGMSCLPGAETVADFWRNLCEGHNAIREIPPDRWSLDGFYDPDPSVAARSYSKWGGFLDNIGDFDPLFFGIS
PLEAELTDPQQRLFLQEAWKAFEDAGYSAEALSGQRCCVFGCKDGDYVYKLGPSADASYRLIGNTSLILAARISY
FLNLKGPSVPVDTACSSSLMAIHLACQSLISGSSDLAVAGGVALMTTPVSHIMLSKTGMLSPGTGSCRTFDDSDAGL
VPAEGVAAVILKPLDAALDRNHIYGVIRGSEANQDGKSNGITAPSTPSQAALVEVEYRKFGVHPETIGYVETHGT
GTLKGDPIEIHALTDAAFTDKKGFVPGSVKTGIGHTLAASGAASLIKVLCLQHRTLVP SLHYDRPNRHIHFE
NSPFYVNTARRHWAHAGDLPRRAAISSFGMSGTNVHLIVEEAP

>Dis_KS4

IAIIGIGGALPKSSDLAFAWQHLVDGRSLVSELPADRWDWRAYDNGDANRKGRLRWGSFYEDMDKFDPMFFGLSPRE
AELMDPQHRVFLETVWKAIEDAGYRPSDLARSNTGVFVGASSLDYLELMNGHRTEAYALTGTPHSILANRISFLLN
LHGPSEPINTACSSALIAVHRAAETLRSGACDLAIAGGVNAILSPATALAIKAGMLSPDGKCKTFDRSANGYVRG
EGAGALLKPLRRALADGDHVAAILRGSANHGGRANSLTAPNPRAQADLI IAAFRAAGVDPATVGYIETHGTGTA
LGDPIEINGLKTAFEQIYKDHGRPPPQAPHCGLSVKTNVGHLEAAAGIPSLFKVLLAMKHKRLPGTLHLHDLNPY
IELEGSPFYIVTRTEDWKPALDADGRPLPLRAGISSFGVGGSNAHLVLEEY

>Dis_KS5

IAVIGYGGFRFPKADDPEAFWRILKEGIDCITEIPRERWDWRAYHDDVPGTPGKIYCKWGGFINDFDRFDPLFFRLS
PRAAHSMQPQERLFLTVAWETLEHAGYTLDRNLNRGSDGPPGGAGRRNRVGVFAGVMWSDYGKHGQDELHKGNPVIA
SADYSSIANRVSYALNLHGPSIASDTACSSSLVAIHLACESLRRGECHYAIAGGVSLSLHPAKYLQMSNLKALSAE
GKCRSFGAGGAGYVPGEGAGALLKPLRQAIADGDYIHAVIRGTAVNHDGKTNGYTVPNPNAQADVISOALRQAGV
DARTISYVEAHGTGTALGDPIEVTGLSKSYRTDTKDRQFCALGSAKSNVGHLEGAAGVAGVIKVLQMKHKQIAPS
LHSRELNPSIDFASSPFKVPQELSAWERPRLARPDGAGEIPRRAGVSSFGAGGTNAHVILEEF

>Dis_KS6

IAIIGMSGRYPMAPDLDAFWANLKAGRDCVVEEIPAERWDHRRYFDPEPGKEGKSYCAWGGFIEDVDKFDPLFFQIS
PKQVATMDPQERLFLLETAWATLEHGGYGRVQEDAARIGVFAGVMWDDYGLLGLEQAALGNHVPAGSDHASIANRIS
FVMNLRGPSLTVSTACSSSLAVHLAVESLRRGECAMAIAGGVNLSIHP SKYTRLCQLQMLAPDGRCSRFGAGGKG
YVPGEGVGAVLLKPLSRAEADGDTIYAVIKGSAVNHGGKTHGYTVPSPKAQADVIGRALERAGVHARTISYVEAHG
TGTALGDPIEVGGLEESFRDRTGDRQYCALGSVKSNIHGLESAAGIAALTKVALQLHHRQIVPSLHAEVLNPNIH
ESTPFYVQRTLDARWQPEVREGGVTEVHPRRAGISSFGAGGTNVHVMVVEEY

>Dis_KS7

IAIVGLSGRYPMAPDLDAFWENLAAGRDCVVEIPADRWDHGRYFDPNPGAAGKSYSKWGGFLDDVDRFDPLFFNIA
PREAEAMDPQERVFLVAVWAHLEDAGYARSP LANRATGVFVGMVYGHYQLFGAEALALDRPVSAAGSSFASIANRVS
YFFDFRGPSVALDTMCSSSLTAIHLACAALQRGEIEMALAGGVNLSLHPQKYILLSRGKFMATDGRCSRFGEGGDG
YVPGEGAGAVVLKRLDRAIADGDRIHGVVKASALNHGGKTSGYTVPNPSAQADVAAAALAQSGVDPRTITYVEAHG
TGTSLGDPIEIALGLTRAFEA SPKERPTCAIGSVKSNVGHLESAAGVAGLTKVLLQMAHEQLVPSIHADPPNPNINF
AESPFVRVQRELGPWRAPVDERGQRLPLRAGLSSFGAGGANAHVLVEAY

>Dis_KS8

IAIIGVSGRYPQAEDLRALWARLQAGESCIEEIPAERWDKDRYFDPQKGRSGKSESKWGGFLRDVDQFDPLLFNIP
PARARIMDPMQRLFLESVYETLEDAGYTRAMLSKDGGKVG VYVGAIYHHYAMLAADSTRSLLLSAFGAHIANHVS
HFFDLHGPCMAVDTT CASSLTAIHLACEGLLLGRD LAIAGGVNLSLIPEKYLGLSQLQFMSSGALS RPF GDS DGM
IPGEGVGAVLLKPLDRAVRDRDHIHAIIRSSAVSHGGASTGFTAPNLKAQSDMFVEAIERAGIDPRTISYVEAAAN
GAPLGDPIEVNALTRAFFRFTADTGFCALGTVKSNIGHLEGASGVSQ LAKVLLQLRHGALAPTINAEPRNPNLHLD
DTPFYLQERLDDWRRPIISGREVPRRAMINSFGAGGGYATLVVEEH

>Dis_KS9

IAVIGLAGRYPGADTPRQLWRALRSGQSAVTRPPAGRF GASAPQGD EPRGGGASPGWGGYLERLDRFDSLFFGISP
AEAKLMDPQERLFLIEVAWECLEDAGYTPEELRRAAPRVGVFVGAMWSDYQSVGLEAWQRDRRAKAVAFHSSIANRI
SYLFDLHGSPVAIDTSCSSGLTALHLASRSLR LGEC DVALVGGVNLLGHPFHPDLLEGLNLTSRDDKTRAFGAGGS
GWVPGEGVGAVLLRRLPEAEERGEHIRCVLKG TALAHAGKAPRYGMPSTRAQAGSIRDALADGGVAASEIDYVECA
ATGSGIADASEVDALKQAFEGRSPDGPCLLGSVKPNIGHLESASALSQ LTKVILQLEHGEIAPTLHTEPRNPLIQ
LDGTPFRINRALSPWPRAAGADAPRRALINAFGATGSSAHAVVEEY

>Dis_KS10

IAIVGLSGRYPGADTIDAFWSNLRQGRDSVTEVPADRWDAAAIFDPEGPGKTRQRWGGFLDRVDRFDALLFNISP
REAAGMDPQERLFLIEIAWCAFEDAVYTRERLAE EQARAGVGAGVFVGS MYQQYSMLARTPDAGASSSFWSIANRVS
YFFDLRGPSLAVDTACASSLTALHLACESLRRGECCLALAGGVNLLHLP HKYVALDRLGLLGSGAASKSLGDGDGY
VPGEAVGAVVLKPLDRAVADNDRIYGVIKGSFANHAGKTAGYGVPS PAAQADLIAALRRTGIDPETIGYIEVAAN
GSSLGDAIELAGLTQAFRRFTARKHFC AVGSVKSNIGHPEAASGIAQLTKVLGQLHHRTLVP TLHAEPHNPNIDLR
DSPFYVQRELGPWTAPTLAGEGGTAELPRRAA ISSFGAGGANTHLLVEEY

>Ery_KS4

EPIAIVGIGCRFPGGIGSPEQLWRVLAEGANLTTGFPADR GWDIGRLYHPDPDNPGTSYVDKGGFLTDAADFDPGF
FGITPREALAMPQQRLMLETAWEAVERAGIDPDALRGTD TG VFVGMNGQSYMQLLAGEAERVDGYQGLGNSASVL
SGRIAYTFGWEGPALTVDTACSSSLVGIHLAMQALRRGEC SLALAGGVTVMSDPYTFVDFSTQRGLASDGRCKAFS
ARADGFALSEGVAALVLEPLSRARANGHQVLAVLRGS AVNQDGASNGLAAPNGPSQERVIRQALAASGVPAADVDV
VEAHGTGTALGDPIEAGAL IATY GQDRDRPLRLGSVKTNIGHTQAAAGAAGVIKVV LAMRHGMLPRSLHADELSPH
IDWESGAVEVLR EEPWPAGERPRRAGVSSFGVSGTNAHVIVEEAP

>Lkc_KS1

AIVGLSAVLPGGPDPAFWQTLDDGRDCVTPAPAGRGLPGEFAGFLPGVVRGFDARFFSISPREASWMDPRQRLLLQ
SAWHTLEDAGYAPSDLSGSRTGCYIAATGNDYALLQARADARQIPYSLVGHSLSLIANRVSSWFDWHGPSAVLDTA
CSGSLVALVRACRDLRAGVCDAAALVGGVNLIILDSQINEGLHAARFLSPEHRCATFDAAADGYVRGEGYGTFLVKRL
ADALADGDDIRAVVESVAENHGGGRANSLTAPNPNAQYRLLLDAYTPELAARTGYIETHGTGTALGDAIEIDALKRA
WRHLVPRSAGGRVRLGAVKSHIGHLEPAAGVASLTKVVKAFEHRTL PANLHFQDPNPGIALEEGPF EAVRKTVPWG
EDGGELVAGISSFGFGGSNAHVVL SA

>Lkc_KS2

IADVGVIAARLPQASDVRQFWDNLLDGLDCTSTVPPERFATRLTDGAAPLSYTDRGAFVDDIDAFDHTFFGLTPHDA
ARMDPQERLVLEQTYLAMLDAGYSRRLAGSDTGVFVGMNGGYAWHTTTEPGAQPPTSAFWSMANRASYHFDWHG
PSMAVDTACSASLTALHLACQSLRTGECDRVVSGVNLITHPRQYQLLCGLEMLSRAGECRPFSGADGFVDGEGV
ISLMLRPAEDALRDGDRVYAVISGSASVNAAGGRANGYTAPNPEAQSAVAKALAAARTSPEEVGYVEAHGTGTALGD
PIELRSLAKAYAAAGTGRIRLGSVKSNIGHLESAAGLSGVLKAVLQMRHGSLVPSLHAEPNPHLDFDATPFTLAA
RTERWPADLPLVSAVSSYGAGGANAHVVLR

>Lkc_KS3

IAVIGMAGEFFGGADTEAFWQALLRGDDAVRVIPGDRWDWRENHSFAPDEPGTAYGRHGGFLDHALDFDPVFFNIA
PLEARFMDPQERRFLQSVYHALEDAGYFARPTGDMGVFVAAMFGHYQDLTAADRVISSFAAIANRVSYAFDLHGP
SIALDTMCSGGLTALHLAVRSIRAGDCALAVAGGVNLMTHPGKYRLLSEGRFLSPTGHQCQAFGVEADGYVPGEETA
AVVLKPLSDALRDGDRVHAVIRATAVNSGGRTAGFTVPSERAQHRVIAAALAEAEIEPGAVTYVEAHGTGTRLGDP
IEVRALSRAYGGPEQGRAYLGSVKSNIGHLESAAMAGLVKVVKQLAHRTLAPTTLHCTLENPDHLADSRFALVKE
TLPWPKSGSPTRFAGLSSFGAGGANHAIVQEF

>Lkc_KS4

AVVGMSGIMPAGENLADFWRLLVENGSAIRPVERWKNRDRQYFAGTIDDHDAFDHSFFGLSAREAMLMDPQHRLFL
QSAYNALLDAGYAPGSLREVGVFAGVQFSEYQ TALQHSEDRAPYTVTGNAHAMLANRVSHLLDFTGPSQTVDTAC
SSGLVALNRGVLSLAAGECDVALVGAVSVLVDPAATDAASELGVLSPDFRCATFDKDANGYVRAEGVGCVVVKRLD
DARRDGAVALVIEAVAENHDGRSNSLTAPNPDAQVALLNRVYTPELAERVSHIEAHGTGTNLGDP IEIGALRTAF
GRLAPHREPGSITLGAVKTNVGHLEPAAGMAGLLKLLLCLRHRRRLPANINFKELNPLVELVGSPFRLLLENEPWER
GTPLVAGVSSFGFGGSNAHAVLSEAP

>Lkc_KS5

VVGMACRFAGSDGLGEYWERLRLGRSALGTTGRWTEEDAGSFTGGFLDGHQEFDARFFRISPNEAQCMDPQQRIIL
LQTVQHAVDDGYLTAADLRDLDCGVFAAGLPDYRTLVARRADLVYGTHSFLGNAPSTLSGRISYFYDVNGPSLTL
DSACSSSLAALHEAALNIRAGQCRAAIVGAVSVFSTPEVLRFAQRSRMSSPEGASLPFTDAADGFVPAEGAAALVV
MRHDEARARGRLRVYGAVQATGTNHNGTTNGLMAPSSKAQSRLIAELYDREKIDASQIAYLETHGTGTPLGDP IELE
GLRSAFRRAGADGCHLGAVKPLIGHTLVASGLASVVKALLAFRHATIPPVAAAGEAVSYLDVAPFKVNREPLPWPE
DKPLCAISAFGFTGSNGHVVLRL

>Lnm_KS1

AVIGMAGRLPGAGDLDAFWDNLVSGRTAIGPAPASRPETAPSGARATGGFLPHIDRFDSLLFHVSPQEAPALDPQA
RLMLESVWQCLDDAGHTADSLRRSAGRVGVFIGSMWHDYRQQGADRWNNGDSAEVAATASDIANRVSHFFDFRGPS
LAVDTSCSSSFAALHLAVESLRRGECGAAVVGAVNLLAHPYHWGLLDGLELLAADAPPAAYAAEGSGWHPGEGVGV
LLLRPADAARRAKDTVHGLIEGTRIGHAGRAPRYGAPHTAALADSLARALADASVIPDEVYVECAAAGAGIADAA
ELEALGSVLARCAGASPVVGTLPKNIGHLEAASGLSQLIKVLLQIRHGRIAPTLVSGELSPLDWDGLPVELVDT
PRALTPRAADGRATVLVNAVATGSYGHVVVRA

>Lnm_KS2

IAVIGIAGRYPGAGDLETFSWNLAEVDSVGPLPAERARDGWPTQMWGGFLDGVDREFDALFFGIAPRDAQLMMDPQ
ERQFLQVWVWETLEDAGCTRARIREQLGSDVGVFVGTMYNEYPPFFGVERSLAGESADTGSAVAGIANRVSYFLDLHG
PSLAVDTMCSSSLTALHLAVESLRRGECAAAVAGGVNLSLHPHKFRQQTRLMSSSDHRCRSFGAGGDGFVPAEGV
GAVLLKPLSAAEADGDRIHAVIRGTAVNHGKTINGYMPNPVAQGD LVRAALRRAGADPATIGYVEAHGTGTQLGD
PVEINGLNRAFAGASVAPASRAIGSVKANIGHAEAAAGIAGLTKVVLQLRHRHLVPSLHTEELNDAVDWASSPFEV
VREGRWPAPLTGADGAPLPRRAGLSAFGAGGANAHVVVEEY

>Lnm_KS3

IAVIGLSCRFPGAEDAAAFARNLLGGTCSVTEVPPSRWDVGELYRPELEPGRSTSKWGGFLDGIEDFDPEWFGMSE
DEARCLDPAVRLFLEGSATCLTDAGYGARELAGRDVGVFAGARMSHYGRRVGERRGLVGMGSDQNFIAARIAHHFD
LHGPNLVVDSACSSSLVALQLACRSLLDGESELALAGGVVDVLLDEEPLYLDFSAAKALSRHGRCATFDEDADGFVPG
EGCGVLLKPLEKALRDGDRIHAVIDAVAVNNDGRTMGLTTPNPAAQAKVVRRALAAAGRRADEVGLIEAHGTGTM
IGDPIELRALTEVFREETGRTGFCAGSVKTNVGHLLSAAGMAGLIKAVLAVRDGRIAPTLFCERPNNPRFDFAASP
FYPSRTAHDWVPEPGRVVRVAGVSAFGLGGTNAHAVVSQI

>Lnm_KS4

IAIIGVAGRYPEAEDLEAFWRNLAEGRDCVGEVPADRWDHAAYYDPERGKEGRTYGRRGGFLDGVDRFDAASFGIS
RREAELMDPQERLFLTVGRQAVENAGYRPEELARTRVGVFAGVMWNHYQLCTDGS AEPVAPTALHCSVANRLSYCL
DLSGPSMAVD TACSSSLTSLHLAVESIRRGE CALAVAGGVNVA AHPQKYLQLAQGRFLSSDGR CRAFTGADGDGYVP
GEGVGAVLLKPLADALADGDH VHAVIKGSFLNHSGR TSGFTVPSPAAQATLIADALDRSGVAADSVGYIEAHGTGT
ALGDP I EIEGLRQAFADAGLAPGSCAIGSVKSGIGHLESAAGIAAVTKVLLQMRHRELVP SLHSEQPNPHIDFAAT
PFAVQRTRAPWVPRPGSTVLRAGVSAFGAGGSNAHV LLESAP

>Lnm_KS5

IAVIGMSGRFPGAEDLDAFWENIAAGRDSFTEVPAQRWDVGPVFDADRLVPDRTYSKWAAMLPEVGRFDAAFFNHS
PLEAEVMDPQQR LFLEQSWAALEHAGYAVGADDRTSCGVFVGCAPGDYSTLLTEAGRADTGHAF LGTTSSLLPARI
GYFLNLDGPTMAVD TACSSSLVAVHLAADSIRRGE CAMALAGGVALMVTPQLHVRASKVGMLSPRGTCVPFDASAD
GTVLGEGVGAVVLKRLDRAVADGDHIHGVIKATGVNGDGR TNGITAPSALSQAALIADVHRRAGVGADDIGYVEAH
GTGTALGDP I EVRALTEVFRRSTDRSGYCGIGTVKANIGHTTMAAGIAGLLKTL LALRHSELPPAPAFDTPNPKTE
LDSSPFFVVRDRQEWEPGPGGQRIATVSSFGSGTNAHAVLAQAP

>Lnm_KS6

IAVIGVVGRYPQSPDLEAFWRNLSGRSCITEIPSERWDWRRNFD PDKSRKHRSYSRWGGFLEDIEMFDAPLFGIL
PRDAADIDPQERLFLESCWELLETAGYLGTYTHEPQTGVFAGLMYGEYGLLAAATDWPEGRYATGHSAYWSMANRV
SYTFDLQGPSLAVDSACSSALS A IQLACESLRRGESRMAIAGGTNLI LHPAHFAALCARNMLSAADACRVFDDGAD
GFVPGEGAGAVLLKPLAQAEADGDTIWGVVKGAFSNAGGKVS GYTVPNPNAQARLVERTLRRSGVHPRTVSYVEAH
GTGTALGDP I ELGGLTKAFRAAGATGDGYCAVGSVKSNIHGLEGAAGIAAVTKVLLQLKHRALAPT IHLDRLNPKI
DFAGSPFGPQRTAEPWDRPVAGVDGAERSWPRRAGISSFGAGGANVHMILEEY

>Lnm_KS7

IAVIGIAGVFPGSADTDEFWEHLAGGVDLVRPVPKDRTAIRANPATREL RGGFLDSVDTFDARLFGISPNEAALMD
PQQR LFLQTAWRVFEDAGYRPADLAGAPCGLFVGVATHDYDDLKENGVA VQAHTATGIAHSVLANRVSYLFDLNG
PSEAVDTACSSSLVAIHRALRAIQDGECELA VAGGVNVILTPGLLESFTQSGMLSPDGRCKTFDADADGYVRGEGV
GAVLLKPLARAEADGDHIYAVVKGTA VNHGGRSNLTAPNPESQARVVA AAVREAGVEPDTITYIEAHGTGTRLGD
PIEIEGLKKAFTTLHEERGEAVPDTGRIAGAVKTNIGHLETA SGIAGVLKVQSMRHRVLPASLHLRRLSPYLRL
DGTPTFTVNDRHRPWEPA LTPDGRQVLRAGVSSFGFGGSNAHVLEAYP

>Mln_KS1

IAIIGVACRFPPADHYHEFWENINSGKDSIREVP IERWDPDLYYSADISIPNKTISKWGGFIHKADHFDHKFFNIS
PREAKNMDPEQRILLEETWRCIEDSGVSLQDLQRKTTSVFAGIMNSDYRQTGHAESEIDSYACLGSFEAMLSNRLS
YTFGLTGKSMSVNAACASSLVALHEAVKSLRTKESDYA IASGVNLNFQPGKYISFSKARMLSPDGKCKTFDAAANG
YVPGEAGAVVLLQRLGDAVKAGHHIYGIIKGTAVNHG GKSRSITAPRAEAQCRVISEALHNAAVDAATVSYVEAHG
TGTS LGDP I EIEALTKAYRQYTEDTQYCRIGSVKTNIGHTEAAAGMAGLIKVLMMM KHRRVPKSLNVHTVNP I IQF
EKTPFRPALDSSDWKAADGAPLRAGISSFGFGGVNSHVIIEEF

>Mln_KS2

IAVIGISGRYPGAENIEELWELLSKERTAITEIPKERWNYETYYDP DPAKAHEGKIYCKWGGFLKNAESFDSLFFQ
ISPREAEAMDPQERIFLET VWKAFEDSGYTIEGLRKQTEKHVG VFAGVTTNSYKLLGERIPTDKNDVLPNSFPWSL
ANRVSYTFDFTGPSVPVDTACSSSLTAIHM AQC SLTKGECSVAVAGGVNLYLHPSDYLYRCQMGLSKSGKCRSFG
EGGDGFVPGEGVGAVILKPLKDAIRDNDTVYAVIKGTAINHG GKTNGYTVPNPAAQADLIQ GALKAAGWSARSVSF
IEAHGTGTPLGDP I EVRGLTKAFRAYTEDVSYCSLGSIKSNIGHLEAAAGIAGLTKIILQMKYK K I AATLHAERVH
PDLYLEETPFCLQOETADWIKPAN EKHS DSKYPRRAGLSSFGAGGANAHILVEEY

>Mln_KS3

VAIVGISGRFPQTDLTLEDFWEGIEKGRDMITDIPEDRWDWKEFDGDP I RDVNRTKIKKGGFIKGADNFDPLFFGIS
PAEAEELMDPQQRIFMETVWKTIEDAGYKPSDLAGTKTAVFAGVATTDYAERL NENGVS VQAQTATGLNHCILANRI
SYQLNLTGPSEP IDTACSSSLVALHRAAEGIQRGDFEMAIAGGVHIMTSP TLFIAFDKAGMLSKDGKCKTFDKSAD
GYVRSEGAAAVLLKPLSKAQADGDHIYGLIKGS AVNHGGRANSLTAPNPNAQADLLTEAWRKAGVSPATAGYIEAH
GTGTSLGDP I EVNSIIKAFKTLYQDWDIPFAKQKCCGIGSVKTNIGHLETAAGIAGVLKVLLAFKYRKLPLGLAHFS
ELNPYIKLENTPFYITETAQKWNPIKDEENNDLPRRAGVSSFGFGGVNAHIVLEEY

>Mln_KS4

IAIIGVSGRYPNSDTLEEFWENIAGGKNCII EIP EERWDFRSNYSPDRMEKGKINSKWGGFISGVDQFDPLFFHIS
HKEAELMDPQERIFLETSWHTFEDSGYTKEKLDGMKAGVFGAMYQQYQLFGAEETARGNP IALSSFFSSIANRV
YFFNLSGPSIALDTCSSSLTAIHLACESIKRGESEIALAGGVNVS IHP SKYLWLSQGNFVSTEGLCRSFGEGGDG
YVPGEGSGAVLLKPLEKAIADQDHIYGVIKGTSVNHGGKTNGFTV PNPNAQAELIAENFKKSGISPRSVSYLEAHG
TGTSLGDP I E IAGLTAFEFKFTDDKQFCAIGSVKSNIGHLESAAGIAALTKVLLQFKHQKLAPSIHSEQLNQNI
RFEKTPFYVQQKEEEWRKESGASNRRAAISSFGAGGANAHVIVEEY

>Mln_KS5

IAIIGISGRYPMANDLDTLWENLLNGKDCITEIPEDRWDSGLHYQPAAGDEVKNQSKWGGFIDDVYHFDPLFFNIS
PAEAE LIDPQERLFLETVWHTIEDAGYAKKTLERKNVGVFAGVMYQQYQLYSVGHEAAVSSSYASIANRVSYFFNF
SGPSIALDTCSSSLTAVHFACESLIRNECEIAIAGGVNLSIHPHKYELLTQGGFLSSDGRCSRFGSGGDGYVPGE
GTGAVLLKPVKKA IADGDQIYSVIKATAINHGAKTNGYTV PNPKAQSEVITRALKKGFIDPKSISYIEAHGTGTAL
GDPIEITGLTRAFSDAERDKKTC AIGSIKSNIGHLEAAAAGIAGITKVILQMKHKTI VPSLTHSAELNENIPFQKTP
FYVPDSAEKWESSVPRRAGISSFGAGGANAHVILEEF

>Mln_KS6

VAIIGMSCVFP GAKNADEFWLNLINEKDLIQEIPDRWDWKKYAEKGGSSEVHSKWGGFITDADKFDEAFFNINPR
EAE LMDPQHRIYLQETWKAIEDAGYKASKLSGKNIGVFTGIQFNDYRQLLMRHS DGAHAFAGTGNSQALISNRVSH
YFNFRGPSESIDTACSSSLVAIHRAVRSIQNGESELAVAGGVSLLLDPVTHMYTDKLGILSRDGRCKTFDKLADGY
VRGEGA AVLLKPLQAAMNDRDNIYGVLRGTGENHGGRSASLTAPNPEAQAE LLTSVYKNADIPVDTISYIEAHGT
GTELGDPIEIEGLKKA FGSFEPRSGKNHDQYCGIGSVKTNIGHLEPASGMPGLIKVLLSMKYKTLPATLHVKE LNP
YIQLSGTPFHIVNKTMKWATLKD RKGNEIPRRAGVSSFGFGGANAHVIVEEF

>Mln_KS7

IAIIGIAGRYPMAKDVEQFWENISSGKDCITEIPKERWDFRKYHYHTGDNARHDSKWGGFIKDADKFDPLFFSISPR
DAELIDPQERLFLETAWHTFEDAGYTKKKLKRHKTGVFVGVTYSHYQLFAAGASDDEERQALLSSYSSIANRVSYF
FDLHGPSLAIDTCSSSLSAVHFACESLKRGESTLAIAGGVNLSLHPDKYTLLSQNHVSSDGRCSRFGAGGDGYV
PGEVGAVLLKLSAAKADGDRIYGVIKGTSVNHGGKTNGYTV PNPGEQANVISETLDKAGIDADSISYIEAHGTG
TSLGDP I E I SGLTKALHSSKSDYRCAIGSVKSNIGHLEAAAAGIASITKVLQM KYKQLAPSLHSGNLNPNIDFEET
PFYVQSELTDWETPQNQARRSGISSFGAGGSNAHIIIEEY

>Mln_KS8

IAIIGMGCEFPDAPDTETFTWNLKKGQNSVREVPASRWDISSYSDTYEKGKSIK WGGFLQDIESFDPAFFNMNK
SEASELDPLIKKCLEVSVQTLRDGGYTKEEVSNKEVG VFIGSRTGTFSKIGSPSKNTIVGIGQNF IGAHISHFFN
LKGP NLVVDTACSSSVSVHLACQSLMSKESDMAIAGGV DILLDQKPYVMLSEARALSPEGKCHTFDEKADGFVPG
EGCGAVLLKRLDDALAEGDRIYAVIDSSAVNNDGQTMGMTTPNPKAQSAVIKKALKKGGIDADTLSYVETHGTGT
MIGDPIELKALTEVFREVTEETQFCGVGSVKTNF GHLMSAAGIASI I KVALSIKNQMLPPTLHCKTPNPRFKFDQSP
FFPNTSLKEWRPRKGVLRAGISSFGFGGTNAHMILSD

>Mln_KS9

IAIIGLSGKYPMAEDLPEFWENL KSGKDCITEIPDRWNMDDFFSEDRDMKGKSYSKWGGFISGADQFDPLFFHIS
PREAE LMDPQERLFLETAKHCFEDSGYPRNMLEKMKVG VFGAMWQQYQLFEGEENGVA FSPASVYSSIANRVSY
FHLKGPSLALDTCSSSLTSIHYACQSIHCGESDMALAGGVNLSIHPNKYKFLSMGQFLSSDGRCSRFGKDGSGYV
PGEVGAVLLKPLKKAIEDQDQIYGVIKGSAVNHGGKTSGYSIPNPDAQAEVISEALRKADIDPNTVNYIEAHGTG
TSLGDP I E IQGLKDSYQLNHPCAIGSVKSNIGHLESAAGIAAVTKVLLQMKNKQLVPSLHSDIVNPFIDFDQVPFQ
VQRKAAEWNIPQNSNAVHPLRAGVSAFGAGGTNAHLILEAY

>Mln_KS10

IAIIGVSGRYPGAENIREFQNVLMNGRDCVSEIPDDRKEMLEGSCYKWGGFLKNPDRFDPLFFRISPKEAAFLDPQ
ERLFLETVYNTIEDAGYKPSDLTRKKVG VFGVTYGSYQFFGVEESLKGNELAVGSPFSAIANRISYFFNFKGP
SM AVDTMCSSSLNAIHLACESIRRGESTLAVAGGVNLT LHPNKYTLLNQSRFFASDGRCTRFGEGGDGYVP
GEGVGSV LLKPAVEAVRDGDHIYALIKATAVNHGGRTNGFTV PNPNGQSELIQDALQKACIDPRTISYIEAHGT
GTSLGDP I E ITGLTKAFREFTEHTQYCSIGSVKSNIGHLEAAAAGIAGLTKVLLQMKLKKLFPSIHAETLNP
NIDFKASPFYVQRS LQDWKKPKLQENGKTVTVPRRAGISSFGAGGTNVHIIIEEY

>Mln_KS11

IAVIGIGCKFPGAADKEEFWDNLRKGNHIKEVPDSRWNIENYSPVQQKGKSISKWGGFINGIGSFDPEYFRMEE
EKAIQTDPLIRHFLETSVQTVRDAGYEETELSGKKVGVFVGSRMGGYGHKLPKESTSHIVGLSQNFIASHVSHFFN
FHGSPMVSdTACSSSLVSIHLACQSIKNGDSEMALAGGADLLLDEIPYMLLTEGGALSPDGQCFTFDERANGFVPG
EGFGAVLLKPLEKAKTDGDRIYGIIEASAINNDGATMGITTPNPKLQEQVIQDAFEKADITPGSVSYVETHGTGTM
IGDPIELQALTKVFRRDNTKTQFCGVGSVKTNIGHLLSAAGAASFVKVLSIWHKEIPPTLNCETPNPRFEFEKSP
FYPNTELRSWKDGKRRAGISAFGFGGTNAHLLVS

>Mmp_KS5

IAIIGMACRVPGAGDYQQFWENLANARDSVTEIPASRWDWRAFWGDPTSEDDRSARHAGCIDAVDAFDARFFGIA
PASARIMDPQQRIMLELSWACLEDAQVVPVSALAGSRTGVFVAAFNYDYKQLLESAGLPIDAHHSTGNAAVIANRI
SHFYDLHGPSVLVDTACSGSLSAIHHAQVSLRLGETELALAGGVNLLLTPTRHIAFAKTGMLSPGTACKSFDEAAD
GYVRSEAGLLELLKPLAKALADGDP IHGVIKGSVAVNHCGKTHLTYPSSAAQAQVIEQALGDAHIPASSVSYIEAH
GTGTPKGDPIEIQGLRQAFQCPQASEPQTCGVGSAKSNIGHLEAAAGVAGVIKVLVLSFKAGQLAPLCHFSALESSRID
LQGSFPFYVTRLQWPWEPASGVRRAGVSSFGFGGTNGHLILEQP

>Mmp_KS6

IAIVGISGRFPQSRDLDAFWEHLAGADLVSTVQRWDPRHCYAGADQGCDRGGFIERIDEFDPLFFNISPLEATYM
DPQQRFLFQEAWNALADAGCLGEQRRAEVSVYVGCEQGDYDQLFDDMPPPPQSFWGNAPSIVPARIAYYLDLQGP
TVDTACSSALVAIHMACQSLLAGDTKVALAGGVFIQSTPAFYQKANRASMLSLTGACHTFDSRADGFVPGEGAGAV
VLKRLADALADRDHIHGLIRGSGINQDGASNGITAPSALSQQLRHESVYARYGIDPATVQLVEAHGTGTRLGDP
IEFQALKGAFSRYTQRKGYCAIGSVKSNMGHAATAAAMAGLFKVLLAMRHRQLPPSLHFQHTNPAIDFADSPFFLNQH
LGDWPAIDGAPRRAAISSFGFGGTNAHMLVLEQP

>Mmp_KS7

IAIVGLSGRYPKAEDLQAFWRNLAEGVDCVTEVPAERWSLGDLAQPGRLPGGKTLRSWGGFLDDVDKFDPLFFNIS
PHDAEYMDPQERVFLCAYATFEDAGMALGLRSPSALRRTGVYVGVMYQEYQLFGAEQTLLGRPMALSGSSASIAN
RVSWSLGLSGPSLAVDSMCSASLTAIHLACQGIRSGDCDVALAGGVNVSVHPNKYLGLAQGNFASSQGRCSFGE
GDGYVPAEGVGAVLLKSLSQAVADGDRIYGVIRGSQINHGKANGFTVPNPNAQADVITQALAAAGVDAADVGYVE
AHGTGTALGDP IELAGLAKAYRHYTDQTAFCALGSVKSNLGHCEAAGIAGLTKVLLQMKGQLVPSLHSEVLNPA
IDFAQSPFVVQRHLAPWPRRVRVEGVTEECPRLAGLSSFGAGGSNAHLIEEY

>Mmp_KS8

IAIIGMGRFPGAESLEQLWEHLAQGRDLTTPVERWDLRGSQADVSGKGLCQRGGLLSRIDEFDASFFNISGLEAT
CMDPQQRFLFLEQAWTALEDAGYVGQATEGQPVGVYVGASASDYRSLEFAEAPPAQAFWGNASSIIPARIAYHLDLQ
PAIAVDTACSSSLVAIHLACQALWTEEIGMALAGGVFVQSTAGFYQAAQTAGMLSPSGHCHAFDARADGFVPAE
GVVLILKRLRQAQADGDYIHGVISGIGSNQDGASNGITAPSAQSQERLIRQVHRDFAIEPGTISMVEAHGTGTPLG
DPIEFEGLTRAFARPQQAGYCALGSIKSNLGHCVTAAGVAGVLKVALALRHGQLPPAAGFTQANAAIAVQGSFPYV
PDQLRPWATLDGVPRRASVSSFGFGGTNAHLVMEQAP

>Mmp_KS1

VAIIGLSANVAQSASVRQFWQALDDDRSLIEEIPATRFDFTSWYAGSNIEEGKMRTRWGGFIPAIDQFDPVFFGML
PAEARKMDPQQRLLMSVRQTFEDAGYRHTDWKGSATGVFIAAERNEYHLNLLQAQIDPGEGLDQAASMLANRVSH
FYDLRGPSEIDAMCAGGAVALHHAVALRSGQINAAIVGACNLLLRPDVFTLSQSGQMSPEPTVRSFGAGADGY
LRGEGVCSLLKPLSKAEADGDHIYGLIRNTAVNYNGDAASIAAPSVSAHSSLVQDCYRRAGIDPRHVSYIEAQ
GMNPVADIAEWDALNHGLLALGREQGVQLQEGQCAISTLKPMMSGHMHAASAIGALFKIIRSLQTEKIHKILDFEQ
NLHLHTAGQPCRLATHTVDWPRQATPRLAGLHSGYAGGNNAHILVEEY

>Mmp_KS2

IAIIGMAGVYPKSADLSAFWDCLANAGDCIETVPEQRWSLDEHFNADRQRAIQEGKSYGKWGGFIEGLDDFDPMFF
NFSLAEATYMHKPERQFIQCAWHALEDAGYTPASLEQEKVGVFVGVSKAGHDNYKDSFFSIANRVSYRFGFTGPS
PVDTACSSSLTAVHEACLHLQAGECTVAVVGGVNAYTHPSTFAEFARLGVLSADGKSRAFGAGANGFVPGEGV
GALLKPLERLALADGDMVHGVIASAVNHGGKANGYTPVPNEAQRAMIRLALDRAGVSADQVTYVEAHGTGTALG
DPIEFRGLVEAFRQDTERGTGFCRLGSVKSNIGHLEAAAGIAGLSKVLLQMRHGQIAPSLHSQQMNPIDIDASLSP
FRVPQALEPVDVDGEGAQERIAACLSSFGAGGANAHVILRQAP

>Mmp_KS3

VAIIIGLAGRYPQARTLEEFWQVLSQGRDCISEIPTERWDHSRYSADEDAPGKTYARWGGFIDGVAEFDPAFFGIS
PREAMAMEPQERLFLQTAHEAIEDAGYTRQGLAASARHEDAEGMVGVFVGVTYEEYQLYGAQQTAEGRPLVLSMSP
SSIANRVSVFVNGFHGPSMAIDAMCASSLTTHLACQSLHSGECQVALAGGVNVSHPAKFLMLGAGKFASRRGRCE
SFGASGSGYVPSEGVGAVLLKPLHQAQADGDRIYGVIRGSAINHGGRTNGYAVPNPAAQAAVISRALRQANVQPRQ
IGYVEAHGTGTVLGDP IEVAGLSRAWRAYTPDRQFCALGSVKSNIHGCESAAGIAGLTKVLLQMKHGLLVSSLHAE
TLNPNIDFSETPFRVQRTLAPWERPLGSDGVPGLRMAAISSFGAGGANAHLLIVSEAP

>Mmp_KS4

IAIIIGLAGRYPQAENIEELWENLKLGRDCITTVPSQRWDHDAIYDPSKGVSGKTYSKWGGFLRGVDEFDPRFFNIS
PREAEIMDPQERLFLQCAHYVLEDAGYTRQSLSAKGRVGVYVGVQYTEYATAFSTAQTLVAALPASIANRVSFCD
RGPSLTLDSCSSSLTTHLACQSLRSGESEYAIAGGVNVSHPNPKYLLHAQGRFASSVGCCKTFGQGGDGYVPAE
GVGAVLLKPLPQAIADGDRIHAVIKGSSINHGGRTATGFTVPKSSAQAVAVRSALHQAAGLASSDLSYIEAHGTGTAL
GDLIEIEGLRTVFEADGFEPQTCAIGSIKSNIGHGCESAAGIAGLTKVLLQLKHRQLVPSLHSTQLNRNIDFAGSPF
HVQQTLEPWLPGAADAVQPRRAGISSFGAGGSNAHLVVEEY

>Ped_KS1

VAIVGMACRLPGGVDSPTAFWQCLQEGASLIGDLPVERWEWPDDIDPQRAHKGIARGGFIEDVKAFDAPFFRISPA
EAQSMDFPQQRMLLELCWQTEHAGYAPDALAGTDGTFIGASGSDYARLLERSESPDAHYGTGSSMAVLANRLSY
FYDFTGPSLLLDTACSSSLVAVHKAVQSIWAGESVQALVGGVNLIHLPANSIAYYKAGMLAKDGLCKTFDQQADGY
VRGEGAVMLLLKPLARALESRDRVYAVIKGTACNHGGQAGGLTVPNPERQSTLLCSAWQSAGIDPSDLGYIEAHGT
GTSLGDP IEVRGLKDAFAATRCGAGQNCGLGSVKTNLGHLEAAAAGIAGLLKVVLCQLHRQLPASLHFQQLNHIEL
ERGLYVVDRLQPWTPPSSGRVRFAGVSSFGSGGANAHVVVAE

>Ped_KS2

IAVIGMSGRFASAADLDEYWQLLAAGESCISEVPAERWAVEDFFHPDPDEAIVQGKSYSKWGGFLQGVTEFDPLFF
NISPKERSIDPQERLFLRASWEVLEDAGYTRERLTKDFQQQLGVFAGITRTGFDLFGPELWRQGYTVYPHTSFSS
VANRVSYFLNARGPSVPVDTMCSSSLTAVHQACQSLRNCECRMAIAGGVNVYLHPSGYVGLSAAHMLS KDGVCRSF
GKGANGFVPGEGVGAVLLKPLSQALADNDQIHAIIRSTQVNHGGKTNGYTVPNPLAQAEIIRRALDKAGLNARAVS
YVEAHGTGTDLGDP IEVSGLTQAFRHD IQENGFALGSVKSNIHGLEAAAAGIAGMIKVILQMRHGQLVPSLNAAEI
NPNIDFSRTPFVLQRELAPWTPPYTLGQNGEREEGTRIAGVSSFGAGGGNAHVILEE

>Ped_KS3

IAIIIGMSGQFPQAPDVKAFWRNIVEGRDCVSEIPAERWSIEEYYDSDRNADGKTVCRRMGALSDREVFDP LFFNIS
PSEAELMDPQQRLLFLNSWHCIEDAGYDPTRLSGSLCGIFVGCASDYSQLAESQTQTAQGLLGESVAMLPARVAY
YLNQGPCLAI DTACSASLVALASACDSLVLGNSDVALAGGVYVINGPDIQVKMSKAGMLSPDGRCSFDQRGNGF
VPGEVGVMLMKRLEQAQRDGGDIYAVIRGWGVNQDGKTNGITAPNQESQTRLETGIYRKFGINPEHIQLVEAHGT
ATRLGDP IEVEALSESFRFSDRKQYCALGSVKSNIHGLATAAGVTSVIKSALALQHRILPPTINFQTLNEHIRLQ
DSPFYINTERRLWEMPQGHSRQVAVSSFGFSGTNAHMLVEE

>Ped_KS4

IAIVGLSGYFPQSASVDEFWRHLDQDATLIEEIPDSRFDWRKVFDPTGERPGSSCSKWGGFIPDIRGFDPAFFNIP
GAEAITLDPRQRLLLMSAYQTLNDAGYASQALRQSKTGVFVALQDNEYLQLLADAGIDPGQWYAQTCLLANRISYF
FDWRGTSEVVDAQCPGAAVA IHRVAVSALRNGEIELALVGAANLLLRPEPFVLLSESGQLSESASVHSFGAQAQGH
RAEGVCSLLLKPLTKALADGDP IYASIKHSAVNFNQGGASIAAPNVDSHVDLIKSCYQQARVDPRQVRYIEAQGM
GNVLADLVEWQAFNRALTDIARQQRVSLPPGNCLISTLKPMGMHESASALGALFKVIRSLHTRTIHKIAHFTQYH
PDMDYQGQPCA IAGETVAWFPQMEGLRLAGIH CYGMGGVNAHLLVEE

>Ped_KS5

AIIGISCNMPGARTLRQFWENLRQGKESSTRLSERELRRAGVPEELIRHPDFVPMQYSMEGKELFDPDFFNLSAKN
ALFMDPQYRVLLQQAQAIEDAGYVAQDIPETAVFMSASNIFYKTLLHSAGAVETTDEYAAWIAGQGGTIPTMISY
QLGFKGPSFAVHSNCSSSLVGLYLASQCLRLKEAKYALVGGATLFPVAGTGHL YTPDMNLSSDGHCKAFDADADGL
VGEGAVVLMVRKALDAIRDGDP IYALIRGVAVNNDGSDKVGFYAPSVNGQAAVIQKALDITGVDPQSVAYVEAHG
TGTRLGDPVEIMALNEVYRRYTEKRQFCRIGSVKPNIGHLDTVAGLAGMLKVVLSLKHAEFFPSINYREP NPAIDF
TSSPFEVVTQLTPWPAGNEPRRAALSSFGIGGTNTHAILEEY

>Ped_KS6

IAIIGLSGRYPQAETLEEFWENLQAGKDCVSEIPEDRWRLNFFHPDPKEAVAQGKSYSKWGGFIEGFAEFDPLFF
NISPREALAMPQERLFLQCAWHVLEDAGYTRQSLQQGGHKVGVFVGITKTGFDLYGPELWHRGERLFPHTSFSSV
ANRVSYCLNLKGPSMPIDTMCSSSLTAIHEACQHRLRQGD CDMAIVGGVNMVYVHPSTYVGLCSAYMLSRDQQCRSFG
QGGNGFVPGEGIGAVLLKPLARAQEDDDLIHAVIRSSSVNHGGRTNGYTVPNPNAQAEILGDCLKKAGVDARSIGY
IEAHGTGTELGDPIEVNGLAQAFGQGEAGEHSRCFLGSVKS NLGHLEAAAGMAGLTKVILQMRHGQIVPSLHAQVLN
PNIDFAATPFTVPQQLVWEWRRTILQESGRSRELPRRAGLSSFGAGGSNAHLILEEY

>Ped_KS7

IAVIGMAGQFFGADSV DALWQNMVAGVNPVTELS ELYLPYHAYSPEKQPGKSYCKWGGALQGRDCFDPLFFNISPR
EAESMNPHQRLILQESWKALEDAGYAPRSLSDSRTGIFVGAEP SAYVHESFVGASDAIVASRLSYFLDLKGPAFVV
NTGCS SSGVALHLACESLRNGETEVALAGGVFAVMGQTILVGLAQTDMLSRTGCCCTFDADADGMVMSEGVGMVVL
KRLDQALSDGDTIYG VIRASGINQDGASNGITAPSGIAQQQLITDVYRRYAIDPRRITYVEAHGTGTRLGDPVEAN
ALVRAFRSFTESTGYCAVGSIKSHIGHTSSSSGVIGLISILLCLKHHQLPGMRHFKRNLNPLIEFERSPFYVNARMM
PWRSGSGEPLMAALNSFGHSGTNVHLVVEEF

>Ped_KS8

VAVIGMAGKFFPGCEDLEDFWTCLQSCQDLISEVPEQRWDWRRFYGDPHQE PGKTKIKWGGFVADADCFDARFFGIS
PVEAEVMDPQRLRLFLETVWAALEDAGYPAGRLAGSRTGVFAGVATADYKDLLIEARARGLVQTPSEPPFPMIANRI
SYWFNFNGPSE AIDTACSSSLIAVHKAIESLRLGSC EMALAGGVNVLGSPRITIASSQAGMLSEDGRCMTFDERAN
GYVRSEGVAI LLLKPLRKAIADNDRIHGLIRGSGENHGGRSASPTAPNGNAQKRLLVDIYSRADIDPRTISYIEAH
GTGTVLGDPVEV NGLKAAFQELYQSRGLDVPEQPHCGLNSVKANVGHLEAAAGAVGIVKVLMLKHKRIPGNPHLR
RPNPYLQLEGTPFYLVRETLDWPQPTDVRGNPLARRAGVSSFGVGGSNAHVILEEY

>Ped_KS9

IAIIGLSGRFPQARTIEELWRILEQGRDAIQEVPIDRFDWRSYYSQSQEMSKSNSKWGGCIPGIAEFDPLFFFEISPR
LEAERMDPRQRHLMQEAWLALEDAGYGPEQLECNKISM FVGVEEGCDYQRRLTQQTSLTSMHNGILASRLAYFLNL
KGPVMAINTACSSALVAVHQACQSLRHGECDTAIAAGVNLLVAPEAYVGMTQAGMLSPDGKCYVFDKRANGLVPGE
AVAVVVLKRLSKALADGDP IKALIRGSGIN YDGKTNGITAPSGASQTELEGIYRQCALQPQDISYIVTHGTGTQL
GDPIEINALYDVFKGKTDKQGFCA LTSIKSNLGH TFAASGLVSLISLVLAIRHRTIPSSLHCEQKNDYIRWQESPF
YVNTKRKKHWEALGQPRIGAVSAFGMSGTNAHVVVQEH

>Ped_KS10

IAIIAMDGVPFQ SADDLEFERHLRQGDDCISEIPADRW DWREVYGD PKEGEFTRVKYGGFAPDIDKFDPLFFFGMSP
REAQLMDPQHRQFIQCVWR LIESAGYAPKALS GSKVGLFIGINLQDYAHLVDRADAMDALHLTSLGHMFCPNRLSF
LLNLHGPSQVIDTACSSSSVALHRAVLSIQYEGCEMAIAGGANLLISPDMHIMYSKVG MICEDGRCKTFSKEANGY
VRSDGIGAVLLKSLHRAEEDGDIILAVIRGSAENHGGMSTSLTAPNPKAQASLIVEAHRKAKVDPRSIGYIECHGT
GTS LGDPIE INGLKLA FEQLYREAGHELPMRPS CGLGSVKS NIGHAETSAGIAGVIKTVLSLRNKRLYQSLHSADI
NPMIDLEQSPFFILQQGRDWQRPLIEGQE QPRRAGISSFGAGGSNAHIVIEEY

>Ped_KS11

VAIIGMSGRFPMAEDIQAFWSNLLEGKDCISEIPEDRWDRAIYGDPTKEANKSDVKWGGFIDGVAHFDARFFGIS
PREAELMDPQQRLLMQYVWKAVEDAGYAPASLSGSRTAIFVGTASSGYGELMAQEGLAIESYSTGVVGSVGP NRM
SYFLNLHGPSEP VETACSSSLVAIHRALSAMAIGDCDQAIVGGVNLLISPQTHISFNKAGMLCSDGRCKTFSSKAN
GYVRGEGVGMLMLKKLKAAEQAGNHIYAVIRGSAENHGGRSSLTAPNPKAQ TQLIKAAYERAGIDPRSVSYIEAH
GTGTELGDPIEINALKAAFKDLYQATGSVEVTAPHCALGAVKTNIGHLELAAGVAGVIKVLQLKHKTLVKS LHCD
EVNPIYIQLQGS PFYLLSETQPWSTLRDAQGRELPRRAGISSFGFGGVNAHLVLEEYP

>Ped_KS12

IAVIGISGRYPMANDLDEFWLN LREGKDCVSEVPSQRWNWRDHYSEEHSRAGGHFCKWGGFID DIDKFDPLFFNIS
PSAAEYMDPQERLFL EHAWMAMEDAGYRREDLRKLARGSAAEDLP GQVGVYAGVMYSEYQLLGIEAARQKGATVA
NFHASVANRVSYVLDLHGPSMTVD TMCSSSLTALHLACQDLKTGR TDMALAGGVNLSVHPNKYSVLSLNEFISSQG
RCTSFGE GGDGYVPSEGVGVLLKRLVDAERDRDHIHAVIKSSVLNHGGKTHGFSVPNPKAQQH LISRALREAEVD
PRAITYVEAHGTGTPLGDPIEVTALSKAFAQYSLGGQPYWIGSVKSNIGHTESTAGIAGLSKVILQ MREGQLAPSL
HSQTLNPNIDF ASSPFQVNRQLREWPRPVL DGR LQPRVASLSSFGAGGSNAHLVISEY

>Ped_KS13

IAIIGMSGRFPFAPDLEAFWENLSQGDCITEIPPTRWKHQEYFDPEKGKPGKTYCKWGGFLESIDQFDPLFFKIP
PAQAEVLDPQERLFLFTVWNLESSGYLGETLQRIAQSRVGVFVGSMSSQQYHAFQADLTRESLVTMSSHSSIANRV
SYFFDFQGPSVAVDTMCSSALVAVHMACESLLRDDCKAAVAGGVNLSIHPKKYIGLSASQILGSHPDSSSFQGGDG
YLPSEGVGAVLLKPLREAVADNDTILGVIKSTTINHSGQSNGYFVPNGAAQTELMVSNFTKAGIDPRTLSYVESAA
NGSSLGDAIEINALTAGFGRYTADKQFCALGSVKSNIGHGEAASGIAQLIKVLLQLKHRQLVPTIKAQPLNSNIDF
THTPFCLQRRLEPWRRPSLALGDGPMREYPLRATVSSFGAGGSNAHLILEEFP

>Ta_KS1

AVIGISQCLPGAADPWRFWKNLREGRDSVVAYRHEELRELGVPEEVLDRDSRYVAVRSSIEDKECFDPQFFGLTARD
ASFMDPQFRLLLMHAWKAVEDAATTPERLGPCGVFMTASNSFYHQGSPQFPADGQPVLRTADEYVLWVLAQAGSIP
TMVSYKLGLKGPSLFVHTNCSSSLSALYVAQQAIAAGDCQTALVGAATVFP SANLGYLHQRLNFSSAGRVKAFDA
AADGMIAGEGVAVLVVKDAAA AVR DGP IYCLVRKVGINNDGQDKVGFYAPSATGQAEVIRRLFDRTGIDPASIGY
VEAHGTGTL LGDPVEVSALSEAFRTFTDRRGYCR LGSVKSNLGHLDTVAGLAGLIK TALSLRQGEVPPTLHVTQVN
PKLELTDSPFVIADRLAPWPSLPGPRRAAVSAFGLGGTNTHAILEHYP

>Ta_KS2

IAVIGMSGRYPGAENLTEFWERLSRGDDCITEIPPERWSLDGFFYPDKKHAAARGMSYSKWGGFLGGFADFDP LFF
NISPREATSM DPQERLFLQSCWEVLEDAGYTRDSL AQRF GSAVGVFAGITKTGYELYGAELEGRDASVRPYTSFAS
VANRVSYLLDLKGPSMPVDTMCSASLTAVHMA CEALQRGACVMAIAGGVNLYVHPSSYVSLSGQQLSTDGRCRSF
GAGGNGFVPGEGV GAVLLKPLSKAIADGDSIYAVIRSTSVNHGGKTNGYTVDPDQAQAALIRSALDKAGLSARDVS
YLEAHGTGTEL GDI EVAGLTQA FR RD TARAYCRIGSLKSNIGHLEAAAAGIAGLTKVILQLRHKRLVPSLHAESL
NANIAFGETPFV VQRG FEDWARPRVEVDGVL SERPRLAGVSSFGAGGANAHVLVEEF

>Ta_KS3

VAIVGAAGFFPGCQSLQAFWDALDAEQTLLEEIPPNRFDYRPLFPDKSRSKWGGFIPDVASFDPGFFNILPAEAE
LDPRQRLLLMAVYHCLEDAGQAPEKLKGSRTGVFVGAEENEYLLHLREQGVD TASGFDQAASMVANRLSYFFDL SG
PSELVNTMCSSAAVAIHRAVLAIRSGEIDRAIVAAANVILRPDGF IKLSQLQQLSPSVRVQSF GKDASGHQRAEGV
ASVLLMPLEQAEREGHP IHAVLRGSAVNYNRSGVSI AAPSRQSHSELIQSCYRSAGIDVRDVEYIEAQGMANPVA
DIAEWEAINDALKRLATAQGVDVVP GHCRVSSLKPLTGHMESASALGALFKVIHSFRDRDKVYGIAGFESANSYLEL
DRQPARLATRTEPWRRNGKPRLAGLHSFGAGGNNAHLLEVEY

>Ta_KS4

IAIIGLSGRYPEAHDLTAFWSNLARGADCVSELP SDRWPLDVFFDADKDAAIASGKSYGKWGGFLGGLYDFDPLFF
RISPVEVEI IH PESRLFLQCAWHVVEDAGYTPTALASERVGVFVGASKVGVAEQHHTFFTIPNRVSYALNLKGPSL
AIDTACSSSLVAIHLACQQLQSGDCTLA IAGGVNTYTHPHYFADLSKLQMLSTEGRSKAFGAGANGFVPGEVGAV
LLKPLGRALRDGDHIYGVIRGSEINHGGKTNGFTVPNPRAQAEVITRALARAKVPARHITYVEAHGTGTD LGDP IE
IRGLTEAFAAQTPDLAYCRIGSVKTNIGHLEAAAAGIAGLSKILLQGQHRKYVPSLHSSTLNPHIDFGKTPFV VQQT
CEDWLPCDAQQSIPRIACISSFGAGGSNAHLIEEAP

>Ta_KS5

IAVIGMAGRFP SADDLDAFWGNLVAGKDCIREVPNSRWDWRAYDGDPIREPKNKTDVKWGGFIDGIDEFDPAFFGIS
PREARLIDPQQRLLMMYAWKAIEDAGYAPSSLAGSNTAIYVGTGHFGYGD LIKEAGIP IEGYTSAGLVPSMGPNRL
SYLLDLHG PSEP VETACSSSLVALHRAMTSLADGTCDLAI VGGVNTIVTPDGHICFSKAGMLSRDGRCKTFSDRAD
GYGRGEGAGFVVLKTL SRAEADGDAIHGLILGSAENHGGHANS LTSPNPASQADVLMAAYRKAGVPMSTVGFIEAH
GTGTALGD PVEVTALTSAYQTLVKADGDAASAQPRCIGSVKTNIGHLELAAGIAGVIKVLQMKHATLVKSLGCE
TLNPHIRLDDTPFYV VRETAPWPRLTDRRGVELPRRAGVSSFGFGGVNAHVVEEY

>Ta_KS6

IAVIGMSGRYPGAENLRQYWDNLRDGVSGISELPYTRWDEATAKQFRQDRNYCHRMGALSDIESFDPLFFRMSPAE
AEVTD PQHRLFWQEGYRAFEDAGYAGEALDGRRCGVYLGIMGSEYATLLQRSGAQAIN TTGNSYAI A AARLAYHLN
LKGP AIAIDTACSSSLVATHLACQALTSHEIDMALVGGVTLYLAPESYLA MCDAGMLSTGGACRPF DNGADGFIPG
EGVGAIVLKRLEDAERDRDAILGVII GSGTNQDGKTNGITAPSAASQMELEREYRRFEVDPATIGYVEMHGTGTR
LGDP IELEALSSVFKERTDR TQFCAIGSVKSSIGHTSAAAGVASIHKVLLAMQHGS LVP SLNYSEPNQHDFDQRSP
FYVNT EHKPWKPNGHALRRAAISSFGSGTNAHLVLEEYP

>Ta_KS7

V A I I G L A G R Y P G A R D L N A F W R N L R E G V D S I G E V P Q D R W D H S A I F D P D K S R P G K T Y S K W G G F I E G A A E F D P R F F N I P
P K E A H F I D P Q E R L F L E C A Y A C C E D A G Y T R E S L A K L G G D R A G G S V G V F V G V M Y Q E Y Q L Y G A Q E T I Q G R P L S L P G N A S
S I A N R V S Y W F D F H G P S M A V D T M C S S S L T A L H L A M Q S L A N G D C E A A L V G G V N L S V H P N K Y L G L S Q G R F V S S K G R C E S
F G A G G D G Y V P A E G V G A V L L K P L E R A K A D G D R I Y G V I K A T A V N H G G R T A G F S V P N P N A Q A Q V I G R A L R R A G V D A R T V
G Y V E A H G T G T S L G D P V E I A G L Q K A F S E F T S D K A F C A I G S V K S N I G H C E S A A G I A G L T K V L L Q M K H R Q L V P S L H S Q V
L N P H I D F D G T A F V V Q Q R L T E W K S P V Q E H E G R R V T Q P R R A A L S S F G A G G A N A H V V F E E Y

>Ta_KS8

V A V I G M A G K F P R A S D L A Q F W Q N I A R G V D C I S E V P A G R W S V A E H Y D A D G N T P G K S Y S K W L G V L E D A E S F D P L F F G I S
P A E A E R M D P Q Q R L F L A A C W H C I E D A A I R P S S L S D T R C G V F V G C G P T D Y G R D L R G G D L N A Q A L M G G A T S I L A A R I S Y
L L N L K G P C L A I E T A C S S S L V A I S Q A C D S L V L R N C D L A L A G G V N V A F G P A M H I M S S D A G M L S K D G R C F T F D A R A N G F
V P G E G V G V L L L K R L S D A V R D D D P I A G V I R G W G V N Q D G K T N G I T A P S A K S Q A A L E R E V Y R R F G I D A D T I S L V E A H G T
G T R L G D P I E V E A L V E S F R E H S A R K H Y C A L G S V K S N I G H L M T A A G V S G V L K V L M A M R H Q S L P P T L H F E A V N P H L A L E
G S P F Y V N T E L K P W T G V P V R R A C V S S F G F S G T N A H V V L E E A P

>Ta_KS9

V A V V G M S G A F P G A P D L A A F W R N L A A G R D C I E E I P A D R W N W R D Y F G D P A A E D N K T R I R H G G F I E G V G E F D P L F F G I S
P S E A E I M D P Q Q R L L M T H V W R A I E D A G H A P Q S L A G S N T A I F V G T G N T G Y A S L L E R S G V A I K G S T A T G S V P S V G P N R L
S Y L L D L H G P S E P I E T A C S S S L V A V H R A L L A I E L G L C D A A L V G G V N T I V T P D A H I G F G K A G M L S E D G R C K A F A R G A D
G Y V R G E G V G V L Y L K R L S L A E R D G D H I Y G L L L G S A E N H G G R A N S L T A P N P K A Q A D L I E A A W L R A G V D P R T A G Y I E A H
G T G T S L G D P V E I N G L K S A F H S L Y E K T G A A E G T D A H I G I G S V K S N I G H L E L A A G V A G L V K V L L Q M R H G V L A K S L H C E
E L N P Y I A L K G S P F Y V V Q E G R P W L A L K D A S G R P L P R R A G V S S F G F G G V N A H V V V E E Y

>Ta_KS10

A V I G M S G R F P M A E D L E A Y W R N L R D G V D C I Q E I P A S R W D W R E I Y G D A N Q E P G K T L I K W G G F I D G I D E F D P L F F G V S P
S E A E L M D P Q Q R L L M T Y V W L A M E D A G Y S A S S L S G T R T A L F I G T G Q A G Y G S L I E Q A N A E I K S Y A S T A A V P S V G P N R M S
Y F L N I K G P S E P I E T A C S S S L V A V H K A M L A I H R G E C D T A I V G G V N T L P T P A G H I G F D K A G M L S P D G R C K T F S D Q A N G
Y V R G E G V G M L M L K R L S L A E A D G D H I Y G V I R G S A A G H G G R T N S P T A P S P K S Q A E L L H A T Y T Q A G I D P R T V T F I E A H G
T G T S L G D P I E I D G L K S A F T A L D P T L G A G P V D R A F C G L G S V K T N I G H L E L A A G V A G V I K V L L Q M K Y K T L A K S L H S E Q
L N R H I R L D G S P F F I V R E T Q P W P A E D G A G N V V P R R A G V S S F G I G G V N A H V V V E E Y

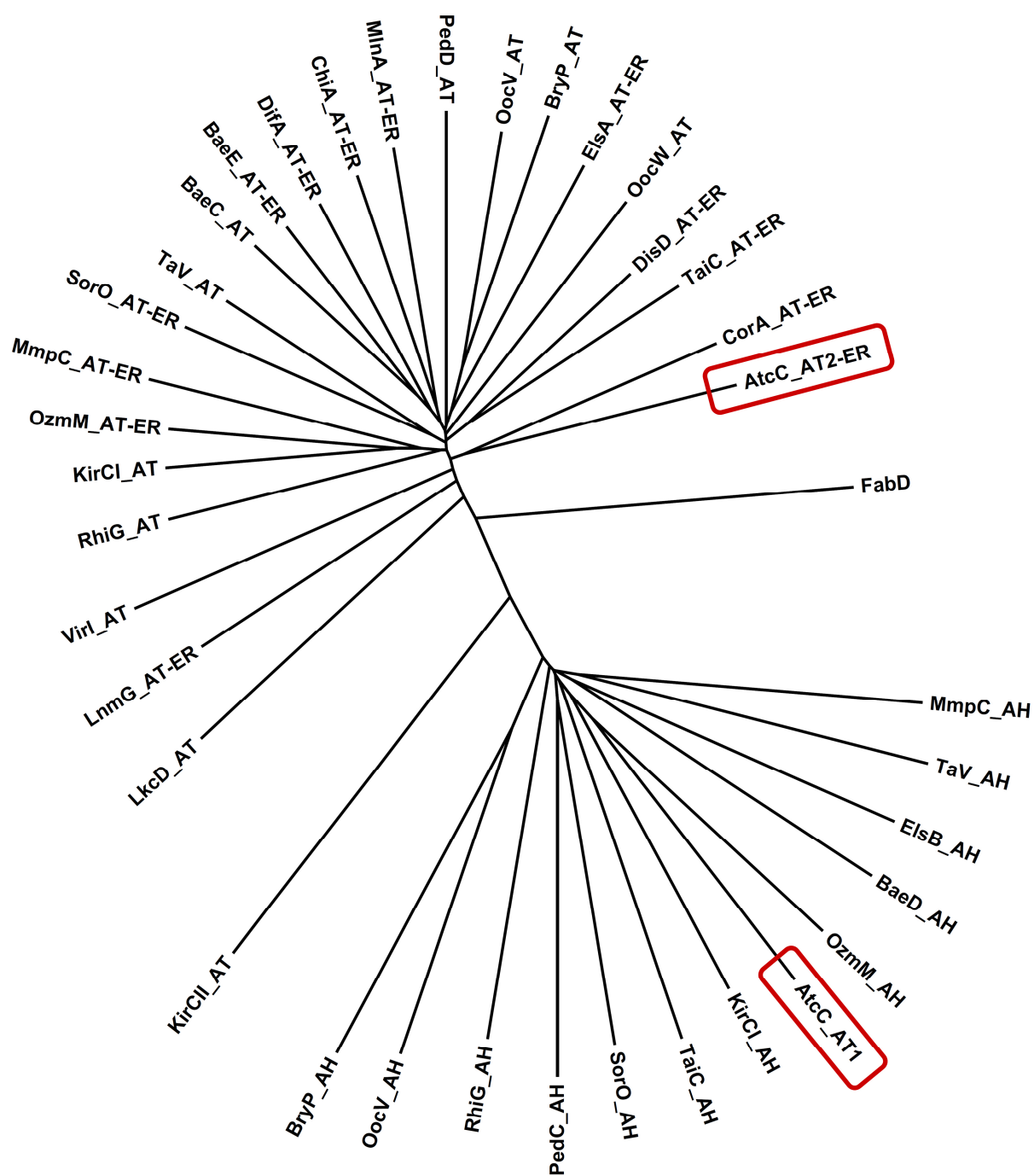
>Ta_KS11

A V V G M S G C F P G A R D L E Q F W T N L A G G V D S I T E V P A S R W D W R E L Y G D P R K E G N K T K V K W G G F I E G V E E F D P L F F G I S P
V E A E V M D P Q Q R L L M M H V W R A I E D A G Y A P H S L S G T R T G I F V G T G I T G Y N S L V E R A N L A I Q G Y S S T A V V P S I G P N R M S
Y L L N L H G P S E P V E T A C S S S L V A L H R A M E A I D S G S C D M A L A G G V N T I V T P G G H I A F D K A G M L S E D G R C K T F S A T A N G
Y A R G E G V G V V F L K R L A D A E R D G D P I Y G V I R S S A E N H G G R A N S L T A P N P N A Q S Q L L Q D A Y R K A D I D P R T I G Y V E A H G
T G T E L G D P V E V N G L K S A F A A Q I E A R G G G T S L E K H C G L G S V K S N I G H L E L A A G M A G V I K V L L Q M K H R M L V K T L H C E R
L N P Y I K L E D S P F F I V Q Q T Q D W P A L M D E R G Q P L P R R A G V S S F G F G G V N A H V V M E E Y

>Ta_KS12

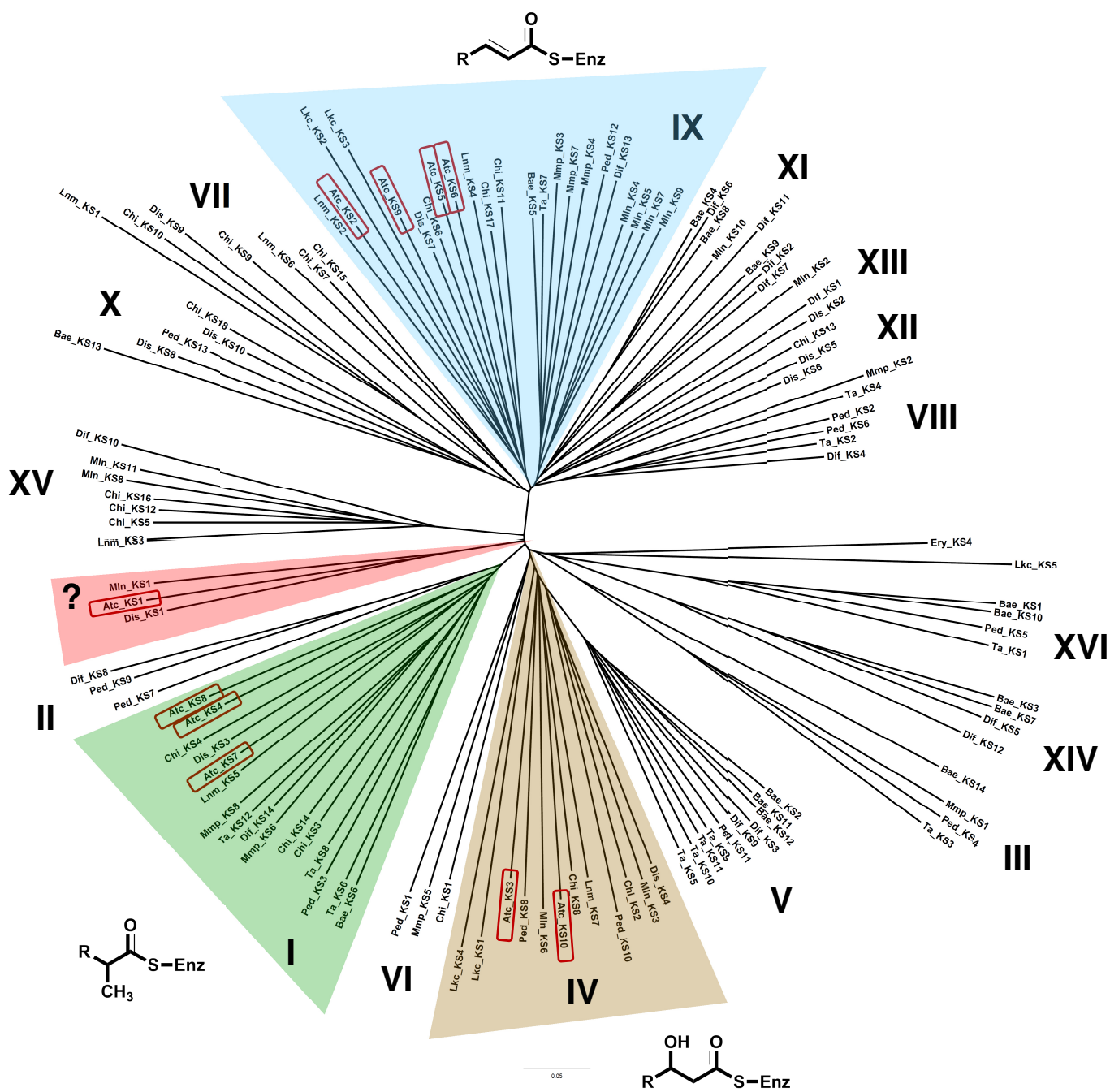
I A I V G M S A R F A Q S D S V E A L W R H L E A G R D L V E D V R R W D L A S H Y A S T L S G E G D R C M R G S F I E G I D R F D P S F F N I S A L E
A R C M D P Q Q R L F L E E S Y K A L E D A G Y A G S T P Y H Q R C G V Y V G C A N G D Y A T L L P R Q A P A Q A F W G N A S S V I P A R I A Y F L N L
Q Q P A L A V D T A C S S S L I A I H L A C Q G L W R R E T N M A L A G G V H L N S T P T F Y V L S S R G G M L S R K G R C G T F S D E A D G F V P G E
G V G V V V L K R L S D A I A D G D H V R G V I R G T G V N Q D G T T N G L T A P S G K S Q E R L E R E V Y E R F G V N P E D I Q M V E A H G T G T R L
G D P I E F D A L T K S F G A Y T R K R G Y C A L G S I K T N L G H T A T A A G V A G I I K V L L S M Q H R K I P A S L H C N A T N P A I D L E R S P F
F V N T Q T R G W D V E P G K P R C A A V S S F G F S G T N G H V I L E E A P

A



0.06

B



REFERENCES

- (1) Grant, S. G., Jessee, J., Bloom, F. R., and Hanahan, D. (1990) Differential plasmid rescue from transgenic mouse DNAs into *Escherichia coli* methylation-restriction mutants. *Proc. Natl. Acad. Sci. U. S. A.* **87**, 4645-4649.
- (2) MacNeil, D. J., Gewain, K. M.; Ruby, C. L., Dezeny, G., Gibbons, P. H., and MacNeil, T. (1992) Analysis of *Streptomyces avermitilis* genes required for avermectin biosynthesis utilizing a novel integration vector. *Gene* **111**, 61-68.
- (3) Gomez-Escribano, J. P. and Bibb, M. J. (2011) Engineering *Streptomyces coelicolor* for heterologous expression of secondary metabolite gene clusters. *Microb. Biotechnol.* **4**, 207-215.
- (4) Sosio, M., Giusino, F., Cappellano, C., Bossi, E., Puglia, A. M., and Donadio, S. (2000) Artificial chromosomes for antibiotic-producing actinomycetes. *Nat. Biotechnol.* **18**, 343-345.
- (5) Nguyen, T., Ishida, K., Jenke-Kodama, H., Dittmann, E., Gurgui, C., Hochmuth, T., Taudien, S., Platzer, M., Hertweck, C., and Piel, J. (2008) Exploiting the mosaic structure of trans-acyltransferase polyketide synthases for natural product discovery and pathway dissection. *Nat. Biotechnol.* **26**, 225-233.