

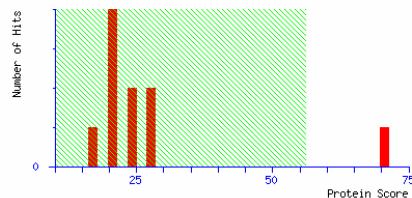
I. Exclusive expression of C7orf24 (Results from D435_131IEF):

a.

```
Database : SwissProt 2010_04 (516081 sequences; 181677051 residues)
Taxonomy : Homo sapiens (human) (20280 sequences)
Timestamp : 8 Apr 2010 at 09:12:03 GMT
Top Score : 71 for GGCT_HUMAN, Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1
```

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 56 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold $p <$ <input type="text" value="0.05"/>		Max. number of hits <input type="text" value="10"/>
Re-Search All Search Unmatched		

```
1. GGCT_HUMAN Mass: 21226 Score: 71 Expect: 0.0018 Matches: 4
Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1
ATPK_HUMAN Mass: 11027 Score: 36 Expect: 5.5 Matches: 2
ATP synthase subunit f, mitochondrial OS=Homo sapiens GN=ATP5J2 PE=1 SV=3
CC051_HUMAN Mass: 15770 Score: 27 Expect: 40 Matches: 2
Uncharacterized protein C3orf51 OS=Homo sapiens GN=C3orf51 PE=2 SV=2
YU004_HUMAN Mass: 31838 Score: 26 Expect: 51 Matches: 2
Uncharacterized protein FLJ46757 OS=Homo sapiens PE=2 SV=1
```

b.

{MATRIX} SCIENCE Mascot Search Results

Protein View

Match to: GGCT_HUMAN Score: 71 Expect: 0.0018
Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1

Nominal mass (M_r): 21226; Calculated pI value: 5.07
NCBI BLAST search of GGCT_HUMAN against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Fixed modifications: Carboxymethyl (C)
Variable modifications: Acetyl (Protein N-term), Oxidation (M), Propionamide (C)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 6
Number of mass values matched: 4
Sequence Coverage: 27%

Matched peptides shown in **Bold Red**

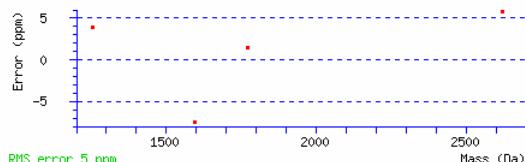
```
1 MANGCKDVT GPDEEESFLYF AYGNSNLTER IHLRNPSAAF FCVARLQDFK
51 LDFGNSQGKT SQTWHGGIAT IFQSPGDEVW GVVWKMNKSN LNSLDEQEGV
101 KSGMYVVIIEV KVATQECKEI TCRSYLMNTY ESAPPSPQYK KIICMGAKEN
151 GLPLEYQEKL KAIEPNNDYTG KVSEEEIEDII KKGETQTL
```

[Show predicted peptides also](#)

[Sort Peptides By](#) Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
35 - 45	1253.6144	1252.6071	1252.6023	4	0	R.NPSAAFFCVAR.L Propionamide (C)
46 - 59	1596.7898	1595.7825	1595.7944	-7	1	R.LQDFKLDGFNSQGK.T
31 - 45	1772.9404	1771.9331	1771.9304	2	1	R.IHLRNPSAAFFCVAR.L Propionamide (C)
8 - 30	2623.2352	2622.2279	2622.2126	6	0	K.DVTGPDEEESFLYFAYGSNLTER.I

No match to: 726.4232, 1148.5822



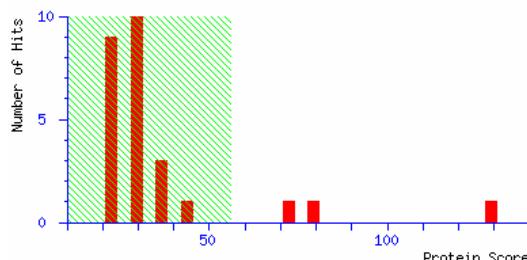
II. The result from co-migration of C7orf24 and ANXA2 (Results from H819_022IEF)

a

Database : SwissProt 2010_04 (516081 sequences; 181677051 residues)
 Taxonomy : Homo sapiens (human) (20280 sequences)
 Timestamp : 8 Apr 2010 at 09:43:08 GMT
 Top Score : 129 for **Mixture 1**, ANXA2_HUMAN + GGCT_HUMAN

Mascot Score Histogram

Protein score is $-10 \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 56 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<		0.05
Max. number of hits		10

[Re-Search All](#) [Search Unmatched](#)

1. Mixture 1 Total score: 129 Expect: 2.6e-09 Matches: 11
 Components (only one family member shown for each component):
ANXA2_HUMAN Mass: 38812 Score: 78 Expect: 0.00029 Matches: 6
 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2
GGCT_HUMAN Mass: 21226 Score: 76 Expect: 0.00057 Matches: 5
 Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1

b.1

(*MATRIX*) Mascot Search Results

Protein View

Match to: ANXA2_HUMAN Score: 78 Expect: 0.00029
 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2
 Nominal mass (M_r): 38812; Calculated pI value: 7.57
 NCBI BLAST search of **ANXA2_HUMAN** against nr
 Unformatted sequence string for pasting into other applications
 Taxonomy: **Homo sapiens**
 Fixed modifications: Carboxymethyl (C)
 Variable modifications: Acetyl (Protein N-term), Oxidation (M), Propionamide (C)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Number of mass values searched: 11
 Number of mass values matched: 6
 Sequence Coverage: 19%

Matched peptides shown in **Bold Red**

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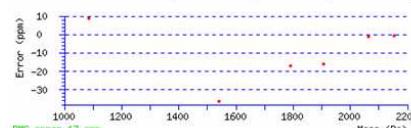
1 MSTVHEILCK LSLEGDHSTP PSAYGSVKAY TNFDAERDAL NIETAIKTKG
51 VDEEVTIVNLL THRSNAQRQRI AFAVQRRRK KELASALKSA LSGHLETVIL
101 GLLKTPTAQYD ASELKASMKG LTDEDSLIE IICSRNTQEL QEINRNUVKEM
151 YKTDLEKDIID SDTSGDFRKL MVALAKGRRA EDGSVIDYEL IDQDARDLYD
201 AGVKKRGKTIDV PKWISIMTER SVPHLQKVFD RYKSYSYIMM LESIRKEVKG
251 DLENNAFLNLV QCIGQNPKLYF ADRLYDSMKGKTRDKVLLR INVSRSEVDM
301 LKIRSEFKRK YGKSLYYVIQ QDTIKGDYQKA LLYLCGGDD
  
```

Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
29 - 37	1086.4945	1085.4873	1085.4778	9	0	K.AYTNFDAER.D
50 - 63	1542.7928	1541.7855	1541.8413	-36	0	K.GVDEEVTIVNLLTNR.S
120 - 135	1791.8493	1790.8420	1790.8720	-17	0	K.GLCTDEEDSLLIEI C SR.T Propionamide (C)
180 - 196	1908.8515	1907.8443	1907.8748	-16	0	R.AEDGSVIDY E LIDQ D AR.D
173 - 196	2064.3809	2063.9736	2063.9760	-1	1	R.RAEDGSVIDY E LIDQ D AR.D
29 - 47	2155.0636	2154.0584	2154.0593	-0	1	K.AYTNFDAERDALNIETAIK.T

No match to: 1253.5956, 1596.7312, 1772.9007, 1975.8828, 2623.2076



b.2

{MATRIX
SCIENCE} Mascot Search Results

Protein View

```

Match to: GCGT_HUMAN Score: 76 Expect: 0.00057
Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GCGT PE=1 SV=1

Nominal mass (Mr): 21226; Calculated pI value: 5.07
NCBI BLAST search of GCGT_HUMAN against nr
Unformatted sequence string for pasting into other applications

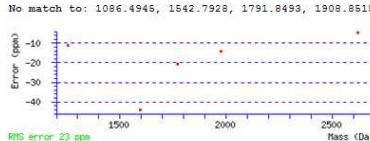
Taxonomy: Homo sapiens

Fixed modifications: Carboxymethyl (C)
Variable modifications: Acetyl (Protein N-term),Oxidation (M),P
Cleavage by Trypsin: cuts C-term side of KR unless next residue
Number of mass values searched: 11
Number of mass values matched: 5
Sequence Coverage: 36%
```

Matched peptides shown in **Bold Red**

51 LDGFGNSQGKT SQTHWGGIAT IFQSPGDFEW GVUVKQANNSN LNSLDEQGV
101 KSGMTVVIEV KVATQEKGKI ICRSYLMTNY ESAPPSPQYK KIICMGAKEN
151 GLBLEYQEKL KAIEPNNDYTG KVSEEIEDII KKGETQTL

Sort Peptides By	C Residue Number	Increasing Mass	Decreasing Mass
Start - End	Observed	Mr (expt)	Mr (calc)
35 - 45	1258.5956	1252.5883	1252.6023
46 - 59	1596.7312	1595.7239	1595.7944
31 - 45	1727.9007	1771.8934	1771.9304
124 - 140	1978.8828	1974.8755	1974.9033
8 - 30	2623.2079	2622.2003	2622.2126
		ppm	Miss
		-11	0
		-44	1
		-21	1
		-14	0
		-5	0
			DVTGHDDEESFPSSPPSQVK.K
			NPSAAFFCVC.R
			L Propionamide (C)
			YVQHLSRPAFFCVC.R
			L Propionamide (C)



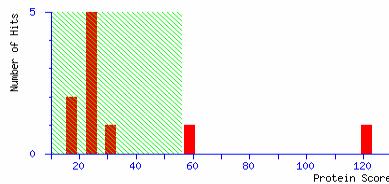
III. Exclusive expression of ANXA2 (results from b02_B692_IEF)

a.

Database	: SwissProt 2010_04 (516081 sequences; 181677051 residues)
Taxonomy	: Homo sapiens (human) (20280 sequences)
Timestamp	: 8 Apr 2010 at 11:06:05 GMT
Top Score	: 121 for ANXA2_HUMAN , Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=

Mascot Score Histogram

Protein score is $-10 \times \text{Log}(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 56 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As Concise Protein Summary Help

	Re-Search All	Search Unmatched
1.	ANXA2_HUMAN	Mass: 38812 Score: 121 Expect: 1.6e-08 Matches: 8 Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2
	ANXA2L_HUMAN	Mass: 38809 Score: 47 Expect: 0.39 Matches: 4 Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2
	FWCH1_HUMAN	Mass: 81276 Score: 31 Expect: 16 Matches: 4 FLYWNC1-type zinc finger-containing protein 1 OS=Homo sapiens GN=FLYWNC1 PE=1 SV=1

b

{MATRIX SCIENCE} Mascot Search Results

Protein View

Match to: ANXA2_HUMAN Score: 121 Expect: 1.6e-08
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2

Nominal mass (M_r): 38612; Calculated pI value: 7.57
NCBI BLAST search of [ANXA2_HUMAN](#) against nr
Unformatted sequence string for pasting into other application

Taxonomy: [Homo sapiens](#)

Fixed modifications: Carboxymethyl
Variable modifications: Acetyl (Pr)

Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr (expt)	Mr (cal)	ppm	Miss Sequence
137 - 205	1036.6430	1540.5451	1539.5449	+10	K...L...YD...V...I...
138 - 206	1036.6430	1540.5451	1539.5449	+10	K...L...YD...V...I...
80 - 63	1542.8252	1541.8179	1541.8413	-15	K...GVDEETV...P...T...W...
153 - 168	1811.8548	1810.8479	1810.8565	-6	K...T...LELD...II...SDTS...R...
11 - 28	1844.8773	1843.8901	1843.8956	-3	K...L...SE...G...V...A...V...A...
180 - 196	1963.8548	1962.8549	1962.8549	+0	K...L...SE...G...V...I...L...D...
179 - 196	2065.0014	2063.9942	2063.9760	+9	K...RAEDGSV...I...L...D...Q...D...

