Identified Human Platelet Proteins

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
1.	IPI00327469	Y	Y	0.97	1	5	4	22	31

*Des: Alpha-2-HS-glycoprotein precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 5 2 22.06%

Seq	Charge	Xcor	Delta	Probility	PepHits
LGGEEVSVACK	+2	3.357	0.384	0.9998	5
QQAEHAVEGDCDFHILK	+3	3.405	0.387	0.9997	1
QQAEHAVEGDCDFHILKQDGQFR	+3	3.147	0.472	1.0000	5
HAFSPVASVESASGEVLHSPK	+3	5.625	0.611	1.0000	10
VGQPGDAGAAGPVAPLCPGR	+2	4.644	0.620	1.0000	6

MASCOT:(PepMatched Observed.Hits Coverage) 4 2 22.06%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LGGEEVSVACK	+2	546.2737	1090.5329	1090.5328	0	66	7
HAFSPVASVESASGEVLHSPK	+3	712.6939	2135.0599	2135.0647	0	86	13
QQAEHAVEGDCDFHILKQDGQFR	+3	891.0836	2670.2288	2670.2244	0	42	4
VGQPGDAGAAGPVAPLCPGR	+2	895.4554	1788.8962	1788.8940	0	101	6

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
2.	IPI00200886	Y	Y	0.14	3	2	3	4	6

*Des: Neuronal C-SRC tyrosine-specific protein kinase

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 9.23%

Seq	Charge	Xcor	Delta	Probility	PepHits
KEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL	+3	4.124	0.518	1.0000	1
SDVWSFGILLTELTTK	+2	2.977	0.489	0.9982	3

MASCOT:(PepMatched Observed.Hits Coverage) 3 3 6.7%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EVLDQVER	+2	494.2628	986.5110	986.5032	0.01	55	6
LIEDNEYTAR	+2	612.3037	1222.5929	1222.5829	0.01	42	4
SDVWSFGILLTELTTK	+2	905.5005	1808.9865	1808.9560	0.03	57	2

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
3.	IPI00358351	Y	Y	0.37	2	12	12	17	21

*Des: PREDICTED: similar to Diap1 protein

SEQUEST:(PepMatched Observed.Hits Coverage) 12 2 13.1%

Seq	Charge	Xcor	Delta	Probility	PepHits
EMVSQYLHTSK	+2	3.771	0.480	0.9999	1
FPDELAHVEK	+2	2.998	0.402	0.9988	3
KSEGVTTILEEAK	+2	2.792	0.288	0.9810	1
SAMMYIQELR	+2	2.702	0.305	0.9894	2
TAQNLSIFLGSFR	+2	3.552	0.499	0.9998	1
VQLNVFDEQGDEDFFDLK	+2	5.578	0.634	1.0000	1
KLSVEEFFMDLHNFR	+3	4.407	0.393	0.9999	2
HLQIDIEGLVDQMIDK	+2	5.830	0.457	1.0000	3
TMLETEEGILLLVR	+3	3.607	0.198	0.9919	2
AEPHFLSILQHLLLVR	+2	5.420	0.658	1.0000	4
SENFSSLLELTLLVGNYMNAGSR	+2	5.234	0.693	1.0000	1
LQDLQGEKDALDSEK	+2	4.193	0.514	0.9930	2

MASCOT:(PepMatched Observed.Hits Coverage) 12 2 10.92%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
FPDELAHVEK	+2	592.81	1183.61	1183.59	0.02	60	3
EMVSQYLHTSK	+2	661.83	1321.64	1321.63	0.01	48	1
LQDLQGEKDALDSEK	+2	844.93	1687.84	1687.83	0.01	89	1
KSEGVTTILEEAK	+2	702.89	1403.76	1403.75	0.01	56	1
SAMMYIQELR	+2	621.30	1240.59	1240.59	0	54	3
ELGDYFVFDPK	+2	665.32	1328.63	1328.63	0	43	1
TAQNLSIFLGSFR	+2	727.40	1452.78	1452.77	0.01	54	3
TMLETEEGILLLVR	+3	539.64	1615.89	1615.89	0	45	2
LSVEEFFMDLHNFR	+2	892.43	1782.84	1782.84	0	100	2
HLQIDIEGLVDQMIDK	+2	933.99	1865.97	1865.96	0.01	112	3
AEPHFLSILQHLLLVR	+2	943.56	1885.10	1885.09	0.01	110	4
KLSVEEFFMDLHNFR	+3	637.99	1910.94	1910.93	0.01	42	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
4.	IPI00231770	Y	Y	0.29	1	3	4	6	6

*Des: cAMP-dependent protein kinase type I-alpha regulatory subunit

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 14.72%

Seq	Charge	Xcor	Delta	Probility	PepHits
RSENEEFVEVGR	+2	3.195	0.234	0.9873	1
GAISAEVYTEEDAASYVR	+2	2.841	0.301	0.9857	1
IVVQGEPGDEFFIILEGTAAVLQR	+3	5.853	0.476	1.0000	4

MASCOT:(PepMatched Observed.Hits Coverage) 4 2 17.57%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SENEEFVEVGR	+2	647.80	1293.58	1293.58	0	55	2
VSILESLDKWER	+2	737.90	1473.79	1473.78	0.01	47	2
LTVADALEPVQFEDGQK	+2	930.48	1858.94	1858.93	0.01	89	1
IVVQGEPGDEFFIILEGTAAVLQR	+3	867.81	2600.40	2600.38	0.02	62	3

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
5.	IPI00359084	Y	N	0.17	1	2	0	2	0

*Des: 53 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 5.27%

Seq	Charge	Xcor	Delta	Probility	PepHits
IASEQHILQR	+2	3.170	0.310	0.9967	1
VYAALGNHDFHPK	+2	3.018	0.453	0.9990	1

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
6.	IPI00192302	Y	Y	0.38	4	7	6	12	22

*Des: 99 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 7 5 14.76%

Seq	Charge	Xcor	Delta	Probility	PepHits
NSYPHFYDGSEIVVAGR	+3	3.850	0.403	0.9999	1
EQGYIFGDYIER	+2	2.719	0.444	0.9983	1
SLPEGVVDGIEIYSTK	+2	4.505	0.607	1.0000	1

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                        VIFELTYEELLK    +2          4.071       0.372       0.9995      1
                        ESPGNVQIVNGYFVHFFAPQGLPVVPK             +3          4.799       0.636       1.0000      2
                        FPLYNLGFGNNLNYNFLESLALENHGFAR+3                     7.288       0.560       1.0000      1
                        LWAYLTIEQLLEK   +2          4.988       0.504       1.0000      2
            MASCOT:(PepMatched Observed.Hits Coverage)          6           6           11.32%
                        Seq         Charge      ObservedMS                  ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        NSYPHFYDGSEIVVAGR           +3          637.64      1909.90     1909.90     0           41          2
                        SLPEGVVDGIEIYSTK            +2          853.95      1705.89     1705.88     0.01        76          2
                        VIFELTYEELLK    +2          748.92      1495.83     1495.82     0.01        65          2
                        LWAYLTIEQLLEK   +2          810.46      1618.90     1618.90     0           74          2
                        ESPGNVQIVNGYFVHFFAPQGLPVVPK             +3          980.86      2939.55     2939.53     0.02        72          4
                        SMTNINDGLLR     +2          617.31      1232.61     1232.62     0           46          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
7.          IPI00372792             Y           Y           0.32        1           2           5           3           5
*Des:       Serine
            SEQUEST:(PepMatched Observed.Hits Coverage)         2           1           9.55%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        NLLIFEVQQPFLFLLWDQR         +3          5.013       0.468       1.0000      1
                        AETNMAFSPFSIASLLTQVLLGAGDSTK            +2          5.380       0.669       1.0000      2
            MASCOT:(PepMatched Observed.Hits Coverage)          5           2           16.17%
                        Seq         Charge      ObservedMS                  ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        INELLDSLPSDTR   +2          736.89      1471.76     1471.75     0.01        71          1
                        LVLLNAVYLSAK    +2          652.40      1302.79     1302.79     0           60          1
                        DSSEATLSEALTDFSVK           +2          900.43      1798.84     1798.85     0           41          1
                        GVTSVSQIFHSPDLAIR           +2          913.99      1825.97     1825.97     0           64          3
                        NLLIFEVQQPFLFLLWDQR         +3          807.11      2418.32     2418.31     0.01        49          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
8.          IPI00362160             N           Y           0.26        2           0           4           0           44
*Des:       PREDICTED: tubulin, beta 3
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)          4           2           13.31%
                        Seq         Charge      ObservedMS                  ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        IMNTFSVVPSPK    +2          660.4000    1318.7854 1318.6955 0.09        54          1
                        MSSTFIGNSTAIQELFK           +2          937.5349    1873.0552 1872.9291 0.13        61          2
                        FPGQLNADLR      +2          565.8393    1129.6640 1129.5880 0.08        77          76
                        GHYTEGAELVDSVLDVVR          +2          980.0594    1958.1042 1957.9744 0.13        58          16

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
9.          IPI00191502             Y           Y           1.46        1           4           3           5           4
*Des:       Proteasome subunit alpha type 5
            SEQUEST:(PepMatched Observed.Hits Coverage)         4           1           28.04%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        PFGVALLFGGVDEK +2           4.385       0.606       1.0000      2
                        GVNTFSPEGR      +2          2.790       0.245       0.9845      2
                        AIGSASEGAQSSLQEVYHK         +2          4.539       0.608       1.0000      4
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                    LNATNIELATVQPGQNFHMFTK      +3          3.146       0.372       0.9987      1
          MASCOT:(PepMatched Observed.Hits Coverage)    3           1           21.95%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                    GVNTFSPEGR  +2          532.26      1062.51     1062.51     0           41          2
                    AIGSASEGAQSSLQEVYHK     +2          981.49      1960.97     1960.95     0.02        100         5
                    LNATNIELATVQPGQNFHMFTK              +3          825.43      2473.26     2473.24     0.02        56          1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
10.       IPI00190701         Y           Y           2.16        4           14          14          35          79
*Des:     Apolipoprotein E precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)   14          8           45.59%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    MEEQTQQIR   +2          3.689       0.313       0.9990      4
                    GRLEEVGNQAR +2          3.633       0.420       0.9982      8
                    IQASVATNSIASTTVPLENQ    +2          3.819       0.506       1.0000      1
                    GWFEPLVEDMQR +2         3.164       0.399       0.9986      3
                    LGADMEDLR   +2          3.426       0.371       0.9993      4
                    ELEEQLGPVAEETR +2       4.623       0.480       1.0000      2
                    IQASVATNSIASTTVPLEN     +2          3.299       0.478       0.9920      1
                    NEVNTMLGQSTEELR         +2          4.614       0.592       1.0000      2
                    IKGWFEPLVEDMQR +2       4.237       0.518       1.0000      4
                    SKMEEQTQQIR +2          3.681       0.472       1.0000      3
                    DRLEEVREQMEEVR +2       3.552       0.459       0.9980      3
                    LGQYRNEVNTMLGQSTEELR    +3          4.413       0.506       1.0000      1
                    TANLGAGAAQPLR +2        3.605       0.443       0.9996      6
                    LGPLVEQGR   +2          3.494       0.453       1.0000      10
          MASCOT:(PepMatched Observed.Hits Coverage)    14          10          38.99%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                    EVQAAQAR    +2          436.7358    871.4570    871.4511    0.01        68          4
                    DADDLQKR    +2          480.7439    959.4733    959.4672    0.01        51          2
                    GWFEPLVEDMQR +2         753.8603    1505.7060   1505.6972   0.01        47          4
                    LEEVGNQAR   +2          508.2668    1014.5191   1014.5094   0.01        47          4
                    MEEQTQQIR   +2          581.7835    1161.5525   1161.5448   0.01        59          12
                    LGADMEDLR   +2          510.2483    1018.4820   1018.4753   0.01        86          12
                    ELEEQLGPVAEETR +2       800.4036    1598.7926   1598.7787   0.01        62          8
                    GRLEEVGNQAR +2          614.8276    1227.6407   1227.6319   0.01        59          12
                    NEVNTMLGQSTEELR         +2          860.9189    1719.8233   1719.8097   0.01        97          8
                    IKGWFEPLVEDMQR +2       874.4535    1746.8924   1746.8763   0.02        72          8
                    SKMEEQTQQIR +2          689.3481    1376.6817   1376.6718   0.01        71          6
                    TANLGAGAAQPLR +2        620.3486    1238.6827   1238.6731   0.01        71          6
                    LGPLVEQGR   +2          484.7828    967.5511    967.5450    0.01        58          11
                    TANLGAGAAQPLRDR         +3          504.2769    1509.8090   1509.8011   0.01        61          6

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
11.       IPI00363974         Y           Y           0.81        4           20          16          45          41
*Des:     Gelsolin
          SEQUEST:(PepMatched Observed.Hits Coverage)   20          12          39.11%
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                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        DGGQTTPASTR             +2          3.442       0.407       0.9993      5
                        AGALNSNDAFVLK           +2          3.750       0.571       1.0000      5
                        EVQGFESSTFQGYFK                     +2          4.579       0.620       1.0000      7
                        VSNSGGSMSVSLVADENPFAQSALR           +3          5.736       0.461       1.0000      4
                        DSQEEEKTEALTSAK                     +2          4.512       0.531       1.0000      2
                        TPSAAYLWVGTGASDAEKTGALELLK          +3          4.788       0.584       1.0000      1
                        VEKFDLVPVPPNLYGDFFTGDAYVILK         +3          3.951       0.485       0.9998      1
                        GGTSRDGGQTTPASTR                    +3          3.386       0.252       0.9865      1
                        DSQEEEKTEALTSAKR                    +3          4.356       0.496       1.0000      1
                        AALKTASDFISK            +3          3.390       0.320       0.9991      4
                        VPFDAATLHTSTAMAAQHGMDDDGTGQK                                +3          6.460       0.620       1.0000      4
                        SEDCFILDHGR             +2          2.959       0.504       0.9996      2
                        QTQVSVLPEGGETPLFK                   +2          4.013       0.516       1.0000      3
                        AQHVQVEEGSEPDGFWEALGGK                          +2          6.459       0.587       1.0000      4
                        KGGVASGFK               +2          2.689       0.335       0.9950      9
                        HVVPNEVVVQR             +2          3.061       0.531       0.9998      21
                        VSETRPSTMVVEHPEFLK                  +3          4.017       0.310       0.9997      2
                        RTPITVVR                +2          2.837       0.231       0.9880      9
                        AGKEPGLQIWR             +3          3.967       0.324       0.9999      15
                        KMDAHPPR                +2          2.740       0.340       0.9968      16
            MASCOT:(PepMatched Observed.Hits Coverage)                  16          9           21.63%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        DGGQTTPASTR             +2          545.7634    1089.5123   1089.5051   0.01        55          4
                        DSQEEEKTEALTSAK                     +2          833.4040    1664.7934   1664.7740   0.02        76          4
                        TASDFISK                +2          434.7271    867.4397    867.4338    0.01        50          5
                        AGALNSNDAFVLK           +2          660.3582    1318.7019   1318.6880   0.01        57          5
                        EVQGFESSTFQGYFK                     +2          877.4142    1752.8138   1752.7994   0.01        88          8
                        TGALELLK                +2          423.2472    844.4798    843.5065    0.97        46          3
                        SEDCFILDHGR             +2          646.2953    1290.5761   1290.5663   0.01        59          1
                        QTQVSVLPEGGETPLFK                   +2          915.4914    1828.9682   1828.9570   0.01        58          3
                        LKATQVSK                +2          437.7749    873.5353    873.5283    0.01        63          4
                        KGGVASGFK               +2          426.4628    850.9110    849.4708    1.44        63          9
                        DSQEEEKTEALTSAKR                    +3          607.9705    1820.8897   1820.8752   0.01        56          1
                        AALKTASDFISK            +2          626.3539    1250.6933   1250.6870   0.01        41          2
                        HVVPNEVVVQR             +2          638.3660    1274.7174   1274.7095   0.01        64          10
                        AGKEPGLQIWR             +3          418.9058    1253.6955   1253.6880   0.01        46          7
                        RTPITVVR                +2          471.3008    940.5870    940.5818    0.01        41          4
                        KMDAHPPR                +2          476.2481    950.4817    950.4756    0.01        44          13

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
12.         IPI00372796             Y           Y           0.33        1           3           2           4           2
*Des:       PREDICTED: similar to mitochondrial carrier homolog 2
            SEQUEST:(PepMatched Observed.Hits Coverage)                 3           1           9.22%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        SAATLITHPFHVITLR+2          3.434       0.417       0.9984      2
                        VLIQVGYEPLPPTIGR                    +2          3.506       0.481       0.9994      1
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		EEGIVGFFAGLIPR		+3	3.075	0.442	0.9993	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	6.4%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VLIQVGYEPLPPTIGR			+2	876.51	1751.00	1751.00	0	52	1	
		SAATLITHPFHVITLR		+2	889.01	1776.01	1776.00	0.01	43	2		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
13.	IPI00363976		Y	Y	1.3	4	6	6	21	30		
*Des:	Stomatin											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	7	30.1%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VIAAEGEMNASR		+2	4.192	0.637	1.0000	3				
		LLAQTTLR		+2	2.825	0.206	0.9850	9				
		VQNATLAVANITNADSATR			+2	6.514	0.630	1.0000	4			
		YLQTLTTIAAEK		+2	4.130	0.422	0.9999	2				
		EASMVITESPAALQLR			+2	4.331	0.382	0.9998	2			
		TISFDIPPQEVLTK		+2	3.435	0.425	0.9997	6				
	MASCOT:(PepMatched Observed.Hits Coverage)					6	4	29.75%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AMAAEAEAAR		+2	495.7462	989.4779	989.4600	0.02	54	14		
		VIAAEGEMNASR		+2	624.3132	1246.6119	1246.5975	0.01	67	7		
		YLQTLTTIAAEK		+2	676.3815	1350.7484	1350.7395	0.01	43	2		
		VQNATLAVANITNADSATR			+2	965.5125	1929.0105	1928.9915	0.02	137	5	
		LLAQTTLR		+2	459.2699	916.5252	914.5549	1.97	52	12		
		ALKEASMVITESPAALQLR			+3	677.0509	2028.1309	2027.1084	1.02	48	2	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
14.	IPI00205036		Y	Y	1.54	4	5	5	27	40		
*Des:	Alpha-2-globin chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	5	48.96%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IGGHGGEYGEEALQR			+2	4.392	0.557	1.0000	14			
		FLASVSTVLTSK		+2	3.055	0.482	0.9999	7				
		TYFSHIDVSPGSAQVK			+2	5.139	0.640	1.0000	17			
		AADHVEDLPGALSTLSDLHAHKLR				+3	3.992	0.457	1.0000	3		
		AADHVEDLPGALSTLSDLHAHK				+3	3.904	0.494	1.0000	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					5	4	54.48%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MFAAFPTTK		+2	507.2886	1012.5626	1012.5052	0.06	41	6		
		FLASVSTVLTSK		+2	626.9042	1251.7938	1251.7074	0.09	66	2		
		IGGHGGEYGEEALQR			+3	524.9478	1571.8216	1571.7327	0.09	58	6	
		TYFSHIDVSPGSAQVK			+2	868.4940	1734.9734	1734.8577	0.12	58	10	
		AADHVEDLPGALSTLSDLHAHK				+4	575.0763	2296.2761	2296.1447	0.13	40	2
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
15.	IPI00191366		Y	Y	0.24	1	2	2	3	2		
*Des:	Megakaryocyte-associated tyrosine-protein kinase											

	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	9.89%					
		Seq	Charge	Xcor	Delta	Probility	PepHits						
		SVGVAAPAGGQEAEGSAPTR			+2	4.158	0.569	1.0000	1				
		ALVSTSQLLQFALHVAEGMEYLESK				+3	5.004	0.566	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	9.89%					
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits	
		SVGVAAPAGGQEAEGSAPTR			+2	906.45	1810.89	1810.88	0.01	71	1		
		ALVSTSQLLQFALHVAEGMEYLESK				+3	922.15	2763.42	2763.42	0	64	2	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)											
16.	IPI00554303		N	Y	0.08	1	0	5	0	13			
*Des:	PREDICTED: hypothetical protein XP_579477												
	SEQUEST:(PepMatched Observed.Hits Coverage)												
	MASCOT:(PepMatched Observed.Hits Coverage)					5	1	5.62%					
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits	
		TPLVTIQSSGSFSQK		+2	790.42	1578.83	1578.83	0	102	1			
		GGEFEMMPLGVNK		+2	704.83	1407.65	1407.65	0	61	2			
		DMGLTAFTNLK		+2	605.81	1209.60	1209.61	0	63	5			
		MLIYTILPDGEVIADSVTFQVEK			+3	861.13	2580.36	2580.34	0.02	51	2		
		NLHPLNELFPLAYIEDPK			+3	708.38	2122.12	2122.11	0.01	41	7		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)											
17.	IPI00565738		N	Y	0.25	1	0	7	0	58			
*Des:	Phosphoglycerate kinase 1												
	SEQUEST:(PepMatched Observed.Hits Coverage)												
	MASCOT:(PepMatched Observed.Hits Coverage)					7	1	27.35%					
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits	
		NNQITNNQR		+2	551.2769	1100.5392	1100.5323	0.01	64	12			
		VLNNMEIGTSLYDEEGAK			+2	991.9767	1981.9389	1981.9302	0.01	102	10		
		LGDVYVNDAFGTAHR			+2	817.9078	1633.8010	1633.7848	0.02	66	13		
		VDFNVPMKNNQITNNQR			+2	1016.5145	2031.0144	2030.9955	0.02	65	11		
		AHSSMVGVNLPQK	+2		684.3630	1366.7114	1366.7027	0.01	78	20			
		ALESPERPFLAILGGAK			+2	885.0076	1768.0007	1767.9882	0.01	74	21		
		SVVLMSHLGRPDGVPMPDKYSLEPVAAELK					+3	1079.2491	3234.7256	3234.6780	0.05	72	3

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)											
18.	IPI00337168		Y	Y	0.23	2	2	3	6	8			
*Des:	T-complex protein 1, delta subunit												
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	2	4.02%					
		Seq	Charge	Xcor	Delta	Probility	PepHits						
		IDDVVNT	+2	3.029	0.380	0.9888	1						
		VIDPATATSVDLR		+2	3.829	0.532	1.0000	2					
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	7.31%					
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits	
		VIDPATATSVDLR		+2	679.3769	1356.7392	1356.7249	0.01	45	2			
		GIHPTIISESFQK		+3	486.2693	1455.7862	1455.7721	0.01	41	2			
		SGPPAAGPGNR		+2	490.7530	979.4914	979.4835	0.01	52	13			

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No.       Protein      Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
19.       IPI00393058        Y          Y          0.61       3          6          5          13         16
*Des:     43 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)   6          4          21.21%
                       Seq        Charge     Xcor       Delta      Probility  PepHits
                       GGSLSNGDPDLQLK                   +2         4.240      0.415      0.9997     4
                       IVEENALAPDFSK    +2         3.056      0.355      0.9961     1
                       LVSDSLANIVKPQK   +2         3.953      0.439      0.9997     1
                       YPPVTTFSGYLLYR   +2         2.833      0.403      0.9955     1
                       IPYLGVYIFK       +2         3.081      0.475      0.9997     1
                       SLTELVESIVEMK    +2         3.883      0.497      0.9999     3
          MASCOT:(PepMatched Observed.Hits Coverage)    5          4          17.42%
                       Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                       GGSLSNGDPDLQLK                   +2         700.86     1399.70    1399.69    0.01       73         4
                       IVEENALAPDFSK    +2         716.87     1431.73    1431.72    0.01       55         1
                       LVSDSLANIVKPQK   +2         756.44     1510.87    1510.87    0          81         3
                       IPYLGVYIFK       +2         606.86     1211.70    1211.70    0          43         1
                       SLTELVESIVEMK    +2         739.39     1476.77    1476.77    0          76         4

No.       Protein      Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
20.       IPI00368053        Y          Y          0.31       1          3          2          4          2
*Des:     Hypothetical LOC363644
          SEQUEST:(PepMatched Observed.Hits Coverage)   3          1          15.84%
                       Seq        Charge     Xcor       Delta      Probility  PepHits
                       VTLAVSDLQK       +2         2.923      0.302      0.9913     1
                       VAEGVFETEAPGGYK                  +2         3.342      0.418      0.9982     1
                       LGNDFMGLTLASSQAVSNAR  +2         4.502      0.606      1.0000     2
          MASCOT:(PepMatched Observed.Hits Coverage)    2          1          12.21%
                       Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                       VAEGVFETEAPGGYK                  +2         777.38     1552.74    1552.74    0          50         1
                       LGNDFMGLTLASSQAVSNAR  +3         684.67     2051.00    2051.01    0          56         1

No.       Protein      Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
21.       IPI00471645        Y          Y          0.43       1          3          2          4          4
*Des:     Dolichyl-di-phosphooligosaccharide-protein glycotransferase
          SEQUEST:(PepMatched Observed.Hits Coverage)   3          1          8.9%
                       Seq        Charge     Xcor       Delta      Probility  PepHits
                       NTLLIAGLQAR      +2         3.516      0.350      0.9992     1
                       LPDVYGVFQFK      +2         3.304      0.500      0.9999     2
                       WVPFDGDDIQLEFVR                  +2         3.392      0.367      0.9983     2
          MASCOT:(PepMatched Observed.Hits Coverage)    2          1          5.34%
                       Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                       NTLLIAGLQAR      +2         585.36     1168.70    1168.69    0.01       52         2
                       LPDVYGVFQFK      +2         656.85     1311.69    1311.69    0          48         4

No.       Protein      Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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22.	IPI00200898		Y	Y	0.3	1	5	3	7	12		
*Des:	Ezrin-radixin-moesin binding phosphoprotein 50											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	2	18%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AVDPDSPAEASGLR		+2	3.893	0.414	0.9995	1				
		AQEKSEHTEPPAAADTKK			+3	3.382	0.325	0.9987	4			
		AQEKSEHTEPPAAADTK			+3	3.154	0.426	0.9999	2			
		KAGDQNEAEKSHLER			+3	3.892	0.416	1.0000	4			
		LLVVDKETDEFFKK		+3	3.187	0.459	1.0000	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	2	9.41%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AVDPDSPAEASGLR		+2	692.8450	1383.6754	1383.6630	0.01	80	4		
		AQEKSEHTEPPAAADTKK			+4	485.2481	1936.9633	1936.9490	0.01	42	6	
		AQEKSEHTEPPAAADTK			+3	603.9642	1808.8709	1808.8540	0.02	43	4	

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
23.	IPI00285606		Y	Y	0.7	1	3	2	3	2		
*Des:	Cell division cycle 42											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	22.56%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TPFLLVGTQIDLRDDPSTIEK			+2	4.430	0.606	0.9955	2			
		GLKNVFDEAILAALEPPEPKK			+3	4.481	0.671	1.0000	2			
		GLKNVFDEAILAALEPPEPK			+3	3.153	0.443	0.9863	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	22.56%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GLKNVFDEAILAALEPPEPKK			+3	760.43	2278.27	2278.26	0.01	41	1	
		TPFLLVGTQIDLRDDPSTIEK			+3	786.76	2357.25	2357.25	0	45	1	

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
24.	IPI00188505		Y	Y	0.6	1	4	4	11	12		
*Des:	Enoyl Coenzyme A hydratase domain containing 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	1	18.04%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DVLETLWGGPANLEAIAK			+2	3.744	0.335	0.9919	2			
		ILEQFPGGSIDLQK		+2	4.608	0.259	0.9992	3				
		VIELENWTEGK		+2	3.414	0.501	1.0000	5				
		ELYLEEALQNER		+2	4.169	0.452	1.0000	3				
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	14.98%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LVEIIGSR	+2	443.77	885.53	885.53	0	51	4			
		VIELENWTEGK		+2	659.33	1316.65	1316.66	0	60	5		
		ILEQFPGGSIDLQK		+2	772.93	1543.84	1543.82	0.02	94	3		
		ELYLEEALQNER		+2	753.88	1505.75	1505.74	0.01	71	4		

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
25.	IPI00371204		Y	N	0.22	1	2	0	2	0		
*Des:	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa											

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 10.32%

Seq	Charge	Xcor	Delta	Probility	PepHits
VIGLSSDLQQVGGASAR	+2	4.873	0.623	1.0000	1
IQDALSTVLQYAEDVLSGK	+2	6.077	0.647	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
26.	IPI00231925	Y	Y	0.54	1	5	9	23	111

*Des: Guanine nucleotide-binding protein G(i), alpha-2 subunit

SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 21.66%

Seq	Charge	Xcor	Delta	Probility	PepHits
YDEAASYIQSK	+2	4.312	0.507	1.0000	7
IAQSDYIPTQQDVLR	+2	4.433	0.536	1.0000	5
AMGNLQIDFADPQR	+2	4.005	0.446	0.9998	4
EYQLNDSAAYYLNDLER	+3	3.998	0.431	0.9999	3
AVVYSNTIQSIMAIVK	+2	5.668	0.632	1.0000	5

MASCOT:(PepMatched Observed.Hits Coverage) 9 1 31.94%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
YDEAASYIQSK	+2	637.80	1273.59	1273.58	0.01	81	9
MFDVGGQR	+2	454.25	906.49	908.42	-1.92	47	36
IAQSDYIPTQQDVLR	+2	873.96	1745.91	1745.89	0.02	68	5
TTGIVETHFTFK	+2	690.87	1379.72	1379.71	0.01	66	12
LLLLGAGESGKSTIVK	+3	529.32	1584.94	1584.94	0	47	63
AMGNLQIDFADPQR	+2	788.39	1574.76	1574.75	0.01	72	4
LLLLGAGESGK	+2	529.32	1056.62	1056.62	0	78	54
AVVYSNTIQSIMAIVK	+2	868.99	1735.97	1735.95	0.02	139	5
NVQFVFDAVTDVIIK	+2	854.48	1706.94	1706.92	0.02	96	9

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
27.	IPI00199867	Y	Y	0.21	2	4	4	4	5

*Des: PREDICTED: similar to Elastin microfibril interfacer 1

SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 5.6%

Seq	Charge	Xcor	Delta	Probility	PepHits
LDTVAGGLQGLR	+2	2.907	0.380	0.9722	2
VSEILSALER	+2	2.876	0.278	0.9894	1
YLLSAVLTGHR	+3	2.311	0.406	0.9993	2
AETAGEAQQAMLEGLQGILGR	+2	5.507	0.622	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 4 2 4.64%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LDTVAGGLQGLR	+2	600.84	1199.67	1198.67	1	66	2
VSEILSALER	+2	558.82	1115.62	1115.62	0	58	2
VAFSAALSLPR	+2	566.33	1130.65	1130.64	0.01	51	1
YLLSAVLTGHR	+2	615.81	1229.60	1228.69	0.91	42	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
28.	IPI00471577	Y	Y	0.59	1	5	4	8	5

*Des: Ubiquinol-cytochrome c reductase core protein I

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          SEQUEST:(PepMatched Observed.Hits Coverage)   5         2         15.36%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    IEEVDAQMVR          +2        3.862     0.431     0.9999    3
                    EVESIGAHLNAYSTR               +2        4.363     0.443     0.9999    2
                    RIPLAEWESR          +3        3.348     0.364     0.9993    3
                    NNGAGYFLEHLAFK      +2        3.286     0.451     0.9995    2
                    VVELLADIVQNISLEDSQIEK         +3        5.950     0.563     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    4         2         12.09%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    IEEVDAQMVR          +2        595.30    1188.58   1188.58   0         65        3
                    EVESIGAHLNAYSTR               +2        823.92    1645.82   1645.81   0.01      58        2
                    IPLAEWESR           +2        550.79    1099.57   1099.57   0         52        1
                    VVELLADIVQNISLEDSQIEK         +3        785.76    2354.26   2354.26   0         50        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
29.       IPI00231927         N         Y         0.21      2         0         6         0         49
*Des:     ADP,ATP carrier protein 1
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)    6         2         23.17%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    GNLANVIR            +2        428.76    855.50    855.49    0.01      42        6
                    VKLLLQVQHASK        +2        682.43    1362.85   1362.83   0.02      74        10
                    AAYFGVVYDTAK        +2        603.30    1204.58   1204.58   0         44        2
                    GAWSNVLR            +2        451.75    901.48    901.48    0         42        6
                    DFLAGGIAAAVSK       +2        610.34    1218.67   1218.66   0.01      86        2
                    YFPTQALNFAFK        +2        723.88    1445.75   1445.73   0.02      85        49

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
30.       IPI00212401         Y         N         0.33      1         3         0         3         0
*Des:     Calumenin precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         1         20.56%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    MDKEETKDWILPSDYDHAEAEAR                 +3        5.384     0.512     1.0000    2
                    EEFTAFLHPEEYDYMK              +2        3.868     0.374     0.9993    1
                    EEIVDKYDLFVGSQATDFGEALVR                +3        5.012     0.504     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
31.       IPI00208454         Y         Y         0.41      2         3         4         9         11
*Des:     PREDICTED: similar to actin-related protein complex 1b
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         2         12.1%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    EHNGQVTGIDWAPESNR             +2        3.043     0.265     0.9949    2
                    TQIAICPNNHEVHIYEK             +2        4.795     0.580     1.0000    4
                    NSVSQISVLSGGK       +2        3.332     0.593     1.0000    8
          MASCOT:(PepMatched Observed.Hits Coverage)    4         1         13.31%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
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		NSVSQISVLSGGK		+2	638.3543	1274.6941	1274.6830	0.01	72	4		
		GSTEGGAATGAGLDSLHK			+2	814.9053	1627.7961	1627.7801	0.02	93	2	
		LDVPKQNSQR		+2	592.8272	1183.6399	1183.6309	0.01	47	1		
		TWKPTLVILR		+3	409.5946	1225.7621	1225.7547	0.01	60	12		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
32.	IPI00207725		Y	Y	0.73	2	7	8	21	21		
*Des:	PREDICTED: similar to purine-nucleoside phosphorylase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					7	3	40.47%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		FEVGDIMLIR		+2	3.835	0.315	0.9996	3				
		LEQFVSILMESIPPR		+3	3.959	0.338	0.9995	4				
		FPAMSDAYDR		+2	3.144	0.361	0.9992	5				
		LTQPQAFDYNEIPNFPQSTVQGHAGR				+3	4.279	0.501	1.0000	1		
		MLGADAVGMSTVPEVIVAR			+2	5.821	0.530	1.0000	7			
		VFGFSLITNK		+2	2.838	0.297	0.9947	9				
		VFHLLGVDTLVVTNAAGGLNPK				+3	4.663	0.454	1.0000	6		
	MASCOT:(PepMatched Observed.Hits Coverage)					8	3	43.87%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		FPAMSDAYDR		+2	586.32	1170.63	1171.50	-0.86	64	5		
		MLGADAVGMSTVPEVIVAR			+2	958.51	1915.01	1914.99	0.02	112	7	
		LTQPQAFDYNEIPNFPQSTVQGHAGR				+3	972.48	2914.43	2914.40	0.03	79	1
		LVFGFLNGR		+2	511.80	1021.58	1021.57	0.01	45	7		
		VFGFSLITNK		+2	563.32	1124.63	1124.62	0.01	43	10		
		FEVGDIMLIR		+2	596.83	1191.64	1191.63	0.01	71	3		
		VFHLLGVDTLVVTNAAGGLNPK				+3	745.76	2234.26	2234.24	0.02	57	5
		LEQFVSILMESIPPR		+3	586.99	1757.95	1757.94	0.01	46	5		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
33.	IPI00206850		Y	Y	0.1	3	3	4	5	5		
*Des:	Unc-13 homolog D											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	3	3.43%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AVQMDSLVPLGELTK			+2	3.781	0.441	0.9990	2			
		IQQQAETTSER		+2	3.548	0.429	0.9992	2				
		HEFPELAPR		+2	2.766	0.432	0.9976	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					4	3	4.33%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NSSLASSR		+2	411.2115	820.4085	820.4039	0	51	1		
		IQQQAETTSER		+2	645.8251	1289.6357	1289.6211	0.01	49	2		
		KDKGQDDFLGNVMLR			+3	579.3022	1734.8847	1734.8722	0.01	44	1	
		LGQPEPNHVK		+2	559.8044	1117.5942	1117.5880	0.01	41	2		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
34.	IPI00231929		N	Y	0.77	1	0	7	0	50		
*Des:	Pyruvate kinase, muscle											
	SEQUEST:(PepMatched Observed.Hits Coverage)											

	MASCOT:(PepMatched Observed.Hits Coverage)					7	1	20.11%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IYVDDGLISLQVK		+2	731.4581	1460.9016	1461.8078	-0.9	65	11		
		LDIDSAPITAR		+2	586.3193	1170.6240	1170.6244	0	65	29		
		GADYLVTEVENGGSLGSK			+2	898.4398	1794.8651	1794.8635	0	90	4	
		GSGTAEVELKK		+2	560.2437	1118.4729	1117.5978	0.88	48	5		
		VNLAMNVGK		+2	473.2630	944.5114	944.5113	0	44	4		
		RFDEILEASDGIMVAR			+2	911.4614	1820.9082	1820.9090	0	59	10	
		KGVNLPGAAVDLPAVSEKDIQDLK				+3	826.4589	2476.3548	2476.3536	0	78	2
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
35.	IPI00231783		Y	Y	0.33	1	2	2	2	2		
*Des:	L-lactate dehydrogenase B chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	11.2%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LIAPVADDETAVPNNK			+2	3.545	0.504	0.9998	1			
		GYTNWAIGLSVADLIESMLK			+2	5.352	0.554	1.0000	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	7.96%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IVVVTAGVR		+2	457.30	912.58	912.58	0	48	2		
		LIAPVADDETAVPNNK			+2	833.94	1665.86	1665.86	0	60	1	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
36.	IPI00365657		Y	Y	1.02	4	11	12	44	37		
*Des:	PREDICTED: similar to vasodilator-stimulated phosphoprotein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					11	11	36.81%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ATVMLYDDSNKR		+2	2.977	0.424	0.9986	6				
		GTGGGLMEEMNAMLAR			+2	4.131	0.516	1.0000	3			
		SSSSVTTSEAHPSVPSSSDDSDLER				+3	4.121	0.552	1.0000	2		
		MKEEIIEVFVQELR		+2	5.249	0.541	1.0000	6				
		RQPEHLER		+2	2.813	0.269	0.9926	2				
		VQIYHNPTANSFR		+2	3.770	0.393	0.9993	5				
		LQPDQQVVINCAIIR		+2	3.732	0.507	0.9998	1				
		VSKQEEASGGPLAPK			+3	4.422	0.464	1.0000	10			
		YNQATPIFHQWR		+2	3.814	0.430	0.9997	8				
		KLQPDQQVVINCAIIR			+3	4.941	0.364	1.0000	8			
		KVSKQEEASGGPLAPK			+2	4.896	0.493	1.0000	9			
	MASCOT:(PepMatched Observed.Hits Coverage)					12	10	36.81%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GTGGGLMEEMNAMLAR			+2	819.3817	1636.7489	1636.7370	0.01	63	3	
		ATVMLYDDSNKR		+2	706.8490	1411.6834	1411.6765	0.01	54	3		
		MKEEIIEVFVQELR		+2	881.9844	1761.9542	1761.9334	0.02	97	5		
		VKQELVEEVRK		+2	678.9028	1355.7911	1355.7772	0.01	50	2		
		LQPDQQVVINCAIIR		+2	855.4744	1708.9342	1708.9294	0	78	1		
		RQPEHLER		+2	532.7866	1063.5586	1063.5523	0.01	44	1		
		YNQATPIFHQWR		+2	780.8950	1559.7755	1559.7633	0.01	75	10		

		VSKQEEASGGPLAPK			+2	749.4046	1496.7947	1496.7834	0.01	77	10	
		VQIYHNPTANSFR		+2	773.8975	1545.7804	1545.7688	0.01	64	3		
		WLPAGTGPQAFSR		+2	694.3640	1386.7134	1386.7044	0.01	62	4		
		KLQPDQQVVINCAIIR			+2	919.5259	1837.0372	1837.0243	0.01	91	8	
		KVSKQEEASGGPLAPK			+2	813.4525	1624.8905	1624.8784	0.01	90	7	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
37.	IPI00209258		Y	Y	0.14	5	15	14	18	19		
*Des:	Spectrin alpha chain, brain											
	SEQUEST:(PepMatched Observed.Hits Coverage)					15	6	9.74%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		HQLLEADISAHEDR		+3	3.698	0.465	1.0000	1				
		SSEEIESAFR		+2	2.884	0.336	0.9617	1				
		KFEEFQTDLAAHEER			+3	3.118	0.430	0.9999	1			
		NQALNTDNYGHDLASVQALQR			+3	4.341	0.491	1.0000	1			
		DVTGAEALLER		+2	2.974	0.306	0.9931	2				
		GVIDMGNSLIER		+2	3.028	0.357	0.9955	2				
		KVEDLFLTFAK		+2	3.222	0.399	0.9990	1				
		AQLADSFHLQQFFR		+2	3.889	0.473	0.9998	2				
		LAALADQWQFLVQK			+2	4.899	0.523	1.0000	2			
		AGTFQAFEQFGQQLLAHGHYASPEIK				+3	5.363	0.496	1.0000	1		
		DLMSWINGIR		+2	2.978	0.328	0.9961	1				
		IAALQAFADQLIAVDHYAK			+3	3.491	0.483	1.0000	1			
		ALINADELANDVAGAEALLDR			+3	3.970	0.476	1.0000	1			
		MTLVASEDYGDTLAAIQGLLK			+2	5.603	0.678	1.0000	1			
		VLETAEDIQER		+2	3.447	0.471	0.9998	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					14	7	8.38%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LFGAAEVQR		+2	495.77	989.53	989.53	0	53	1		
		VLETAEDIQER		+2	651.83	1301.65	1301.65	0	67	1		
		HQLLEADISAHEDR		+3	545.27	1632.80	1632.79	0.01	65	1		
		SSEEIESAFR		+2	578.31	1154.61	1153.53	1.08	45	1		
		DVTGAEALLER		+2	587.31	1172.60	1172.60	0	54	2		
		GVIDMGNSLIER		+2	652.34	1302.66	1302.66	0	52	2		
		KFEEFQTDLAAHEER			+3	617.30	1848.88	1848.86	0.02	43	1	
		NQALNTDNYGHDLASVQALQR			+3	776.72	2327.13	2327.13	0	46	1	
		KVEDLFLTFAK		+2	655.87	1309.73	1309.73	0	56	1		
		LAALADQWQFLVQK			+2	815.96	1629.91	1629.89	0.02	87	2	
		AQLADSFHLQQFFR		+2	854.44	1706.86	1706.85	0.01	62	2		
		DLMSWINGIR		+2	602.81	1203.60	1203.61	0	45	1		
		IAALQAFADQLIAVDHYAK			+3	686.71	2057.11	2057.09	0.02	50	2	
		AGTFQAFEQFGQQLLAHGHYASPEIK				+3	959.15	2874.44	2874.41	0.03	65	1

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
38.	IPI00362243		Y	Y	0.83	1	5	2	6	3		
*Des:	GTP:AMP phosphotransferase mitochondrial											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	1	33.04%				

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                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    VYQIDTVINLNVPFEVIK                  +2          3.503       0.373       0.9992      1
                    GVLETFSGTETNK       +2              3.105       0.347       0.9829      1
                    AYEAQTEPVLQYYQK                     +2          5.040       0.597       1.0000      2
                    VYNIEFNPPK          +2              3.097       0.411       0.9996      2
                    TVGIDDLTGEPLIQR     +2              3.675       0.384       0.9995      1
          MASCOT:(PepMatched Observed.Hits Coverage)    2           1           13.91%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                    AYEAQTEPVLQYYQK                     +2          915.96      1829.90     1829.88     0.02        86          2
                    TVGIDDLTGEPLIQR     +2              813.95      1625.88     1625.86     0.02        64          1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
39.       IPI00214945           Y           Y           0.21        1           3           2           5           4
*Des:     Heparanase
          SEQUEST:(PepMatched Observed.Hits Coverage)   3           2           9.9%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    LYGPDIGQPR              +2          2.730       0.325       0.9936      2
                    LDLIFGLNALLR            +2          3.882       0.341       0.9991      1
                    QVFFGAGNYHLVDENFEPLPDYWLSLLFK                   +3          4.963       0.411       0.9998      1
          MASCOT:(PepMatched Observed.Hits Coverage)    2           2           4.4%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                    LYGPDIGQPR              +2          558.30      1114.58     1114.58     0           49          2
                    LDLIFGLNALLR            +2          679.42      1356.82     1356.81     0.01        52          2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
40.       IPI00207657           Y           Y           0.24        1           7           4           10          6
*Des:     PREDICTED: similar to Ubiquitin carboxyl-terminal hydrolase 5 (Ubiquitin thiolesterase 5) (Ubiquitin-specific processing protease 5)
(Deubiquitinating enzyme 5) (Isopeptidase T)
          SEQUEST:(PepMatched Observed.Hits Coverage)   7           1           14.2%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    SAADSISESVPVGPK                     +2          3.377       0.489       0.9997      1
                    IFQNAPTDPTQDFSTQVAK                 +2          4.856       0.528       1.0000      1
                    DGLGGLPDIVR             +2          2.763       0.379       0.9974      2
                    VTSAVEALLSADSASR                    +2          3.876       0.459       0.9998      1
                    FASFPDYLVIQIK           +2          3.604       0.523       0.9999      2
                    IGEWELIQESGVPLKPLFGPGYTGIR                      +3          5.479       0.425       0.9999      2
                    QQDAQEFFLHLINMVER                   +3          3.675       0.444       0.9999      1
          MASCOT:(PepMatched Observed.Hits Coverage)    4           1           8.47%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                    SAADSISESVPVGPK                     +2          722.37      1442.73     1442.73     0           52          1
                    VTSAVEALLSADSASR                    +2          788.92      1575.82     1575.81     0.01        62          1
                    FASFPDYLVIQIK           +2          770.93      1539.84     1539.83     0.01        85          2
                    IGEWELIQESGVPLKPLFGPGYTGIR                      +3          952.85      2855.53     2855.52     0.01        75          2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
41.       IPI00230986           N           Y           0.35        1           0           3           0           13
*Des:     Splice Isoform 2 of Reticulon 4
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           SEQUEST:(PepMatched Observed.Hits Coverage)
           MASCOT:(PepMatched Observed.Hits Coverage)   3         1         13.66%
                     Seq       Charge    ObservedMS              ExpectedMS          CalculatedMS                  Pepscore  PepHits
                     SPAAPAPSLPPAAAVLPSK           +2        871.50    1740.99   1740.98   0.01      61        6
                     AYLESEVAISEELVQK              +2        904.48    1806.94   1806.93   0.01      44        5
                     LFLVDDLVDSLK        +2        688.89    1375.77   1375.76   0.01      57        2

No.        Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
42.        IPI00193983         Y         Y         0.89      4         34        29        56        49
*Des:      Clathrin heavy chain
           SEQUEST:(PepMatched Observed.Hits Coverage)  34        7         34.46%
                     Seq       Charge    Xcor      Delta     Probility PepHits
                     RPISADSAIMNPASK +2  4.061     0.442     0.9997    2
                     VANVELYYK           +2        2.937     0.344     0.9974    1
                     VSQPIEGHAASFAQFK              +2        3.933     0.543     0.9999    2
                     KFNALFAQGNYSEAAK              +2        5.103     0.555     1.0000    2
                     LLYNNVSNFGR         +2        3.372     0.554     0.9999    3
                     IVLDNSVFSEHR        +2        3.497     0.514     0.9999    1
                     VVGAMQLYSVDR        +2        3.535     0.539     0.9999    1
                     LHIIEVGTPPTGNQPFPK            +2        5.066     0.638     1.0000    2
                     LASTLVHLGEYQAAVDGAR           +2        5.271     0.653     1.0000    3
                     GQFSTDELVAEVEKR               +2        4.393     0.513     0.9999    2
                     TSIDAYDNFDNISLAQR             +2        5.334     0.569     1.0000    2
                     GQFSTDELVAEVEK +2   3.347     0.433     0.9992    1
                     ALEHFTDLYDIK        +2        3.622     0.454     0.9997    2
                     NNLAGAEELFAR        +2        3.350     0.391     0.9899    2
                     VGEQAQVVIIDMNDPSNPIR          +3        3.344     0.420     0.9998    1
                     LAELEEFINGPNNAHIQQVGDR +3     3.783     0.483     1.0000    1
                     ISGETIFVTAPHEATAGIIGVNR +3    5.146     0.624     1.0000    1
                     TLQIFNIEMK          +2        3.147     0.331     0.9974    1
                     SVNESLNNLFITEEDYQALR          +2        5.588     0.562     1.0000    3
                     WLLLTGISAQQNR +2    3.509     0.518     0.9998    2
                     RPLIDQVVQTALSETQDPEEVSVTVK              +3        4.685     0.490     1.0000    1
                     AHMGMFTELAILYSK               +2        4.372     0.533     0.9999    2
                     NLQNLLILTAIK        +2        4.515     0.428     0.9999    1
                     LLEMNLMHAPQVADAILGNQMFTHYDR             +3        7.042     0.619     1.0000    2
                     KFDVNTSAVQVLIEHIGNLDR +3      6.092     0.610     1.0000    2
                     VGYTPDWIFLLR        +2        3.489     0.442     0.9996    1
                     YHEQLSTQSLIELFESFK            +2        6.567     0.619     1.0000    2
                     HNIMDFAMPYFIQVMK              +2        4.530     0.707     1.0000    4
                     WISLNTVALVTDNAVYHWSMEGESQPVK +3         4.706     0.545     1.0000    1
                     FDFVHDLVLYLYR +2    5.200     0.525     1.0000    3
                     FQSVPAQPGQTSPLLQYFGILLDQGQLNK                     +3        5.615     0.614     1.0000    1
                     AFMTADLPNELIELLEK             +3        5.835     0.553     1.0000    2
                     DTELAEELLQWFLQEEK             +3        6.828     0.590     1.0000    4
                     IYIDSNNNPER         +2        3.128     0.398     0.9988    1
           MASCOT:(PepMatched Observed.Hits Coverage)   29        7         26.89%
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Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
IYIDSNNNPER		+2	667.83	1333.64	1333.63	0.01	64	2		
RPISADSAIMNPASK		+2	779.41	1556.81	1556.80	0.01	42	2		
VANVELYYK		+2	549.80	1097.58	1097.58	0	60	1		
LLYNNVSNFGR		+2	648.84	1295.67	1295.66	0.01	54	4		
VVGAMQLYSVDR		+2	669.35	1336.68	1336.68	0	59	2		
IVLDNSVFSEHR		+2	708.37	1414.73	1414.72	0.01	82	1		
VSQPIEGHAASFAQFK			+2	858.94	1715.87	1715.86	0.01	87	4	
KFNALFAQGNYSEAAK			+2	879.95	1757.88	1757.87	0.01	67	2	
LHIIEVGTPPTGNQPFPK			+2	973.03	1944.05	1944.05	0	83	2	
LASTLVHLGEYQAAVDGAR			+2	986.03	1970.05	1970.02	0.03	103	5	
TLQIFNIEMK		+2	618.84	1235.66	1235.66	0	53	2		
NNLAGAEELFAR		+2	653.34	1304.67	1303.65	1.02	69	4		
ALEHFTDLYDIK		+2	732.87	1463.73	1463.73	0	53	4		
WLLLTGISAQQNR		+2	750.42	1498.83	1498.83	0	65	2		
GQFSTDELVAEVEK		+2	776.39	1550.76	1550.75	0.01	60	1		
GQFSTDELVAEVEKR			+2	854.44	1706.86	1706.85	0.01	113	1	
TSIDAYDNFDNISLAQR			+2	971.96	1941.91	1941.91	0	102	2	
ISGETIFVTAPHEATAGIIGVNR			+3	785.09	2352.26	2352.24	0.02	70	1	
LAELEEFINGPNNAHIQQVGDR			+3	822.08	2463.23	2463.21	0.02	58	1	
RPLIDQVVQTALSETQDPEEVSVTVK				+3	961.18	2880.52	2880.51	0.01	54	1
NLQNLLILTAIK		+2	677.43	1352.84	1352.84	0	82	2		
VGYTPDWIFLLR		+2	740.41	1478.80	1478.79	0.01	67	1		
FDFVHDLVLYLYR		+2	850.45	1698.88	1698.88	0	93	3		
AHMGMFTELAILYSK			+2	856.43	1710.85	1710.85	0	80	2	
AFMTADLPNELIELLEK			+2	974.02	1946.02	1946.01	0.01	86	2	
HNIMDFAMPYFIQVMK			+2	992.98	1983.95	1983.94	0.01	94	4	
DTELAEELLQWFLQEEK			+3	707.68	2120.03	2120.03	0	62	2	
YHEQLSTQSLIELFESFK			+3	733.71	2198.10	2198.09	0.01	42	1	
KFDVNTSAVQVLIEHIGNLDR			+3	790.10	2367.27	2367.25	0.02	81	1	

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
43.	IPI00387720	Y	N	0.22	2	3	0	5	0

*Des: 36 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 15.88%

Seq	Charge	Xcor	Delta	Probility	PepHits			
ILGLLDTHLK		+2	2.841	0.272	0.9903	1		
EYFSWEGAFQHVGK			+2	3.375	0.472	0.9997	2	
NAFASVILFGTNNSSSISGVWVFR				+3	4.042	0.436	0.9997	1

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
44.	IPI00191444	Y	Y	0.55	3	6	4	20	8

*Des: 31 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 6 3 27.04%

Seq	Charge	Xcor	Delta	Probility	PepHits		
SGSGTMNLGGSLTR			+2	4.280	0.450	1.0000	2

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                        YDPPLEDGAMPSAR+2        3.020       0.424       0.9992      3
                        KLEVEANNAFDQYR+2        5.279       0.536       1.0000      5
                        SPWSNKYDPPLEDGAMPSAR +3 3.658       0.501       0.9983      1
                        STLNEIYFGK  +2          3.290       0.469       0.9999      4
                        LTSTVMLWLQTNK +2        4.197       0.453       1.0000      10
            MASCOT:(PepMatched Observed.Hits Coverage)      4           2           16.37%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        STLNEIYFGK  +2          586.3450    1170.6754 1170.5920 0.08        41          2
                        YDPPLEDGAMPSAR+2        759.9116    1517.8086 1517.6820 0.13        60          2
                        LEVEANNAFDQYR +2        784.9346    1567.8546 1567.7266 0.13        62          2
                        SPWSNKYDPPLEDGAMPSAR +3             740.0704    2217.1894 2217.0160 0.17        46          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
45.         IPI00202570             Y           Y           0.02        1           2           2           3           4
*Des:       Ras-related protein Rab-2A
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           13.42%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LQIWDTAGQESFR +2        4.516       0.593       1.0000      1
                        TASNVEEAFINTAK +2       4.353       0.583       1.0000      2
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           13.42%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        LQIWDTAGQESFR +2        775.8918    1549.7691 1549.7525 0.02        75          2
                        TASNVEEAFINTAK +2       747.8864    1493.7582 1493.7361 0.02        85          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
46.         IPI00556929             N           Y           0.58        1           0           5           0           17
*Des:       Splice Isoform 1 of Voltage-dependent anion-selective channel protein 3
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      5           2           29.16%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        AEDFQLHTHVNDGTEFGGSIYQR             +3          874.41      2620.22     2620.19     0.03        76          2
                        LTLSALVDGK  +2          508.81      1015.60     1015.59     0.01        74          9
                        LTVDTIFVPNTGK +2        702.90      1403.78     1403.77     0.01        62          6
                        IETSINLAWTAGSNNTR       +2          924.47      1846.93     1846.92     0.01        100         9
                        WNTDNTLGTEISWENK        +2          954.45      1906.89     1906.87     0.02        84          3

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
47.         IPI00390733             N           Y           0.29        1           0           2           0           14
*Des:       PREDICTED: similar to Adenylate kinase 2
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           10.59%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        NGFLLDGFPR  +2          568.30      1134.59     1134.58     0.01        77          16
                        LVSDEMVVELIEK +2        752.41      1502.80     1502.79     0.01        85          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
48.         IPI00471727             Y           Y           0.78        3           4           16          27          150
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Identified Human Platelet Proteins

*Des:	49 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	2	13.86%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VAQLEAQCQEPCKDSVR			+2	4.829	0.537	1.0000	11			
		IHDTTGKDCQDIANKGAK			+2	5.655	0.527	1.0000	41			
		IHDTTGKDCQDIANK		+2	4.867	0.591	1.0000	13				
		ATQQFLVYCEIDGSGNGWTVLQK				+3	4.564	0.475	1.0000	12		
	MASCOT:(PepMatched Observed.Hits Coverage)					16	10	40.22%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DCQDIANKGAK		+2	581.7843	1161.5541	1161.5448	0.01	53	10		
		VGPESDKYR		+2	525.7686	1049.5226	1049.5141	0.01	92	28		
		TSTADYAMFR		+2	581.7669	1161.5193	1161.5124	0.01	46	10		
		DNCCILDER		+2	540.7250	1079.4355	1079.4376	0	46	4		
		YLQDIYTSNK		+2	622.8163	1243.6181	1243.6084	0.01	61	24		
		ITNLKQK	+2	422.7692	843.5239	843.5178	0.01	41	12			
		IHDTTGKDCQDIANK		+2	829.9010	1657.7875	1657.7730	0.01	94	4		
		LDGSVDFKK		+2	504.7743	1007.5340	1007.5287	0.01	44	4		
		YLQDIYTSNKQK		+2	750.8957	1499.7768	1499.7620	0.01	72	6		
		VAQLEAQCQEPCKDSVR			+2	952.4628	1902.9111	1902.8927	0.02	90	14	
		IQLKDWSGR		+2	551.8074	1101.6002	1101.5931	0.01	47	12		
		LDGSVDFKKNWIQYK			+2	920.9908	1839.9670	1839.9519	0.02	60	4	
		IHDTTGKDCQDIANKGAK			+2	957.9788	1913.9431	1913.9265	0.02	111	24	
		KMVEEILKYEALLLTHESSIR			+4	626.3499	2501.3706	2501.3563	0.01	78	8	
		LSIGDGQQHHMGGSK			+2	776.3764	1550.7383	1550.7259	0.01	97	44	
		AIQVYYNPDQPPKPGMIEGATQK				+2	1273.1544	2544.2943	2544.2682	0.03	84	52
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
49.	IPI00471584		Y	Y	0.19	3	4	17	9	71		
*Des:	Heat shock 90kDa protein 1, beta											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	1	11.39%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		KHLEINPDHPIVETLR			+2	4.870	0.511	1.0000	6			
		YHTSQSGDEMTSLSEYVSR			+2	5.837	0.668	1.0000	4			
		HSQFIGYPITLYLEK		+2	4.506	0.527	1.0000	2				
		AVKDLVVLLFETALLSSGFSLEDPQTHSNR					+3	5.637	0.608	1.0000	2	
	MASCOT:(PepMatched Observed.Hits Coverage)					17	7	34.05%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YIDQEELNK		+2	576.28	1150.55	1150.55	0	50	4		
		YESLTDPSKLDSGK		+2	770.39	1538.76	1538.75	0.01	46	3		
		SIYYITGESK		+2	580.80	1159.58	1159.58	0	51	8		
		KHLEINPDHPIVETLR			+2	956.04	1910.06	1910.04	0.02	63	3	
		IDIIPNPQER		+2	597.83	1193.65	1193.64	0.01	55	8		
		VILHLKEDQTEYLEER			+3	672.36	2014.05	2014.04	0.01	41	10	
		DNSTMGYMMAK		+2	624.76	1247.50	1247.50	0	57	4		
		TLTLVDTGIGMTK		+2	675.37	1348.73	1348.73	0	81	3		
		YHTSQSGDEMTSLSEYVSR			+3	726.32	2175.93	2175.94	0	42	2	
		GVVDSEDLPLNISR		+2	757.40	1512.78	1512.78	0	82	4		

		ADLINNLGTIAK		+2	621.86	1241.70	1241.70	0	56	16		
		HFSVEGQLEFR		+2	674.84	1347.66	1347.66	0	66	16		
		NPDDITQEEYGEFYK			+2	924.40	1846.79	1846.79	0	93	9	
		SLTNDWEDHLAVK		+2	764.37	1526.73	1526.74	0	62	6		
		APFDLFENK		+2	540.78	1079.54	1079.53	0.01	42	1		
		HSQFIGYPITLYLEK		+2	904.99	1807.96	1807.95	0.01	80	2		
		DLVVLLFETALLSSGFSLEDPQTHSNR				+3	996.85	2987.54	2987.52	0.02	134	4

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
50.	IPI00365734		N	Y	0.3	1	0	4	0	6		
*Des:	PREDICTED: similar to RIKEN cDNA 2410004H02											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	6.49%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GLDGAVDMGAR		+2	531.26	1060.50	1060.50	0	84	2		
		LLIQESVWDEAMK		+2	781.40	1560.79	1560.79	0	55	2		
		ASLLWALAAALER		+2	692.90	1383.79	1383.79	0	51	1		
		LLWTLESLVTGR		+2	694.40	1386.79	1386.79	0	63	1		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
51.	IPI00364932		Y	Y	1.37	5	8	9	68	63		
*Des:	31 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					8	10	52.12%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ALYLSDNDFEILPPDIGK			+2	4.314	0.571	1.0000	12			
		LTVLPPELGNLDLTGQK			+3	5.739	0.490	1.0000	50			
		NLEVLNFFNNQIEELPTQISSLQK				+3	7.399	0.526	1.0000	11		
		AENNPWVTPIADQFQLGVSHVFEYIR				+4	4.168	0.479	1.0000	5		
		GISSMLDVNGLFSLAHITQLVLSHNK				+3	4.771	0.561	1.0000	9		
		EIGELTQLK		+2	2.693	0.343	0.9974	10				
		DNDLISLPK		+2	3.772	0.292	0.9995	15				
		NQPEVDMSDR		+2	2.801	0.505	0.9999	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					9	12	50%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NQPEVDMSDR		+2	595.76	1189.51	1189.50	0.01	52	2		
		DNDLISLPK		+2	507.78	1013.55	1013.54	0.01	72	7		
		EIGELTQLK		+2	515.80	1029.58	1029.57	0.01	55	10		
		LTTVPPNVAELK		+2	641.38	1280.74	1280.73	0.01	41	9		
		LQILSLR	+2	421.78	841.54	841.54	0	48	32			
		LTVLPPELGNLDLTGQK			+2	904.52	1807.02	1807.01	0.01	99	47	
		ALYLSDNDFEILPPDIGK			+3	674.02	2019.03	2019.02	0.01	44	3	
		GISSMLDVNGLFSLAHITQLVLSHNK				+3	932.18	2793.52	2793.48	0.04	60	6
		NLEVLNFFNNQIEELPTQISSLQK				+3	940.17	2817.48	2817.45	0.03	74	10

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
52.	IPI00209261		N	Y	0.1	1	0	3	0	3		
*Des:	cGMP-inhibited 3',5'-cyclic phosphodiesterase A											

	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	2.41%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		FLVIEAILATDLK		+2	723.44	1444.87	1444.85	0.02	102	1		
		LFEDMGLFEAFK		+2	723.85	1445.69	1445.69	0	65	1		
		FLVIEAILATDLKK		+2	787.48	1572.95	1572.95	0	66	2		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
53.	IPI00390595		N	Y	0.45	1	0	4	0	21		
*Des:	Serine/threonine kinase 25											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	12.67%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AANVLLSEQGDVK		+2	672.80	1343.58	1342.71	0.87	54	18		
		VLFLIPK	+2	415.28	828.55	828.55	0	53	2			
		LADFGVAGQLTDTQIK			+2	838.95	1675.88	1675.88	0	72	2	
		ADIWSLGITAIELAK		+2	800.95	1599.89	1599.89	0	52	8		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
54.	IPI00231864		Y	Y	0.56	1	2	2	3	9		
*Des:	Cytochrome c, somatic											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	17.92%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GITWGEDTLMEYLENPKK			+2	5.030	0.461	1.0000	2			
		GITWGEDTLMEYLENPK			+2	4.960	0.349	0.9999	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	29.24%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TGPNLHGLFGR		+2	584.3656	1166.7167	1167.6148	-0.89	39	4		
		GITWGEDTLMEYLENPKK			+2	1062.5375	2123.0604	2123.0244	0.04	99	5	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
55.	IPI00231865		N	Y	1.51	1	0	2	0	7		
*Des:	Cytochrome c, testis-specific											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	15.09%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TGQAPGFSYTDANK		+2	728.84	1455.67	1455.66	0.01	80	5		
		KTGQAPGFSYTDANK			+2	792.89	1583.77	1583.76	0.01	66	3	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
56.	IPI00204322		Y	N	0.08	1	2	0	4	0		
*Des:	Dynamin-1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	2.71%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LDLMDEGTDAR		+2	3.864	0.431	0.9998	3				
		TIMHLMINNTK		+2	2.737	0.403	0.9981	2				
	MASCOT:(PepMatched Observed.Hits Coverage)											

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No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
57.        IPI00389331           Y          Y          0.05       1          2          2          3          4
*Des:      Latent transforming growth factor beta binding protein 1 precursor
           SEQUEST:(PepMatched Observed.Hits Coverage)  2          1          1.83%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      LYQHAQQPGK            +2         2.862      0.261      0.9877     8
                      VKEVQPGQSQVSYQGLPVQK  +3         4.190      0.488      1.0000     1
           MASCOT:(PepMatched Observed.Hits Coverage)   2          1          1.83%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      LYQHAQQPGK            +2         585.3109   1168.6073 1168.5989 0.01       42         11
                      VKEVQPGQSQVSYQGLPVQK  +3         733.7354   2198.1844 2198.1694 0.01       49         2

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
58.        IPI00194939           Y          N          0.11       1          2          0          5          0
*Des:      PREDICTED: similar to C type lectin
           SEQUEST:(PepMatched Observed.Hits Coverage)  2          1          5.17%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      IVSNASCTTNCLAPLAK                +2         4.178      0.351      0.9990     6
                      AGAHLKGGAK            +2         3.042      0.348      0.9889     4
           MASCOT:(PepMatched Observed.Hits Coverage)

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
59.        IPI00327630           Y          Y          0.03       4          2          8          3          12
*Des:      Dynein heavy chain, cytosolic
           SEQUEST:(PepMatched Observed.Hits Coverage)  2          3          0.88%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      LVPLLLEDGGDAPAALEAALEEK          +3         4.037      0.275      0.9973     1
                      FYFVGDEDLLEIIGNSK                +2         5.313      0.548      1.0000     1
           MASCOT:(PepMatched Observed.Hits Coverage)   8          2          2.35%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      KLEHLITELVHQR         +3         539.32     1614.93    1614.92    0.01       43         1
                      MIVLSLPR              +2         465.27     928.53     927.56     0.97       44         1
                      WQALLVQIR             +2         563.84     1125.67    1125.67    0          42         2
                      NTISLLVAGLK           +2         564.86     1127.70    1127.69    0.01       67         2
                      VDDLLIIEEK            +2         593.84     1185.66    1185.65    0.01       47         1
                      VTFVNFTVTR            +2         592.33     1182.64    1182.64    0          66         4
                      EVQALIAEGIALVWESYK               +3         673.70     2018.09    2018.07    0.02       41         1
                      LVAEDIPLLFSLLSDVFPGVQYHR                    +3         910.17     2727.48    2727.46    0.02       48         2

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
60.        IPI00202651           Y          Y          0.97       4          23         8          97         50
*Des:      Splice Isoform Alpha-E of Fibrinogen alpha/alpha-E chain precursor
           SEQUEST:(PepMatched Observed.Hits Coverage)  23         19         36.18%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      SQLQEGPPEWK           +2         3.130      0.388      0.9997     15
                      TSDSDIFTDIENPSSHVPEFSSSSK                   +2         4.715      0.629      1.0000     8
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GDFANANNFDNTFGQVSEDLRR	+3	3.995	0.472	1.0000	11
MADEAASEAHQEGDTRTTKR	+3	3.775	0.506	1.0000	6
MADEAASEAHQEGDTRTTK	+3	3.320	0.384	0.9999	2
MADEAASEAHQEGDTR	+2	4.602	0.545	1.0000	3
SYKMADEAASEAHQEGDTR	+3	3.300	0.453	1.0000	2
EINLKDYEGQQK	+2	3.663	0.408	0.9997	3
GDFANANNFDNTFGQVSEDLR	+2	4.906	0.427	1.0000	1
NIMEYLRGDFANANNFDNTFGQVSEDLRR	+3	4.869	0.536	1.0000	2
TVLGNDGHREVVK	+2	3.119	0.486	0.9998	4
GLIDEANQDFTNRINK	+2	4.301	0.512	1.0000	18
EINLKDYEGQQKQLEQVIAK	+3	5.576	0.500	1.0000	14
GDFANANNFDNTFGQVSEDLRRR	+3	3.117	0.431	0.9999	2
LVTSKGDKELLIGNEK	+2	4.548	0.532	1.0000	19
GDKELLIGNEKVTSTGTSTTR	+3	4.847	0.457	1.0000	5
MKGLIDEANQDFTNRINK	+2	4.986	0.508	1.0000	5
AQQIQVLQKDVRDQLIDMK	+2	4.012	0.454	0.9999	6
NNKDSNSLTR	+2	2.769	0.260	0.9877	20
RLEVDIDIKIR	+3	3.248	0.318	0.9997	28
GLIDEANQDFTNRINKLK	+3	2.485	0.520	1.0000	15
GLIDEANQDFTNR	+2	2.669	0.387	0.9988	15
MKGLIDEANQDFTNR	+2	4.976	0.620	1.0000	9

MASCOT:(PepMatched Observed.Hits Coverage) 8 16 12.81%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
MADEAASEAHQEGDTR	+2	859.3680	1716.7214	1716.7009	0.02	80	16
GLIDEANQDFTNR	+2	746.8620	1491.7094	1491.6953	0.01	62	6
GDLPGDSRGDSATR	+2	702.3364	1402.6583	1402.6436	0.01	49	4
GDKELLIGNEK	+2	608.3407	1214.6668	1214.6506	0.02	52	1
SQLQEGPPEWK	+2	649.8320	1297.6494	1297.6302	0.02	55	14
EINLKDYEGQQK	+2	732.8808	1463.7470	1463.7256	0.02	74	14
MKGLIDEANQDFTNR	+2	876.4352	1750.8558	1750.8308	0.03	99	4
GLIDEANQDFTNRINK	+2	924.4785	1846.9424	1846.9173	0.03	76	6

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
61.	IPI00203528	Y	Y	0.31	1	2	2	2	3

*Des: PREDICTED: similar to stomatin-like protein 2

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 9.47%

Seq	Charge	Xcor	Delta	Probility	PepHits
AEQINQAAGEASAVLAK	+2	4.729	0.548	1.0000	1
ILEPGLNVLIPVLDR	+2	3.170	0.490	0.9995	1

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 9.47%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
AEQINQAAGEASAVLAK	+2	835.95	1669.88	1669.86	0.02	96	2
ILEPGLNVLIPVLDR	+2	831.01	1660.01	1659.99	0.02	55	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
62.	IPI00191385	Y	Y	0.07	1	3	3	4	4

*Des: Phosphoinositide phosphatase SAC1

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          SEQUEST:(PepMatched Observed.Hits Coverage)   3         1         10.55%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    LEEQDEFEK           +2        2.849     0.238     0.9896    2
                    QDSIDLFLGNYSVDELDSHSPLSVPR              +3        4.162     0.350     0.9999    1
                    LSILLDQVAEMQDELSYFLVDSAGK               +3        6.268     0.554     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    3         2         10.55%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    LEEQDEFEK           +2        583.7734  1165.5322 1165.5139 0.02      42        2
                    LSILLDQVAEMQDELSYFLVDSAGK               +3        928.8207  2783.4402 2783.3938 0.05      79        2
                    QDSIDLFLGNYSVDELDSHSPLSVPR              +3        968.4904  2902.4494 2902.3984 0.05      66        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
63.       IPI00422053         N         Y         0.19      1         0         2         0         9
*Des:     Galpha13
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)    2         1         6.51%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    APMAAQGMVETR        +2        631.31    1260.60   1260.60   0         54        1
                    ILLLGAGESGK         +2        529.32    1056.62   1056.62   0         78        9

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
64.       IPI00202658         Y         Y         1.06      1         5         5         9         8
*Des:     3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)   5         1         24.34%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    DLGLAQDSATSTK       +2        4.001     0.576     1.0000    4
                    MGAVFMDAPVSGGVGAAR            +2        5.035     0.540     1.0000    2
                    TPILLGSVAHQIYR      +2        3.595     0.448     0.9998    4
                    EAGEQVASSPADVAEK              +2        3.700     0.423     0.9998    2
                    TPVGFIGLGNMGNPMAK             +2        4.003     0.435     0.9999    1
          MASCOT:(PepMatched Observed.Hits Coverage)    5         1         24.34%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    DLGLAQDSATSTK       +2        653.83    1305.65   1305.64   0.01      69        4
                    EAGEQVASSPADVAEK              +2        794.38    1586.74   1586.74   0         50        2
                    TPILLGSVAHQIYR      +2        784.46    1566.90   1566.89   0.01      67        5
                    MGAVFMDAPVSGGVGAAR            +2        846.92    1691.83   1691.81   0.02      91        2
                    TPVGFIGLGNMGNPMAK             +2        852.44    1702.87   1702.85   0.02      74        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
65.       IPI00200117         Y         N         0.55      1         2         0         6         0
*Des:     Syntenin-1
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         14.42%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    PSSVNYMVAPVTGNDAGIR           +2        5.630     0.535     1.0000    2
                    SVDNGIFVQLVQANSPASLVGLR                 +2        6.263     0.578     1.0000    4
          MASCOT:(PepMatched Observed.Hits Coverage)
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Identified Human Platelet Proteins

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No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
66.        IPI00421326          Y          Y          0.58       2          3          3          4          4
*Des:      LRRGT00084
           SEQUEST:(PepMatched Observed.Hits Coverage)  3          2          13.31%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      LALQLHPDRNPDDPQAQEK   +3         4.441      0.492      1.0000     1
                      TLEVEIEPGVR           +2         3.165      0.410      0.9992     2
                      FQDLGAAYEVLSDSEK      +2         3.920      0.556      1.0000     1
           MASCOT:(PepMatched Observed.Hits Coverage)   3          2          14.4%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      TLEVEIEPGVR           +2         621.3506   1240.6866 1240.6663 0.02       44         1
                      FQDLGAAYEVLSDSEK      +2         886.4402   1770.8659 1770.8311 0.03       118        2
                      DGMEYPFIGEGEPHVDGEPGDLR          +3         839.3854   2515.1345 2515.0961 0.04       35         2

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
67.        IPI00360589          N          Y          0.08       1          0          2          0          2
*Des:      PREDICTED: complement component 7
           SEQUEST:(PepMatched Observed.Hits Coverage)
           MASCOT:(PepMatched Observed.Hits Coverage)   2          1          2.64%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      FIFVSSANQR            +2         584.81     1167.61    1167.60    0.01       44         2
                      FLFFSSSSNR            +2         596.29     1190.58    1190.57    0.01       47         2

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
68.        IPI00554181          Y          Y          0.51       3          8          7          58         30
*Des:      PREDICTED: zyxin
           SEQUEST:(PepMatched Observed.Hits Coverage)  8          12         23.26%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      EVEELEQLTQQLMQDMEHPQR            +3         3.241      0.187      0.9682     2
                      EKVSSIDLEIDSLSSLLDDMTKNDPFK      +3         5.699      0.558      1.0000     5
                      QHPLPPPAQNQNQVR       +3         5.901      0.548      1.0000     20
                      VNPFRPGDSESPVAAGAQR   +2         5.114      0.479      1.0000     19
                      APSSSQPPPQPQAK+2      3.535      0.485      0.9955     15
                      PHVQPQSVSSANTQPR      +2         5.213      0.587      1.0000     6
                      GPLSQAPTPAPK          +2         3.649      0.561      1.0000     7
                      SVPLEAPSSVGTGSPQPPSFTYAQQK       +3         2.797      0.446      0.9999     3
           MASCOT:(PepMatched Observed.Hits Coverage)   7          12         18.7%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      SPGGPGPLTLK           +2         512.29     1022.57    1022.58    0          60         10
                      GPLSQAPTPAPK          +2         582.33     1162.64    1162.63    0.01       74         9
                      FSPGAPSGPGPQPSQK      +2         769.88     1537.75    1537.75    0          66         2
                      QHPLPPPAQNQNQVR       +3         575.31     1722.89    1722.89    0          66         2
                      VNPFRPGDSESPVAAGAQR   +3         652.33     1953.96    1953.97    0          63         7
                      SVPLEAPSSVGTGSPQPPSFTYAQQK       +3         887.45     2659.32    2659.31    0.01       43         4
                      EVEELEQLTQQLMQDMEHPQR            +3         871.08     2610.20    2610.21    0          66         6

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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69.       IPI00326838         Y         Y         0.26      1         3         4         6         17
*Des:     Signal transducer and activator of transcription 5B
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         1         6.12%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    IQAQFAQLAQLNPQER              +2        4.466     0.362     0.9996    3
                    ATQLLEGLVQELQK +2             3.563     0.356     0.9987    2
                    NYTFWQWFDGVMEVLK              +2        4.184     0.569     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    4         1         7.12%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    LGHYATQLQNTYDR +2             840.41    1678.82   1678.81   0.01      55        6
                    IQAQFAQLAQLNPQER              +2        928.00    1853.99   1853.97   0.02      89        3
                    LAEIIWQNR           +2        571.82    1141.63   1141.62   0.01      59        12
                    FSDSEIGGITIAWK      +2        762.39    1522.77   1522.77   0         59        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
70.       IPI00368072         N         Y         0.35      1         0         2         0         2
*Des:     PREDICTED: similar to phosphoserine aminotransferase 1
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)    2         1         7.92%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    IISNTENLVR          +2        579.83    1157.65   1157.64   0.01      43        1
                    ASLYNAVTTEDVEK +2             770.39    1538.76   1538.75   0.01      65        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
71.       IPI00365813         Y         N         0.38      1         2         0         3         0
*Des:     PREDICTED: similar to voltage-dependent anion channel 1
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         8.82%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    VNNSSLIGLGYTQTLKPGIK          +2        3.623     0.473     0.9994    2
                    VNNSSLIGLGYTQTLK              +2        4.234     0.486     0.9990    2
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
72.       IPI00197344         Y         Y         0.43      1         3         2         5         2
*Des:     Monoglyceride lipase
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         1         13.26%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    DLLQHVNTVQK         +2        3.541     0.404     0.9992    2
                    GAYLLMESSPSQDK+2              3.076     0.394     0.9966    2
                    LLNFVLPNISLGR       +2        3.090     0.414     0.9978    1
          MASCOT:(PepMatched Observed.Hits Coverage)    2         1         7.11%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    DLLQHVNTVQK         +2        647.86    1293.71   1293.70   0.01      52        2
                    YDELAQMLK           +2        555.78    1109.54   1109.54   0         42        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
73.       IPI00373764         N         Y         0.13      1         0         3         0         6
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*Des: PREDICTED: similar to mKIAA1601 protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 2.94%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ELVEAQELAR +2 579.31 1156.61 1156.61 0 47 4
ENVLLSSELQR +2 644.35 1286.69 1286.68 0.01 47 1
IEALQADNDFTNER +2 818.39 1634.76 1634.75 0.01 86 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
74. IPI00372027 Y Y 0.55 1 3 4 13 12
*Des: PREDICTED: similar to coiled-coil-helix-coiled-coil-helix domain containing 3
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 12.08%
Seq Charge Xcor Delta Probility PepHits
VAEELALEQAK +2 4.068 0.406 0.9999 10
YSSVYGASVSDEELK +2 4.361 0.529 1.0000 3
VTFEADENENITVVK +2 4.689 0.493 1.0000 3
MASCOT:(PepMatched Observed.Hits Coverage) 4 2 14.56%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LSENVIDR +2 473.26 944.50 944.49 0.01 53 3
VAEELALEQAK +2 600.83 1199.65 1199.64 0.01 97 9
YSSVYGASVSDEELK +2 817.39 1632.76 1632.75 0.01 97 3
VTFEADENENITVVK +2 854.43 1706.85 1706.84 0.01 72 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
75. IPI00195673 Y Y 0.48 4 9 2 91 6
*Des: PREDICTED: similar to Tubulin, beta 6
SEQUEST:(PepMatched Observed.Hits Coverage) 9 9 31.42%
Seq Charge Xcor Delta Probility PepHits
EVDEQMLAIQNK +2 3.292 0.252 0.9922 1
FPGQLNADLR +2 2.943 0.353 0.9980 9
IMNTFSVMPSPK +2 4.472 0.580 1.0000 3
KLAVNMVPFPR +2 3.160 0.461 0.9997 1
NSSYFVEWIPNNVK +2 4.550 0.448 0.9999 5
ALTVPELTQQMFDAK +2 4.159 0.553 1.0000 4
GHYTEGAELVDSVLDVVR +2 7.165 0.599 1.0000 4
MASTFIGNSTAIQELFK +2 5.435 0.421 0.9631 2
LTTPTYGDLNHLVSATMSGVTTSLR +3 4.059 0.610 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 2 2 9.67%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
MASTFIGNSTAIQELFK +2 929.48 1856.94 1856.93 0.01 115 3
LTTPTYGDLNHLVSATMSGVTTSLR +3 879.12 2634.35 2634.33 0.02 51 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
76. IPI00204261 Y Y 0.44 2 8 6 10 7
*Des: Importin beta-1 subunit
SEQUEST:(PepMatched Observed.Hits Coverage) 8 2 16.04%
Seq Charge Xcor Delta Probility PepHits

Seq	Charge	Xcor	Delta	Probility	PepHits
LQQVLQMESHIQSTSDR	+3	4.063	0.601	1.0000	2
LAATNALLNSLEFTK	+2	5.255	0.528	1.0000	2
YMEAFKPFLGIGLK	+2	2.827	0.342	0.9914	2
SDFDMVDYLNELR	+2	3.349	0.418	0.9994	1
SNEILTAIIQGMR	+3	2.758	0.381	0.9991	2
AAVENLPTFLVELSR	+2	4.233	0.384	0.9996	1
GALQYLVPILTQTLTK	+2	3.323	0.393	0.9987	2
MFQSTAGSGGVQEDALMAVSTLVEVLGGEFLK	+3	5.270	0.542	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 6 2 10.43%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
TVSPDRLELEAAQK	+2	778.92	1555.82	1555.82	0	45	1
LQQVLQMESHIQSTSDR	+3	667.34	1998.98	1998.98	0	45	2
LAATNALLNSLEFTK	+2	803.45	1604.89	1604.88	0.01	105	1
SNEILTAIIQGMR	+3	482.60	1444.77	1444.77	0	43	2
SDFDMVDYLNELR	+2	808.87	1615.72	1615.72	0	59	1
AAVENLPTFLVELSR	+2	829.97	1657.92	1657.90	0.02	69	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
77.	IPI00195678	Y	Y	0.36	4	8	8	27	61

*Des: Platelet glycoprotein V precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 8 9 21.31%

Seq	Charge	Xcor	Delta	Probility	PepHits
LMSLDSGLLANLGALTELR	+2	5.573	0.550	1.0000	10
MVLLEQLFLDHNALR	+2	5.529	0.507	1.0000	13
LTLFENPLEELPEVLFGEMAGLR	+3	5.522	0.583	1.0000	4
LMLSDSHISAIDPGTFNDLVK	+2	3.390	0.402	0.9986	3
LMSLDSGLLANLGALTELRLER	+3	4.192	0.480	1.0000	3
TLPGDVFAALPQLTR	+3	2.925	0.401	0.9999	5
AILDKMVLLEQLFLDHNALR	+3	6.158	0.543	1.0000	3
GVLQSHSFSGMTVLQR	+2	4.394	0.307	0.9986	3

MASCOT:(PepMatched Observed.Hits Coverage) 8 9 16.63%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LMSLDSGLLANLGALTELR	+2	994.0585	1986.1024	1986.0819	0.02	105	27
DLDQNLFQK	+2	560.7892	1119.5638	1119.5560	0.01	44	15
MVLLEQLFLDHNALR	+2	906.5040	1810.9934	1810.9763	0.02	91	38
LMSLDSGLLANLGALTELRLER	+3	795.7797	2384.3172	2384.3096	0.01	63	5
TLPGDVFAALPQLTR	+2	799.9541	1597.8937	1597.8828	0.01	63	18
AILDKMVLLEQLFLDHNALR	+3	785.1173	2352.3301	2351.3035	1.03	81	12
GVLQSHSFSGMTVLQR	+2	873.9680	1745.9214	1745.8882	0.03	63	6
NKISHLPR	+2	482.7908	963.5671	963.5614	0.01	45	9

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
78.	IPI00203390	Y	N	0.19	1	2	0	2	0

*Des: Serine/threonine protein phosphatase PP1-beta catalytic subunit

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.5%

Seq	Charge	Xcor	Delta	Probility	PepHits
IVQMTEAEVR	+2	2.896	0.462	0.9994	1

GVSFTFGADVVSK +2 2.953 0.424 0.9985 1

MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

79. IPI00556943 Y N 0.07 1 2 0 3 0

*Des: PREDICTED: similar to AP2 associated kinase 1

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 2.45%

Seq Charge Xcor Delta Probility PepHits

AQATPSQPLQSSQPK +2 3.583 0.347 0.9977 2

VQTTPPPTIQGQK +2 2.704 0.272 0.9689 1

MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

80. IPI00567369 N Y 1.6 3 0 6 0 66

*Des: Tropomyosin isoform 6

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 6 4 21.73%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

EQAEAEVASLNR +2 658.83 1315.64 1315.64 0 67 27

AREQAEAEVASLNR +2 772.40 1542.78 1542.77 0.01 80 4

IQVLQQQADDAEER +2 821.91 1641.80 1641.80 0 105 16

KIQVLQQQADDAEER +2 885.96 1769.90 1769.89 0.01 107 10

TIDDLEDKLK +2 595.32 1188.63 1188.62 0.01 67 18

MLDQTLLDLNEM +2 718.34 1434.68 1434.67 0.01 72 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

81. IPI00324302 Y Y 0.38 3 3 4 8 9

*Des: Acetyl-CoA acetyltransferase, mitochondrial precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 11.57%

Seq Charge Xcor Delta Probility PepHits

EVYMGNVIQGGEGQAPTR +2 4.959 0.476 1.0000 1

LGTIAIQGAIEK +2 2.927 0.368 0.9974 2

TPIGSFLGSLASQPATK +2 4.538 0.623 1.0000 5

MASCOT:(PepMatched Observed.Hits Coverage) 4 3 13.65%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

EVYMGNVIQGGEGQAPTR +2 953.46 1904.91 1904.90 0.01 90 1

AGIPKEEVKEVYMGNVIQGGEGQAPTR +3 953.46 2857.37 2856.44 0.93 43 1

LGTIAIQGAIEK +2 607.37 1212.72 1212.71 0.01 50 2

TPIGSFLGSLASQPATK +2 837.96 1673.91 1673.90 0.01 111 5

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

82. IPI00201792 Y Y 0.18 3 2 5 24 25

*Des: Protein kinase C, alpha type

SEQUEST:(PepMatched Observed.Hits Coverage) 2 7 5.56%

Seq Charge Xcor Delta Probility PepHits

LLNQEEGEYYNVPIPEGDEEGNVELR +3 4.114 0.412 1.0000 2

LSVEIWDWDR +2 3.641 0.476 0.9999 2

```
          MASCOT:(PepMatched Observed.Hits Coverage)     5          6          11.71%
                    Seq         Charge      ObservedMS               ExpectedMS             CalculatedMS                         Pepscore   PepHits
                    LDNVMLDSEGHIK         +2          735.87      1469.72     1469.72     0           55          6
                    STLNPQWNESFTFK        +2          849.91      1697.81     1697.80     0.01        64          2
                    LSVEIWDWDR            +2          660.38      1318.74     1317.64     1.1         53          2
                    NDFMGSLSFGVSELMK                  +2          881.41      1760.81     1760.81     0           76          5
                    LYFVMEYVNGGDLMYHIQQVGK                        +3          869.09      2604.26     2603.26     1           41          4

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
83.       IPI00200054             Y           Y           0.32        2           4           5           8           6
*Des:     Cytoplasmic aminopeptidase P
          SEQUEST:(PepMatched Observed.Hits Coverage)    4          1          9.77%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    IENVVLVVPAK           +2          3.258       0.386       0.9988      2
                    GHIAVSAAVFPTGTK                   +2          4.356       0.590       1.0000      3
                    GSLTFEPLTLVPIQTK                  +2          4.637       0.480       1.0000      3
                    SAGHHLVPVKENLVDK                  +3          3.541       0.274       0.9970      3
          MASCOT:(PepMatched Observed.Hits Coverage)     5          2          11.82%
                    Seq         Charge      ObservedMS               ExpectedMS             CalculatedMS                         Pepscore   PepHits
                    ASYAVSEAIPK           +2          568.30      1134.59     1134.59     0           43          2
                    IENVVLVVPAK           +2          590.87      1179.72     1179.72     0           42          2
                    GHIAVSAAVFPTGTK                   +2          728.40      1454.79     1454.79     0           66          1
                    GSLTFEPLTLVPIQTK                  +2          872.50      1742.98     1742.98     0           72          2
                    TLSLDEVYLIDSGAQYK                 +2          957.99      1913.97     1913.96     0.01        99          2

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
84.       IPI00325975             Y           N           1.15        1           2           0           2           0
*Des:     Vesicle-associated membrane protein 8
          SEQUEST:(PepMatched Observed.Hits Coverage)    2          1          34.31%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    NLQSEVEGVKNIMTQNVER               +3          3.655       0.544       0.9983      1
                    NKTEDLEATSEHFK        +3          3.319       0.517       0.9975      1
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
85.       IPI00554194             N           Y           1.42        1           0           5           0           12
*Des:     PREDICTED: hypothetical protein XP_346694
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)     5          1          28.03%
                    Seq         Charge      ObservedMS               ExpectedMS             CalculatedMS                         Pepscore   PepHits
                    MADKDGDLIATK          +2          639.33      1276.64     1276.63     0.01        50          4
                    SFDQLTPEESKER         +2          783.38      1564.74     1564.74     0           53          3
                    DIVVQETMEDIDK         +2          767.87      1533.73     1533.72     0.01        57          4
                    MDKEETKDWILPSDYDHAEAEAR                       +3          917.09      2748.26     2748.23     0.03        62          2
                    EEIVDKYDLFVGSQATDFGEALVR                      +3          901.12      2700.33     2700.33     0           46          6

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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86.	IPI00393158		N	Y	0.33	1	0	4	0	24		
*Des:	33 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	12.45%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MELQEIQLK		+2	566.31	1130.60	1130.60	0	74	8		
		LVIIEGDLER		+2	578.77	1155.52	1155.65	-0.12	50	10		
		KLVIIEGDLER		+2	642.88	1283.75	1283.74	0.01	66	16		
		TIDDLEDELYAQK		+2	776.87	1551.73	1551.73	0	71	2		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
87.	IPI00480639		Y	Y	0.05	1	3	2	3	3		
*Des:	Complement C3 precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	3.9%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VHQFFNVGLIQPGSVK			+3	4.109	0.267	0.9984	2			
		LTTIELSDDFDEYIMTIEQVIK			+3	4.088	0.348	0.9994	1			
		WEEPGQQLYNVEATSYALLALLLLK				+3	4.073	0.448	0.9999	1		
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	2.89%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LTTIELSDDFDEYIMTIEQVIK			+3	872.78	2615.31	2615.29	0.02	68	1	
		WEEPGQQLYNVEATSYALLALLLLK				+3	954.86	2861.54	2861.52	0.02	59	2

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
88.	IPI00231013		Y	Y	1.65	1	3	2	4	6		
*Des:	Splice Isoform Short of Cytochrome b5											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	44.55%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		FLEEHPGGEEVLR		+2	3.827	0.508	0.9956	3				
		TYIIGELHPDDRSK		+2	4.280	0.631	1.0000	3				
		STWVILHHKVYDLTK			+3	2.724	0.465	0.9874	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	28.71%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		FLEEHPGGEEVLR		+2	756.38	1510.75	1510.74	0.01	42	6		
		TYIIGELHPDDRSK		+2	822.42	1642.84	1642.83	0.01	66	4		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
89.	IPI00187731		Y	Y	1.75	4	11	9	36	51		
*Des:	Splice Isoform 2 of Tropomyosin beta chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)					11	11	32.17%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LEEAEKAADESER		+2	4.316	0.525	1.0000	6				
		RIQLVEEELDRAQER			+3	4.035	0.420	1.0000	13			
		LATALQKLEEAEKAADESER			+2	5.275	0.639	1.0000	17			
		LVILEGELER		+2	3.163	0.449	0.9995	6				
		QLEEEQQALQK		+2	2.909	0.321	0.9942	2				
		IQLVEEELDR		+2	3.423	0.295	0.9974	2				

Seq	Charge	Xcor	Delta	Probility	PepHits
LEEAEKAADESERGMK	+2	4.437	0.516	1.0000	2
KATDAEADVASLNR	+2	3.254	0.366	0.9974	2
RIQLVEEELDR	+2	2.941	0.265	0.9879	1
LATALQKLEEAEK	+2	3.918	0.406	0.9979	3
KLVILEGELER	+3	4.375	0.374	1.0000	3

MASCOT:(PepMatched Observed.Hits Coverage) 9 2 33.21%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
ATDAEADVASLNR	+2	666.83	1331.64	1331.63	0.01	94	10
QLEEEQQALQK	+2	672.35	1342.68	1342.67	0.01	68	2
SLIASEEEYSTK	+2	678.84	1355.66	1355.65	0.01	83	7
MELQEMQLK	+2	575.29	1148.57	1148.56	0.01	50	3
SLIASEEEYSTKEDKYEEEIK	+3	840.74	2519.20	2519.18	0.02	47	1
KLVILEGELER	+3	433.60	1297.77	1297.76	0.01	57	11
IQLVEEELDR	+2	622.33	1242.65	1242.65	0	78	24
RIQLVEEELDR	+2	700.39	1398.76	1398.75	0.01	49	16
TIDDLEETLASAK	+2	703.36	1404.71	1404.70	0.01	94	3

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
90.	IPI00231953	Y	N	0.08	1	3	0	4	0

*Des: Coatomer protein complex, subunit beta 2

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 6.94%

Seq	Charge	Xcor	Delta	Probility	PepHits
AAESLADPTEYENLFPGLK	+2	4.175	0.431	0.9998	1
FELALQLGELK	+2	3.541	0.435	0.9998	1
VLAAQETHEGVTEDGIEDAFEVLGEIQEIVK	+3	3.671	0.429	0.9998	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
91.	IPI00358464	Y	Y	0.62	1	5	6	6	8

*Des: PREDICTED: similar to Deoxyribose-phosphate aldolase-like

SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 14.43%

Seq	Charge	Xcor	Delta	Probility	PepHits
IPVASVATGFPAGQTHLK	+3	3.481	0.434	0.9995	1
LAVEDGATEIDVVINR	+2	4.945	0.557	1.0000	2
IGASSLLSDIER	+2	3.106	0.345	0.9952	1
TILATGELGSLTNIYK	+2	5.042	0.602	1.0000	1
EELGDEWLTPDLFR	+2	3.863	0.478	0.9997	1

MASCOT:(PepMatched Observed.Hits Coverage) 6 1 15.86%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LAVEDGATEIDVVINR	+2	857.46	1712.90	1712.89	0.01	79	2
ESLVWLSLVK	+2	587.35	1172.68	1172.68	0	50	1
IGASSLLSDIER	+2	630.84	1259.67	1259.67	0	73	2
TILATGELGSLTNIYK	+2	847.48	1692.94	1692.93	0.01	103	1
ETVNATFPVAIVMLR	+2	831.46	1660.91	1659.90	1.01	56	1
EELGDEWLTPDLFR	+2	860.42	1718.83	1718.82	0.01	63	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)

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92.      IPI00231954    Y        Y        0.38     2        2        9        4        13
*Des:    Phosphofructokinase, platelet
         SEQUEST:(PepMatched Observed.Hits Coverage)  2        1        4.73%
                  Seq      Charge   Xcor     Delta    Probility PepHits
                  MGVEAVLALLEATPETPACVVSLR           +3       3.951    0.439    1.0000   1
                  LAIKEPDDKIPK      +3       3.673    0.413    1.0000   6
         MASCOT:(PepMatched Observed.Hits Coverage)   9        4        17.58%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
                  SFEGNLNTYK        +2       586.78   1171.55  1171.55  0        44       1
                  YEASYDMSDVGK      +2       682.79   1363.56  1363.56  0        68       1
                  DLQSNVMHLTEK      +2       707.85   1413.69  1413.69  0        61       1
                  AIGVLTSGGDAQGMNAAVR        +2       894.46   1786.90  1786.90  0        105      6
                  ELVVTNLGFDTR      +2       682.36   1362.71  1362.71  0        74       1
                  MFAIYDGFDGLANGQIK          +2       930.45   1858.89  1858.89  0        110      2
                  IIEVVDAIMTTAQSHQR          +2       956.50   1910.99  1910.99  0        107      2
                  TFVLEVMGR         +2       526.28   1050.55  1050.55  0        50       6
                  NINALLIIGGFEAYLGLLELAAAR           +3       839.15   2514.42  2514.42  0        74       1

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
93.      IPI00231955    N        Y        0.3      1        0        2        0        3
*Des:    Calmodulin
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)   2        1        20.52%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
                  DTDSEEEIREAFR     +2       798.8605 1595.7064 1595.7063 0       39       1
                  VFDKDGNGYISAAELR           +2       878.4319 1754.8492 1753.8634 0.99 89       3

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
94.      IPI00209283    Y        N        0.5      1        3        0        4        0
*Des:    Vesicle-associated membrane protein-associated protein B
         SEQUEST:(PepMatched Observed.Hits Coverage)  3        1        21.05%
                  Seq      Charge   Xcor     Delta    Probility PepHits
                  TEAPVAAKPLTSPLDDAEVKK +3   3.955    0.459    0.9999   2
                  ALPSNSPMAALAASGK           +2       2.794    0.487    0.9995   1
                  GPFTDVVTTNLK      +2       3.388    0.409    0.9997   2
         MASCOT:(PepMatched Observed.Hits Coverage)

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
95.      IPI00371308    Y        Y        0.07     1        3        4        3        4
*Des:    PREDICTED: similar to FYVE and coiled-coil domain containing 1
         SEQUEST:(PepMatched Observed.Hits Coverage)  3        1        2.03%
                  Seq      Charge   Xcor     Delta    Probility PepHits
                  ALQAELSQVR        +2       3.068    0.256    0.9902   5
                  LEYLLQFDQK        +2       3.213    0.352    0.9983   1
                  TPGIYLLIFDNTFSR +2         3.894    0.512    0.9988   1
         MASCOT:(PepMatched Observed.Hits Coverage)   4        1        2.56%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
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                        ALQAELSQVR  +2          557.81      1113.60     1113.61     0           44          5
                        LELDQLEVR   +2          557.81      1113.61     1113.60     0.01        42          2
                        LEYLLQFDQK  +2          648.85      1295.69     1295.68     0.01        49          1
                        TPGIYLLIFDNTFSR +2      879.47      1756.94     1755.92     1.02        45          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
96.         IPI00362416             Y           Y           0.39        2           6           6           21          32
*Des:       Serum deprivation response protein
            SEQUEST:(PepMatched Observed.Hits Coverage)     6           3           14.85%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        YQASTSNTVSK +2          3.496       0.501       1.0000      16
                        HVQAAVLHVDQT +2         3.300       0.609       1.0000      2
                        LVNMLDAVR   +2          2.856       0.327       0.9961      1
                        DNSQVNAVTVHTLLDKLVNMLDAVR           +3          5.590       0.600       1.0000      3
                        LENNHAQLLR  +3          2.625       0.301       0.9961      3
                        RLENNHAQLLR +2          3.968       0.441       1.0000      11
            MASCOT:(PepMatched Observed.Hits Coverage)      6           3           16.03%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        YQASTSNTVSK             +2          593.2948    1184.5750   1184.5673   0.01        70          22
                        IVSVERR  +2             429.7644    857.5143    857.5083    0.01        43          5
                        KSLTPNHQK               +2          526.8000    1051.5855   1051.5774   0.01        49          3
                        DNSQVNAVTVHTLLDKLVNMLDAVR           +3          922.4964    2764.4674   2764.4541   0.01        64          2
                        LENNHAQLLR              +2          604.3335    1206.6524   1206.6469   0.01        74          3
                        RLENNHAQLLR             +3          455.2586    1362.7541   1362.7480   0.01        66          8

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
97.         IPI00361541             Y           Y           0.09        1           3           3           5           6
*Des:       PREDICTED: similar to mKIAA1734 protein
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           1           2.91%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        GLQEGYENSR  +2          2.830       0.445       0.9990      2
                        AALLEAGMPESTEDK         +2          3.770       0.497       0.9998      1
                        SGYPDIGFPLFPLSK+2       3.588       0.560       1.0000      4
            MASCOT:(PepMatched Observed.Hits Coverage)      3           1           2.64%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        GLQEGYENSR              +2          576.7687    1151.5229   1151.5207   0           44          2
                        SGYPDIGFPLFPLSK+2                   819.4414    1636.8683   1636.8500   0.02        59          2
                        LLFSHDLVSGR             +2          622.8221    1243.6297   1242.6720   0.96        44          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
98.         IPI00210900             Y           Y           0.15        1           2           2           5           3
*Des:       AMBP protein precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           8.73%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        AFAELWAFDAAQGK          +2          3.533       0.468       0.9996      5
                        TIAACNLPIVQGPCR +2      2.901       0.395       0.9964      1
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           8.73%
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		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AFAELWAFDAAQGK			+2	762.8838	1523.7530	1523.7408	0.01	64	3	
		TIAACNLPIVQGPCR		+2	778.4130	1554.8114	1554.8010	0.01	59	1		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
99.	IPI00371093		Y	Y	0.54	5	13	14	68	61		
*Des:	69 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					13	13	28.37%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AEAAVELR		+2	2.806	0.275	0.9931	6				
		AELQLDLQKPR		+2	3.694	0.321	0.9986	8				
		NSQNPNSEAVLLPVAVR			+2	4.177	0.530	1.0000	6			
		LALCELGNPMK		+2	3.267	0.476	0.9997	3				
		QASLTLSLDLGGR		+2	2.361	0.472	0.9624	2				
		AQPVVMATVQLMVQDSLNPTLK				+2	6.752	0.572	1.0000	33		
		GNSFPASLVVAAEEVDKEQDGLDSWVSR				+3	3.838	0.461	1.0000	3		
		FGSAIAPLGDLNR		+2	3.956	0.551	1.0000	6				
		VYLFLQPK		+2	3.235	0.394	0.9993	11				
		RVLLLASR		+2	3.148	0.298	0.9976	11				
		GLQALSSPTLVLTGTQVYGR			+2	6.269	0.680	1.0000	11			
		GGLLCSTQPPPK		+2	3.153	0.344	0.9969	11				
		SKNSQNPNSEAVLLPVAVR			+2	5.508	0.530	1.0000	6			
	MASCOT:(PepMatched Observed.Hits Coverage)					14	12	25.61%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AEAAVELR		+2	429.7404	857.4662	857.4606	0.01	51	5		
		LALCELGNPMK		+2	594.8130	1187.6114	1187.6042	0.01	63	3		
		QASLTLSLDLGGR		+2	666.8206	1331.6267	1329.7252	1.9	49	1		
		NSQNPNSEAVLLPVAVR			+2	904.4905	1806.9665	1806.9587	0.01	89	7	
		AELQLDLQKPR		+2	655.8801	1309.7457	1309.7354	0.01	61	3		
		FGSAIAPLGDLNR		+2	665.8640	1329.7134	1329.7040	0.01	69	5		
		VYLFLQPK		+2	504.3028	1006.5911	1006.5851	0.01	56	9		
		GLQALSSPTLVLTGTQVYGR			+2	1031.0784	2060.1422	2060.1265	0.02	118	10	
		GGLLCSTQPPPK		+2	599.3209	1196.6273	1196.6223	0.01	52	11		
		RVLLLASR		+2	464.3113	926.6080	926.6025	0.01	50	8		
		LALCELGNPMKK		+2	658.8683	1315.7221	1315.6992	0.02	44	2		
		SKNSQNPNSEAVLLPVAVR			+2	1012.0575	2022.1004	2022.0857	0.01	115	6	
		AQPVVMATVQLMVQDSLNPTLK				+2	1192.1500	2382.2855	2382.2650	0.02	127	28
		NKPICHTIK		+2	527.3007	1052.5869	1052.5801	0.01	42	1		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
100.	IPI00205216		Y	Y	0.28	2	4	3	4	3		
*Des:	P-selectin precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	1	6.91%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TLTAEAENWADNEPNNKR			+2	4.412	0.429	0.9998	2			
		HFTDLVAIQNK		+2	3.125	0.427	0.9992	3				
		TLTAEAENWADNEPNNK			+2	3.819	0.457	0.9997	1			

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                   NEIAHLNDVIPYVNSYYWIGIR  +3          3.636     0.374     0.9996    1
          MASCOT:(PepMatched Observed.Hits Coverage)   3         2         3.96%
                   Seq       Charge    ObservedMS      ExpectedMS          CalculatedMS                  Pepscore PepHits
                   HFTDLVAIQNK         +2        643.35    1284.69   1284.68   0.01      51        2
                   TLTAEAENWADNEPNNK   +2        958.94    1915.87   1915.85   0.02      62        1
                   TLTAEAENWADNEPNNKR  +3        691.66    2071.97   2071.96   0.01      47        1

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
101.      IPI00195685        Y         N         0.21      1         4         0         8         0
*Des:     CD44 protein
          SEQUEST:(PepMatched Observed.Hits Coverage)  4         1         6.8%
                   Seq       Charge    Xcor      Delta     Probility PepHits
                   EPTETPDQFMTADETR              +2        3.012     0.488     0.9995    2
                   SQEMVHLVNKEPTETPDQFMTADETR    +3        6.902     0.587     1.0000    3
                   YGFIEGHVVIPR        +3        3.289     0.473     0.9999    3
                   LVINSGNGTVEDR       +2        3.680     0.496     0.9982    3
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
102.      IPI00569987        N         Y         0.85      1         0         7         0         16
*Des:     60 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)   7         1         16.11%
                   Seq       Charge    ObservedMS      ExpectedMS          CalculatedMS                  Pepscore PepHits
                   INQDGTFLVR          +2        581.81    1161.62   1161.61   0.01      45        2
                   FLNLTENDIQK         +2        667.85    1333.68   1333.69   0         64        2
                   YQEESQVYLLGTGLR               +2        878.45    1754.89   1754.88   0.01      99        8
                   TVNNPYVLMVLYK       +2        777.43    1552.84   1552.83   0.01      74        2
                   EDFLSVSDIIDYFR      +2        859.92    1717.83   1717.82   0.01      90        2
                   GKEDFLSVSDIIDYFR              +2        952.48    1902.94   1902.94   0         124       2
                   SEVLAWNPDNLADYFR              +2        955.45    1908.89   1908.90   0         50        4

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
103.      IPI00205076        N         Y         0.09      1         0         2         0         2
*Des:     Lon
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)   2         1         2.69%
                   Seq       Charge    ObservedMS      ExpectedMS          CalculatedMS                  Pepscore PepHits
                   VLEFIAVSQLR         +2        638.00    1273.99   1273.74   0.25      41        2
                   AQLSATVLTLLIK       +2        685.94    1369.86   1369.85   0.01      82        1

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
104.      IPI00557753        N         Y         0.16      1         0         2         0         4
*Des:     61 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)   2         1         5.6%
                   Seq       Charge    ObservedMS      ExpectedMS          CalculatedMS                  Pepscore PepHits
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                    YVLDDEYTSSVGSK +2        781.86    1561.72   1561.71   0.01      80        2
                    EGSMSEDEFIEEAK +2        800.84    1599.66   1599.66   0         62        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
105.      IPI00203479         Y         Y         0.15      1         2         2         3         3
*Des:     Glia derived nexin precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)       2         1         10.39%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    SESLHVSHILQK        +2        3.199     0.299     0.9945    4
                    SQPHENVVISPHGIASILGMLQLGADGR  +3        6.021     0.634     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)        2         1         10.39%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    SESLHVSHILQK        +2        689.3839  1376.7533 1376.7412 0.01      55        4
                    SQPHENVVISPHGIASILGMLQLGADGR  +3        966.1873  2895.5401 2895.5024 0.04      72        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
106.      IPI00464532         N         Y         0.35      1         0         2         0         3
*Des:     Pyrroline-5-carboxylate reductase 2
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)        2         1         7.66%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    LGAQALLGAAK         +2        507.76    1013.51   1011.61   1.9       68        2
                    GFTAAGVLSAHK        +2        579.82    1157.63   1157.62   0.01      62        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
107.      IPI00422076         Y         Y         1.18      5         38        39        189       238
*Des:     Thrombospondin 1
          SEQUEST:(PepMatched Observed.Hits Coverage)       38        28        36.8%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    CEGSSVQTR           +2        2.876     0.449     0.9993    5
                    SCDSLNNR            +2        3.292     0.435     0.9997    8
                    SCDSLNNRCEGSSVQTR             +3        3.807     0.453     1.0000    2
                    KIMADSGPIYDK        +3        2.378     0.428     0.9998    7
                    GQDLSSPAFR          +2        3.328     0.459     0.9997    20
                    DNCQYVYNVDQR        +2        4.062     0.531     1.0000    2
                    IMADSGPIYDKTYAGGR             +2        5.206     0.568     1.0000    9
                    GTLLAVER            +2        2.829     0.370     0.9983    6
                    GTSQNDPNWVVR        +2        3.204     0.374     0.9981    11
                    QVTQSYWDTNPTR       +2        4.278     0.570     1.0000    11
                    DNSGQIFSVVSNGK      +2        3.321     0.402     0.9986    5
                    VAKGDVNDNFQGVLQNVR            +3        5.658     0.330     1.0000    15
                    SITLFVQEDR          +2        3.413     0.305     0.9977    4
                    TIVTTLQDSIR         +2        3.796     0.486     1.0000    18
                    AGTLDLSLSLPGK       +2        4.485     0.330     0.9993    14
                    FVFGTTPEDILR        +2        3.592     0.541     1.0000    19
                    QQVVSVEEALLATGQWK             +2        5.516     0.522     1.0000    25
                    TKDLQAICGLSCDELSSMVLELR                 +3        4.377     0.401     0.9999    3
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	GVEHAMANK		+2	3.046	0.425	0.9993	31				
	AGTLDLSLSLPGKQQVVSVEEALLATGQWK					+3	6.229	0.610	1.0000	12	
	IPESGGDNGVFDIFELIGGAR			+2	5.992	0.576	1.0000	3			
	NPCTDGTHDCNKNAK			+3	2.526	0.401	0.9992	5			
	NPCTDGTHDCNK		+2	3.558	0.468	0.9997	1				
	GRSCDSLNNR		+2	2.829	0.350	0.9833	2				
	LCNSPSPQMNGKPCEGEAR			+3	3.022	0.487	1.0000	6			
	KVTEENRELASELR		+2	3.847	0.391	0.9966	5				
	FTGSQPFGR		+2	2.541	0.337	0.9930	10				
	DTDMDGVGDQCDNCPLEHNPDQLDSDSDR					+3	6.130	0.583	1.0000	1	
	GTLLAVERK		+2	2.777	0.266	0.9890	9				
	NTDPGYNCLPCPPR		+2	3.289	0.531	0.9997	6				
	TIVTTLQDSIRK		+2	3.454	0.383	0.9989	2				
	FQMIPLDPK		+2	3.362	0.408	0.9995	16				
	GFIFLASLR		+2	2.886	0.344	0.9971	3				
	LVKGQDLSSPAFR		+2	3.441	0.499	0.9988	9				
	NALWHTGNTPGQVR			+3	4.073	0.469	1.0000	25			
	SRLCNNPTPQFGGK		+2	3.746	0.474	0.9987	1				
	KIMADSGPIYDKTYAGGR			+2	5.394	0.552	1.0000	7			
	HIGWKDFTAYR		+3	3.009	0.424	0.9999	10				
MASCOT:(PepMatched Observed.Hits Coverage)					39	35	29.24%				
	Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
	SCDSLNNR		+2	454.7010	907.3874	907.3818	0.01	68	5		
	CEGSSVQTR		+2	483.7220	965.4294	965.4236	0.01	69	7		
	FVFGTTPEDILR		+2	697.8741	1393.7336	1393.7241	0.01	54	14		
	GVEHAMANK		+2	478.2863	954.5581	955.4545	-0.89	57	33		
	AQGYSGLSVK		+2	505.2725	1008.5305	1008.5240	0.01	41	5		
	GQDLSSPAFR		+2	539.2734	1076.5322	1076.5250	0.01	66	25		
	IMADSGPIYDK		+2	605.2989	1208.5833	1208.5747	0.01	71	15		
	GTSQNDPNWVVR		+2	686.8390	1371.6634	1371.6531	0.01	56	15		
	QVTQSYWDTNPTR		+2	798.3820	1594.7494	1594.7376	0.01	94	16		
	DNSGQIFSVVSNGK		+2	726.3679	1450.7213	1450.7052	0.02	68	12		
	GDVNDNFQGVLQNVR			+2	837.9201	1673.8257	1673.8121	0.01	97	20	
	SITLFVQEDR		+2	604.3232	1206.6318	1206.6244	0.01	56	5		
	TIVTTLQDSIR		+2	623.8588	1245.7030	1245.6929	0.01	72	15		
	QQVVSVEEALLATGQWK			+2	943.5131	1885.0116	1884.9945	0.02	120	38	
	SCDSLNNRCEGSSVQTR			+3	619.2775	1854.8106	1854.7948	0.02	55	1	
	KIMADSGPIYDK		+2	669.3469	1336.6792	1336.6696	0.01	59	5		
	GTLLAVER		+2	429.7588	857.5030	857.4970	0.01	58	4		
	DNCQYVYNVDQR		+2	758.8339	1515.6532	1515.6412	0.01	79	2		
	IMADSGPIYDKTYAGGR			+2	907.9481	1813.8817	1813.8668	0.01	146	17	
	KDNSGQIFSVVSNGK			+2	790.9079	1579.8012	1578.8001	1	76	1	
	VAKGDVNDNFQGVLQNVR			+2	987.0223	1972.0301	1972.0125	0.02	119	16	
	AGTLDLSLSLPGK		+2	636.3677	1270.7208	1270.7132	0.01	94	12		
	FYVVMWK		+2	486.7570	971.4995	971.4939	0.01	46	8		
	NPCTDGTHDCNKNAK			+2	809.3479	1616.6812	1616.6671	0.01	69	5	
	GRSCDSLNNR		+2	561.2621	1120.5097	1120.5043	0.01	45	2		

NPCTDGTHDCNK	+2	652.7591	1303.5036	1303.4921	0.01	68	1
TNYIGHK	+2	416.3509	830.6873	831.4239	-0.73	55	23
FTGSQPFGR	+2	498.7522	995.4899	995.4824	0.01	54	13
VTEENRELASELR	+2	773.4012	1544.7879	1544.7794	0.01	47	2
KVTEENRELASELR	+2	837.4514	1672.8883	1672.8743	0.01	55	4
NTDPGYNCLPCPPR	+2	773.8490	1545.6834	1545.6704	0.01	73	6
FQMIPLDPK	+2	544.7974	1087.5803	1087.5736	0.01	53	10
TIVTTLQDSIRK	+2	687.9068	1373.7990	1373.7878	0.01	69	3
GTLLAVERK	+2	493.8068	985.5990	985.5920	0.01	58	6
AGTLDLSLSLPGKQQVVSVEEALLATGQWK	+3	1046.9149	3137.7229	3137.6971	0.03	75	4
LVKGQDLSSPAFR	+2	709.3984	1416.7823	1416.7725	0.01	67	8
NALWHTGNTPGQVR	+2	775.9003	1549.7861	1549.7749	0.01	71	23
SRLCNNPTPQFGGK	+2	759.8849	1517.7553	1517.7408	0.01	57	1
KIMADSGPIYDKTYAGGR	+2	971.9980	1941.9814	1941.9618	0.02	119	8

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
108.	IPI00560835	N	Y	0.06	1	0	2	0	2

*Des: 181 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 1.2%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EITALPIFEK	+2	580.0213	1158.0280	1159.6488	-1.61	43	3
CASLKCAK	+2	412.5416	823.0686	822.4091	0.66	41	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
109.	IPI00200067	Y	N	0.42	1	2	0	4	0

*Des: Junctional adhesion molecule JAM

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 11.8%

Seq	Charge	Xcor	Delta	Probility	PepHits
GSVYSPQTAVQVPENDSVK	+2	5.278	0.572	1.0000	2
VTFSSSGITFSSVTR	+2	4.422	0.583	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
110.	IPI00464535	Y	Y	0.22	1	2	2	2	4

*Des: Splice Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.26%

Seq	Charge	Xcor	Delta	Probility	PepHits
SAAQAAAQTNSNAAGK	+2	4.495	0.534	1.0000	1
RPDQQLQGDGK	+2	3.168	0.482	0.9996	2

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 7.26%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
RPDQQLQGDGK	+2	621.3174	1240.6203	1240.6160	0	48	2
SAAQAAAQTNSNAAGK	+2	730.8640	1459.7135	1459.7015	0.01	94	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
111.	IPI00198232	N	Y	0.19	1	0	3	0	6

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*Des:      83 kDa protein
           SEQUEST:(PepMatched Observed.Hits Coverage)
           MASCOT:(PepMatched Observed.Hits Coverage)    3        1        5.17%
                     Seq        Charge     ObservedMS        ExpectedMS        CalculatedMS                    Pepscore PepHits
                     IYGISFPDPK            +2         568.80     1135.59  1135.59  0        41       3
                     NELSGALTGLTR          +2         616.34     1230.66  1230.66  0        47       3
                     FLGDIEIWNQAEK         +2         781.90     1561.78  1561.78  0        56       2

No.        Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
112.       IPI00188610          Y          N          0.39       1        2        0        6        0
*Des:      17 kDa protein
           SEQUEST:(PepMatched Observed.Hits Coverage)   2        1        18.42%
                     Seq        Charge     Xcor       Delta      Probility PepHits
                     GDFCIQVGR             +2         3.235      0.415    0.9995   3
                     VMLGETNPADSKPGTIR                +2         4.725    0.548    1.0000   15
           MASCOT:(PepMatched Observed.Hits Coverage)

No.        Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
113.       IPI00196703          Y          Y          0.2        1        5        4        6        5
*Des:      Dynactin-1
           SEQUEST:(PepMatched Observed.Hits Coverage)   5        1        6.14%
                     Seq        Charge     Xcor       Delta      Probility PepHits
                     SPSAQLMEQVAQLK                   +2         3.175    0.437    0.9990   1
                     VDELTTDLEILK          +2         3.662      0.373    0.9992   2
                     ETVTQRPGATVPTDFATFPSSAFLR                   +3       3.413    0.335    0.9986   1
                     DSPLLLQQISAMR         +2         2.704      0.322    0.9863   1
                     SLDFLIELLHK           +2         3.300      0.513    0.9998   2
           MASCOT:(PepMatched Observed.Hits Coverage)    4        1        3.76%
                     Seq        Charge     ObservedMS        ExpectedMS        CalculatedMS                    Pepscore PepHits
                     LEETQTLLR             +2         551.81     1101.60  1101.60  0        63       2
                     VDELTTDLEILK          +2         694.89     1387.76  1387.74  0.02     45       2
                     DSPLLLQQISAMR         +2         736.40     1470.79  1470.79  0        41       1
                     SLDFLIELLHK           +2         664.39     1326.76  1326.75  0.01     55       2

No.        Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
114.       IPI00372040          Y          Y          2.72       2        7        6        13       8
*Des:      PREDICTED: similar to actin related protein 2/3 complex, subunit 4
           SEQUEST:(PepMatched Observed.Hits Coverage)   7        4        57.3%
                     Seq        Charge     Xcor       Delta      Probility PepHits
                     EKVLIEGSINSVR         +2         3.156      0.504    0.9742   1
                     SSKELLLQPVTISR        +2         4.472      0.679    1.0000   5
                     AENFFILR              +2         2.779      0.523    0.9938   2
                     KPVEGYDISFLITNFHTEQMYK +3        6.567      0.694    1.0000   1
                     IVAEEFLKN             +2         2.706      0.695    0.9847   3
                     LVDFVIHFMEEIDKEISEMKLSVNAR                  +3       6.389    0.643    1.0000   3
                     LVDFVIHFMEEIDKEISEMK             +2         5.495    0.722    1.0000   4
           MASCOT:(PepMatched Observed.Hits Coverage)    6        4        49.12%
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Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
VLIEGSINSVR		+2	593.84	1185.67	1185.67	0	65	3		
EKVLIEGSINSVR		+2	722.41	1442.81	1442.81	0	41	1		
SSKELLLQPVTISR		+2	785.96	1569.91	1569.91	0	76	4		
IVAEEFLKNF		+2	605.33	1208.64	1208.64	0	47	3		
KPVEGYDISFLITNFHTEQMYK			+3	887.44	2659.30	2659.30	0	81	1	
LVDFVIHFMEEIDKEISEMK			+3	818.08	2451.21	2451.21	0	53	1	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)								
115.	IPI00364021		N	Y	0.2	1	0	2	0	2

*Des: Angiopoietin-1 precursor

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 5.13%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
EDGSLDFQR		+2	533.74	1065.47	1065.47	0	46	1		
SGIYTIYFNNMPEPK		+2	887.44	1772.86	1772.84	0.02	43	2		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)								
116.	IPI00188541		Y	Y	0.18	4	11	12	26	54

*Des: Inter-alpha-inhibitor H4 heavy chain

SEQUEST:(PepMatched Observed.Hits Coverage) 11 5 15.91%

Seq	Charge	Xcor	Delta	Probility	PepHits			
LGDGLVGSR		+2	2.637	0.246	0.9799	6		
TTFELIYQELLQR		+2	3.797	0.442	0.9997	4		
VVEQEGTTPEESPNPDHPR			+3	4.173	0.641	1.0000	1	
LGMYELLLK		+2	2.879	0.378	0.9982	4		
IPAQGGTNINK		+2	3.050	0.398	0.9985	3		
QYTAAVGRGESAGLVK			+2	4.126	0.379	0.9968	1	
AVDYASKIPAQGGTNINK			+2	4.723	0.530	1.0000	2	
LRDQGPDVLLAK		+3	3.963	0.343	0.9999	8		
VLDLPSLSSQDPAGPSLAMLPK				+2	5.601	0.588	1.0000	5
TLFSVLPGLK		+2	2.843	0.342	0.9947	2		
AHIQFKPTLSQQR		+2	3.702	0.463	0.9997	3		

MASCOT:(PepMatched Observed.Hits Coverage) 12 5 16.12%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
LGDGLVGSR		+2	437.2462	872.4778	872.4715	0.01	61	10		
LALDNGGLAR		+2	500.7779	999.5412	998.5508	0.99	50	4		
LGMYELLLK		+2	540.3126	1078.6106	1078.6096	0	47	4		
TTFELIYQELLQR		+2	827.4501	1652.8856	1652.8773	0.01	70	4		
IPAQGGTNINK		+2	556.8109	1111.6072	1111.5985	0.01	45	6		
QYTAAVGRGESAGLVK			+2	803.9388	1605.8631	1605.8474	0.02	69	2	
AVDYASKIPAQGGTNINK			+2	923.9955	1845.9765	1845.9584	0.02	89	4	
VLDLPSLSSQDPAGPSLAMLPK				+2	1118.6064	2235.1983	2235.1820	0.02	91	10
LRDQGPDVLLAK		+2	662.8893	1323.7641	1323.7510	0.01	61	14		
TLFSVLPGLK		+2	537.8340	1073.6535	1073.6484	0.01	41	4		
HFKTPTTGSK		+2	552.2989	1102.5833	1102.5771	0.01	41	8		
AHIQFKPTLSQQR		+2	777.4371	1552.8596	1552.8474	0.01	56	6		

Identified Human Platelet Proteins

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No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
117.      IPI00209436          Y          Y          1.17       3          17         8          46         108
*Des:     PREDICTED: similar to pyruvate kinase (EC 2.7.1.40) isozyme M2 - rat
          SEQUEST:(PepMatched Observed.Hits Coverage)  17         8          47.77%
                     Seq        Charge     Xcor       Delta      Probility  PepHits
                     LDIDSAPITAR           +2         3.938      0.421      0.9997     7
                     GADYLVTEVENGGSLGSK               +2         6.045      0.455      1.0000     2
                     IYVDDGLISLQVK         +2         4.100      0.475      1.0000     4
                     LAPITSDPTEAAAVGAVEASFK +2        5.811      0.641      1.0000     6
                     AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR         +3         5.945      0.616      1.0000     2
                     ITLDNAYMEK            +2         2.791      0.325      0.9942     3
                     DAVLDAWAEDVDLR                   +2         4.884      0.533      1.0000     3
                     KAADVHEVR             +2         2.908      0.273      0.9925     4
                     RFDEILEASDGIMVAR                 +2         4.491      0.496      1.0000     4
                     KAADVHEVRK            +2         3.174      0.128      0.9573     1
                     LNFSHGTHEYHAETIK                 +3         4.983      0.434      1.0000     10
                     APIIAVTR +2           2.684      0.317      0.9949     11
                     NTGIICTIGPASR         +2         3.670      0.463      0.9997     9
                     TGLIKGSGTAEVELKK                 +3         3.758      0.448      1.0000     1
                     AGKPVICATQMLESMIK                +3         3.934      0.436      1.0000     2
                     LNFSHGTHEYHAETIKNVR              +3         3.928      0.424      1.0000     1
                     KGDVVIVLTGWRPGSGFTNTMR                      +3         3.654      0.400      0.9999     1
          MASCOT:(PepMatched Observed.Hits Coverage)   8          5          24.25%
                     Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                     GADYLVTEVENGGSLGSK               +2         898.4408   1794.8670  1794.8635  0          52         4
                     RFDEILEASDGIMVAR                 +2         910.7737   1819.5328  1820.9090  -1.37      62         12
                     LNFSHGTHEYHAETIK                 +3         628.6400   1882.8982  1882.8962  0          63         56
                     AATESFASDPILYRPVAVALDTKGPEIR     +3         996.5350   2986.5833  2986.5763  0.01       81         8
                     KAADVHEVR             +2         512.7808   1023.5471  1023.5461  0          55         27
                     GSGTAEVELKK           +2         559.8065   1117.5984  1117.5978  0          55         33
                     IISKIENHEGVR          +2         697.8914   1393.7683  1393.7677  0          48         58
                     NTGIICTIGPASR         +2         651.8461   1301.6777  1301.6761  0          53         18

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
118.      IPI00209290          Y          Y          0.42       1          2          2          2          6
*Des:     Vesicle-associated membrane protein-associated protein A
          SEQUEST:(PepMatched Observed.Hits Coverage)  2          1          14.17%
                     Seq        Charge     Xcor       Delta      Probility  PepHits
                     QDGPLPKPHSVSLNDTETR              +3         3.201      0.492      0.9999     3
                     HEQILVLDPPSDLK +2     3.517      0.495      0.9999     3
          MASCOT:(PepMatched Observed.Hits Coverage)   2          1          11.33%
                     Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                     GPFTDVVTTNLK          +2         646.35     1290.69    1290.68    0.01       79         4
                     HEQILVLDPPSDLK        +2         802.44     1602.87    1602.86    0.01       58         6

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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119.        IPI00206020 N           Y           0.42        1           0           2           0           2
*Des:       Similar to ribosome-binding protein p34-rat
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)                  2           1           7.66%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        LQQLPADFGR              +2          572.8547    1143.6948   1143.6036   0.09        37          1
                        LVTLPVSFAQLK            +2          658.4535    1314.8924   1314.7911   0.1         46          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
120.        IPI00390695 Y           Y           0.66        1           2           2           4           4
*Des:       PREDICTED: similar to RIKEN cDNA 1810009N02
            SEQUEST:(PepMatched Observed.Hits Coverage)                 2           1           11.73%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        GYHVVLASASPR            +2          3.420       0.397       0.9996      6
                        LLPSGPGQEVESQ           +2          2.953       0.512       0.9993      4
            MASCOT:(PepMatched Observed.Hits Coverage)                  2           1           12.17%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        GYHVVLASASPR            +2          628.85      1255.68     1255.67     0.01        54          4
                        LLPSGPGQEVESQT          +2          721.37      1440.72     1440.71     0.01        61          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
121.        IPI00209291 Y           Y           0.05        2           4           2           8           4
*Des:       GLUT4 vesicle protein
            SEQUEST:(PepMatched Observed.Hits Coverage)                 4           1           8.03%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        SPEEGAGPEPSGQSPATDSTR               +2          3.856       0.450       0.9992      1
                        SQELDVQVKDDSR           +2          3.908       0.447       0.9976      3
                        YKVGLTTVLNSGFLDEWLTLEDVPSGR                     +3          5.027       0.503       1.0000      2
                        LSPRPTAAELEEVLQVNSLIQTQK                        +3          4.600       0.495       1.0000      3
            MASCOT:(PepMatched Observed.Hits Coverage)                  2           2           2.25%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        QLLDDEER                +2          509.2538    1016.4930   1016.4774   0.02        37          1
                        DLPDPYVSVLLLPDK                     +2          842.4769    1682.9392   1682.9131   0.03        34          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
122.        IPI00364890 Y           Y           0.39        1           4           4           9           6
*Des:       Similar to SPI6
            SEQUEST:(PepMatched Observed.Hits Coverage)                 4           1           16.53%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        IPELLSGGSVDSETR         +2          4.226       0.511       1.0000      1
                        GQTQVQISQALGLNK                     +2          3.802       0.488       0.9998      1
                        LGIVDVFQEAK             +2          3.385       0.500       0.9998      4
                        DLHQGFQLLLSNLNKPER                  +3          4.590       0.564       1.0000      3
            MASCOT:(PepMatched Observed.Hits Coverage)                  4           1           16.53%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        IPELLSGGSVDSETR         +2          780.41      1558.80     1558.78     0.02        86          1
                        GQTQVQISQALGLNK                     +2          792.94      1583.87     1583.86     0.01        87          1
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                    LGIVDVFQEAK         +2          609.84      1217.67     1217.67     0           59          4
                    DLHQGFQLLLSNLNKPER              +3          708.06      2121.15     2121.13     0.02        58          3

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
123.        IPI00231965             N           Y           0.71        2           0           4           0           11
*Des:       ADP-ribosylation factor 5
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      4           2           19.23%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                    VQESADELQK              +2          573.7900    1145.5654 1145.5564 0.01    43          1
                    ILMVGLDAAGK             +2          544.3168    1086.6190 1086.6107 0.01    70          13
                    KQMRILMVGLDAAGK                     +3          544.3168    1629.9285 1629.9058 0.02    46          4
                    LGLQHLR+2   418.7610    835.5075    835.5028    0           50          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
124.        IPI00198168             Y           N           0.19        3           3           0           3           0
*Des:       81 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           3           6.86%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    PLVETIFER               +2          2.832       0.503       0.9986      2
                    FSLIDLAGNER             +2          3.467       0.306       0.9981      1
                    ALLEMTEEVDYDVDSYATQLEAILEQK         +3          6.050       0.609       1.0000      1
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
125.        IPI00231966             N           Y           0.44        1           0           2           0           6
*Des:       ADP-ribosylation factor 4
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           17.58%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                    HYFQNTQGLIFVVDSNDRER    +3          813.3997    2437.1773 2437.1774 0               46          10
                    IQEGAAVLQK              +2          528.8080    1055.6015 1055.5975 0           47          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
126.        IPI00193151             Y           Y           0.29        1           2           2           2           2
*Des:       Dihydropteridine reductase
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           14.63%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    RPNSGSLIQVVTTDGK                    +2          3.797       0.596       1.0000      2
                    MTDSFTEQADQVTAEVGK                  +2          4.791       0.579       1.0000      1
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           14.63%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                    RPNSGSLIQVVTTDGK                    +2          836.46      1670.92     1670.90     0.02        75          2
                    MTDSFTEQADQVTAEVGK                  +2          978.96      1955.90     1955.88     0.02        92          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
127.        IPI00231968             Y           Y           0.35        1           3           3           3           6
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*Des:	Annexin A4											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	13.53%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VLVSLTAGGR		+2	2.701	0.322	0.9894	2				
		AASGFNATEDAQVLR			+2	3.880	0.475	0.9996	1			
		SETSGSFEDALLAIVK			+2	4.567	0.549	1.0000	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	13.84%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GLGTDDSTLIR		+2	574.31	1146.60	1146.59	0.01	50	2		
		AASGFNATEDAQVLR			+2	775.39	1548.76	1548.75	0.01	59	2	
		SETSGSFEDALLAIVK			+2	833.93	1665.85	1665.85	0	74	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
128.	IPI00208568		Y	Y	1.03	3	8	6	24	22		
*Des:	PREDICTED: similar to pleckstrin											
	SEQUEST:(PepMatched Observed.Hits Coverage)					8	12	42.41%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GCVVTSVESNPDGK		+2	4.845	0.574	1.0000	4				
		NRQEGLMISASLLSEGYLQPASDLSK				+3	4.872	0.610	1.0000	8		
		EDPAYLHYYDPAGGEDPLGAIHLR				+3	6.063	0.515	1.0000	3		
		GSVFNTWKPMWVVLLEDGIEFYK				+3	3.489	0.356	0.9997	4		
		GSTLTSPCQDFGKR		+2	2.789	0.348	0.9922	2				
		KFILREDPAYLHYYDPAGGEDPLGAIHLR				+4	5.848	0.550	1.0000	11		
		VFNHCFTGSGVIDWLVSNK			+2	5.554	0.626	1.0000	8			
		GMIPLKGSTLTSPCQDFGK			+2	4.672	0.622	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					6	10	27.24%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LPETIDLGALYLSMKDPEK			+2	1067.0813	2132.1480	2132.1075	0.04	115	4	
		EDPAYLHYYDPAGGEDPLGAIHLR				+3	890.4421	2668.3046	2668.2557	0.05	98	2
		GSVFNTWKPMWVVLLEDGIEFYK				+3	919.9932	2756.9577	2757.3875	-0.42	52	8
		KGSVFNTWKPMWVVLLEDGIEFYK				+3	962.8497	2885.5272	2885.4825	0.04	54	2
		SDEENLFEIITADEVHYYMQAATAK				+3	963.4688	2887.3846	2887.3221	0.06	61	2
		KSDEENLFEIITADEVHYYMQAATAK				+3	1006.1652	3015.4738	3015.4171	0.06	112	2

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
129.	IPI00187747		Y	Y	1.18	4	9	4	19	27		
*Des:	Ras-related protein Rap-1A											
	SEQUEST:(PepMatched Observed.Hits Coverage)					9	15	63.82%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LVVLGSGGVGK		+2	3.127	0.559	0.9955	4				
		MREYKLVVLGSGGVGK			+2	5.029	0.570	0.9959	5			
		VVGKEQGQNLAR		+2	3.116	0.568	0.9862	3				
		SALTVQFVQGIFVEKYDPTIEDSYRK				+3	5.420	0.626	1.0000	4		
		SALTVQFVQGIFVEK			+3	5.699	0.690	1.0000	3			
		SALTVQFVQGIFVEKYDPTIEDSYR				+3	6.113	0.699	1.0000	1		
		SKINVNEIFYDLVR		+2	4.415	0.622	1.0000	5				
		INVNEIFYDLVRQINRK			+3	3.342	0.599	0.9991	2			

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                NGQGFALVYSITAQSTFNDLQDLREQILR +3        5.600     0.678     1.0000    6
          MASCOT:(PepMatched Observed.Hits Coverage)    4         7         28.19%
                Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                LVVLGSGGVGK         +2        493.31    984.60    984.60    0         49        10
                SALTVQFVQGIFVEK               +2        833.47    1664.92   1664.91   0.01      97        4
                SKINVNEIFYDLVR      +2        855.47    1708.92   1708.91   0.01      68        4
                SALTVQFVQGIFVEKYDPTIEDSYR               +3        969.16    2904.47   2904.45   0.02      73        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
130.      IPI00364895         Y         Y         0.59      2         9         9         10        20
*Des:     PREDICTED: similar to Mitochondrial inner membrane protein (Mitofilin)
          SEQUEST:(PepMatched Observed.Hits Coverage)   9         1         17.5%
                Seq       Charge    Xcor      Delta     Probility PepHits
                VVSQYHELVVQAR       +2        3.757     0.423     0.9997    2
                GIEQAVQSHAVAEEEAR             +2        4.914     0.569     1.0000    3
                EIAGATPYITAAEEK     +2        2.772     0.411     0.9963    1
                AVDEAADALLK         +2        2.719     0.243     0.9762    2
                SLEDALNQTATVTR      +2        3.865     0.571     1.0000    1
                TSSAEMPTIPLGSAVEAIR           +2        4.066     0.506     0.9999    1
                LFGMVLGSAPYTVPLPK             +2        3.395     0.496     0.9997    1
                QTITAQNAAVQAVK      +2        3.634     0.471     0.9998    1
                NSLYQYFLSYLQSLLLFPPK          +3        4.154     0.547     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    9         3         15.51%
                Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                LSEQELEFHR          +3        429.88    1286.63   1286.63   0         52        2
                QTITAQNAAVQAVK      +2        721.90    1441.80   1441.79   0.01      65        2
                VVSQYHELVVQAR       +2        764.42    1526.83   1526.82   0.01      47        4
                GIEQAVQSHAVAEEEAR             +2        912.46    1822.90   1822.88   0.02      82        8
                AVDEAADALLK         +2        558.30    1114.59   1114.59   0         52        4
                SLEDALNQTATVTR      +2        759.90    1517.78   1517.77   0.01      74        2
                EIAGATPYITAAEEK     +2        782.40    1562.79   1562.78   0.01      45        2
                FEFEQDLSEK          +2        636.29    1270.57   1270.57   0         56        2
                TSSAEMPTIPLGSAVEAIR           +2        965.51    1929.00   1928.99   0.01      75        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
131.      IPI00213172         Y         Y         0.48      2         5         6         12        9
*Des:     PREDICTED: similar to Phospholipid transfer protein
          SEQUEST:(PepMatched Observed.Hits Coverage)   5         2         13.27%
                Seq       Charge    Xcor      Delta     Probility PepHits
                INMAFGGTFR          +2        2.564     0.277     0.9832    2
                FLEQELEDINIPDVYGAK            +2        4.255     0.568     1.0000    2
                ATYFGSIVLQSPTVINSPLK          +2        4.857     0.499     1.0000    2
                TLLQIGVMPLLNER      +2        3.168     0.487     0.9996    2
                MYNFFSTFITSGMR      +2        4.834     0.695     1.0000    1
          MASCOT:(PepMatched Observed.Hits Coverage)    6         3         12.78%
                Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                VTSAALELVK          +2        516.26    1030.50   1029.61   0.89      55        2
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                        INMAFGGTFR  +2          557.28      1112.54     1112.54     0           49          2
                        DPVVSNGNLDMEFR+2        796.87      1591.73     1591.73     0           64          1
                        VPNDLDMLLR  +2          593.32      1184.62     1184.62     0           53          3
                        TLLQIGVMPLLNER +2       798.96      1595.91     1595.91     0           65          3
                        MYNFFSTFITSGMR +2       851.39      1700.77     1700.77     0           97          3

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
132.        IPI00205157             Y           N           0.42        1           2           0           3           0
*Des:       Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor
            SEQUEST:(PepMatched Observed.Hits Coverage) 2           1           16.87%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LGAGYPMGPFELLDYVGLDTTK              +2          4.653       0.569       1.0000      1
                        TLSSLSTSTDAASVVHSTDLVVEAIVENLK+3    5.762       0.654       1.0000      2
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
133.        IPI00558635             N           Y           0.77        1           0           5           0           22
*Des:       43 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)  5           1           17.09%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        AGIATHFVDSEK +2         637.83      1273.65     1273.63     0.02        70          12
                        AGQTLSQDLFR +2          617.35      1232.69     1234.63     -1.93       49          3
                        SPSAEDVAGVLESYHAK       +2          880.44      1758.86     1758.84     0.02        67          2
                        DPDTFLIIIK  +2          587.84      1173.67     1173.66     0.01        65          8
                        LHVLEEELLALK +2         703.92      1405.83     1405.82     0.01        47          6

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
134.        IPI00566583             N           Y           1.12        2           0           9           0           36
*Des:       Malate dehydrogenase, mitochondrial
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)  9           3           38.95%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        VNVPVIGGHAGK +2         574.33      1146.65     1146.65     0           59          10
                        ANTFVAELK   +2          496.77      991.53      991.53      0           59          3
                        AGAGSATLSMAYAGAR        +2          727.86      1453.70     1453.70     0           90          14
                        MIAEAIPELK  +2          557.81      1113.61     1113.61     0           47          4
                        VDFPQDQLATLTGR +2       780.91      1559.80     1559.79     0.01        91          4
                        IFGVTTLDIVR +2          617.36      1232.71     1232.71     0           65          5
                        FVFSLVDAMNGK +2         664.34      1326.67     1326.66     0.01        86          4
                        LTLYDIAHTPGVAADLSHIETR  +3          798.42      2392.25     2392.24     0.01        56          1
                        VAVLGASGGIGQPLSLLLK     +2          897.05      1792.09     1792.08     0.01        104         6

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
135.        IPI00204359             Y           Y           2.34        3           3           3           11          13
*Des:       Beta-2-microglobulin precursor
            SEQUEST:(PepMatched Observed.Hits Coverage) 3           2           21.48%
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Seq Charge Xcor Delta Probility PepHits
KIPNIEMSDLSFSK +3 3.459 0.407 1.0000 4
HVTLKEPK +2 2.924 0.361 0.9930 26
VKHVTLKEPK +2 3.301 0.389 0.9961 7
MASCOT:(PepMatched Observed.Hits Coverage) 3 4 20.66%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
TPQIQVYSR +2 546.2571 1090.4997 1090.5771 -0.07 67 3
IPNIEMSDLSFSK +2 740.8844 1479.7542 1479.7279 0.03 79 2
KIPNIEMSDLSFSK +2 804.9322 1607.8498 1607.8228 0.03 84 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
136. IPI00558494 N Y 2.14 1 0 4 0 8
*Des: PREDICTED: similar to ARP2/3 complex 16 kDa subunit (p16-ARC) (Actin-related protein 2/3 complex subunit 5)
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 4 1 44.53%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ALAAGGVGSIVR +2 535.82 1069.62 1069.62 0 77 4
AVQSLDKNGVDLLMK +2 815.95 1629.88 1629.88 0 45 6
YIYKGFESPSDNSSAMLLQWHEK +3 910.77 2729.27 2729.28 0 49 4
AVQSLDKNGVDLLMKYIYK +3 733.40 2197.19 2197.18 0.01 55 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
137. IPI00190759 Y Y 0.62 3 10 2 52 4
*Des: Splice Isoform Gamma-B of Fibrinogen gamma chain precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 10 10 37.52%
Seq Charge Xcor Delta Probility PepHits
YLQDIYTSNK +2 3.711 0.457 0.9999 10
LSIGDGQQHHMGGSK +2 3.052 0.533 0.9998 3
TSTADYAMFR +2 3.325 0.573 1.0000 5
AIQVYYNPDQPPKPGMIEGATQK +2 4.589 0.535 1.0000 6
FFTSHNGMHFSTWDNDNDK +3 4.705 0.554 1.0000 2
YEALLLTHESSIR +2 4.330 0.526 1.0000 4
EGFGHLSPTGTTEFWLGNEK +2 5.563 0.594 1.0000 3
SSTPNGYDNGIIWATWK +2 5.076 0.497 1.0000 3
LTYAYFIGGDAGDAFDGYDFGDDPSDK +2 6.246 0.709 1.0000 1
MVEEILKYEALLLTHESSIR +3 5.511 0.548 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 10.15%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
DNCCILDER +2 539.7262 1077.4378 1079.4376 -1.99 35 2
FGSYCPTTCGISDFLNSYQTDVDTDLQTLENILQR +3 1319.2954 3954.8644 3956.8084 -1.93 43 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
138. IPI00421428 Y Y 0.71 3 5 4 17 14
*Des: Pgam1 protein
SEQUEST:(PepMatched Observed.Hits Coverage) 5 3 35.9%
Seq Charge Xcor Delta Probility PepHits
ALPFWNEEIVPQIK +2 3.977 0.298 0.9989 5

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                        HLEGLSEEAIMELNLPTGIPIVYELDK         +3          5.133       0.506       1.0000      1
                        HGESAWNLENR +2          3.953       0.354       0.9998      7
                        FSGWYDADLSPAGHEEAK      +2          5.378       0.390       1.0000      5
                        NLKPIKPMQFLGDEETVR      +2          4.448       0.642       1.0000      5
            MASCOT:(PepMatched Observed.Hits Coverage)      4           3           25.09%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        HGESAWNLENR +2          656.81      1311.61     1311.60     0.01        74          5
                        FSGWYDADLSPAGHEEAK      +2          990.45      1978.89     1978.87     0.02        107         5
                        NLKPIKPMQFLGDEETVR      +3          705.72      2114.13     2114.12     0.01        52          2
                        ALPFWNEEIVPQIK +2       842.47      1682.92     1682.90     0.02        67          5

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
139.        IPI00200147             Y           Y           0.68        1           3           2           5           5
*Des:       60S acidic ribosomal protein P0
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           2           13%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        IIQLLDDYPK  +2          3.526       0.448       0.9998      1
                        VLALSVETDYTFPLAEK       +2          3.806       0.515       0.9999      2
                        TSFFQALGITTK +2         3.072       0.543       0.9998      2
            MASCOT:(PepMatched Observed.Hits Coverage)      2           2           9.9%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        GTIEILSDVQLIK +2        714.92      1427.83     1427.82     0.01        60          3
                        VLALSVETDYTFPLAEK       +2          948.51      1895.01     1894.99     0.02        83          3

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
140.        IPI00421429             Y           Y           0.02        1           2           4           3           6
*Des:       Plakoglobin
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           3.56%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        VSVELTNSLFK +2          3.128       0.459       1.0000      1
                        NEGTATYAAAVLFR +2       3.007       0.292       0.9923      2
            MASCOT:(PepMatched Observed.Hits Coverage)      4           1           6.99%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        LNYGIPAIVK  +2          544.2744    1086.5343 1086.6437 -0.1        41          3
                        VSVELTNSLFK +2          618.8446    1235.6747 1235.6761 0           51          1
                        ALMGSPQLVAAVVR+2        706.4079    1410.8012 1410.8016 0           46          1
                        NEGTATYAAAVLFR +2       742.3823    1482.7501 1482.7466 0           52          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
141.        IPI00421357             Y           N           0.04        1           2           0           2           0
*Des:       170 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           1.88%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        DQVDSAVQELLQLK+2        4.324       0.355       0.9994      1
                        GVLEDIQLNLFTR +2        3.246       0.339       0.9965      1
            MASCOT:(PepMatched Observed.Hits Coverage)
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No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
142. IPI00369117 Y Y 0.78 1 4 3 6 3
*Des: PREDICTED: similar to LDL receptor adaptor protein
SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 17.89%
Seq Charge Xcor Delta Probility PepHits
VAQAVTLTVAQAFK +2 2.733 0.333 0.9913 2
TSVATGNLLDLEELAK +2 3.800 0.454 0.9997 1
VAFEFWQVSK +2 2.997 0.393 0.9989 3
ETLLEGMVFSLK +2 3.438 0.512 0.9998 1
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 13.09%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VAFEFWQVSK +2 620.83 1239.64 1239.63 0.01 41 4
TSVATGNLLDLEELAK +2 837.46 1672.91 1672.89 0.02 64 1
ETLLEGMVFSLK +2 683.88 1365.74 1365.72 0.02 54 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
143. IPI00367445 Y N 0.3 2 4 0 6 0
*Des: 48 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage) 4 2 17.84%
Seq Charge Xcor Delta Probility PepHits
GMGGAMDLVSSSK +2 3.596 0.549 0.9995 2
GGHVNLTMLGAMQVSK +3 3.770 0.338 0.9988 1
AAGTTVVEVEEIVDIGSFAPEDIHIPK +3 4.688 0.482 0.9999 2
DLTAVSNNAGVDNFGLGLLLR +2 5.916 0.447 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
144. IPI00365914 Y N 0.14 1 2 0 2 0
*Des: PREDICTED: similar to Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS)
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 6.12%
Seq Charge Xcor Delta Probility PepHits
DMNQILDAYENK +2 3.428 0.348 0.9987 1
DLTLEQAYSYTVENAK +2 4.073 0.585 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
145. IPI00231106 Y Y 1.84 1 5 5 6 7
*Des: 3-mercaptopyruvate sulfurtransferase
SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 26.57%
Seq Charge Xcor Delta Probility PepHits
THEDILENLDAR +2 3.056 0.473 0.9991 2
YWLSQNLPISSGK +2 3.980 0.586 1.0000 1
LLDASWYLPK +2 3.411 0.399 0.9927 3
ALVSAQWVAEALK +2 3.271 0.390 0.9978 1
DGIEPGHIPGSVNIPFTEFLTSEGLEK +3 6.642 0.571 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 5 1 26.57%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

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                    THEDILENLDAR  +2          713.35      1424.69     1424.69     0           54          2
                    LLDASWYLPK    +2          603.81      1205.60     1204.65     0.95        51          2
                    ALVSAQWVAEALK +2          694.34      1386.67     1384.77     1.9         79          2
                    YWLSQNLPISSGK +2          746.89      1491.77     1491.77     0           77          1
                    DGIEPGHIPGSVNIPFTEFLTSEGLEK           +3          961.82      2882.45     2882.43     0.02        87          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
146.        IPI00372125 Y           Y           0.11        1           3           2           6           3
*Des:       PREDICTED: similar to T-Brain-1
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           1           5.3%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        AVEEEDKMTPEQLAIK                    +2          4.372       0.400       0.9923      2
                        VIDVFAMPQSGTGVSVEAVDPVFQAK          +3          3.901       0.500       0.9998      1
                        AGVPMEVMGLMLGEFVDDYTVR              +2          5.846       0.602       1.0000      4
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           3.16%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        AVEEEDKMTPEQLAIK                    +2          915.96      1829.91     1829.91     0           55          2
                        AGVPMEVMGLMLGEFVDDYTVR              +3          810.39      2428.14     2428.15     0           49          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
147.        IPI00365918 Y           N           0.06        2           2           0           3           0
*Des:       PREDICTED: similar to RIKEN cDNA 2610204M08
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           2           2.52%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        SFSEDAVTDSSGSGTLPR                  +2          3.585       0.559       0.9998      2
                        KQQLAEEEAR  +2          3.096       0.344       0.9942      3
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
148.        IPI00231108 Y           Y           0.56        1           3           2           4           4
*Des:       5'-AMP-activated protein kinase, beta-1 subunit
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           1           20.8%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        APEKEEFLAWQHDLEVNEK                 +3          3.677       0.462       0.9986      2
                        SQNNFVAILDLPEGEHQYK                 +3          4.292       0.370       0.9997      2
                        APPILPPHLLQVILNK                    +3          2.620       0.461       0.9996      5
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           11.67%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        DGVMVLSATHR +2          593.31      1184.61     1184.60     0.01        60          8
                        SQNNFVAILDLPEGEHQYK     +3          734.70      2201.08     2201.08     0           46          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
149.        IPI00208645 Y           Y           0.46        1           2           2           3           4
*Des:       LOC84013 protein
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           10.37%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LGEWAVVTGGTDGIGK                    +2          4.277       0.513       0.9999      1
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                  GIFVQSVLPFFVATK +2      4.700     0.477     0.9998    2
          MASCOT:(PepMatched Observed.Hits Coverage)  2         1         10.37%
                  Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                  LGEWAVVTGGTDGIGK        +2        780.41    1558.81   1558.80   0.01      89        2
                  GIFVQSVLPFFVATK +2      826.97    1651.93   1651.93   0         76        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
150.      IPI00196645         Y         Y         0.35      1         4         4         9         18
*Des:     5'-AMP-activated protein kinase, gamma-1 subunit
          SEQUEST:(PepMatched Observed.Hits Coverage) 4         1         16.36%
                  Seq       Charge    Xcor      Delta     Probility PepHits
                  TYNNLDVSVTK         +2        3.076     0.495     0.9997    3
                  LVVVDEHDVVK         +2        2.790     0.282     0.9895    10
                  LPVIDPESGNTLYILTHK  +3        4.538     0.582     1.0000    2
                  AFFALVTNGVR         +2        3.772     0.439     0.9998    3
          MASCOT:(PepMatched Observed.Hits Coverage)  4         1         16.07%
                  Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                  TYNNLDVSVTK         +2        627.33    1252.64   1252.63   0.01      60        6
                  FDVINLAAEK          +2        560.31    1118.60   1118.60   0         42        4
                  AFFALVTNGVR         +2        597.84    1193.66   1193.66   0         76        6
                  LPVIDPESGNTLYILTHK            +3        670.71    2009.10   2009.08   0.02      78        4

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
151.      IPI00231038         Y         Y         0.66      1         2         2         4         5
*Des:     26S proteasome non-ATPase regulatory subunit 9
          SEQUEST:(PepMatched Observed.Hits Coverage) 2         1         9.29%
                  Seq       Charge    Xcor      Delta     Probility PepHits
                  ANYDVLESQK          +2        3.001     0.462     0.9998    4
                  ADVDLYQVR           +2        3.569     0.226     0.9977    3
          MASCOT:(PepMatched Observed.Hits Coverage)  2         1         9.29%
                  Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                  ANYDVLESQK          +2        583.79    1165.57   1165.56   0.01      64        4
                  ADVDLYQVR           +2        539.78    1077.55   1077.55   0         68        3

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
152.      IPI00189358         Y         Y         0.46      1         2         2         4         4
*Des:     Transcription factor Pur-beta
          SEQUEST:(PepMatched Observed.Hits Coverage) 2         1         14.86%
                  Seq       Charge    Xcor      Delta     Probility PepHits
                  GGGGGGPGSFQPAPR               +2        2.504     0.361     0.9895    3
                  GGGGFGGGPGPGGLQSGQTIALPAQGLIEFR         +3        4.632     0.432     0.9999    3
          MASCOT:(PepMatched Observed.Hits Coverage)  2         1         14.86%
                  Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                  GGGGGGPGSFQPAPR               +2        649.82    1297.63   1297.62   0.01      80        3
                  GGGGFGGGPGPGGLQSGQTIALPAQGLIEFR         +3        951.84    2852.49   2852.46   0.03      57        3

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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153.     IPI00196648    Y       Y       0.58    1       2       2       2       4
*Des:    Syntaxin-7
         SEQUEST:(PepMatched Observed.Hits Coverage)    2       1       11.69%
                 Seq     Charge  Xcor    Delta   Probility PepHits
                 TLNQLGTPQDTPELR         +2      3.740   0.324   0.9980  1
                 LVAEFTTALTNFQK  +2      4.252   0.554   1.0000  1
         MASCOT:(PepMatched Observed.Hits Coverage)     2       1       11.69%
                 Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 TLNQLGTPQDTPELR         +2      841.94  1681.87 1681.86 0.01    50      2
                 LVAEFTTALTNFQK  +2      791.93  1581.85 1581.84 0.01    71      2

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
154.     IPI00212523    Y       Y       0.63    2       4       2       6       4
*Des:    DJ-1 protein
         SEQUEST:(PepMatched Observed.Hits Coverage)    4       3       31.08%
                 Seq     Charge  Xcor    Delta   Probility PepHits
                 GAEEMETVIPVDIMR+2       3.675   0.480   0.9997  1
                 GPGTSFEFALAIVEALSGKDMANQVK      +3      4.786   0.623   1.0000  1
                 GPGTSFEFALAIVEALSGK     +2      5.442   0.692   1.0000  3
                 VTVAGLAGKDPVQCSR        +3      3.417   0.413   0.9954  3
         MASCOT:(PepMatched Observed.Hits Coverage)     2       1       13.98%
                 Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 GPGTSFEFALAIVEALSGK     +2      947.5086 1893.0027 1892.9883 0.01  130     2
                 GPGTSFEFALAIVEALSGKDMANQVK      +3      894.1235 2679.3486 2679.3577 0     61      2

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
155.     IPI00210920    Y       Y       0.43    2       5       6       9       34
*Des:    Aspartate aminotransferase, mitochondrial precursor
         SEQUEST:(PepMatched Observed.Hits Coverage)    5       1       15.52%
                 Seq     Charge  Xcor    Delta   Probility PepHits
                 DAGMQLQGYR      +2      3.404   0.473   0.9998  4
                 PLYSNPPLNGAR    +2      3.127   0.372   0.9935  7
                 ASAELALGENSEVLK         +2      3.719   0.418   0.9994  1
                 FVTVQTISGTGALR  +2      4.016   0.479   0.9998  2
                 IAATILTSPDLR    +2      3.390   0.448   0.9996  1
         MASCOT:(PepMatched Observed.Hits Coverage)     6       2       16.89%
                 Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 DAGMQLQGYR      +2      569.77  1137.53 1137.52 0.01    55      25
                 MNLGVGAYR       +2      490.76  979.50  979.49  0.01    44      1
                 VGASFLQR        +2      439.74  877.46  876.48  0.98    59      20
                 IAATILTSPDLR    +2      635.88  1269.74 1269.73 0.01    63      1
                 FVTVQTISGTGALR  +2      725.41  1448.81 1448.80 0.01    90      2
                 ASAELALGENSEVLK         +2      765.91  1529.81 1529.79 0.02    57      1

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
156.     IPI00565930    N       Y       0.02    1       0       5       0       61
*Des:    52 kDa protein
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SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 5 1 9.83%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
EVATNSELVQSGK +2 681.3493 1360.6841 1360.6834 0 56 2
ILNEMRDQYEK +2 719.8541 1437.6937 1437.6922 0 42 2
VTMQNLNDR +2 545.7686 1089.5227 1089.5237 0 67 58
LAADDFR +2 403.7300 805.4455 806.3922 -0.94 48 12
ILNEMRDQYEKMAEK +2 949.4388 1896.8630 1896.9073 -0.03 55 7

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
157. IPI00370456 Y Y 0.17 2 4 3 9 8
*Des: PREDICTED: similar to Proteasome 26S non-ATPase subunit 2
SEQUEST:(PepMatched Observed.Hits Coverage) 4 2 10.6%
Seq Charge Xcor Delta Probility PepHits
MNLASSFVNGFVNAAFGQDK +3 4.974 0.537 1.0000 2
AELATEEFLPVTPILEGFVILR +3 5.460 0.608 1.0000 3
EAPADMGAHQGVAVLGIALIAMGEEIGAEMALR +3 5.001 0.612 1.0000 2
GEAIEAILAALEVVSEPFR +3 4.993 0.575 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 3 2 6.92%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
MNLASSFVNGFVNAAFGQDK +3 706.35 2116.02 2116.00 0.02 72 1
AELATEEFLPVTPILEGFVILR +3 819.80 2456.38 2456.36 0.02 54 2
GEAIEAILAALEVVSEPFR +3 672.04 2013.09 2013.08 0.01 81 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
158. IPI00213329 Y N 0.38 1 3 0 3 0
*Des: PREDICTED: similar to methylenetetrahydrofolate dehydrogenase (NAD) (EC 1.5.1.15) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) precursor - mouse
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 10.42%
Seq Charge Xcor Delta Probility PepHits
EGATVIDVGINR +2 3.132 0.409 0.9990 2
LVGDVDFEGVK +2 2.817 0.340 0.9958 2
VLRPEELEVLK +3 3.201 0.392 0.9996 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
159. IPI00205166 Y Y 0.06 3 2 3 7 14
*Des: Integrin alpha 6 subchain
SEQUEST:(PepMatched Observed.Hits Coverage) 2 2 3.48%
Seq Charge Xcor Delta Probility PepHits
NSYPDVAVGSLSDSVTIFR +2 3.604 0.258 0.9653 1
VNSLPEVLPILNSNEAK +2 3.983 0.529 0.9998 2
MASCOT:(PepMatched Observed.Hits Coverage) 3 2 3.84%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
WSNVKPVR +2 493.2852 984.5558 984.5505 0.01 41 2
SRPVINILK +2 520.3377 1038.6609 1038.6549 0.01 46 2
ASIDVTAAAQNIKLPHAGTQVR +3 754.4280 2260.2621 2260.2287 0.03 49 2

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No.      Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
160.     IPI00204365       Y          Y       0.02      2          2        2         4         4
*Des:    Ribophorin I
         SEQUEST:(PepMatched Observed.Hits Coverage)   2          3        4.05%
                 Seq        Charge    Xcor      Delta     Probility  PepHits
                 GEDEEDNNLEVR  +2     3.109     0.427     0.9994     2
                 SEDILDYGPFK   +2     3.731     0.380     0.9997     2
         MASCOT:(PepMatched Observed.Hits Coverage)    2          3        5.18%
                 Seq        Charge    ObservedMS          ExpectedMS           CalculatedMS                Pepscore PepHits
                 FVDHVFDEQVIDSLTVK    +2        996.0189  1990.0232 1990.0047 0.02      98        3
                 DTYIENEKLSSGK +2     742.3766  1482.7387 1482.7202 0.02      60        1

No.      Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
161.     IPI00360767       Y          N       0.07      1          2        0         2         0
*Des:    PREDICTED: similar to beta1-syntrophin
         SEQUEST:(PepMatched Observed.Hits Coverage)   2          1        5.08%
                 Seq        Charge    Xcor      Delta     Probility  PepHits
                 SMTLADPENR    +2     2.906     0.359     0.9930     1
                 GSGTGHPGTGVPQAPDSPAGVR         +3        3.196      0.452    0.9997    1
         MASCOT:(PepMatched Observed.Hits Coverage)

No.      Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
162.     IPI00476855       N          Y       0.07      1          0        2         0         3
*Des:    LRRGT00050
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)    2          1        1.91%
                 Seq        Charge    ObservedMS          ExpectedMS           CalculatedMS                Pepscore PepHits
                 DQVDSAVQELLQLK +2    793.43    1584.84   1584.84   0         108       1
                 GVLEDIQLNLFTR  +2    759.43    1516.84   1516.82   0.02      50        2

No.      Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
163.     IPI00387771       Y          Y       3.95      4          9        6         35        38
*Des:    Peptidyl-prolyl cis-trans isomerase A
         SEQUEST:(PepMatched Observed.Hits Coverage)   9          10       72.89%
                 Seq        Charge    Xcor      Delta     Probility  PepHits
                 KITISDCGQ     +2     2.925     0.490     0.9953     1
                 VNPTVFFDITADGEPLGR   +2        5.418     0.628      1.0000   14
                 KITISDCGQL    +2     2.846     0.420     0.9987     2
                 VKEGMSIVEAMER +3     3.127     0.310     0.9983     3
                 SIYGEKFEDENFILK +2   4.604     0.464     1.0000     2
                 TEWLDGKHVVFGK +2     4.190     0.499     1.0000     4
                 IIPGFMCQGGDFTR +2    4.036     0.655     1.0000     5
                 VCFELFADKVPK  +2     2.751     0.500     0.9966     2
                 ALSTGEKGFGYKGSSFHR   +2        4.819     0.529      1.0000   9
         MASCOT:(PepMatched Observed.Hits Coverage)    6          9        46.38%
                 Seq        Charge    ObservedMS          ExpectedMS           CalculatedMS                Pepscore PepHits
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		VKEGMSIVEAMER		+2	739.8755	1477.7365	1477.7268	0.01	50	8		
		SIYGEKFEDENFILK		+2	916.4663	1830.9181	1830.9039	0.01	76	4		
		ALSTGEKGFGYK		+2	629.3298	1256.6450	1256.6400	0	48	6		
		VCFELFADKVPK		+2	698.3768	1394.7391	1394.7267	0.01	54	1		
		IIPGFMCQGGDFTR		+2	771.3717	1540.7289	1540.7166	0.01	79	5		
		ALSTGEKGFGYKGSSFHR			+2	964.9895	1927.9645	1927.9540	0.01	105	18	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
164.	IPI00422092		Y	Y	0.73	2	2	3	3	4		
*Des:	Ras-related C3 botulinum toxin substrate 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	8.16%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LTPITYPQGLAMAK		+2	2.792	0.415	0.9970	4				
		KLTPITYPQGLAMAK			+2	3.021	0.426	0.9981	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	14.28%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GLKTVFDEAIR		+2	624.8932	1247.7718	1247.6873	0.08	35	1		
		LTPITYPQGLAMAK		+2	752.4788	1502.9430	1502.8167	0.13	34	1		
		KLTPITYPQGLAMAK			+2	816.5255	1631.0364	1630.9116	0.12	56	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
165.	IPI00325135		Y	Y	1.34	3	11	13	37	446		
*Des:	14-3-3 protein epsilon											
	SEQUEST:(PepMatched Observed.Hits Coverage)					11	5	58.07%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		YDEMVESMK		+2	3.171	0.182	0.9769	8				
		YLAEFATGNDRK		+2	2.914	0.315	0.9893	4				
		YLAEFATGNDR		+2	3.302	0.382	0.9983	4				
		AASDIAMTELPPTHPIR			+2	4.980	0.512	1.0000	9			
		KVAGMDVELTVEER		+2	4.184	0.533	1.0000	1				
		DNLTLWTSDMQGDGEEQNK			+2	5.533	0.623	1.0000	2			
		AAFDDAIAELDTLSEESYK			+2	6.261	0.588	1.0000	3			
		LGLALNFSVFYYEILNSPDR			+2	5.882	0.565	1.0000	8			
		AAFDDAIAELDTLSEESYKDSTLIMQLLR				+3	6.941	0.674	1.0000	3		
		EALQDVEDEN		+2	2.861	0.384	0.9861	3				
		KEAAENSLVAYK		+2	3.197	0.339	0.9956	3				
	MASCOT:(PepMatched Observed.Hits Coverage)					13	7	58.07%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		QMVETELK		+2	489.26	976.50	976.49	0.01	63	2		
		EALQDVEDENQ		+2	645.28	1288.55	1288.54	0.01	68	5		
		KEAAENSLVAYK		+2	661.86	1321.70	1321.69	0.01	77	4		
		YDEMVESMK		+2	566.24	1130.47	1130.46	0.01	56	5		
		YLAEFATGNDRK		+2	692.85	1383.69	1383.68	0.01	50	8		
		YLAEFATGNDR		+2	628.80	1255.59	1255.58	0.01	75	7		
		VAGMDVELTVEER		+2	724.36	1446.71	1446.70	0.01	102	10		
		KVAGMDVELTVEER		+2	789.37	1576.73	1574.80	1.93	54	3		
		AASDIAMTELPPTHPIR			+2	910.48	1818.95	1818.93	0.02	92	14	

NLLSVAYK	+2	453.37	904.73	906.52	-1.78	53	350
AAFDDAIAELDTLSEESYK	+3	696.66	2086.97	2086.96	0.01	66	3
DSTLIMQLLR	+2	594.70	1187.40	1188.65	-1.24	78	245
LGLALNFSVFYYEILNSPDR	+3	777.74	2330.21	2330.19	0.02	45	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
166.	IPI00557778	N	Y	1.05	1	0	5	0	22

*Des: 59 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 5 1 11.51%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
TSELNLDQFHDK	+2	723.85	1445.69	1445.68	0.01	58	3
VVDDWANDGWGLK	+2	737.85	1473.69	1473.69	0	76	9
APVPTGEVYFADSFDR	+2	885.92	1769.83	1769.83	0	81	6
IPNPDFFEDLEPFR	+2	868.43	1734.84	1734.83	0.01	63	6
KIPNPDFFEDLEPFR	+3	621.98	1862.93	1862.92	0.01	44	6

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
167.	IPI00326948	Y	Y	0.24	3	4	3	6	8

*Des: Hsd17b4 protein

SEQUEST:(PepMatched Observed.Hits Coverage) 4 3 7.32%

Seq	Charge	Xcor	Delta	Probility	PepHits
VVLVTGAGGGLGR	+2	3.826	0.452	0.9996	2
AYALAFAER	+2	3.107	0.414	0.9990	2
SIQESTGGIIEVLHK	+2	3.748	0.488	0.9996	1
LGLLGLANTLVIEGR	+2	4.296	0.610	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 3 3 6.02%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VVLVTGAGGGLGR	+2	578.35	1154.68	1154.68	0	70	4
SIQESTGGIIEVLHK	+2	805.94	1609.87	1609.87	0	88	2
LGLLGLANTLVIEGR	+2	769.97	1537.93	1537.92	0.01	94	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
168.	IPI00201969	Y	Y	0.4	1	6	4	7	4

*Des: PREDICTED: similar to Vesicle amine transport protein 1 homolog (T californica)

SEQUEST:(PepMatched Observed.Hits Coverage) 6 1 25.54%

Seq	Charge	Xcor	Delta	Probility	PepHits
EATEAATVAAAAEAR	+2	3.796	0.380	0.9993	1
ENGVTHPIDYHTTDYVDEIKK	+3	3.557	0.351	0.9983	2
TVENVTVFGTASASK	+2	3.173	0.510	0.9997	1
GVDIVMDPLGGSDTAK	+2	3.443	0.548	0.9999	1
VVTYGMANLLTGPK	+2	2.771	0.256	0.9696	2
TWWNQFSVTALQLLQANR	+2	5.277	0.487	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 16.54%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EATEAATVAAAAEAR	+2	716.36	1430.71	1430.70	0.01	59	1
TVENVTVFGTASASK	+2	755.89	1509.77	1509.77	0	53	1

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                        GVDIVMDPLGGSDTAK        +2          787.89      1573.77     1573.77     0           42          1
                        TWWNQFSVTALQLLQANR      +3          726.05      2175.13     2175.12     0.01        55          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
169.        IPI00464557             N           Y           0.22        1           0           2           0           10
*Des:       Splice Isoform 3 of Drebrin-like protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)          2           1           6.59%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        TGELEQEVVSR             +2          623.8213    1245.6280   1245.6200   0.01        57          4
                        SRQEWESAGQQAPHPR        +3          621.9721    1862.8945   1862.8772   0.02        56          6

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
170.        IPI00187902             Y           Y           1.73        1           3           3           5           3
*Des:       CD9 antigen
            SEQUEST:(PepMatched Observed.Hits Coverage)         3           2           22.27%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        ELQEFYKDTYQK            +2          2.771       0.393       0.9979      1
                        AIHMALNCCGIAGGVEQFISDICPK                       +3          3.645       0.434       0.9988      1
                        NKDEPQRETLK             +2          3.108       0.264       0.9934      16
            MASCOT:(PepMatched Observed.Hits Coverage)          3           1           21.39%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        NKDEPQRETLK             +2          679.3611    1356.7077   1356.6997   0.01        44          1
                        KQVLESFQVK              +2          603.3522    1204.6899   1204.6815   0.01        57          3
                        AIHMALNCCGIAGGVEQFISDICPK                       +3          863.4169    2587.2290   2589.2211   -1.98       44          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
171.        IPI00287338             Y           N           0.08        1           4           0           4           0
*Des:       Nuclear export factor CRM1
            SEQUEST:(PepMatched Observed.Hits Coverage)         4           1           5.31%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LNMILVQILK              +2          2.798       0.346       0.9968      1
                        YYGLQILENVIK            +2          3.516       0.477       0.9998      1
                        YMLLPNQVWDSIIQQATK      +3          4.512       0.444       1.0000      1
                        FLNWIPLGYIFETK          +2          3.008       0.364       0.9969      1
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
172.        IPI00198327             Y           Y           0.5         2           3           3           3           5
*Des:       Voltage-dependent anion-selective channel protein 2
            SEQUEST:(PepMatched Observed.Hits Coverage)         3           1           17%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        YQLDPTASISAK            +2          3.123       0.301       0.9912      5
                        TGDFQLHTNVNNGTEFGGSIYQK                         +3          5.918       0.531       1.0000      1
                        LTFDTTFSPNTGK           +2          3.695       0.581       1.0000      1
            MASCOT:(PepMatched Observed.Hits Coverage)          3           2           17%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
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                YQLDPTASISAK    +2      647.34  1292.66 1292.66 0       51      15
                LTFDTTFSPNTGK   +2      714.86  1427.70 1427.69 0.01    94      1
                TGDFQLHTNVNNGTEFGGSIYQK         +3      843.07  2526.18 2526.18 0       59      1

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
173.    IPI00195851     Y       N       0.33    2       7       0       43      0
*Des:   Hypothetical LOC299052
        SEQUEST:(PepMatched Observed.Hits Coverage)     7       4       25.87%
                Seq     Charge  Xcor    Delta   Probility PepHits
                GILAADESTGSIAKR +2      4.359   0.540   1.0000  7
                GILAADESTGSIAK  +2      4.391   0.596   1.0000  4
                AAQEEYIKR       +2      2.917   0.421   0.9991  3
                ALANSLACQGK     +2      3.661   0.557   1.0000  4
                YASICQQNGIVPIVEPEILPDGDHDLKR    +3      6.195   0.525   1.0000  1
                RLQSIGTENTEENRR         +3      3.788   0.351   0.9999  3
                SKGGVVGIKVDK    +2      3.223   0.483   0.9982  9
        MASCOT:(PepMatched Observed.Hits Coverage)

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
174.    IPI00365929     Y       Y       0.88    4       8       7       15      13
*Des:   Thioredoxin domain conTaining 7
        SEQUEST:(PepMatched Observed.Hits Coverage)     8       6       28.91%
                Seq     Charge  Xcor    Delta   Probility PepHits
                GSTAPVGGGSFPNITPR       +2      4.531   0.571   1.0000  3
                HQSLGGQYGVQGFPTIK       +2      4.848   0.669   1.0000  3
                DVVELTDDTFDK    +2      2.949   0.524   0.9998  1
                LAAVDATVNQVLASR         +2      4.128   0.402   0.9997  2
                GSFSEQGINEFLR   +2      3.578   0.491   0.9999  1
                TGEAIVDAALSALR  +2      4.007   0.426   0.9998  4
                ALDLFSDNAPPPELLEIINEDIAK        +2      4.448   0.547   1.0000  3
                GESPVDYDGGR     +2      2.838   0.451   0.9993  2
        MASCOT:(PepMatched Observed.Hits Coverage)      7       7       26.04%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                GESPVDYDGGR     +2      576.26  1150.50 1150.49 0.01    55      2
                GSTAPVGGGSFPNITPR       +2      807.92  1613.82 1613.82 0       86      3
                HQSLGGQYGVQGFPTIK       +2      908.97  1815.93 1815.93 0       77      3
                GSFSEQGINEFLR   +2      742.37  1482.72 1482.71 0.01    44      1
                LAAVDATVNQVLASR         +2      764.43  1526.85 1526.84 0.01    70      2
                TGEAIVDAALSALR  +2      693.88  1385.75 1385.75 0       83      4
                ALDLFSDNAPPPELLEIINEDIAK        +3      879.80  2636.37 2636.36 0.01    56      1

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
175.    IPI00365783     N       Y       0.05    1       0       2       0       4
*Des:   PREDICTED: similar to isoleucine-tRNA synthetase
        SEQUEST:(PepMatched Observed.Hits Coverage)
        MASCOT:(PepMatched Observed.Hits Coverage)      2       1       1.41%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
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		LFILMEAR		+2	496.78	991.55	991.55	0	51	3		
		LYLINSPVVR		+2	587.85	1173.69	1172.69	1	43	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
176.	IPI00339040		Y	Y	0.64	1	2	2	2	8		
*Des:	Ubiquitin-conjugating enzyme E2 variant 2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	14.96%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LLEELEEGQK		+2	2.834	0.537	0.9930	1				
		WTGMIIGPPR		+2	2.921	0.383	0.9728	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	14.96%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LLEELEEGQK		+2	594.31	1186.61	1186.61	0	54	5		
		WTGMIIGPPR		+2	564.30	1126.59	1126.60	0	46	6		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
177.	IPI00231046		Y	Y	0.87	1	3	3	7	6		
*Des:	Proteasome subunit alpha type 4											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	13.15%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		RPFGVSLLYIGWDK		+2	3.693	0.458	0.9999	2				
		VEIATLTR+2		2.760	0.277	0.9949	4					
		LLDEVFFSEK		+2	3.253	0.407	0.9997	8				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	13.15%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VEIATLTR+2		451.77	901.53	901.52	0.01	44	4			
		LLDEVFFSEK		+2	613.82	1225.63	1225.62	0.01	60	10		
		RPFGVSLLYIGWDK		+2	825.96	1649.91	1649.89	0.02	46	2		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
178.	IPI00364046		N	Y	0.3	2	0	3	0	49		
*Des:	Tubulin alpha-6 chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	2	11.37%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TIQFVDWCPTGFK		+2	771.3825	1540.7505	1540.7384	0.01	68	11		
		VGINYQPPTVVPGGDLAR			+2	927.0067	1851.9988	1851.9842	0.01	69	13	
		GHYTIGKEIIDLVLDRIR			+4	528.8084	2111.2043	2110.1898	1.01	54	10	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
179.	IPI00339114		Y	Y	0.06	1	2	2	5	6		
*Des:	Tyrosine-protein phosphatase, non-receptor type 6											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	4.48%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VNAADIENR		+2	3.113	0.418	0.9987	4				
		TGTIIVIDMLMESVSTK			+2	4.667	0.598	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	4.48%				

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VNAADIENR +2 501.2585 1000.5025 1000.4937 0.01 61 4
TGTIIVIDMLMESVSTK +2 919.5006 1836.9867 1836.9576 0.03 104 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
180. IPI00196656 Y Y 0.09 2 2 8 4 34
*Des: Ba1-667
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 2.8%
Seq Charge Xcor Delta Probility PepHits
EGVCPEGSIDSAPVK +2 2.770 0.299 0.9819 1
HQTVLENTNGK +2 3.658 0.511 1.0000 5
MASCOT:(PepMatched Observed.Hits Coverage) 8 3 11.23%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
GYYAVAVVK +2 485.27 968.53 968.53 0 48 1
ASDSSINWNNLK +2 674.83 1347.64 1347.64 0 51 1
GTDFQLNQLQGK +2 674.85 1347.68 1347.68 0 58 1
LYLGHSYVTAIR +2 696.89 1391.76 1391.76 0 65 2
HTTIFEVLPQK +3 438.25 1311.72 1311.72 0 42 8
DFQLFGSPLGK +2 603.85 1205.68 1207.62 -1.93 58 3
NGDGKEDLIWEILK +2 815.43 1628.84 1628.84 0 43 8
LPEGTTYEEYLGAEYLQAVGNIR +3 862.76 2585.27 2585.26 0.01 43 7

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
181. IPI00195929 Y N 0.16 1 6 0 11 0
*Des: CLIP-115 protein
SEQUEST:(PepMatched Observed.Hits Coverage) 6 1 9.68%
Seq Charge Xcor Delta Probility PepHits
MLDYEMLQR +2 2.705 0.345 0.9958 1
ATLNSGPGAQQK +2 3.218 0.440 0.9993 7
ALVEGIKMEHQLELGNLQAK +3 4.152 0.422 1.0000 2
LLSASKEHQR +2 2.805 0.428 0.9941 2
QASGPSSAGATTTVSEKPGPK +3 3.366 0.487 1.0000 5
HSSPVGRPSIGSASSSVVASASGSK +3 3.757 0.408 0.9999 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
182. IPI00371266 N Y 1.04 1 0 2 0 4
*Des: PREDICTED: similar to alpha NAC/1.9.2. protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 14.15%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
IEDLSQQAQLAAAEK +2 807.92 1613.83 1613.83 0 79 2
SPASDTYIVFGEAK +2 743.37 1484.73 1483.72 1.01 70 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
183. IPI00211731 Y Y 0.13 3 4 4 5 5
*Des: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma 2

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          SEQUEST:(PepMatched Observed.Hits Coverage)  4          2          4.81%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    GILDLNTYNVVK          +2         3.374      0.397      0.9990     1
                    VTFEIYDPNLAFLR        +2         4.400      0.536      1.0000     2
                    VEELFEWFQSIR          +2         4.315      0.307      0.9992     1
                    YYLTDNLTFNSIYALIQHYR  +3         3.665      0.404      0.9998     1
          MASCOT:(PepMatched Observed.Hits Coverage)   4          3          5.98%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore   PepHits
                    GEAEDMLMR             +2         526.2393   1050.4641  1050.4474  0.02       45         1
                    GDVDVNVEDK            +2         545.2631   1088.5116  1088.4985  0.01       47         2
                    DSSVFILGNTDRPDASAVYLQDFQR        +3         938.8098   2813.4074  2813.3620  0.05       48         1
                    LSFSDDIEQTVEEDPVQDTPPTELHFGEK    +3         1101.5314  3301.5723  3301.5150  0.06       135        1

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
184.      IPI00203712           Y          N          0.3        1          2          0          2          0
*Des:     Interferon gamma inducible protein 1
          SEQUEST:(PepMatched Observed.Hits Coverage)  2          1          13.95%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    HMFALLLPNISDASIELK               +3         3.767      0.326      0.9983     1
                    IFLISNFDLDAFDFPK                 +2         4.564      0.525      1.0000     1
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
185.      IPI00213190           Y          Y          1.04       1          6          3          19         12
*Des:     Branched-chain-amino-acid aminotransferase, mitochondrial precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)  6          1          21.25%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    AADLQVQVTR            +2         3.611      0.396      0.9996     4
                    LGGNYGPTVAVQQEAQK                +2         4.875      0.519      1.0000     10
                    KPAPSQPLLFGK          +2         2.993      0.408      0.9987     2
                    AIQYGTSAHDWMLR+2                 3.813      0.471      0.9998     3
                    LFRPWLNMDR            +3         3.295      0.293      0.9983     1
                    QLHIPTMENGPELILR                 +3         3.827      0.427      0.9999     2
          MASCOT:(PepMatched Observed.Hits Coverage)   3          1          11%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore   PepHits
                    AADLQVQVTR            +2         550.81     1099.61    1099.60    0.01       78         4
                    LGGNYGPTVAVQQEAQK                +2         880.46     1758.91    1758.89    0.02       95         10
                    AIQYGTSAHDWMLR+2                 824.91     1647.80    1647.78    0.02       81         4

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
186.      IPI00566742           N          Y          0.18       1          0          2          0          2
*Des:     23 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)   2          1          14.7%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore   PepHits
                    GASQAGMTGYGMPR                   +2         692.3223   1382.6300  1382.6070  0.02       50         1
                    TTDIFQTVDLWEGK +2                826.9251   1651.8357  1651.8093  0.03       45         1
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Identified Human Platelet Proteins

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No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
187.    IPI00193247     Y       N       0.07    1       2       0       2       0
*Des:   PREDICTED: similar to cellular apoptosis susceptibility protein
        SEQUEST:(PepMatched Observed.Hits Coverage)     2       1       5.06%
                Seq     Charge  Xcor    Delta   Probility       PepHits
                SFSLLQEAIIPYIPTLITQLTQK +3      4.225   0.525   1.0000  1
                HGITQANELVNLTEFFVNHILPDLK       +3      5.802   0.591   1.0000  2
        MASCOT:(PepMatched Observed.Hits Coverage)

No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
188.    IPI00192445     N       Y       1.04    1       0       2       0       16
*Des:   Vps24p
        SEQUEST:(PepMatched Observed.Hits Coverage)
        MASCOT:(PepMatched Observed.Hits Coverage)      2       1       10.13%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                IPEIQATMR       +2      529.79  1057.56 1057.56 0       51      3
                ILFEITAGALGK    +2      616.87  1231.73 1231.72 0.01    84      15

No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
189.    IPI00563401     N       Y       0.17    1       0       3       0       5
*Des:   PREDICTED: hypothetical protein XP_579397
        SEQUEST:(PepMatched Observed.Hits Coverage)
        MASCOT:(PepMatched Observed.Hits Coverage)      3       1       3.47%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                STVVSTAVALAAHK +2       678.86  1355.71 1353.76 1.95    45      1
                IPAFGSIPIEFR    +2      673.88  1345.74 1345.74 0       46      2
                TLLRPEEILLSIEIPYSK      +3      705.41  2113.22 2113.20 0.02    48      4

No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
190.    IPI00205248     Y       Y       0.9     1       2       3       4       8
*Des:   Phospholipase A2, membrane associated precursor
        SEQUEST:(PepMatched Observed.Hits Coverage)     2       1       10.73%
                Seq     Charge  Xcor    Delta   Probility       PepHits
                GGQISCSTNQDSCR +2       4.428   0.564   1.0000  3
                GGQISCSTNQDSCRK +2      3.616   0.448   0.9995  1
        MASCOT:(PepMatched Observed.Hits Coverage)      3       1       16.77%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                GGQISCSTNQDSCR +2       728.3088 1454.6030 1454.5878 0.02 100   4
                AAAECFAR        +2      419.6996 837.3846 837.3803 0    43      5
                GGQISCSTNQDSCRK +2      792.3568 1582.6991 1582.6828 0.02 70    1

No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
191.    IPI00555312     Y       Y       1.9     1       7       9       14      17
*Des:   Protease (Prosome, macropain) 28 subunit, alpha
        SEQUEST:(PepMatched Observed.Hits Coverage)     7       1       30.76%
                Seq     Charge  Xcor    Delta   Probility       PepHits
```

NAYAVLYDIILK		+2	3.988	0.501	1.0000	6		
EPALNEANLSNLK		+2	3.002	0.539	0.9999	2		
QLVHELDEAEYQEIR			+2	4.215	0.535	1.0000	4	
APLDIPVPDPVKEK		+2	3.267	0.487	0.9943	3		
APLDIPVPDPVK		+2	2.865	0.319	0.9947	2		
VFELMTSLHTK		+2	3.254	0.343	0.9989	1		
KISELDAFLKEPALNEANLSNLK				+3	5.584	0.471	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 9 1 33.84%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
IVVLLQR	+2	420.79	839.56	839.56	0	41	2			
EPALNEANLSNLK		+2	706.88	1411.74	1411.73	0.01	58	2		
APLDIPVPDPVKEK		+2	759.44	1516.86	1516.85	0.01	52	3		
QLVHELDEAEYQEIR			+2	936.47	1870.92	1870.91	0.01	77	4	
APLDIPVPDPVK		+2	630.87	1259.72	1259.71	0.01	53	2		
ISELDAFLK		+2	519.27	1036.53	1034.56	1.97	56	3		
TENLLGSYFPK		+2	634.83	1267.65	1267.64	0.01	65	6		
KISELDAFLKEPALNEANLSNLK				+3	853.14	2556.40	2556.38	0.02	61	1
NAYAVLYDIILK		+2	698.40	1394.79	1394.78	0.01	93	6		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)								
192.	IPI00211593		N	Y	0.62	1	0	3	0	4

*Des: Superoxide dismutase [Mn], mitochondrial precursor

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 17.69%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
GELLEAIKR		+2	514.8415	1027.6684	1027.6025	0.07	41	2		
GDVTTQVALQPALK		+2	720.9592	1439.9038	1439.7984	0.11	66	1		
AIWNVINWENVSQR		+2	865.0145	1728.0144	1727.8743	0.14	54	1		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)								
193.	IPI00421513		N	Y	0.15	1	0	2	0	3

*Des: Aspartate aminotransferase, cytoplasmic

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 4.53%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
VNLGVGAYR		+2	474.76	947.52	947.52	0	52	1		
IGADFLAR		+2	431.74	861.47	861.47	0	51	2		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)								
194.	IPI00210938		Y	Y	0.21	2	3	6	3	9

*Des: PREDICTED: similar to Ctps protein

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 5.04%

Seq	Charge	Xcor	Delta	Probility	PepHits			
LTKDNNLTTGK		+2	3.251	0.399	0.9954	2		
GVIASSVGTILK		+2	2.934	0.438	0.9987	1		
TSHPVVIDMPEHNPGQMGGTMR				+3	4.330	0.588	1.0000	3

MASCOT:(PepMatched Observed.Hits Coverage) 6 2 8.92%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
FVGQDVEGER	+2	568.77	1135.53	1134.53	1	49	2
LYGDTDYLEER	+2	687.32	1372.62	1372.61	0.01	74	1
GVIASSVGTILK	+2	573.30	1144.59	1143.69	0.9	62	4
YILVTGGVISGIGK	+2	688.91	1375.80	1375.81	0	99	3
NVLGWQDANSTEFDPK	+2	910.93	1819.84	1819.84	0	69	1
VPLLLEEQGVVDYFLR	+2	945.52	1889.03	1889.03	0	97	3

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
195.	IPI00368400	Y	N	0.15	2	2	0	6	0

*Des: PREDICTED: similar to Eno1 protein

SEQUEST:(PepMatched Observed.Hits Coverage) 2 2 9.54%

Seq	Charge	Xcor	Delta	Probility	PepHits
DATNVGDEGGFAPNILENK	+2	5.628	0.557	0.9789	2
DYPVVSIEDPFDQDDWDAWQK	+2	4.812	0.481	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
196.	IPI00555171	Y	Y	3.62	5	18	12	139	112

*Des: Transgelin 2

SEQUEST:(PepMatched Observed.Hits Coverage) 18 12 77.57%

Seq	Charge	Xcor	Delta	Probility	PepHits
NFSDNQLQEGK	+2	4.217	0.428	1.0000	15
DDGLFSGDPNWFPKK	+2	4.381	0.535	1.0000	14
QMEQISQFLQAAER	+3	4.473	0.378	1.0000	8
DDGLFSGDPNWFPK	+2	4.792	0.579	1.0000	8
YGINTTDIFQTVDLWEGKNMACVQR	+3	5.347	0.562	1.0000	3
YGINTTDIFQTVDLWEGK	+2	6.425	0.591	1.0000	22
DGTVLCELINSLYPEGQAPVKK	+2	5.091	0.603	1.0000	7
TLMNLGGLAVARDDGLFSGDPNWFPK	+3	5.824	0.549	1.0000	6
IEKQYDPDLEQILIQWITTQCRK	+3	3.798	0.501	1.0000	2
ENFQNWLKDGTVLCELINSLYPEGQAPVKK	+3	6.976	0.593	1.0000	3
IEKQYDPDLEQILIQWITTQCR	+3	5.178	0.539	1.0000	5
NVIGLQMGTNR	+2	3.619	0.510	1.0000	20
NFSDNQLQEGKNVIGLQMGTNR	+3	4.994	0.425	1.0000	3
TLMNLGGLAVAR	+2	4.294	0.465	1.0000	39
KGVSQPQPGR	+2	3.569	0.502	1.0000	18
GVSQPQPGRENFQNWLK	+2	4.080	0.423	0.9981	3
KGVSQPQPGRENFQNWLK	+3	3.846	0.382	0.9999	3
TLMNLGGLAVARDDGLFSGDPNWFPKK	+3	5.369	0.542	1.0000	13

MASCOT:(PepMatched Observed.Hits Coverage) 12 13 39.71%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
NFSDNQLQEGK	+2	640.3041	1278.5936	1278.5840	0.01	86	23
DDGLFSGDPNWFPKK	+2	861.9175	1721.8205	1721.8049	0.02	70	20
DDGLFSGDPNWFPK	+2	797.8690	1593.7234	1593.7099	0.01	75	12
QMEQISQFLQAAER	+2	839.9217	1677.8288	1677.8144	0.01	91	11
NVIGLQMGTNR	+2	601.8231	1201.6316	1201.6237	0.01	68	18

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                    TLMNLGGLAVAR    +2      608.3513        1214.6881       1214.6805       0.01    87      32
                    GVSQPQPGR       +2      463.2493        924.4840        924.4777        0.01    51      8
                    NFSDNQLQEGKNVIGLQMGTNR          +3      821.7457        2462.2154       2462.1971       0.02    69      1
                    KGVSQPQPGR      +2      527.2972        1052.5798       1052.5726       0.01    62      18
                    GVSQPQPGRENFQNWLK       +2      993.0129        1984.0113       1983.9914       0.02    50      3
                    KGVSQPQPGRENFQNWLK      +2      1057.0580       2112.1014       2112.0864       0.01    50      3
                    TLMNLGGLAVARDDGLFSGDPNWFPKK     +3      973.8380        2918.4922       2918.4748       0.02    81      12

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
197.    IPI00288140     Y       Y       0.44    1       2       3       2       22
*Des:   Ribose-phosphate pyrophosphokinase II
        SEQUEST:(PepMatched Observed.Hits Coverage)     2       1       11.45%
                    Seq     Charge  Xcor    Delta   Probility       PepHits
                    FSNQETSVEIGESVR         +2      4.479   0.519   1.0000  1
                    INNAAFEAVVVTNTIPQEDK    +2      5.660   0.546   1.0000  1
        MASCOT:(PepMatched Observed.Hits Coverage)      3       2       15.47%
                    Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore        PepHits
                    FSNQETSVEIGESVR         +2      841.41  1680.80 1680.80 0       81      1
                    VYAILTHGIFSGPAISR       +2      901.50  1800.98 1800.99 0       118     3
                    IQVIDISMILAEAIR +2      842.99  1683.97 1683.96 0.01    120     18

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
198.    IPI00562537     N       Y       1.08    2       0       19      0       252
*Des:   PREDICTED: similar to pyruvate kinase (EC 2.7.1.40) isozyme M2 - rat
        SEQUEST:(PepMatched Observed.Hits Coverage)
        MASCOT:(PepMatched Observed.Hits Coverage)      19      2       46.95%
                    Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore        PepHits
                    GSGTAEVELK      +2      495.7615        989.5085        989.5029        0.01    59      20
                    LDIDSAPITAR     +2      586.3235        1170.6324       1170.6244       0.01    84      69
                    ITLDNAYMEK      +2      599.2990        1196.5835       1196.5747       0.01    62      24
                    KGATLKITLDNAYMEK        +3      599.2990        1794.8752       1794.9549       -0.07   44      24
                    GDLGIEIPAEK     +2      571.3123        1140.6101       1140.6026       0.01    56      22
                    IYVDDGLISLQVK   +2      731.9163        1461.8180       1461.8078       0.01    86      34
                    GADYLVTEVENGGSLGSK      +2      898.4412        1794.8679       1794.8635       0       127     10
                    DAVLDAWAEDVDLR          +2      794.3924        1586.7702       1586.7576       0.01    93      20
                    VNLAMNVGK       +2      473.9076        945.8006        944.5113        1.29    56      9
                    RFDEILEASDGIMVAR        +2      911.4714        1820.9283       1820.9090       0.02    76      16
                    KAADVHEVR       +2      512.7838        1023.5531       1023.5461       0.01    64      15
                    GSGTAEVELKK     +2      559.8112        1117.6079       1117.5978       0.01    43      10
                    APIIAVTR +2     420.7714        839.5283        839.5229        0.01    69      30
                    PKPDSEAGTAFIQTQQLHAAMADTFLEHMCR         +4      861.9172        3443.6396       3443.6060       0.03    88      15
                    NTGIICTIGPASR   +2      651.8500        1301.6855       1301.6761       0.01    69      45
                    MQHLIAR +2      434.7472        867.4798        867.4749        0       44      7
                    IISKIENHEGVR    +2      697.8966        1393.7787       1393.7677       0.01    67      14
                    LNFSHGTHEYHAETIK        +2      942.4626        1882.9106       1882.8962       0.01    95      28
                    KGDVVIVLTGWRPGSGFTNTMR          +3      797.7654        2390.2745       2390.2528       0.02    54      5
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Identified Human Platelet Proteins

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
199. IPI00199203 Y N 0.2 2 3 0 16 0
*Des: PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase
SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 17.3%
Seq Charge Xcor Delta Probility PepHits
GAAQNIIPASTGAAK +2 4.266 0.508 0.9999 20
IVSNASCTTNCLTPLAK +2 3.228 0.182 0.9526 1
VIHDNFGIVGGLMTTVHAITATQK +3 5.491 0.499 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
200. IPI00325146 N Y 0.02 1 0 2 0 4
*Des: Annexin A2
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 4.34%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
QDIAFAYQR +2 556.2870 1110.5595 1110.5458 0.01 45 2
SNAQRQDIAFAYQR +3 556.2870 1665.8393 1666.8175 -0.97 37 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
201. IPI00325147 Y N 0.44 1 5 0 10 0
*Des: Farnesyl pyrophosphate synthetase
SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 20.05%
Seq Charge Xcor Delta Probility PepHits
VLTEDELGHPEK +2 2.895 0.382 0.9977 4
EVLEYNTVGGK +2 3.250 0.478 0.9997 4
ALYEELDLR +2 2.851 0.394 0.9988 3
GLTVVQTFQELVEPR +3 4.567 0.472 1.0000 4
PGIGLDAINDALLLEAAIYR +3 4.013 0.496 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
202. IPI00480673 N Y 0.32 1 0 2 0 5
*Des: Similar to Ras-related protein Rab-1B
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 16.58%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VVDNTTAKEFADSLGVPFLETSAK +3 847.1664 2538.4774 2538.2853 0.19 43 1
TITSSYYR +2 495.7809 989.5472 989.4818 0.07 38 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
203. IPI00197605 Y Y 1.09 1 4 4 4 5
*Des: SynaptoSomal-aSSociated protein 23
SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 29.9%
Seq Charge Xcor Delta Probility PepHits
IEEGMDQINK +2 2.622 0.231 0.9685 2
ITNGQPQQTTGAASGGYIK +2 2.940 0.417 0.9906 1

```
                  ATWGDGGDSSPSNVVSK        +2       4.445    0.609    1.0000   1
                  TITMLDEQGEQLNR +2        4.277    0.355    0.9997   1
         MASCOT:(PepMatched Observed.Hits Coverage)  4        1        29.9%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
                  ITNGQPQQTTGAASGGYIK      +2       946.98   1891.94  1890.94  1        95       1
                  IEEGMDQINK        +2       588.79   1175.56  1175.55  0.01     55       4
                  ATWGDGGDSSPSNVVSK        +2       832.39   1662.76  1662.75  0.01     98       1
                  TITMLDEQGEQLNR +2        824.41   1646.80  1646.79  0.01     85       1

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
204.     IPI00366735       N        Y        0.13     1        0        2        0        3
*Des:    PREDICTED: similar to mKIAA0089 protein
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)  2        1        5.36%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
                  LQGPQTSAEVYR      +2       674.85   1347.68  1347.68  0        44       1
                  LGLMEMIAFAK       +2       612.33   1222.65  1222.65  0        67       2

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
205.     IPI00198191       Y        Y        1.42     1        5        5        11       11
*Des:    Calcyclin binding protein
         SEQUEST:(PepMatched Observed.Hits Coverage)  5        1        43.77%
                  Seq      Charge   Xcor     Delta    Probility PepHits
                  ISNYGWDQSDK       +2       3.563    0.373    0.9997   5
                  KPEFDNEKPAAVVAPLTTGYTVK           +3       5.233    0.589    1.0000   1
                  IYITLTGVHQVPAENVQVHFTER           +3       6.730    0.597    1.0000   4
                  EKPSYDTEADPSEGLMNVLK     +3       3.336    0.273    0.9932   1
                  NYSMIVNNLLKPISVESSSK     +3       4.412    0.432    0.9999   3
         MASCOT:(PepMatched Observed.Hits Coverage)  5        1        38.19%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
                  ISNYGWDQSDK       +2       656.80   1311.58  1311.57  0.01     75       5
                  KPEFDNEKPAAVVAPLTTGYTVK           +3       825.78   2474.33  2474.31  0.02     49       1
                  SFDLLVK +2        411.25   820.48   820.47   0.01     47       1
                  IYITLTGVHQVPAENVQVHFTER           +3       884.48   2650.42  2650.39  0.03     96       3
                  NYSMIVNNLLKPISVESSSK     +3       741.73   2222.18  2222.16  0.02     61       2

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
206.     IPI00196661       Y        Y        0.69     5        6        6        79       41
*Des:    14-3-3 protein tau
         SEQUEST:(PepMatched Observed.Hits Coverage)  6        6        39.6%
                  Seq      Charge   Xcor     Delta    Probility PepHits
                  TAFDEAIAELDTLNEDSYK      +2       5.959    0.635    1.0000   7
                  DSTLIMQLLR        +2       3.890    0.244    0.9988   37
                  AVTEQGAELSNEER +2        5.299    0.397    1.0000   18
                  YLIANATNPESK      +2       4.410    0.352    0.9999   24
                  QTIENSQGAYQEAFDISKK      +3       3.713    0.441    0.9999   1
                  KQTIENSQGAYQEAFDISK      +2       6.242    0.600    1.0000   5
```

	MASCOT:(PepMatched Observed.Hits Coverage)					6	5	35.2%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AVTEQGAELSNEER		+2	766.87	1531.72	1531.71	0.01	106	19		
		YLIANATNPESK		+2	660.85	1319.68	1319.67	0.01	85	24		
		QTIENSQGAYQEAFDISK			+3	676.99	2027.96	2027.94	0.02	57	2	
		KQTIENSQGAYQEAFDISK			+3	719.69	2156.05	2156.04	0.01	53	4	
		QTIENSQGAYQEAFDISKK			+3	719.69	2156.06	2156.04	0.02	43	1	
		TAFDEAIAELDTLNEDSYK			+3	715.67	2144.00	2143.98	0.02	93	4	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
207.	IPI00365792		Y	Y	0.17	1	2	3	5	5		
*Des:	PREDICTED: similar to Stromal interaction molecule 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	3.29%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		YAEEELEQVR		+2	2.850	0.394	0.9986	4				
		QALSEVTAALR		+2	3.083	0.321	0.9969	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	2	4.73%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YAEEELEQVR		+2	633.31	1264.60	1264.59	0.01	48	4		
		QALSEVTAALR		+2	579.83	1157.64	1157.64	0	46	1		
		LISVEDLWK		+2	551.81	1101.61	1101.61	0	43	1		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
208.	IPI00559603		N	Y	0.11	2	0	4	0	13		
*Des:	75 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	2	8.19%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YEISESLLAQR		+2	654.84	1307.67	1307.67	0	56	4		
		DTINPLYDETFR		+2	742.36	1482.70	1482.70	0	45	2		
		DLILSVLQR		+2	528.82	1055.63	1055.63	0	52	6		
		SVIDLRPEDVAQESGILGDR			+3	723.71	2168.10	2168.11	0	42	6	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
209.	IPI00363182		N	Y	0.28	1	0	2	0	9		
*Des:	PREDICTED: similar to solute carrier family 25, member 5											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	10.19%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DFLAGGVAAAISK		+2	610.34	1218.66	1218.66	0	89	5		
		GMGGAFVLVLYDEIKK			+2	870.48	1738.94	1738.93	0.01	66	6	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
210.	IPI00211812		Y	Y	0.12	2	4	2	4	2		
*Des:	Coatomer beta subunit											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	2	6.81%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					

		LPGLLMTIIR		+2	2.711	0.384	0.9978	1				
		NFENLIPDAPELIHDFLVNEK			+3	4.124	0.394	0.9998	1			
		LLLVFWEIVPK		+2	3.162	0.339	0.9980	1				
		QNSFVAEAMLLMATILHLGK			+3	3.923	0.498	1.0000	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	2	2.47%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VLQDLVMDILR		+2	658.3095	1314.6045	1313.7377	0.87	62	3		
		LLLVFWEIVPK		+2	678.9227	1355.8308	1355.8216	0.01	51	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
211.	IPI00211813		Y	Y	0.04	2	2	3	12	67		
*Des:	Neuronal myosin heavy chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	3	1.18%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IAQLEEELEEEQGNTELINDR			+3	5.568	0.459	1.0000	7			
		IAQLEEELEEEQGNTELINDRLK				+3	5.110	0.493	1.0000	5		
	MASCOT:(PepMatched Observed.Hits Coverage)					3	4	2.55%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IAQLEEELEEEQGNTELINDRLK				+3	905.1257	2712.3554	2712.3453	0.01	86	6
		AGVLAHLEEER		+2	612.3242	1222.6339	1222.6305	0	51	2		
		KFDQLLAEEITKSAK		+3	574.3234	1719.9483	1719.9406	0.01	42	4		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
212.	IPI00209397		Y	Y	0.3	1	3	3	5	8		
*Des:	Coronin-1B											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	7.3%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VLVKEQGER		+2	2.721	0.358	0.9849	3				
		NVLSDSKPAGYSR		+2	2.943	0.495	0.9994	1				
		VGIITWHPTAR		+3	3.266	0.402	1.0000	9				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	7.3%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VLVKEQGER		+2	529.3079	1056.6012	1056.5927	0.01	41	3		
		NVLSDSKPAGYSR		+2	697.3632	1392.7119	1392.6997	0.01	59	1		
		VGIITWHPTAR		+3	417.5741	1249.7006	1249.6931	0.01	48	16		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
213.	IPI00210941		Y	Y	0.67	3	5	3	17	13		
*Des:	Tropomyosin											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	6	26.48%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AREQAEAEVASLNR		+2	5.152	0.554	1.0000	1				
		KIQVLQQQADDAEERAER			+3	4.151	0.455	1.0000	9			
		IQVLQQQADDAEERAERLQR			+3	4.130	0.508	1.0000	2			
		LQREVEGERR		+3	3.111	0.300	0.9988	18				
		AREQAEAEVASLNRR			+3	4.453	0.354	1.0000	22			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	3	11.46%				

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
EQAEAEVASLNR +2 658.83 1315.64 1315.64 0 54 6
IQVLQQQADDAEER +2 821.91 1641.80 1641.80 0 99 3
KIQVLQQQADDAEER +2 885.96 1769.90 1769.89 0.01 98 6

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
214. IPI00191728 Y Y 0.44 3 6 7 7 7
*Des: Calreticulin precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 6 8 30.96%
Seq Charge Xcor Delta Probility PepHits
IDDPTDSKPEDWDKPEHIPDPDAK +3 3.544 0.410 0.9992 4
GQTLVVQFTVK +2 3.298 0.472 0.9998 2
KPEDWDEEMDGEWEPPVIQNPEYK +3 5.409 0.570 1.0000 1
IDNSQVESGSLEDDWDFLPPKK +3 3.941 0.396 0.9994 1
SGTIFDNFLITNDEAYAEEFGNETWGVTK +3 5.406 0.595 1.0000 1
IKDPDAAKPEDWDER +2 4.004 0.503 0.9988 4
MASCOT:(PepMatched Observed.Hits Coverage) 7 6 27.42%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
IKDPDAAKPEDWDER +2 892.93 1783.85 1783.84 0.01 42 2
IDDPTDSKPEDWDKPEHIPDPDAK +3 920.77 2759.28 2759.26 0.02 51 2
AKIDDPTDSKPEDWDKPEHIPDPDAK +3 987.14 2958.39 2958.39 0 57 1
GQTLVVQFTVK +2 610.36 1218.70 1218.70 0 67 2
EQFLDGDAWTNR +2 726.33 1450.65 1450.65 0 50 1
IDNSQVESGSLEDDWDFLPPKK +3 840.40 2518.19 2518.19 0 49 1
KPEDWDEEMDGEWEPPVIQNPEYK +3 987.44 2959.30 2959.29 0.01 48 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
215. IPI00210945 N Y 0.68 1 0 4 0 38
*Des: Hepatoma alpha tropomyosin; NCBI gi: 207353
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 4 1 11.07%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LVIIESDLER +2 593.84 1185.67 1185.66 0.01 62 16
KLVIIESDLER +2 657.89 1313.76 1313.76 0 81 12
AELSEGQVR +2 494.76 987.50 987.50 0 42 3
MEIQEIQLK +2 566.31 1130.61 1130.60 0.01 53 19

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
216. IPI00210947 N Y 0.46 1 0 3 0 4
*Des: Heparin cofactor II precursor
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 8.82%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
TLEAQLTPQVVER +2 742.41 1482.81 1482.80 0.01 76 1
YEVTTIHNLFR +2 696.87 1391.72 1391.72 0 44 1
NFGYTLQSVNDLYIQK +2 951.99 1901.96 1901.95 0.01 88 2

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
217.	IPI00555252		N	Y	0.4	1	0	4	0	96		
*Des:	Glyceraldehyde-3-phosphate dehydrogenase											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	2	18.34%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GAAQNIIPASTGAAK		+2	685.38	1368.74	1368.74	0	64	22		
		VGVNGFGR		+2	403.71	805.41	804.42	0.99	47	10		
		VVDLMAYMASK		+2	614.31	1226.61	1226.60	0.01	68	30		
		VIHDNFGIVEGLMTTVHAITATQK				+3	865.79	2594.35	2594.35	0	70	8

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
218.	IPI00191587		Y	Y	0.91	1	2	4	4	7		
*Des:	LOC500282 protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	21.05%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DLPNALDEKQLIEK		+2	4.043	0.648	0.9961	2				
		NELHNLLDKPQLQGIPVLVLGNKR				+3	6.126	0.816	1.0000	4		
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	31.57%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MNLSAIQDR		+2	524.27	1046.52	1046.52	0	41	2		
		IWDIGGQPR		+2	521.28	1040.54	1040.54	0	44	1		
		DLPNALDEKQLIEK		+2	813.44	1624.87	1624.87	0	70	2		
		NELHNLLDKPQLQGIPVLVLGNKR				+3	903.52	2707.54	2707.55	0	69	2

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
219.	IPI00391812		N	Y	0.46	1	0	3	0	7		
*Des:	57 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	8.71%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GTTLNPDSEIAR		+2	637.32	1272.63	1272.63	0	45	9		
		RPTSASSSPTETVYSVVK			+2	948.49	1894.97	1894.96	0.01	51	1	
		WLFNSQSLQLTDR		+2	804.42	1606.82	1606.81	0.01	50	3		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
220.	IPI00555182		Y	Y	0.91	1	2	3	2	3		
*Des:	Splice Isoform 1 of Adaptin ear-binding coat-associated protein 2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	16.04%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ASEWQLDQPSWSGR			+2	3.339	0.333	0.9948	1			
		TSGELFAQAPVDQFPGTAVESVTDSSR				+3	4.812	0.513	0.9999	1		
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	20.14%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ASEWQLDQPSWSGR			+2	823.89	1645.76	1645.75	0.01	43	1	
		AFIGIGFGDR		+2	526.78	1051.54	1051.54	0	44	3		
		TSGELFAQAPVDQFPGTAVESVTDSSR				+3	932.79	2795.34	2795.32	0.02	61	1

Identified Human Platelet Proteins

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
221.	IPI00558598	N	Y	0.2	1	0	2	0	6

*Des: 27 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 10.31%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
DLADELALVDVIEDK	+2	829.4480	1656.8814	1656.8457	0.04	82	2
LVIITAGAR	+2	457.3027	912.5909	912.5756	0.02	56	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
222.	IPI00421528	N	Y	0.34	1	0	4	0	9

*Des: Proteasome (Prosome, macropain) 26S subunit, ATPase 3

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 11.55%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
MSTEEIVQR	+2	546.77	1091.53	1091.53	0	50	2
MNVSPDVNYEELAR	+2	818.89	1635.76	1635.76	0	69	2
VDILDPALLR	+2	562.84	1123.66	1123.66	0	43	3
QTYFLPVIGLVDAEK	+2	846.96	1691.91	1691.91	0	50	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
223.	IPI00555185	N	Y	0.47	1	0	2	0	2

*Des: RAB10, member RAS oncogene family

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 17.64%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
AFLTLAEDILR	+2	631.4083	1260.8020	1260.7077	0.09	50	1
TPVKEPNSENVDISSGGGVTGWK	+3	786.7799	2357.3179	2357.1498	0.17	50	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
224.	IPI00387868	Y	Y	0.09	2	2	2	3	3

*Des: Ischemia responsive 94 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 2 3 4.09%

Seq	Charge	Xcor	Delta	Probility	PepHits
SNLAYDIVQLPTGLTGIK	+2	4.532	0.499	0.9999	2
EFSITDVVPYPISLR	+2	3.039	0.422	0.9986	1

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 3.39%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
ELSTTLNADEAVTR	+2	760.3886	1518.7625	1518.7525	0.01	85	2
VLATAFDTTLGGR	+2	661.3648	1320.7151	1320.7037	0.01	66	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
225.	IPI00358720	N	Y	0.35	1	0	2	0	3

*Des: PREDICTED: similar to GLI pathogenesis-related 2

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 7.3%

Identified Human Platelet Proteins

		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ASASDGSSFVVAR		+2	627.31	1252.61	1252.60	0.01	55	2		
		KLNQEAQQYSEALASTR			+2	968.99	1935.98	1935.96	0.02	115	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
226.	IPI00464645		N	Y	0.34	1	0	5	0	16		
*Des:	Pyruvate dehydrogenase (Lipoamide) beta											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					5	1	21.91%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		EAINQGMDEELERDEK			+2	953.44	1904.86	1904.84	0.02	54	2	
		ILEDNSIPQVK		+2	628.35	1254.68	1254.68	0	57	4		
		VFLLGEEVAQYDGAYK			+3	601.64	1801.90	1800.89	1.01	55	6	
		TIRPMDIEAIEASVMK			+2	902.48	1802.94	1802.93	0.01	62	6	
		TYYMSAGLQPVPIVFR			+2	921.49	1840.97	1840.95	0.02	85	6	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
227.	IPI00390946		Y	N	0.3	3	3	0	5	0		
*Des:	PREDICTED: similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	6	13.27%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LNVVEQEKIDQLMIEMDGTENKSK				+3	3.683	0.473	1.0000	1		
		YNQILRIEEELGSKAK			+3	3.943	0.387	1.0000	2			
		VNQIGSVTESLQACK			+2	2.913	0.461	0.9997	13			
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
228.	IPI00368347		Y	Y	0.78	3	21	21	42	40		
*Des:	Hypothetical LOC314432											
	SEQUEST:(PepMatched Observed.Hits Coverage)					21	3	36.24%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		QMNPYIQVTSHQNR		+2	3.183	0.384	0.9983	4				
		QPAENVNQYLTDSK		+2	2.786	0.522	0.9996	2				
		SPPAVQQDNVDEDLIR			+2	5.469	0.657	1.0000	3			
		LDQPMTEIVSR		+2	3.869	0.483	0.9999	3				
		IHVSDQELQSANASVDDSRLEELK				+3	6.293	0.620	1.0000	2		
		YDGQVAVFGSDLQEK			+2	5.524	0.584	1.0000	1			
		FEVQGLQPNGEEMTLK			+2	4.445	0.519	1.0000	2			
		HQYYNQEWTLWDR		+2	4.667	0.572	1.0000	4				
		NEEDATELVTLAQAVNAR			+3	4.633	0.369	0.9998	1			
		QLLHNFPPDQLTSSGAPFWSGPK				+3	3.377	0.387	0.9992	2		
		NFPNAIEHTLQWAR		+2	3.329	0.439	0.9994	2				
		LAGTQPLEVLEAVQR			+2	3.740	0.465	0.9998	2			
		AVTLHDQGTTQWADLSSQFYLR				+2	5.857	0.625	1.0000	3		
		AAVASLLQSVQVPEFTPK			+2	3.983	0.520	0.9999	2			
		SLPASLAEPDFVMTDFAK			+2	3.562	0.529	0.9999	1			
		GNVQVVIPFLTESYSSSQDPPEK				+2	4.238	0.570	1.0000	3		

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                IYDDDFFQNLDGVANALDNVDAR             +2      6.027   0.481   1.0000  3
                LAYVAAGDLAPINAFIGGLAAQEVMK          +2      6.588   0.674   1.0000  2
                NGFLNLALPFFGFSEPLAAPR       +2      5.298   0.571   1.0000  4
                TEHKLEITMLSQGVSMLYSFFMPAAK          +3      3.186   0.436   0.9948  1
                IHVSDQELQSANASVDDSR         +2      6.949   0.681   1.0000  2
        MASCOT:(PepMatched Observed.Hits Coverage)  21      4       35.4%
                Seq     Charge  ObservedMS          ExpectedMS      CalculatedMS            Pepscore PepHits
                QPAENVNQYLTDSK +2       803.89  1605.77 1605.76 0.01    44      2
                QMNPYIQVTSHQNR +2       858.42  1714.83 1714.82 0.01    51      2
                IHVSDQELQSANASVDDSR         +3      691.00  2069.98 2069.96 0.02    43      1
                LDQPMTEIVSR     +2      644.83  1287.65 1287.65 0       74      3
                NGSEADIDESLYSR  +2      778.84  1555.67 1554.68 0.99    73      1
                SPPAVQQDNVDEDLIR            +2      898.45  1794.89 1794.87 0.02    113     3
                IHVSDQELQSANASVDDSRLEELK            +3      895.12  2682.33 2682.31 0.02    80      1
                YDGQVAVFGSDLQEK             +2      828.40  1654.79 1654.78 0.01    104     2
                FEVQGLQPNGEEMTLK            +2      910.45  1818.89 1818.88 0.01    84      4
                LAGTQPLEVLEAVQR             +2      812.46  1622.90 1622.90 0       81      4
                NFPNAIEHTLQWAR +2       848.94  1695.86 1695.85 0.01    47      2
                HQYYNQEWTLWDR +2        919.92  1837.83 1837.82 0.01    81      6
                AAVASLLQSVQVPEFTPK          +2      943.03  1884.04 1884.04 0       61      4
                SLPASLAEPDFVMTDFAK          +2      969.98  1937.94 1937.94 0       56      4
                NEEDATELVTLAQAVNAR          +3      648.66  1942.97 1942.96 0.01    62      2
                AVTLHDQGTTQWADLSSQFYLR              +3      846.42  2536.25 2536.23 0.02    42      4
                NGFLNLALPFFGFSEPLAAPR       +3      760.08  2277.20 2277.19 0.01    41      4
                GNVQVVIPFLTESYSSSQDPPEK             +3      841.09  2520.24 2520.24 0       41      2
                IYDDDFFQNLDGVANALDNVDAR             +3      867.41  2599.19 2599.18 0.01    82      2
                LAYVAAGDLAPINAFIGGLAAQEVMK          +3      868.47  2602.39 2602.38 0.01    84      2
                TEHKLEITMLSQGVSMLYSFFMPAAK          +3      987.17  2958.50 2958.47 0.03    63      2

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
229.    IPI00198417     Y       Y       0.26    2       10      8       23      16
*Des:   PREDICTED: similar to FYN binding protein
        SEQUEST:(PepMatched Observed.Hits Coverage) 10      5       14.83%
                Seq     Charge  Xcor    Delta   Probility PepHits
                VAGQNSPSGIQSK   +2      3.281   0.491   0.9996  4
                LHNLNQESDLK     +2      3.264   0.264   0.9933  1
                FGTQPNSVSRDPEVK         +3      3.132   0.401   0.9998  3
                FMPAPQDADSKPR   +2      2.997   0.597   1.0000  4
                LNQEEPARFPK     +2      3.074   0.315   0.9796  4
                NLFDNQGNASPPAGPSNMSK +2 5.342   0.660   1.0000  2
                VGFLKPVSPKPTSLTK        +3      3.548   0.405   1.0000  7
                FGTTKPPLAAKPTYEEK       +3      3.451   0.389   0.9999  5
                LTGPIQVIHHAK    +2      2.935   0.388   0.9975  3
                KNLFDNQGNASPPAGPSNMSK           +2      5.689   0.650   1.0000  2
        MASCOT:(PepMatched Observed.Hits Coverage)  8       2       11.61%
                Seq     Charge  ObservedMS          ExpectedMS      CalculatedMS            Pepscore PepHits
                VAGQNSPSGIQSK   +2      636.8347 1271.6549 1271.6469 0.01 74    4
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		LHNLNQESDLK		+2	655.8451	1309.6756	1309.6626	0.01	47	1		
		FGTQPNSVSRDPEVK			+2	830.9252	1659.8359	1659.8216	0.01	44	3	
		LNQEEPARFPK		+2	664.8571	1327.6996	1327.6884	0.01	58	3		
		FMPAPQDADSKPR		+2	730.3597	1458.7048	1458.6925	0.01	60	5		
		NLFDNQGNASPPAGPSNMSK			+2	1023.4807	2044.9468	2044.9272	0.02	99	2	
		FGTTKPPLAAKPTYEEK			+2	939.5112	1877.0079	1876.9934	0.01	55	4	
		KNLFDNQGNASPPAGPSNMSK				+2	1087.5299	2173.0453	2173.0221	0.02	96	2
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
230.	IPI00197616		Y	Y	1.23	5	23	20	129	144		
*Des:	CAP, adenylate cyclase-associated protein 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					23	14	60.99%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GAVPYVQAFDSLLANPVAEYLK				+2	6.390	0.645	1.0000	13		
		LSDLLAPISEQIQEVITFR			+2	6.227	0.696	1.0000	16			
		TDGCHAYLSK		+2	3.170	0.394	0.9990	2				
		INSITVDNCK		+2	3.000	0.310	0.9954	5				
		NSLDCEIVSAK		+2	3.914	0.529	1.0000	8				
		SSEMNVLIPTEGGDFNEFPVPEQFK				+2	5.048	0.581	1.0000	4		
		VENQENVSNLVIDDTELK			+2	4.180	0.500	1.0000	1			
		KLGLVFDDVVGIVEIINSR			+2	6.489	0.599	1.0000	33			
		GKINSITVDNCK		+2	3.629	0.428	0.9980	2				
		ALLVTASQCQQPAGNK			+2	5.305	0.529	1.0000	16			
		GKINSITVDNCKK		+3	4.280	0.502	1.0000	5				
		KEPALLELEGKK		+3	4.762	0.398	1.0000	14				
		ALLVTASQCQQPAGNKLSDLLAPISEQIQEVITFR					+3	6.400	0.616	1.0000	4	
		AVGRLEAVSHTSDMHCGYGDSPSK				+3	5.152	0.658	1.0000	7		
		SALFAQINQGESITHALK			+2	5.249	0.476	1.0000	12			
		AYLSIWTELQAYIK		+2	4.239	0.497	1.0000	1				
		PQTSPSPKPATK		+2	3.461	0.435	0.9928	3				
		HAEMVHTGLK		+2	2.668	0.567	0.9997	13				
		VQVMGKVPTISINK		+2	4.542	0.433	1.0000	3				
		VPTISINKTDGCHAYLSK			+2	4.491	0.599	1.0000	6			
		HAEMVHTGLKLER		+3	4.320	0.586	1.0000	10				
		EIGGDVQKHAEMVHTGLKLER			+3	3.582	0.461	1.0000	2			
		DVKVQVMGKVPTISINK			+2	4.472	0.576	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					20	14	44.19%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		INSITVDNCK		+2	553.7825	1105.5505	1105.5437	0.01	78	14		
		NSLDCEIVSAK		+2	589.7939	1177.5733	1177.5649	0.01	68	28		
		TDGCHAYLSK		+2	547.7538	1093.4930	1093.4862	0.01	66	4		
		ALLVTASQCQQPAGNK			+2	814.9308	1627.8470	1627.8351	0.01	116	32	
		AYLSIWTELQAYIK		+2	849.9659	1697.9173	1697.9028	0.01	73	3		
		LGLVFDDVVGIVEIINSR			+2	979.5610	1957.1074	1957.0883	0.02	116	29	
		GKINSITVDNCK		+2	646.3450	1290.6754	1290.6601	0.02	78	4		
		KEPALLELEGKK		+3	452.2725	1353.7957	1353.7867	0.01	67	32		
		INSITVDNCKK		+2	617.8348	1233.6550	1233.6387	0.02	47	2		

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                    GKINSITVDNCKK       +2        710.3913  1418.7680 1418.7551 0.01      68        6
                    SALFAQINQGESITHALK            +2        964.5253  1927.0360 1927.0163 0.02      93        24
                    KLGLVFDDVVGIVEIINSR           +2        1043.6118 2085.2091 2085.1833 0.03      125       4
                    AVGRLEAVSHTSDMHCGYGDSPSK                +3        835.3881  2503.1424 2503.1219 0.02      67        12
                    HAEMVHTGLK          +2        561.7934  1121.5722 1121.5651 0.01      57        16
                    VQVMGKVPTISINK      +2        757.4464  1512.8781 1512.8697 0.01      78        3
                    VPTISINKTDGCHAYLSK            +2        974.0156  1946.0167 1945.9931 0.02      80        8
                    ALLVTASQCQQPAGNKLSDLLAPISEQIQEVITFR               +3        1261.3523 3781.0351 3781.0083 0.03      91        16
                    DVKVQVMGKVPTISINK             +2        928.5464  1855.0783 1855.0600 0.02      70        8
                    HAEMVHTGLKLER       +2        760.9095  1519.8045 1519.7929 0.01      80        18
                    EIGGDVQKHAEMVHTGLKLER +3      783.0837  2346.2292 2346.2113 0.02      52        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
231.      IPI00471794         Y         N         0.24      1         2         0         2         0
*Des:     Hypothetical LOC304860
          SEQUEST:(PepMatched Observed.Hits Coverage)       2         1         11.96%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    SLNFLSFPGLK         +2        3.185     0.471     0.9994    1
                    ESQELAQHAAEIGADGIAVIAPFFFK              +3        3.576     0.341     0.9961    1
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
232.      IPI00207003         Y         N         0.13      1         3         0         3         0
*Des:     Iron-responsive element binding protein 1
          SEQUEST:(PepMatched Observed.Hits Coverage)       3         1         6.74%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    QAPQTVHLPSGETLDVFDAAER                  +3        3.190     0.444     0.9995    1
                    FVEFFGPGVAQLSIADR             +2        4.585     0.577     1.0000    1
                    VILQDFTGVPAVVDFAAMR           +3        3.781     0.427     0.9874    2
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
233.      IPI00365944         Y         N         1.25      1         6         0         17        0
*Des:     PREDICTED: similar to myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
          SEQUEST:(PepMatched Observed.Hits Coverage)       6         1         58.44%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    ALGQNPTNAEVLK       +2        3.977     0.581     0.9979    7
                    NKDQGTYEDYVEGLR               +2        4.596     0.789     1.0000    4
                    ALGQNPTNAEVLKVLGNPK           +2        5.341     0.762     1.0000    3
                    NKDQGTYEDYVEGLRVFDK           +3        4.773     0.605     0.9997    1
                    VFDKEGNGTVMGAEIRHVLVTLGEK               +3        4.907     0.691     1.0000    1
                    SDEMNVKVLDFEHFLPMLQTVAK                 +3        4.942     0.627     1.0000    3
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
234.      IPI00231207         N         Y         0.31      1         0         2         0         32
*Des:     Myosin light chain 3, skeletal muscle isoform
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          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)   2          1          11.18%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore  PepHits
                    EGNGTVMGAELR          +2         617.3065   1232.5984  1232.5819  0.02       58         8
                    VFDKEGNGTVMGAELR                 +2         861.9345   1721.8545  1721.8406  0.01       75         40

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
235.      IPI00231134          Y          Y          0.73       1          3          5          5          7
*Des:     Guanine nucleotide-binding protein beta subunit 2-like 1
          SEQUEST:(PepMatched Observed.Hits Coverage)  3          1          17.17%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    IIVDELKQEVISTSSK +2   5.003      0.546      1.0000     3
                    DGQAMLWDLNEGK +2      3.315      0.447      0.9991     1
                    GHNGWVTQIATTPQFPDMILSASR         +3         4.253      0.301      0.9962     2
          MASCOT:(PepMatched Observed.Hits Coverage)   5          1          24.23%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore  PepHits
                    VWQVTIGTR             +2         530.30     1058.59    1058.59    0          42         1
                    DVLSVAFSSDNR          +2         655.32     1308.63    1308.63    0          50         1
                    IIVDELKQEVISTSSK +2   895.01     1788.00    1787.99    0.01       86         3
                    GHNGWVTQIATTPQFPDMILSASR         +3         876.44     2626.30    2626.30    0          42         2
                    DGQAMLWDLNEGK +2      738.84     1475.67    1475.67    0          67         4

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
236.      IPI00195871          Y          Y          0.18       3          4          4          6          8
*Des:     Splice Isoform LYN B of Tyrosine-protein kinase Lyn
          SEQUEST:(PepMatched Observed.Hits Coverage)  4          3          12.62%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    VLEEHGEWWK            +2         2.848      0.441      0.9994     1
                    TNADVMTALSQGYR+2      3.213      0.521      0.9998     1
                    LIDFSAQIAEGMAYIER                +2         3.441      0.461      0.9997     1
                    SDVWSFGILLYEIVTYGK               +2         5.644      0.677      1.0000     3
          MASCOT:(PepMatched Observed.Hits Coverage)   4          2          11.62%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore  PepHits
                    SLDNGGYYISPR          +2         671.33     1340.64    1340.64    0          55         2
                    VLEEHGEWWK            +2         656.82     1311.63    1311.62    0.01       57         2
                    TNADVMTALSQGYR+2      763.87     1525.72    1525.72    0          69         2
                    SDVWSFGILLYEIVTYGK               +3         697.37     2089.08    2089.08    0          44         2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
237.      IPI00362534          N          Y          0.1        1          0          3          0          6
*Des:     PREDICTED: similar to RNA helicase
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)   3          1          5.83%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore  PepHits
                    VGNLGLATSFFNER +2     762.90     1523.78    1523.77    0.01       57         2
                    HVINFDLPSDIEEYVHR                +3         695.01     2082.02    2082.02    0          73         2
                    DLLDLLVEAK            +2         564.83     1127.64    1127.64    0          50         2
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Identified Human Platelet Proteins

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
238. IPI00360930 Y Y 1.49 1 7 7 14 15
*Des: PREDICTED: similar to Carbonic anhydrase I (Carbonate dehydratase I) (CA-I)
SEQUEST:(PepMatched Observed.Hits Coverage) 7 1 46.61%
Seq Charge Xcor Delta Probility PepHits
ADGLAIIGVLMK +2 4.443 0.469 1.0000 3
HDSSLKPVSVSYNPATAK +2 4.203 0.573 1.0000 3
VLDALSSVK +2 2.716 0.370 0.9985 4
LYPIANGNNQSPIDIK +2 4.840 0.456 1.0000 4
GLLSSAEGEPAVPVLSNHRPPQPLK +3 5.254 0.588 1.0000 4
EIVNVGHSFHVVFDDSSNQSVLK +3 4.515 0.380 0.9998 3
ESISLSPEQLAQLR +2 3.805 0.300 0.9985 1
MASCOT:(PepMatched Observed.Hits Coverage) 7 1 46.61%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
HDSSLKPVSVSYNPATAK +2 951.00 1899.98 1899.97 0.01 78 4
VLDALSSVK +2 466.28 930.54 930.54 0 50 3
LYPIANGNNQSPIDIK +2 878.97 1755.93 1755.92 0.01 76 4
GLLSSAEGEPAVPVLSNHRPPQPLK +3 865.15 2592.43 2592.40 0.03 63 2
ESISLSPEQLAQLR +2 785.93 1569.85 1569.84 0.01 69 1
EIVNVGHSFHVVFDDSSNQSVLK +3 853.10 2556.28 2556.26 0.02 49 1
ADGLAIIGVLMK +2 600.86 1199.70 1199.69 0.01 91 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
239. IPI00231139 Y Y 0.16 3 5 7 12 15
*Des: TranskeTolase
SEQUEST:(PepMatched Observed.Hits Coverage) 5 5 14.11%
Seq Charge Xcor Delta Probility PepHits
SVPMSTVFYPSDGVATEK +2 3.242 0.243 0.9826 1
NMAEQIIQEIYSQVQSK +3 4.527 0.566 1.0000 3
SKDDQVTVIGAGVTLHEALAAAEMLKK +3 7.737 0.622 1.0000 8
MFGIDKDAIVQAVK +2 3.817 0.537 1.0000 4
KISSDLDGHPVPK +2 3.403 0.450 0.9995 7
MASCOT:(PepMatched Observed.Hits Coverage) 7 2 14.41%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
IIALDGDTK +2 473.2688 944.5230 944.5178 0.01 41 2
VGDKIATR +2 430.2578 858.5011 858.4923 0.01 44 4
LAVSQVPR +2 435.2663 868.5181 868.5130 0.01 45 4
MFGIDKDAIVQAVK +2 767.9232 1533.8319 1533.8224 0.01 48 3
LQALKDTANR +2 565.3236 1128.6327 1128.6251 0.01 48 5
SKDDQVTVIGAGVTLHEALAAAEMLKK +3 932.5128 2794.5166 2794.4898 0.03 93 3
KISSDLDGHPVPK +2 696.8830 1391.7514 1391.7408 0.01 86 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
240. IPI00212622 Y N 0.07 1 2 0 3 0
*Des: Trifunctional enzyme alpha subunit, mitochondrial precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 4.38%

```
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        TGLEQGNDAGYLAESEK                   +2          4.878       0.554       1.0000      2
                        ADMVIEAVFEDLAVK                     +2          3.454       0.336       0.9977      1
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
241.        IPI00205332             Y           Y           0.28        1           6           2           12          4
*Des:       Electron transfer flavoprotein alpha-subunit, mitochondrial precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)                 6           1           36.87%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        AAVDAGFVPNDMQVGQTGK                 +2          5.146       0.586       1.0000      2
                        APSSSSAGISEWLDQK                    +2          4.888       0.457       0.9998      1
                        GLLPEELTPLILETQK                    +2          3.632       0.495       0.9996      2
                        TIVAINKDPEAPIFQVADYGIVADLFK                     +3          6.024       0.600       1.0000      2
                        IVAPELYIAVGISGAIQHLAGMK             +2          6.027       0.667       1.0000      8
                        GTSFEAAAASGGSASSEK                  +2          4.929       0.592       1.0000      1
            MASCOT:(PepMatched Observed.Hits Coverage)                  2           3           12.97%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        AAVDAGFVPNDMQVGQTGK                 +2          952.97      1903.92     1903.91     0.01        55          2
                        IVAPELYIAVGISGAIQHLAGMK +3                      784.12      2349.33     2350.31     -0.97       44          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
242.        IPI00389610             Y           N           0.25        1           2           0           4           0
*Des:       55 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)                 2           1           4.77%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        DNSTMGYMMAK             +2          3.234       0.520       0.9999      2
                        RAPFDLFENK              +2          2.869       0.268       0.9877      4
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
243.        IPI00370486             N           Y           0.42        1           0           2           0           20
*Des:       25 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)                  2           1           14.34%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        ANGAPISQGVDTANPTK                   +2          821.42      1640.82     1639.82     1           91          10
                        FSGSSSGTTATLTIR +2                  743.39      1484.76     1484.75     0.01        89          10

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
244.        IPI00361738             Y           N           0.28        1           2           0           2           0
*Des:       Hypothetical LOC317191
            SEQUEST:(PepMatched Observed.Hits Coverage)                 2           1           9.65%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        YVEEQPGYLQR             +2          2.919       0.353       0.9948      2
                        TPDLEHSVFLLK            +3          3.485       0.369       0.9991      1
            MASCOT:(PepMatched Observed.Hits Coverage)
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Identified Human Platelet Proteins

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No.           Protein       Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
245.          IPI00421600                 Y             Y             0.17          1             2             2             3             2
*Des:         26S protease regulatory subunit 7
              SEQUEST:(PepMatched Observed.Hits Coverage)             2             1             5.89%
                            Seq           Charge        Xcor          Delta         Probility     PepHits
                            QTLQSEQPLQVAR               +2            3.487         0.412         0.9995        1
                            ALDEGDIALLK                 +2            2.852         0.405         0.9986        2
              MASCOT:(PepMatched Observed.Hits Coverage)              2             1             5.89%
                            Seq           Charge        ObservedMS                  ExpectedMS                  CalculatedMS                              Pepscore      PepHits
                            QTLQSEQPLQVAR               +2            749.41        1496.80       1496.79       0.01          41            1
                            ALDEGDIALLK                 +2            579.33        1156.64       1156.63       0.01          44            2

No.           Protein       Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
246.          IPI00362395                 Y             Y             0.65          1             4             3             6             5
*Des:         PREDICTED: similar to esterase D/formylglutathione hydrolase
              SEQUEST:(PepMatched Observed.Hits Coverage)             4             1             22.25%
                            Seq           Charge        Xcor          Delta         Probility     PepHits
                            AFNGYLGPDQSK                +2            3.546         0.482         0.9996        3
                            SYSGPQIDILIDQGK             +2            3.446         0.513         0.9996        1
                            MYSYVTEELPQLINANFPVDPQR                                 +3            4.124         0.458         0.9997        1
                            LQEGYDHSYYFIATFITDHIR                     +3            5.811         0.453         0.9999        2
              MASCOT:(PepMatched Observed.Hits Coverage)              3             1             15.13%
                            Seq           Charge        ObservedMS                  ExpectedMS                  CalculatedMS                              Pepscore      PepHits
                            AFNGYLGPDQSK                +2            649.31        1296.61       1295.61       1             59            3
                            SYSGPQIDILIDQGK             +2            817.43        1632.84       1632.84       0             62            1
                            LQEGYDHSYYFIATFITDHIR                     +3            863.76        2588.25       2588.23       0.02          53            1

No.           Protein       Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
247.          IPI00396906                 Y             Y             0.37          1             2             2             3             6
*Des:         ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
              SEQUEST:(PepMatched Observed.Hits Coverage)             2             2             8.58%
                            Seq           Charge        Xcor          Delta         Probility     PepHits
                            VYGTGSLALYEK                +2            3.002         0.470         0.9997        2
                            ELIEIISGAAAL                +2            2.925         0.442         0.9979        2
              MASCOT:(PepMatched Observed.Hits Coverage)              2             1             8.25%
                            Seq           Charge        ObservedMS                  ExpectedMS                  CalculatedMS                              Pepscore      PepHits
                            VYGTGSLALYEK                +2            650.84        1299.67       1299.67       0             73            4
                            THSDQFLVSFK                 +2            654.84        1307.66       1307.65       0.01          55            6

No.           Protein       Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
248.          IPI00191737                 Y             Y             0.82          4             20            18            90            80
*Des:         Serum albumin precursor
              SEQUEST:(PepMatched Observed.Hits Coverage)             20            10            43.13%
                            Seq           Charge        Xcor          Delta         Probility     PepHits
                            TCVADENAENCDK               +2            4.453         0.493         1.0000        1
                            YMCENQATISSK                +2            4.367         0.575         1.0000        6
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LVQEVTDFAK	+2	3.401	0.368	0.9990	6
TVMGDFAQFVDK	+2	4.100	0.615	1.0000	9
LPCVEDYLSAILNR	+2	3.985	0.549	1.0000	3
DVFLGTFLYEYSR	+2	3.607	0.557	1.0000	2
CCTLPEAQRLPCVEDYLSAILNR	+3	4.609	0.452	0.9998	1
TPVSEKVTK	+2	2.797	0.348	0.9853	12
AADKDNCFATEGPNLVAR	+3	5.146	0.427	1.0000	3
AETFTFHSDICTLPDKEK	+3	3.225	0.345	0.9830	1
GLVLIAFSQYLQK	+2	4.553	0.552	1.0000	19
FKDLGEQHFK	+3	3.820	0.285	0.9996	15
LQACCDKPVLQK	+2	3.437	0.318	0.9972	1
KQTALAELVK	+2	3.302	0.372	0.9989	3
MSQRFPNAEFAEITK	+2	4.169	0.533	1.0000	9
RPCFSALTVDETYVPK	+2	3.030	0.390	0.9969	3
APQVSTPTLVEAAR	+2	3.495	0.575	1.0000	7
YTQKAPQVSTPTLVEAAR	+2	4.859	0.508	1.0000	12
RHPDYSVSLLLR	+3	5.254	0.435	1.0000	20
SIHTLFGDKLCAIPK	+2	3.432	0.535	0.9990	1

MASCOT:(PepMatched Observed.Hits Coverage) 18 12 37.64%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LPCVEDYLSAILNR	+2	803.4247	1604.8348	1604.8232	0.01	65	4
YMCENQATISSK	+2	687.8101	1373.6057	1373.5955	0.01	93	8
LVQEVTDFAK	+2	575.3148	1148.6151	1148.6077	0.01	51	9
TCVADENAENCDK	+2	706.2803	1410.5461	1410.5391	0.01	80	1
TVMGDFAQFVDK	+2	679.3316	1356.6487	1356.6383	0.01	75	10
DVFLGTFLYEYSR	+2	805.4083	1608.8020	1608.7823	0.02	49	5
AADKDNCFATEGPNLVAR	+2	946.4615	1890.9085	1890.8893	0.02	92	3
TPVSEKVTK	+2	495.4859	988.9573	987.5600	1.4	50	11
EAHKSEIAHR	+2	589.3110	1176.6074	1176.5999	0.01	55	1
KQTALAELVK	+2	550.8409	1099.6672	1099.6601	0.01	80	2
MSQRFPNAEFAEITK	+2	884.9463	1767.8780	1767.8613	0.02	73	10
GLVLIAFSQYLQK	+2	740.4373	1478.8600	1478.8496	0.01	87	18
FKDLGEQHFK	+2	624.8270	1247.6395	1247.6298	0.01	58	15
LQACCDKPVLQK	+2	673.3571	1344.6996	1344.6893	0.01	51	2
APQVSTPTLVEAAR	+2	720.4003	1438.7860	1438.7780	0.01	71	7
YTQKAPQVSTPTLVEAAR	+2	980.5359	1959.0573	1959.0425	0.01	91	10
RHPDYSVSLLLR	+3	485.9428	1454.8067	1454.7994	0.01	89	19
SIHTLFGDKLCAIPK	+2	821.9601	1641.9057	1641.8912	0.01	51	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
249.	IPI00190862	Y	N	0.33	1	2	0	3	0

*Des: Golgi phosphoprotein 3

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 9.9%

Seq	Charge	Xcor	Delta	Probility	PepHits
LTLMEEVLLLGLK	+2	3.328	0.352	0.9978	1
ANTNEVLWAVVAAFT	+2	3.620	0.640	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
250.	IPI00421602	N	Y	1.78	1	0	4	0	29

*Des: Ferritin light chain 1

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 32.25%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
DDVALEGVGHFFR	+2	731.37	1460.73	1460.70	0.03	67	3
NLNQALLDLHALGSAR	+2	853.48	1704.94	1704.93	0.01	98	18
TLEAMEAALALEK	+2	695.37	1388.73	1388.72	0.01	89	4
ASYTYLSLGFFFDR	+2	843.92	1685.82	1685.81	0.01	50	10

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
251.	IPI00362469	Y	Y	1.16	2	7	6	15	13

*Des: PREDICTED: similar to 6-phosphogluconolactonase

SEQUEST:(PepMatched Observed.Hits Coverage) 7 2 45.6%

Seq	Charge	Xcor	Delta	Probility	PepHits
LPIPDSQVLTIDPALPVEDAAEDYAR	+3	4.075	0.290	0.9974	1
FALGLSGGSLVSMLAR	+2	4.261	0.478	1.0000	2
VTLTLPVLNAAQSVIFVATGEGK	+3	4.475	0.529	1.0000	1
IVAPIGDSPKPPPQR	+2	3.758	0.521	1.0000	8
DLPAATAPAGPASFAR	+2	4.597	0.520	1.0000	4
ILEDQESALPAAMVQPR	+2	4.889	0.409	1.0000	2
LVPFDHAESTYGLYR	+2	3.540	0.604	1.0000	3

MASCOT:(PepMatched Observed.Hits Coverage) 6 2 31.41%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
IVAPIGDSPKPPPQR	+2	786.46	1570.90	1570.88	0.02	80	8
DLPAATAPAGPASFAR	+2	756.90	1511.79	1511.77	0.02	68	4
ILEDQESALPAAMVQPR	+2	934.49	1866.96	1866.95	0.01	81	2
LLSVPFEK	+2	466.78	931.54	931.54	0	41	1
LVPFDHAESTYGLYR	+2	884.45	1766.88	1766.86	0.02	80	3
FALGLSGGSLVSMLAR	+2	789.94	1577.87	1577.86	0.01	101	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
252.	IPI00211756	Y	Y	0.96	1	6	10	13	48

*Des: Prohibitin

SEQUEST:(PepMatched Observed.Hits Coverage) 6 1 36.1%

Seq	Charge	Xcor	Delta	Probility	PepHits
FGLALAVAGGVVNSALYNVDAGHR	+3	4.954	0.575	1.0000	4
AATFGLILDDVSLTHLTFGK	+2	5.528	0.668	1.0000	2
DLQNVNITLR	+2	3.380	0.325	0.9992	3
FDAGELITQR	+2	3.696	0.444	0.9996	8
KLEAAEDIAYQLSR	+2	5.363	0.491	1.0000	5
NITYLPAGQSVLLQLP	+2	3.513	0.471	0.9994	3

MASCOT:(PepMatched Observed.Hits Coverage) 10 2 56.67%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EFTEAVEAK	+2	512.26	1022.50	1022.49	0.01	46	6

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                        IYTSIGEDYDER            +2          730.84      1459.66     1459.65     0.01        74          4
                        FDAGELITQR              +2          575.30      1148.59     1148.58     0.01        72          12
                        DLQNVNITLR              +2          593.34      1184.66     1184.65     0.01        66          9
                        KLEAAEDIAYQLSR          +2          803.94      1605.86     1605.84     0.02        120         10
                        VLPSITTEILK             +2          607.38      1212.74     1212.73     0.01        46          11
                        NITYLPAGQSVLLQLPQ                   +2          928.03      1854.04     1854.03     0.01        44          3
                        AAELIANSLATAGDGLIELR                +2          999.56      1997.10     1997.08     0.02        115         21
                        AATFGLILDDVSLTHLTFGK                +3          707.06      2118.15     2118.14     0.01        67          1
                        FGLALAVAGGVVNSALYNVDAGHR                        +3          791.09      2370.26     2370.24     0.02        75          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
253.        IPI00202790             Y           Y           0.1         1           2           2           4           4
*Des:       PREDICTED: similar to GAS2-related protein isoform beta
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           4.59%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        VGDSSLLIFVR             +2          3.699       0.351       0.9987      5
                        AELGVPEVLMFETEDLVLR                 +2          4.132       0.638       1.0000      1
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           3.29%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        LVQFEQEIER              +2          645.84      1289.67     1289.66     0.01        41          2
                        VGDSSLLIFVR             +2          603.66      1205.31     1204.68     0.63        45          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
254.        IPI00476880             N           Y           0.21        1           0           2           0           4
*Des:       22 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           12.31%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        GLFIIDDKGILR            +2          680.4042    1358.7939 1358.7921 0           46          2
                        ATAVMPDGQFK             +2          582.7889    1163.5632 1163.5645 0           45          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
255.        IPI00555262             N           Y           0.46        1           0           2           0           4
*Des:       Hypothetical protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           15.13%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        GAEEMETVIPVDIMR+2                   845.4179    1688.8213 1688.8113 0.01        48          2
                        VTVAGLAGKDPVQCSR                    +2          800.9339    1599.8532 1599.8402 0.01        55          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
256.        IPI00421539             Y           Y           0.3         3           5           4           9           8
*Des:       Aconitate hydratase, mitochondrial precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)     5           3           11.6%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        IVYGHLDDPANQEIER                    +3          3.175       0.283       0.9947      1
                        SQFTITPGSEQIR           +2          2.746       0.353       0.9944      2
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NAVTQEFGPVPDTAR +2 3.530 0.542 0.9999 1
QGLLPLTFADPSDYNK +2 3.369 0.434 0.9994 1
NDANPETHAFVTSPEIVTALAIAGTLK +3 5.007 0.573 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 4 3 6.93%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
DLEDLQILIK +2 600.3557 1198.6969 1198.6809 0.02 58 2
FKLEAPDADELPR +2 750.9008 1499.7871 1499.7620 0.03 41 2
IVYGHLDDPANQEIER +2 934.9783 1867.9420 1867.9064 0.04 71 4
LQLLEPFDKWDGKDLEDLQILIK +3 924.5041 2770.4906 2768.5000 1.99 39 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
257. IPI00200258 Y Y 0.27 3 7 7 15 21
*Des: EH-domain containing protein 2
SEQUEST:(PepMatched Observed.Hits Coverage) 7 6 27.57%
Seq Charge Xcor Delta Probility PepHits
LFEAEEQDLFK +2 3.449 0.336 0.9990 2
LDISDEFSEVIK +2 3.860 0.463 0.9999 2
LADIDKDGMLDDEEFALANHLIK +3 6.401 0.478 1.0000 4
GGAFEGTLQGPFGHGYGEGAGEGIDDAEWVVAR +3 7.087 0.526 1.0000 2
DKPMYDEIFYTLSPVDGK +3 3.413 0.301 0.9981 1
IGPEPTTDSFIAVMQGDVEGIIPGNALVVDPK +3 4.615 0.357 1.0000 1
GYDFAAVLEWFAER +2 3.316 0.286 0.9949 4
MASCOT:(PepMatched Observed.Hits Coverage) 7 6 27.57%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LFEAEEQDLFK +2 684.8484 1367.6823 1367.6608 0.02 43 1
DKPMYDEIFYTLSPVDGK +2 1059.5282 2117.0418 2117.0027 0.04 73 3
LADIDKDGMLDDEEFALANHLIK +3 862.7794 2585.3162 2585.2683 0.05 75 1
IGPEPTTDSFIAVMQGDVEGIIPGNALVVDPK +3 1093.9236 3278.7489 3278.6743 0.07 56 2
GGAFEGTLQGPFGHGYGEGAGEGIDDAEWVVAR +3 1102.8619 3305.5640 3305.5012 0.06 102 2
GYDFAAVLEWFAER +2 837.4125 1672.8104 1672.7885 0.02 55 11
LDISDEFSEVIK +2 697.8672 1393.7198 1393.6976 0.02 87 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
258. IPI00197550 Y N 0.24 1 2 0 4 0
*Des: cAMP-dependent protein kinase, beta-catalytic subunit
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 3.65%
Seq Charge Xcor Delta Probility PepHits
LKQIEHTLNEK +2 3.335 0.249 0.9679 2
LKQIEHTLNEKR +3 3.540 0.298 0.9992 4
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
259. IPI00607114 N Y 0.23 1 0 2 0 12
*Des: Ig gamma-2A chain C region
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 7.31%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

SVSELPIVHR +2 568.83 1135.64 1135.63 0.01 45 6
VNSGAFPAPIEK +2 615.33 1228.65 1228.65 0 49 6

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
260. IPI00358660 N Y 0.05 1 0 2 0 2
*Des: PREDICTED: similar to NF-kappa-B-repressing factor (NFKB-repressing factor) (Transcription factor NRF)
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 3.25%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
FEGEPTTHTQPGVQLR +2 898.96 1795.90 1795.89 0.01 44 2
EDSYKPIVEFIDAQFEAYLQEELK +3 968.81 2903.42 2903.41 0.01 49 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
261. IPI00188804 N Y 1.04 1 0 2 0 7
*Des: 60S acidic ribosomal protein P2
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 40.17%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK +3 925.48 2773.43 2773.42 0.01 64 3
NIEDVIAQGVGK +2 622.82 1243.63 1241.66 1.97 41 8

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
262. IPI00196751 Y N 0.16 1 2 0 11 0
*Des: Heat shock 70 kDa protein 1A/1B
SEQUEST:(PepMatched Observed.Hits Coverage) 2 2 3.98%
Seq Charge Xcor Delta Probility PepHits
VEIIANDQGNR +2 3.400 0.379 0.9995 4
TTPSYVAFTDTER +2 2.757 0.421 0.9986 3
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
263. IPI00480698 Y Y 0.47 1 5 2 8 3
*Des: 37 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 28.34%
Seq Charge Xcor Delta Probility PepHits
SFDQLTPEESKER +2 3.176 0.448 0.9925 2
IDGDKDGFVTVDELK +2 3.710 0.362 0.9843 2
DIVVQETMEDIDK +2 4.059 0.565 1.0000 2
GHDLNEDGLVSWEEYK +2 4.685 0.517 1.0000 1
NADGFIDLEEYIGDMYSHDGNADEPEWVK +3 4.891 0.486 0.9999 2
MASCOT:(PepMatched Observed.Hits Coverage) 2 2 11.52%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
SFDQLTPEESK +2 640.80 1279.59 1279.59 0 45 4
EEIVDKYDLFVGSQATDFGEALVR +3 901.12 2700.33 2700.33 0 41 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
264. IPI00464587 Y Y 0.28 3 3 4 4 14

Identified Human Platelet Proteins

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*Des:     Tubulin alpha-8 chain
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         2         11.37%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    AVMVDLEPTVVDEVR               +2        4.740     0.431     0.9999    1
                    INDDDSFTTFFSETGNGK            +2        5.488     0.605     1.0000    1
                    IHFPLVTYAPIVSAEK              +2        3.728     0.571     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    4         3         14.66%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    AVMVDLEPTVVDEVR               +2        835.9443  1669.8741 1670.8549 -0.97     51        2
                    LDHKFDLMYAK         +3        460.9067  1379.6982 1379.6907 0.01      49        24
                    QLFHPEQLITGKEDAANNYAR +3      805.7475  2414.2207 2414.1978 0.02      58        3
                    IHFPLVTYAPIVSAEK              +2        893.0076  1784.0006 1783.9872 0.01      51        3

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
265.      IPI00370703         Y         Y         0.04      2         3         2         4         10
*Des:     PREDICTED: similar to Myosin, light polypeptide kinase, telokin isoform
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         2         1.36%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    DLEVVEGSAAR         +2        3.478     0.414     0.9996    1
                    VSDVYDIEER          +2        3.113     0.210     0.9868    1
                    IEGYPDPEVVWFK       +2        2.936     0.431     0.9989    1
          MASCOT:(PepMatched Observed.Hits Coverage)    2         2         0.91%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    RLENAGSLK           +2        494.2860  986.5575  986.5508  0.01      45        5
                    LFAPIFLQGLSDLK      +2        781.4584  1560.9023 1560.8915 0.01      52        5

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
266.      IPI00364144         Y         Y         0.13      1         2         2         2         2
*Des:     PREDICTED: similar to RIKEN cDNA 1110067D22
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         5.87%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    IQTLSAIDTIK         +2        2.727     0.596     0.9946    2
                    LDDGHLNNSLGSPVQADVYFPR                  +3        4.665     0.706     1.0000    1
          MASCOT:(PepMatched Observed.Hits Coverage)    2         1         5.87%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    IQTLSAIDTIK         +2        601.85    1201.69   1201.69   0         47        2
                    LDDGHLNNSLGSPVQADVYFPR                  +3        805.40    2413.17   2413.17   0         43        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
267.      IPI00215107         Y         Y         0.32      1         2         3         3         5
*Des:     40S ribosomal protein SA
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         2         10.03%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    FAAATGATPIAGR       +2        3.166     0.330     0.9974    4
                    FTPGTFTNQIQAAFR+2             3.001     0.327     0.9945    1
          MASCOT:(PepMatched Observed.Hits Coverage)    3         2         13.04%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
```

FAAATGATPIAGR +2 603.24 1204.48 1202.64 1.84 45 2
LLVVTDPR +2 457.78 913.54 911.54 2 41 3
FTPGTFTNQIQAAFR+2 849.94 1697.87 1697.85 0.02 60 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
268. IPI00364072 Y Y 0.36 1 2 2 3 5
*Des: PREDICTED: similar to proteasome 26S non-ATPase subunit 8
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.52%
Seq Charge Xcor Delta Probility PepHits
LVLLELNFLPTTGTK+2 5.002 0.619 1.0000 2
VAEFHTELER +2 2.903 0.328 0.9974 5
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 7.52%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VAEFHTELER +2 615.82 1229.62 1229.60 0.02 50 5
LVLLELNFLPTTGTK+2 830.00 1657.98 1657.97 0.01 90 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
269. IPI00372166 Y N 0.06 1 2 0 3 0
*Des: PREDICTED: similar to Traf2 and NCK interacting kinase, splice variant 4
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 2.45%
Seq Charge Xcor Delta Probility PepHits
SQGPALTASQSVHEQPTK +2 3.668 0.564 1.0000 2
NHGQRPATEQLMK +2 3.284 0.364 0.9978 4
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
270. IPI00196684 Y N 0.23 2 2 0 4 0
*Des: cAMP-dependent protein kinase type II-alpha regulatory subunit
SEQUEST:(PepMatched Observed.Hits Coverage) 2 2 8.22%
Seq Charge Xcor Delta Probility PepHits
GQYFGELALVTNKPR +2 4.758 0.605 1.0000 4
GSFGELALMYNTPR +2 3.193 0.384 0.9975 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
271. IPI00396910 Y Y 0.84 4 15 14 33 24
*Des: ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1
SEQUEST:(PepMatched Observed.Hits Coverage) 15 10 39.78%
Seq Charge Xcor Delta Probility PepHits
VVDALGNAIDGK +2 4.256 0.488 1.0000 6
LELAQYR +2 2.715 0.258 0.9935 2
PAINVGLSVSR +2 2.811 0.463 0.9964 3
ILGADTSVDLEETGR +2 5.501 0.613 1.0000 2
GIRPAINVGLSVSR +3 4.015 0.347 0.9993 4
AVDSLVPIGR +2 3.201 0.408 0.9995 2
TGTAEMSSILEER +2 4.260 0.452 0.9999 3
HALIIYDDLSK +2 3.198 0.607 1.0000 4

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                        NVQAEEMVEFSSGLK         +2          5.128       0.630       1.0000      4
                        TGAIVDVPVGDELLGR        +2          2.736       0.376       0.9947      1
                        FESAFLSHVVSQHQSLLGNIR   +3          4.897       0.539       1.0000      2
                        GMSLNLEPDNVGVVVFGNDK    +2          5.604       0.593       1.0000      2
                        QGQYSPMAIEEQVAVIYAGVR   +2          5.078       0.512       1.0000      2
                        LKEIVTNFLAGFE   +2          3.778       0.526       0.9962      4
                        EVAAFAQFGSDLDAATQQLLSR              +2          7.070       0.627       1.0000      4
            MASCOT:(PepMatched Observed.Hits Coverage)      14          10          37.12%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        VLSIGDGIAR  +2          500.79      999.57      999.57      0           62          1
                        VVDALGNAIDGK +2         586.32      1170.63     1170.62     0.01        65          7
                        GIRPAINVGLSVSR +3       480.91      1439.70     1437.84     1.86        50          4
                        ILGADTSVDLEETGR                     +2          788.40      1574.79     1574.78     0.01        101         3
                        HALIIYDDLSK +2          644.35      1286.69     1286.69     0           74          2
                        TSIAIDTIINQK +2         658.88      1315.74     1315.73     0.01        59          1
                        TGTAEMSSILEER +2        712.34      1422.67     1422.67     0           57          1
                        NVQAEEMVEFSSGLK         +2          834.41      1666.80     1666.79     0.01        90          3
                        TGAIVDVPVGDELLGR        +2          805.94      1609.87     1609.87     0           57          2
                        QGQYSPMAIEEQVAVIYAGVR   +3          770.40      2308.16     2308.15     0.01        47          1
                        FESAFLSHVVSQHQSLLGNIR   +3          790.42      2368.23     2368.23     0           62          1
                        EIVTNFLAGFEP +2         668.85      1335.68     1335.67     0.01        47          1
                        LKEIVTNFLAGFEP +2       789.44      1576.86     1576.85     0.01        61          3
                        EVAAFAQFGSDLDAATQQLLSR              +3          780.06      2337.17     2337.16     0.01        55          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
272.        IPI00339148             Y           Y           4.78        4           4           33          15          73
*Des:       60 kDa heat shock protein, mitochondrial precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)     4           2           13.2%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LVQDVANNTNEEAGDGTTTATVLAR           +3          3.817       0.404       0.9996      2
                        ALMLQGVDLLADAVAVTMGPK+2             5.496       0.588       1.0000      13
                        VGEVIVTKDDAMLLK                     +2          3.214       0.374       0.9691      2
                        NAGVEGSLIVEK +2         3.626       0.469       0.9995      2
            MASCOT:(PepMatched Observed.Hits Coverage)      33          5           61.74%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        IGIEIIK     +2          393.26      784.51      784.51      0           55          2
                        DDAMLLK                 +2          403.21      804.41      804.41      0           42          1
                        IPAMTIAK+2              422.75      843.49      843.49      0           41          2
                        VGEVIVTK                +2          422.76      843.51      843.51      0           73          2
                        GANPVEIR                +2          428.24      854.46      854.46      0           44          2
                        LSDGVAVLK               +2          451.27      900.53      900.53      0           83          4
                        VGLQVVAVK               +2          457.29      912.56      911.58      0.98        79          4
                        IGIEIIKR    +2          471.31      940.61      940.61      0           58          2
                        VTDALNATR               +2          480.76      959.50      959.50      0           77          3
                        LKVGLQVVAVK             +2          577.39      1152.76     1152.76     0           65          7
                        NAGVEGSLIVEK            +2          608.33      1214.65     1214.65     0           68          4
                        DRVTDALNATR             +2          616.32      1230.63     1230.63     0           42          2
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VGGTSDVEVNEK	+2	617.30	1232.59	1232.59	0	73	2
TVIIEQSWGSPK	+2	672.86	1343.71	1343.71	0	76	4
GYISPYFINTSK	+2	695.36	1388.70	1388.70	0	71	2
GVMLAVDAVIAELK	+2	714.91	1427.81	1427.81	0	59	2
TLNDELEIIEGMK	+2	752.88	1503.75	1503.75	0	97	2
GVMLAVDAVIAELKK	+2	778.96	1555.90	1555.90	0	118	4
VGEVIVTKDDAMLLK	+2	815.96	1629.90	1629.90	0	69	4
RGVMLAVDAVIAELKK	+3	571.67	1712.00	1712.00	0	85	2
ISSVQSIVPALEIANAHR	+2	953.03	1904.05	1904.05	0	103	6
TLNDELEIIEGMKFDR	+3	641.66	1921.94	1921.95	0	63	1
LKVGLQVVAVKAPGFGDNR	+3	656.72	1967.13	1967.13	0	59	1
KISSVQSIVPALEIANAHR	+3	678.39	2032.14	2032.14	0	65	2
ALMLQGVDLLADAVAVTMGPK	+3	705.05	2112.13	2112.13	0	55	2
IQEITEQLDITTSEYEKEK	+3	766.39	2296.13	2296.13	0	55	5
KPLVIIAEDVDGEALSTLVLNR	+3	789.12	2364.32	2364.33	0	60	5
QSKPVTTPEEIAQVATISANGDK	+3	795.42	2383.23	2383.22	0.01	47	2
RIQEITEQLDITTSEYEKEK	+3	818.42	2452.24	2452.23	0.01	106	2
TALLDAAGVASLLTTAEAVVTEIPK	+3	818.80	2453.37	2453.36	0.01	66	1
ILQSSSEVGYDAMLGDFVNMVEK	+3	844.74	2531.20	2531.19	0.01	47	1
LVQDVANNTNEEAGDGTTTATVLAR	+3	854.09	2559.25	2559.24	0.01	80	3
TALLDAAGVASLLTTAEAVVTEIPKEEK	+3	947.52	2839.55	2839.54	0.01	78	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
273.	IPI00210961	N	Y	0.18	1	0	2	0	6

*Des: PREDICTED: similar to zinc finger protein Sp5

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 4.01%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
KLGKALIK	+2	436.2639	870.5133	869.6062	0.91	53	6
FPASAAAAAAAAALQR	+3	510.5858	1528.7357	1527.8157	0.92	43	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
274.	IPI00190943	Y	Y	0.13	1	2	2	8	45

*Des: Glial fibrillary acidic protein, astrocyte

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 5.25%

Seq	Charge	Xcor	Delta	Probility	PepHits
ALAAELNQLR	+2	3.270	0.378	0.9998	3
LALDIEIATYR	+2	3.019	0.546	1.0000	6

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 5.25%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
ALAAELNQLR	+2	549.8168	1097.6190	1097.6193	0	58	12
LALDIEIATYR	+2	639.3601	1276.7057	1276.7027	0	58	41

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
275.	IPI00203674	Y	Y	1.04	2	5	5	13	18

*Des: PREDICTED: similar to regulator of G-protein signaling RGS18

SEQUEST:(PepMatched Observed.Hits Coverage) 5 3 28.87%

Seq Charge Xcor Delta Probility PepHits
DGVDAFTR +2 2.456 0.222 0.9650 9
SIAQPTLHSFDAAQSR +2 4.610 0.540 1.0000 12
LSLLLQRPDFHGETHTSR +3 3.861 0.484 1.0000 4
SFTYNEFQDVK +2 3.185 0.542 1.0000 1
SEIYLHLIEGR +3 2.877 0.486 0.9995 9
MASCOT:(PepMatched Observed.Hits Coverage) 5 3 28.03%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
DGVDAFTR +2 440.71 879.41 879.41 0 63 9
EVNLDFHTK +2 551.78 1101.55 1101.55 0 59 9
SIAQPTLHSFDAAQSR +2 864.94 1727.87 1727.86 0.01 92 12
SFTYNEFQDVK +2 689.33 1376.64 1376.62 0.02 52 2
LSLLLQRPDFHGETHTSR +3 703.05 2106.11 2106.10 0.01 53 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
276. IPI00191748 Y Y 0.36 1 3 2 5 2
*Des: Proteasome subunit alpha type 1
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 15.67%
Seq Charge Xcor Delta Probility PepHits
ETLPAEQDLTTK +2 3.083 0.446 0.9988 1
IHQIEYAMEAVK +3 3.525 0.352 0.9988 4
NQYDNDVTVWSPQGR +2 3.578 0.452 0.9992 1
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 10.82%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ETLPAEQDLTTK +2 673.35 1344.68 1344.68 0 62 1
NQYDNDVTVWSPQGR +2 889.91 1777.81 1777.80 0.01 50 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
277. IPI00213299 Y Y 0.78 2 6 3 11 6
*Des: Microtubule-associated protein RP/EB family member 1
SEQUEST:(PepMatched Observed.Hits Coverage) 6 2 30.88%
Seq Charge Xcor Delta Probility PepHits
LEHEYIQNFK +2 2.921 0.473 0.9992 2
QGQETAVAPSLVAPALSKPK +3 3.870 0.553 0.9999 4
QGQETAVAPSLVAPALSK +2 5.062 0.485 1.0000 1
KNPGMGNGDDEAAELMQQVK +2 3.579 0.410 0.9885 2
HDMLAWINESLQLNLTK +2 5.201 0.625 1.0000 4
FQDNFEFVQWFK +2 3.938 0.534 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 16.54%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LTVEDLEKER +2 617.31 1232.61 1230.65 1.96 44 6
QGQETAVAPSLVAPALSKPK +3 664.65 1990.93 1991.11 -0.17 64 4
FQDNFEFVQWFK +2 817.89 1633.76 1633.76 0 98 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
278. IPI00191749 N Y 0.3 1 0 2 0 2
*Des: Proteasome subunit beta type 1

SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 15.57%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
AGGSASAMLQPLLDNQVGFK +2 1002.5233 2003.0321 2003.0145 0.02 92 1
AGGSASAMLQPLLDNQVGFKNMQNVEHVPLTLDRAMR +4 1002.5233 4006.0642 4008.0131 -1.94 41 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
279. IPI00201137 Y Y 1.29 1 6 5 12 9
*Des: PREDICTED: similar to nonclathrin coat protein epsilon-COP
SEQUEST:(PepMatched Observed.Hits Coverage) 6 1 37.26%
Seq Charge Xcor Delta Probility PepHits
DSIVLELDR +2 2.863 0.273 0.9881 1
YGVVLDEIKPSSAPELQAVR +3 4.808 0.513 0.9999 1
WETAEGVLQEALDK +2 4.799 0.509 1.0000 2
LQEAYYIFQELADK +2 4.851 0.614 1.0000 3
SVDVTNTTFLLMAASIYFHDQNPDAALR +3 5.547 0.551 1.0000 2
MQEQDEDATLTQLATAWVNLAMGGEK +3 6.110 0.656 1.0000 3
MASCOT:(PepMatched Observed.Hits Coverage) 5 1 28.02%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
DSIVLELDR +2 530.29 1058.56 1058.56 0 49 1
YGVVLDEIKPSSAPELQAVR +3 724.40 2170.16 2170.16 0 47 1
WETAEGVLQEALDK +2 794.90 1587.79 1587.78 0.01 79 2
LQEAYYIFQELADK +2 865.94 1729.86 1729.86 0 80 3
MQEQDEDATLTQLATAWVNLAMGGEK +3 950.78 2849.33 2849.32 0.01 71 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
280. IPI00555272 N Y 0.21 1 0 7 0 74
*Des: Liver regeneration-related protein LRRG03
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 7 1 12.11%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
EGVCPEGSIDSAPVK +2 744.3617 1486.7088 1486.6973 0.01 53 5
NGDGKEDLIWEILK +2 815.9247 1629.8348 1628.8409 0.99 48 8
DGGGDVAFVK +2 482.1836 962.3527 963.4661 -1.1 43 7
VAQEHFGK +2 457.7788 913.5430 914.4610 -0.91 47 31
HQTVLENTNGK +2 620.8223 1239.6301 1239.6207 0.01 68 23
LYLGHSYVTAIR +2 696.8915 1391.7685 1391.7561 0.01 47 8
IPSHAVVAR +2 475.2852 948.5559 948.5505 0.01 54 30

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
281. IPI00211698 Y Y 0.07 1 3 2 7 3
*Des: Flightless I homolog
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 4.02%
Seq Charge Xcor Delta Probility PepHits
NAEAVLQGPGISGK +2 3.740 0.571 0.9999 2
FVFLLDQGLDIYVWR +2 3.185 0.340 0.9948 1
LVTLPEAIHFLTEIEVLDVR +2 5.488 0.596 1.0000 5

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 2.78%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
NAEAVLQGPGISGK +2 670.86 1339.71 1339.71 0 73 2
LVTLPEAIHFLTEIEVLDVR +3 769.77 2306.30 2306.29 0.01 52 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
282. IPI00359611 Y Y 0.29 1 3 3 5 5
*Des: PREDICTED: similar to 26S proteasome non-ATPase regulatory subunit 7 (26S proteasome regulatory subunit rpn8) (26S proteasome regulatory subunit S12) (Proteasome subunit p40) (Mov34 protein)
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 10.83%
Seq Charge Xcor Delta Probility PepHits
SVVALHNLINNK +2 2.788 0.322 0.9931 1
VVGVLLGSWQK +2 3.382 0.108 0.9547 4
VVVHPLVLLSVVDHFNR +3 5.358 0.650 1.0000 6
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 10.83%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
SVVALHNLINNK +2 661.39 1320.76 1320.75 0.01 48 1
VVGVLLGSWQK +2 593.36 1184.70 1184.69 0.01 55 5
VVVHPLVLLSVVDHFNR +3 648.38 1942.13 1942.12 0.01 71 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
283. IPI00476899 Y Y 0.61 1 4 3 8 13
*Des: PREDICTED: similar to Eukaryotic translation elongation factor 1 beta 2
SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 34.93%
Seq Charge Xcor Delta Probility PepHits
YGPVSVADTTGSGAADAK +2 4.805 0.572 1.0000 3
SIQADGLVWGSSK +2 3.829 0.620 1.0000 3
SSILLDVKPWDDETDMTK +2 5.157 0.607 1.0000 2
VGTDMLEEQITAFEDYVQSMDVAAFNK +3 6.058 0.635 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 3 2 21.39%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
YGPVSVADTTGSGAADAK +2 833.90 1665.79 1665.78 0.01 96 3
SIQADGLVWGSSK +2 674.35 1346.68 1346.68 0 67 3
TPAGLQVLNDYLADK +2 809.43 1616.85 1616.84 0.01 110 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
284. IPI00197703 Y Y 1.02 3 9 5 25 10
*Des: Apolipoprotein A-I precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 9 5 46.96%
Seq Charge Xcor Delta Probility PepHits
DSGRDYVSQFESSTLGK +2 4.898 0.663 1.0000 4
QLNLNLLDNWDTLGSTVGR +2 5.527 0.616 1.0000 8
LQEQLGPVTQEFWANLEK +2 4.705 0.524 1.0000 1
AKPALDDLGQGLMPVLEAWK +2 6.302 0.708 1.0000 12
LQEQLGPVTQEFWANLEKETDWLR +3 3.769 0.470 1.0000 3
NEMNKDLENVKQK +3 4.335 0.285 0.9996 3
NEMNKDLENVK +2 3.152 0.309 0.9750 1

VKDFATVYVDAVK		+2	3.764	0.485	1.0000	2
NHPTLIEYHTK		+3	3.888	0.322	0.9999	9

MASCOT:(PepMatched Observed.Hits Coverage) 5 2 26.89%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
NEMNKDLENVKQK		+2	795.4005	1588.7865	1588.7878	0	64	4		
NEMNKDLENVK		+2	667.3243	1332.6341	1332.6343	0	53	2		
VKDFATVYVDAVK		+2	728.8602	1455.7059	1453.7816	1.92	44	2		
DSGRDYVSQFESSTLGK			+2	938.4404	1874.8663	1874.8646	0	112	2	
LQEQLGPVTQEFWANLEKETDWLR				+3	977.4918	2929.4535	2929.4610	0	61	4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
285. IPI00560892 N Y 0.41 1 0 8 0 22
*Des: Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (Trifunctional protein), alpha subunit
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 8 1 17.52%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
DTTASAVAVGLK		+2	566.81	1131.61	1131.61	0	61	2		
TGLEQGNDAGYLAESEK			+2	891.42	1780.82	1780.81	0.01	100	1	
LPAKPEVSSDEDIQYR			+3	616.31	1845.91	1845.91	0	44	1	
MGLVDQLVDPLGPGIK			+2	826.46	1650.91	1650.90	0.01	81	4	
TIEYLEEVAVNFAK		+3	542.62	1624.82	1624.83	0	69	4		
NLNSEIDNILVNLR		+2	813.94	1625.88	1625.87	0.01	75	6		
ADMVIEAVFEDLAVK			+2	825.42	1648.83	1648.84	0	90	2	
TVQQLAILGAGLMGAGIAQVSVDK				+3	780.77	2339.28	2339.29	0	43	2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
286. IPI00372241 N Y 0.13 1 0 6 0 7
*Des: PREDICTED: similar to RIKEN cDNA 1200009I06
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 6 1 11.85%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
VTDGVSQQAATGVEAEDLER			+3	692.34	2073.98	2073.98	0	41	1	
LESDYTSFLETK		+2	716.85	1431.68	1431.68	0	62	1		
DHILAILALR		+2	567.85	1133.69	1133.69	0	45	2		
RDHILAILALR		+3	430.94	1289.79	1289.79	0	42	1		
HLLQIAQQDIQPLFK		+2	896.51	1791.01	1791.00	0.01	88	2		
VIPGAAEGASDLAQLLAELGGVVR				+3	769.43	2305.27	2305.26	0.01	48	1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
287. IPI00391695 Y Y 0.17 1 3 4 6 5
*Des: PREDICTED: similar to Programmed cell death 6 interacting protein (ALG-2 interacting protein X) (ALG-2 interacting protein 1) (E2F1-inducible protein) (Eig2)
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 9.19%

Seq	Charge	Xcor	Delta	Probility	PepHits		
ATLVKPTPVNVPISQK			+2	3.744	0.520	0.9999	2
MVPVSVQQSLAVFSQR			+2	4.096	0.522	0.9999	3

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                        EPTVDISPDTVGTLSLIMLAQAQEVFFLK  +3      6.318   0.609   1.0000  1
            MASCOT:(PepMatched Observed.Hits Coverage)  4       1       8.62%
                        Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                        ATLVKPTPVNVPISQK        +2      846.51  1691.00 1691.00 0       61      2
                        LALASLGYEK      +2      532.80  1063.59 1063.59 0       45      2
                        LANQAADYFGDAFK  +2      766.73  1531.45 1529.71 1.74    61      1
                        MVPVSVQQSLAVFSQR        +2      888.48  1774.94 1774.94 0       85      3

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
288.        IPI00369169         Y       Y       0.06    2       2       2       3       2
*Des:       PREDICTED: similar to FNBP1-like
            SEQUEST:(PepMatched Observed.Hits Coverage)  2      1       3.88%
                        Seq     Charge  Xcor    Delta   Probility PepHits
                        LAETMNNIDR      +2      3.172   0.315   0.9969  1
                        MKDVYEKNPQMGDPGSLQPK +3 4.741   0.436   1.0000  2
            MASCOT:(PepMatched Observed.Hits Coverage)  2       1       4.37%
                        Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                        ESPEGSYTDDANQEVR        +2      898.9019 1795.7893 1795.7496 0.04  76      1
                        EGEVLYIIEEDKGDGWTR      +3      703.6887 2108.0443 2108.0061 0.04  37      2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
289.        IPI00373045         Y       Y       0.22    1       3       2       4       4
*Des:       Eukaryotic translation initiation factor 4B
            SEQUEST:(PepMatched Observed.Hits Coverage)  3      2       8.68%
                        Seq     Charge  Xcor    Delta   Probility PepHits
                        STPKEDDSSASTSQSSR       +3      3.471   0.507   1.0000  2
                        SRTGSESSQTGTSATSGR      +3      3.296   0.413   0.9999  1
                        AASIFGGAKPVDTAAR        +2      3.239   0.441   0.9989  1
            MASCOT:(PepMatched Observed.Hits Coverage)  2       1       5.62%
                        Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                        TGSESSQTGTSATSGR        +2      757.3401 1512.6656 1512.6652 0     80      1
                        STPKEDDSSASTSQSSR       +2      885.3943 1768.7740 1768.7711 0     70      4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
290.        IPI00363423         N       Y       0.03    1       0       2       0       5
*Des:       PREDICTED: similar to colonic and hepatic tumor over-expressed protein isoform a
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)  2       1       1.42%
                        Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                        MQGQSPPAPTR     +2      585.2941 1168.5736 1168.5659 0.01  69      6
                        AVSKPMGGSAPAK   +2      600.8271 1199.6397 1199.6332 0.01  42      1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
291.        IPI00206222         Y       Y       0.35    1       2       2       7       4
*Des:       29 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)  2      1       12.08%
                        Seq     Charge  Xcor    Delta   Probility PepHits
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		AAELIANSLATAGDGLIELR			+2	5.767	0.563	1.0000	7			
		VLPSITTEILK		+2	2.764	0.462	0.9994	4				
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	15.01%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		FNAGELITQR		+2	575.31	1148.60	1147.60	1	42	5		
		AAELIANSLATAGDGLIELRKLEAAQLSR				+3	999.56	2995.65	2993.65	2	69	2

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
292.	IPI00361821		Y	Y	0.51	1	2	3	3	6		
*Des:	V-crk sarcoma virus CT10 oncogene homolog (Avian)-like											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	9.06%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VSHYIINSLPNR		+2	2.959	0.310	0.9942	3				
		MNINGQWEGEVNGR			+2	3.977	0.408	0.9996	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	13.26%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VSHYIINSLPNR		+2	706.89	1411.76	1411.76	0	53	6		
		MNINGQWEGEVNGR			+2	802.37	1602.73	1602.72	0.01	51	1	
		TALALEVGDIVK		+2	615.31	1228.60	1227.71	0.89	51	4		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
293.	IPI00231229		Y	Y	0.56	2	5	2	18	8		
*Des:	Glutathione S-transferase P											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	6	38.02%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		EAALVDMVNDGVEDLR			+2	5.392	0.554	1.0000	3			
		SLGLYGKDQK		+2	2.892	0.375	0.9843	3				
		PPYTIVYFPVR		+2	3.707	0.529	1.0000	13				
		AFLSSPDHLNRPINGNGKQ			+3	3.452	0.392	0.9965	5			
		ALPGHLKPFETLLSQNQGGK			+3	4.692	0.373	1.0000	6			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	4	17.84%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		EAALVDMVNDGVEDLR			+2	873.4278	1744.8410	1744.8301	0.01	112	5	
		ALPGHLKPFETLLSQNQGGK			+2	1068.0935	2134.1725	2134.1534	0.02	67	4	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
294.	IPI00198369		N	Y	0.64	1	0	5	0	7		
*Des:	Sorting nexin 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					5	1	13.69%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		KLHAVVETLVNHR		+3	505.96	1514.87	1514.87	0	49	2		
		AVGTQALSGAGLLK		+2	643.38	1284.74	1284.74	0	61	2		
		SLAMLGSSEDNTALSR			+2	826.40	1650.79	1650.79	0	86	1	
		YLETLLHSQQQLAK		+2	836.46	1670.90	1670.90	0	63	1		
		ELALNTALFAK		+2	595.84	1189.67	1189.67	0	52	2		

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
295.	IPI00206224		Y	Y	0.22	1	2	3	2	4		
*Des:	Aspartyl-tRNA synthetase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	6.27%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LPLQLDDAIRPEVEGEEDGR			+3	3.594	0.427	0.9995	1			
		IYVISLAEPR		+2	3.098	0.306	0.9969	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	7.64%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		FGAPPHAGGGIGLER			+3	479.26	1434.75	1434.74	0.01	42	2	
		IYVISLAEPR		+2	580.84	1159.67	1159.66	0.01	46	2		
		ESIIDVEGIVR		+2	615.34	1228.67	1228.67	0	50	1		

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
296.	IPI00363427		Y	Y	0.43	2	9	5	13	9		
*Des:	PREDICTED: similar to Arhgap1 protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					9	3	32.62%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LEQLGIPR		+2	2.726	0.264	0.9916	2				
		EKNPNQEPIPIVLR		+2	4.343	0.501	0.9993	1				
		VEVTQQVLQTLPEENYR			+2	4.408	0.511	1.0000	2			
		FLLDHQGELFPSTDAQG			+2	3.652	0.422	0.9980	2			
		IFYVNYLSELSEHVK		+2	3.904	0.489	0.9999	2				
		YNMGLPVDFDQYNELHLPAVILK				+3	3.350	0.453	0.9995	2		
		VLHFLTAFLVQVSAHSYQNR			+3	3.554	0.457	0.9997	2			
		MNNTNLAVVFGPNLLWAK			+2	4.128	0.616	1.0000	2			
		TLLILFKPLISFK		+3	3.292	0.445	0.9997	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					5	2	16.52%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LEQLGIPR		+2	463.28	924.54	924.54	0	48	3		
		EKNPNQEPIPIVLR		+2	823.97	1645.93	1645.92	0.01	61	1		
		FLLDHQGELFPSTDAQGV			+2	987.49	1972.97	1972.95	0.02	97	2	
		TLLILFKPLISFK		+3	511.67	1531.98	1531.97	0.01	44	2		
		VLHFLTAFLVQVSAHSYQNR			+3	777.42	2329.24	2329.23	0.01	42	1	

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
297.	IPI00197568		Y	Y	0.21	1	8	2	11	9		
*Des:	Rab GDP dissociation inhibitor beta-2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					8	1	29.35%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		YIAIVSTTVETK		+2	3.267	0.443	0.9996	1				
		DLGTDSQIFISR		+2	3.085	0.444	0.9995	2				
		PALELLEPIEQK		+2	4.056	0.466	0.9997	1				
		VLHMDQNPYYGGESASITPLEDLYK				+3	5.064	0.468	0.9999	1		
		EIRPALELLEPIEQK		+3	3.288	0.233	0.9878	2				
		LSAIYGGTYMLNKPIEEIIVQNGK				+3	3.761	0.547	0.9999	1		
		FDLGQDVIDFTGHSLALYR			+2	4.619	0.558	1.0000	2			

VPSTEAEALASSLMGLFEK +2 5.784 0.622 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 6.62%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
MLLFTEVTR +2 555.81 1109.60 1108.60 1 47 6
VPSTEAEALASSLMGLFEK +3 660.67 1979.00 1978.99 0.01 51 6

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
298. IPI00207891 Y N 0.72 1 5 0 9 0
*Des: 31 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage) 5 2 32.52%
Seq Charge Xcor Delta Probility PepHits
AEDFQLHTHVNDGTEFGGSIYQR +3 6.551 0.663 1.0000 3
VNNASLIGLGYTQSLRPGVK +2 4.967 0.555 1.0000 4
IETSINLAWTAGSNNTR +2 5.204 0.643 1.0000 3
WNTDNTLGTEISWENK +2 4.786 0.581 1.0000 1
LTVDTIFVPNTGK +2 3.867 0.585 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
299. IPI00207964 Y Y 0.3 1 2 2 5 6
*Des: Splice Isoform 4 of Tropomyosin 1 alpha chain
SEQUEST:(PepMatched Observed.Hits Coverage) 2 2 10.15%
Seq Charge Xcor Delta Probility PepHits
ETAEADVASLNR +2 3.812 0.417 0.9999 4
SLQEQADAAEER +2 4.383 0.338 0.9998 2
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 10.15%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ETAEADVASLNR +2 638.32 1274.62 1274.61 0.01 60 3
SLQEQADAAEER +2 673.82 1345.62 1345.61 0.01 71 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
300. IPI00212647 Y Y 0.37 3 5 6 14 146
*Des: Glyceraldehyde-3-phosphate dehydrogenase
SEQUEST:(PepMatched Observed.Hits Coverage) 5 6 31.26%
Seq Charge Xcor Delta Probility PepHits
LISWYDNEYGYSNR +2 2.821 0.480 0.9813 1
LVINGKPITIFQER +3 3.383 0.633 0.9998 1
WGDAGAEYVVESTGVFTTMEK +2 6.487 0.855 1.0000 2
VIHDNFGIVEGLMTTVHAITATQK +3 5.788 0.747 1.0000 3
VDIVAINDPFIDLNYMVYMFQYDSTHGK +3 4.330 0.587 0.9996 1
MASCOT:(PepMatched Observed.Hits Coverage) 6 8 35.98%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VDIVAINDPFIDLNYMVYMFQYDSTHGK +3 1103.5455 3307.6148 3307.5569 0.06 69 2
WGDAGAEYVVESTGVFTTMEK +2 1139.0431 2276.0716 2276.0306 0.04 136 14
VPTPNVSVVDLTCR +2 750.4088 1498.8030 1498.7813 0.02 82 7
GAAQNIIPASTGAAK +2 685.3886 1368.7625 1368.7361 0.03 49 9
LISWYDNEYGYSNR +2 890.4166 1778.8186 1778.7900 0.03 79 14

		VIHDNFGIVEGLMTTVHAITATQK				+3	865.8028	2594.3866	2594.3526	0.03	64	14

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)					
301.	IPI00194087		N	Y	0.3	1	0	3	0	35		
*Des:	Actin, alpha cardiac											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	11.71%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YPIEHGIITNWDDMEK			+2	980.9607	1959.9068	1959.9036	0	61	22	
		VAPEEHPTLLTEAPLNPKANR			+3	767.0573	2298.1499	2296.2175	1.93	51	8	
		GILTLKYPIEHGIITNWDDMEK			+3	862.7823	2585.3250	2585.3199	0.01	54	44	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)					
302.	IPI00191681		Y	Y	0.2	2	3	4	5	4		
*Des:	Integrin beta-1 precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	2	5.53%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LPDGVTINYK		+2	3.215	0.455	0.9996	3				
		SLGTDLMNEMR		+2	2.984	0.472	0.9995	1				
		LSENNIQTIFAVTEEFQPVYK			+3	4.478	0.531	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	7.13%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LPDGVTINYK		+2	560.22	1118.43	1118.60	-0.16	42	3		
		SLGTDLMNEMR		+2	633.80	1265.58	1265.57	0.01	53	1		
		GEFFNELVGQQR		+2	712.36	1422.70	1422.69	0.01	44	2		
		LSENNIQTIFAVTEEFQPVYK			+3	824.09	2469.24	2469.24	0	45	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)					
303.	IPI00200410		Y	Y	1.12	1	6	6	9	8		
*Des:	PREDICTED: similar to EF hand domain containing 2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	2	27.15%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LSEIDVSTEGVK		+2	3.929	0.484	0.9998	3				
		AAAGELQEDSGLHVLAR			+2	4.124	0.554	1.0000	2			
		SMIQEVDEDFDSK		+2	3.646	0.379	0.9985	1				
		DGFIDLMELK		+2	2.918	0.408	0.9981	1				
		FEEEIKAEQEER		+2	3.848	0.502	0.9976	2				
		ADLNQGIGEPQSPSR			+2	3.842	0.445	0.9994	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					6	3	27.47%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LGAPQTHLGLK		+2	567.84	1133.66	1133.66	0	41	2		
		LSEIDVSTEGVK		+2	638.84	1275.66	1275.66	0	72	2		
		FEEEIKAEQEER		+2	768.86	1535.71	1535.71	0	64	2		
		ADLNQGIGEPQSPSR			+2	784.89	1567.77	1567.76	0.01	45	1	
		AAAGELQEDSGLHVLAR			+2	868.95	1735.89	1735.89	0	60	2	
		SMIQEVDEDFDSK		+2	771.84	1541.66	1541.66	0	67	1		

Identified Human Platelet Proteins

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
304.	IPI00559637		N	Y	0.75	1	0	3	0	5		
*Des:	Protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	29.65%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ALSTGEKGFGYK		+2	629.3305	1256.6465	1256.6400	0.01	47	5		
		VKEGMSIVEAMER		+3	493.9159	1478.7259	1477.7268	1	42	6		
		SIYGEKFEDENFILK		+2	916.4589	1830.9033	1830.9039	0	64	3		
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
305.	IPI00362487		Y	Y	0.56	1	2	3	3	6		
*Des:	Protein phosphatase V											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	11.57%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TGGQVPDTNYIFMGDFVDR			+2	5.745	0.559	0.9611	2			
		GYYSLETFTYLLALK			+3	5.496	0.610	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	13.82%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VTNEFVHINNLK		+2	714.39	1426.76	1426.76	0	75	2		
		APLDLDKYVEIAR		+2	751.91	1501.81	1501.81	0	53	2		
		GYYSLETFTYLLALK			+2	891.47	1780.93	1780.93	0	64	2	
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
306.	IPI00361686		Y	Y	1.47	1	6	3	11	6		
*Des:	Complement component 1, q subcomponent binding protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	1	43.66%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		EVSFQTTGDSEWR		+2	3.365	0.396	0.9982	3				
		MSGDWELEVNGTEAK			+2	4.952	0.547	1.0000	2			
		AEEQEPELTSTPNFVVEVTK			+2	4.584	0.589	1.0000	2			
		AFVEFLTDEIKEEK		+2	3.394	0.352	0.9537	2				
		DTNYTLNTDSLDWALYDHLMDFLADR				+3	4.540	0.531	0.9999	2		
		GVDNTFADELVELSTALEHQEYITFLEDLK					+3	6.498	0.538	1.0000	3	
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	15.84%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		EVSFQTTGDSEWR		+2	771.35	1540.69	1540.68	0.01	77	3		
		MSGDWELEVNGTEAK			+2	833.38	1664.74	1664.74	0	80	2	
		AFVEFLTDEIKEEK		+2	849.44	1696.86	1696.86	0	67	2		
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
307.	IPI00210975		Y	Y	0.59	1	16	15	23	18		
*Des:	150 kDa oxygen-regulated protein precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					16	1	28.05%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LYQPEYQEVSTEEQR			+2	4.717	0.539	1.0000	1			
		LPATEKPVLLSK		+2	3.120	0.423	0.9990	2				

		FLGDSAAGMAIK		+2	2.759	0.288	0.9825	1				
		TLGGLEMELR		+2	3.211	0.243	0.9911	1				
		AHFNLDESGVLSLDR			+2	4.506	0.574	1.0000	2			
		VAIVKPGVPMEIVLNK			+3	2.161	0.423	0.9988	2			
		NINADEAAAMGAVYQAAALSK			+2	6.055	0.718	1.0000	2			
		AANSLEAFIFETQDK		+2	4.642	0.565	1.0000	3				
		TVLSANADHMAQIEGLMDDVDFK				+3	3.485	0.395	0.9997	2		
		VESVFETLVEDSPEEESTLTK			+2	5.563	0.629	1.0000	2			
		VLQLINDNTATALSYGVFR			+2	5.568	0.635	1.0000	2			
		YSHDFNFHINYGDLGFLGPEDLR				+3	5.527	0.586	1.0000	2		
		LSATSTWLEDEGFGATTVMLK			+2	4.771	0.745	1.0000	1			
		DAVIYPILVEFTR		+2	2.775	0.457	0.9985	1				
		LIPEMDQIFTDVEMTTLEK			+2	6.084	0.693	1.0000	3			
		SRFPEHELNVDPQR		+3	3.793	0.385	0.9971	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					15	1	25.19%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LYQPEYQEVSTEEQR			+2	949.95	1897.88	1897.87	0.01	68	1	
		YFQHLLGK		+2	503.28	1004.55	1004.54	0.01	44	2		
		TLGGLEMELR		+2	559.80	1117.59	1117.58	0.01	50	2		
		AHFNLDESGVLSLDR			+2	836.92	1671.82	1671.82	0	64	2	
		AANSLEAFIFETQDK		+2	842.42	1682.82	1682.82	0	79	3		
		VLQLINDNTATALSYGVFR			+3	699.05	2094.12	2094.11	0.01	61	1	
		VESVFETLVEDSPEEESTLTK			+3	790.05	2367.14	2367.12	0.02	49	1	
		TVLSANADHMAQIEGLMDDVDFK				+3	840.74	2519.19	2519.17	0.02	45	2
		YSHDFNFHINYGDLGFLGPEDLR				+3	909.44	2725.28	2725.26	0.02	95	1
		NINADEAAAMGAVYQAAALSK			+3	693.68	2078.02	2078.01	0.01	50	2	
		DAVIYPILVEFTR		+2	768.43	1534.84	1534.84	0	56	2		
		LIPEMDQIFTDVEMTTLEK			+3	751.71	2252.11	2252.10	0.01	45	1	
		EAGTQPQLQIR		+2	621.34	1240.67	1239.66	1.01	41	5		
		FLGDSAAGMAIK		+2	590.81	1179.60	1179.60	0	73	2		
		VAIVKPGVPMEIVLNK			+3	569.68	1706.00	1706.02	-0.01	49	4	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)					
308.	IPI00421624		Y	Y	0.34	1	2	3	5	7		
*Des:	IMP (Inosine monophosphate) dehydrogenase 2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	6.3%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TSSAQVEGGVHGLHSYEKR			+3	2.799	0.459	1.0000	2			
		VAQGVSGAVQDK		+2	3.718	0.384	0.9999	4				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	6.3%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TSSAQVEGGVHGLHSYEK			+3	629.3063	1884.8970	1884.8965	0	44	2	
		TSSAQVEGGVHGLHSYEKR			+3	681.3403	2040.9992	2040.9976	0	46	2	
		VAQGVSGAVQDK		+2	579.8089	1157.6032	1157.6040	0	78	4		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)					
309.	IPI00421625		Y	N	0.69	3	3	0	5	0		

*Des:	Myosin regulatory light chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	5	22.28%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		FTDEEVDELYR		+2	3.386	0.777	1.0000	1				
		EAPIDKKGNFNYIEFTR			+3	2.706	0.694	0.9995	3			
		ELLTTMGDRFTDEEVDELYR			+3	4.834	0.716	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)											
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
310.	IPI00200344		Y	N	0.19	1	2	0	2	0		
*Des:	Retinoid-inducible serine carboxypeptidase precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	6.3%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AGHMVPADQGDMALK			+2	2.899	0.634	0.9956	2			
		SYENLAFYWILK		+2	4.281	0.502	0.9972	1				
	MASCOT:(PepMatched Observed.Hits Coverage)											
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
311.	IPI00388768		Y	N	0.22	2	3	0	6	0		
*Des:	51 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	2	9.23%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		SIYYITGESK		+2	2.897	0.451	0.9995	5				
		HLEINPDHPIVETLR		+3	3.851	0.528	1.0000	4				
		SLTNDWEDHLAVK		+2	3.864	0.471	0.9999	3				
	MASCOT:(PepMatched Observed.Hits Coverage)											
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
312.	IPI00324452		Y	Y	0.14	1	2	2	7	7		
*Des:	Complement component C1q receptor precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	3.36%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LSAAEAQHR		+2	2.974	0.340	0.9975	6				
		HVQEALAQLLK		+2	3.255	0.502	0.9998	6				
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	3.36%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LSAAEAQHR		+2	491.7599	981.5053	981.4992	0.01	73	4		
		HVQEALAQLLK		+2	625.3710	1248.7275	1248.7190	0.01	66	5		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
313.	IPI00563448		N	Y	0.62	1	0	4	0	38		
*Des:	31 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	2	15.88%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		QLEEEQQALQK		+2	672.3479	1342.6812	1342.6728	0.01	61	6		
		ATDAEADVASLNR		+2	666.8312	1331.6478	1331.6317	0.02	47	2		

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                AMKDEEKMELQEMQLK        +2      990.9874  1979.9602 1979.9366 0.02      115       34
                KATDAEADVASLNR +2       731.3425  1460.6704 1459.7266 0.94      71        6

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
314.      IPI00464815     Y         Y       0.75      5         4         12        10        71
*Des:     Alpha enolase
          SEQUEST:(PepMatched Observed.Hits Coverage)   4         6         16.78%
                Seq       Charge    Xcor    Delta     Probility PepHits
                IDQLMIEMDGTENK  +2  4.337   0.628     1.0000    1
                DATNVGDEGGFAPNILENK     +2      5.780     0.712     1.0000    1
                FTATAGIQVVGDDLTVTNPK    +2      5.507     0.663     1.0000    1
                LAMQEFMILPVGASSFR       +2      3.907     0.707     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    12        11        43.76%
                Seq       Charge    ObservedMS        ExpectedMS          CalculatedMS                  Pepscore PepHits
                YITPDQLADLYK    +2  720.3799  1438.7452 1438.7344 0.01      62        5
                VNQIGSVTESLQACK         +2      788.9098  1575.8050 1575.7926 0.01      116       10
                AVEHINK  +2       405.6685  809.3225  809.4395  -0.11     44        16
                DATNVGDEGGFAPNILENK     +2      980.9747  1959.9348 1959.9173 0.02      80        4
                AGKYDLDFKSPDDASR        +2      892.9344  1783.8542 1783.8376 0.02      69        8
                AAVPSGASTGIYEALELR      +2      902.9826  1803.9507 1803.9366 0.01      126       15
                IGAEVYHNLK      +2      572.3153  1142.6161 1142.6084 0.01      52        8
                LAQSNGWGVMVSHR          +2      771.3907  1540.7668 1540.7568 0.01      58        6
                LAMQEFMILPVGASSFR       +2      948.9965  1895.9784 1895.9637 0.01      101       10
                FGANAILGVSLAVCK         +2      731.9123  1461.8100 1461.8013 0.01      116       10
                AVEHINKTIAPALVSK        +2      846.0027  1689.9909 1689.9777 0.01      65        2
                HIADLAGNPEVILPVPAFNVINGGSHAGNK            +3        1007.8756 3020.6050 3020.5831 0.02      96        17

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
315.      IPI00197711     Y         Y       2.28      5         14        14        44        150
*Des:     L-lactate dehydrogenase A chain
          SEQUEST:(PepMatched Observed.Hits Coverage)   14        14        48.22%
                Seq       Charge    Xcor    Delta     Probility PepHits
                DYSVTANSK       +2  2.841   0.446     0.9992    5
                VIGSGCNLDSAR    +2  3.664   0.597     1.0000    10
                QVVDSAYEVIK     +2  3.261   0.536     1.0000    6
                DLADELALVDVIEDKLK       +2      5.675     0.520     1.0000    3
                VTLTPDEEAR      +2  2.668   0.420     0.9980    10
                DLADELALVDVIEDK+2   5.138   0.492     1.0000    5
                GLYGIKEDVFLSVPCILGQNGISDVVK     +3        4.751     0.448     1.0000    6
                IVSSKDYSVTANSK  +2  4.143   0.500     1.0000    3
                SLNPQLGTDADKEQWKDVHK +3     3.534     0.533     1.0000    3
                SLNPQLGTDADKEQWK        +2      4.559     0.564     1.0000    1
                GEMMDLQHGSLFLK          +2      3.489     0.522     0.9998    3
                LVIITAGAR       +2  3.164   0.393     0.9992    25
                LLIVSNPVDILTYVAWK       +2      5.752     0.574     0.9739    3
                LKGEMMDLQHGSLFLK        +2      4.496     0.491     1.0000    8
          MASCOT:(PepMatched Observed.Hits Coverage)    14        16        52.95%
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Identified Human Platelet Proteins

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VTLTPDEEAR	+2	565.7917	1129.5689	1129.5615	0.01	51	28
SADTLWGIQK	+2	559.7989	1117.5832	1117.5768	0.01	57	12
VIGSGCNLDSAR	+2	596.2971	1190.5796	1190.5713	0.01	89	28
QVVDSAYEVIK	+2	625.8397	1249.6648	1249.6554	0.01	68	24
DLADELALVDVIEDKLK	+2	950.0301	1898.0456	1898.0248	0.02	100	12
SLNPQLGTDADKEQWK	+2	915.4644	1828.9143	1828.8955	0.02	101	2
GEMMDLQHGSLFLK	+2	803.3992	1604.7839	1604.7690	0.01	76	12
DLADELALVDVIEDK	+2	829.4377	1656.8608	1656.8457	0.02	94	13
IVSSKDYSVTANSK	+2	749.8980	1497.7815	1497.7674	0.01	83	7
FIIPNVVK	+2	465.2972	928.5799	928.5745	0.01	45	4
GLYGIKEDVFLSVPCILGQNGISDVVK	+3	955.1894	2862.5463	2862.5200	0.03	58	2
LVIITAGAR	+2	457.2977	912.5809	912.5756	0.01	67	45
LLIVSNPVDILTYVAWK	+2	972.5677	1943.1208	1943.1131	0.01	130	27
LKGEMMDLQHGSLFLK	+2	923.9882	1845.9618	1845.9480	0.01	72	19

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
316.	IPI00387897	N	Y	2.3	2	0	9	0	264

*Des: Ywhaz protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 9 2 43.33%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
YLAEVAAGDDK	+2	576.29	1150.56	1150.55	0.01	72	44
YLAEVAAGDDKK	+2	640.33	1278.65	1278.65	0	70	50
SVTEQGAELSNEER	+2	774.87	1547.72	1547.71	0.01	111	136
FLIPNASQPESK	+2	665.86	1329.70	1329.69	0.01	81	38
GIVDQSQQAYQEAFEISK	+3	681.01	2040.00	2039.98	0.02	69	18
KGIVDQSQQAYQEAFEISK	+3	723.70	2168.09	2168.07	0.02	72	8
NLLSVAYKNVVGAR	+2	752.45	1502.88	1502.86	0.02	73	19
TAFDEAIAELDTLSEESYK	+3	711.34	2131.00	2130.98	0.02	76	28
LGLALNFSVFYYEILNSPEK	+3	773.08	2316.23	2316.20	0.03	91	15

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
317.	IPI00607203	N	Y	1.6	1	0	2	0	20

*Des: Tubulin alpha-2 chain

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 5.88%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
DVNAAIATIK	+2	508.29	1014.57	1014.57	0	59	20
AVFVDLEPTVIDEVR	+2	851.46	1700.90	1700.90	0	57	10

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
318.	IPI00555287	Y	Y	0.07	4	2	11	4	30

*Des: Non-erythroid spectrin beta

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 1.5%

Seq	Charge	Xcor	Delta	Probility	PepHits
SALPAQSAATLPAR	+2	3.511	0.432	0.9993	5

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          AQTLPTSVVTITSESSPGKR      +2        4.656     0.579     1.0000    2
MASCOT:(PepMatched Observed.Hits Coverage)  11        5         6.67%
          Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
          MLTAQDMSYDEAR  +2   765.8387  1529.6629 1529.6490 0.01      65        4
          ETWLSENQR +2        581.7831  1161.5516 1161.5414 0.01      45        3
          MWEVLESTTQTK   +2   726.8611  1451.7076 1451.6966 0.01      76        3
          LTTLELLEVR     +2   593.8610  1185.7075 1185.6969 0.01      49        1
          LWEYLLELLR     +2   674.3929  1346.7712 1346.7598 0.01      71        8
          LQAAYAGDKADDIQKR          +3        588.3115  1761.9127 1761.9009 0.01      42        2
          AKDEQSAVSMLKK  +3   478.9307  1433.7703 1433.7548 0.02      41        4
          SALPAQSAATLPAR +2   677.3823  1352.7500 1352.7412 0.01      76        5
          AQTLPTSVVTITSESSPGKR      +2        1030.0647 2058.1148 2058.0957 0.02      102       2
          LILEVHQFSR     +2   621.3596  1240.7046 1240.6928 0.01      46        2
          SNAHYNLQNAFNLAEQHLGLTK              +3        828.4250  2482.2533 2482.2352 0.02      75        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
319.      IPI00369247         Y         Y         0.15      2         2         2         5         2
*Des:     PREDICTED: similar to RIKEN cDNA 2810457I06
SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         4.16%
          Seq       Charge    Xcor      Delta     Probility PepHits
          TEVHVEPHKK     +2   2.740     0.277     0.9873    4
          HGSALDLLLSMGFPR          +2        4.395     0.632     1.0000    6
MASCOT:(PepMatched Observed.Hits Coverage)  2         1         4.16%
          Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
          FAADFAAEAASK   +2   599.79    1197.57   1197.57   0         46        2
          LVISESYDTYINR  +2   786.90    1571.78   1571.78   0         55        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
320.      IPI00231303         Y         N         0.31      1         2         0         6         0
*Des:     Ribose-phosphate pyrophosphokinase I-like
SEQUEST:(PepMatched Observed.Hits Coverage)   2         2         10.49%
          Seq       Charge    Xcor      Delta     Probility PepHits
          VYAILTHGIFSGPAISR        +2        5.149     0.568     1.0000    3
          IQVIDISMILAEAIR  +2 5.578     0.466     1.0000    3
MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
321.      IPI00325189         Y         Y         0.72      3         2         6         19        65
*Des:     Nucleoside diphosphate kinase B
SEQUEST:(PepMatched Observed.Hits Coverage)   2         2         23.22%
          Seq       Charge    Xcor      Delta     Probility PepHits
          EIGLWFKPEELIDYK +2  3.621     0.492     1.0000    4
          YMNSGPVVAMVWEGLNVVK      +2        5.627     0.534     1.0000    3
MASCOT:(PepMatched Observed.Hits Coverage)  6         3         65.16%
          Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
          NIIHGSDSVESAEK +2   743.37    1484.72   1484.71   0.01      59        4
          VMLGETNPADSKPGTIR        +2        893.47    1784.92   1784.91   0.01      110       10
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                        GLVGEIIKR   +2          492.81      983.61      983.61      0           43          8
                        TFIAIKPDGVQR+3          448.93      1343.76     1343.76     0           45          16
                        ASEEHLKQHYIDLKDRPFFPGLVK            +3          956.52      2866.52     2866.51     0.01        48          1
                        YMNSGPVVAMVWEGLNVVK     +3          698.36      2092.05     2092.05     0           74          6

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
322.        IPI00198444             Y           Y           0.35        1           2           3           2           3
*Des:       Glycine amidinotransferase, mitochondrial precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)         2           1           6.96%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        TPDFESTGLYSAMPR                     +2          3.767       0.473       0.9998      1
                        SQVTNYLGIEWMR           +2          3.346       0.463       0.9997      1
            MASCOT:(PepMatched Observed.Hits Coverage)          3           1           9.97%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        VMVDANEVPIQK            +2          671.86      1341.70     1341.70     0           41          2
                        SQVTNYLGIEWMR           +2          798.90      1595.79     1595.78     0.01        52          1
                        TPDFESTGLYSAMPR                     +2          836.39      1670.76     1670.76     0           61          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
323.        IPI00390975             Y           Y           0.21        2           2           3           2           23
*Des:       57 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)         2           1           3.65%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LENEIQTYR   +2          3.487       0.197       0.9954      1
                        LKYENEVALR  +3          3.220       0.249       0.9983      3
            MASCOT:(PepMatched Observed.Hits Coverage)          3           3           4.87%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        VTMQNLNDR   +2          545.77      1089.53     1089.52     0.01        47          8
                        LENEIQTYR   +2          583.30      1164.58     1164.58     0           44          4
                        LAADDFR+2   404.20      806.40      806.39      0.01        43          12

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
324.        IPI00368449             Y           Y           0.57        1           3           4           8           9
*Des:       PREDICTED: similar to phosphomannomutase
            SEQUEST:(PepMatched Observed.Hits Coverage)         3           1           16.59%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        TVGYTVTAPEDTR           +2          3.377       0.328       0.9873      3
                        IGVVGGSDFEK +2          3.094       0.472       0.9998      6
                        YDYVFPENGLVAYK          +2          4.018       0.540       1.0000      3
            MASCOT:(PepMatched Observed.Hits Coverage)          4           1           21.45%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        TVGYTVTAPEDTR           +2          705.82      1409.63     1408.68     0.95        51          3
                        IGVVGGSDFEK +2          554.29      1106.57     1106.56     0.01        54          5
                        NGMLNVSPIGR +2          579.31      1156.61     1156.60     0.01        48          2
                        YDYVFPENGLVAYK          +2          839.91      1677.81     1676.81     1           46          3

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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325.     IPI00195109   N       Y       0.14    1       0       2       0       3
*Des:    Serine hydroxymethyl transferase 2
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)    2       1       4.67%
                 Seq           Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 NAQAMADALLK   +2      573.30  1144.59 1144.59 0       41      1
                 VLELVSITANK   +2      593.85  1185.70 1185.70 0       66      2

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
326.     IPI00364093   Y       Y       0.27    1       2       2       5       7
*Des:    PREDICTED: similar to cytoskeleton-associated protein 1
         SEQUEST:(PepMatched Observed.Hits Coverage)   2       2       10.84%
                 Seq           Charge  Xcor    Delta   Probility PepHits
                 LSEEEAQASAISVGSR      +2      4.871   0.508   1.0000  2
                 LGPYNEELR     +2      2.767   0.276   0.9768  2
         MASCOT:(PepMatched Observed.Hits Coverage)    2       2       10.84%
                 Seq           Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 LGPYNEELR     +2      545.78  1089.55 1089.55 0       64      4
                 LSEEEAQASAISVGSR      +2      817.41  1632.81 1632.80 0.01    67      3

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
327.     IPI00193361   Y       Y       0.02    1       2       2       3       7
*Des:    PREDICTED: similar to ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1
         SEQUEST:(PepMatched Observed.Hits Coverage)   2       1       4.12%
                 Seq           Charge  Xcor    Delta   Probility PepHits
                 TSNLNEELGQVK  +2      3.724   0.304   0.9948  2
                 HLEQFATEGLR   +2      2.702   0.403   0.9930  1
         MASCOT:(PepMatched Observed.Hits Coverage)    2       1       3.79%
                 Seq           Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 GADTVIYER     +2      512.2628 1022.5110 1022.5032 0.01 43    2
                 TSNLNEELGQVK  +2      666.3523 1330.6900 1330.6728 0.02 60    5

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
328.     IPI00372259   N       Y       1.34    2       0       9       0       110
*Des:    Tropomyosin
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)    9       3       34.38%
                 Seq           Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 IQVLQQQADDAEER +2     821.9104 1641.8062 1641.7958 0.01 84    8
                 TIDDLEDKLK    +2      595.3230 1188.6314 1188.6238 0.01 62    32
                 EQAEAEVASLNR  +2      658.8303 1315.6461 1315.6367 0.01 70    14
                 IQVLQQQADDAEERAER     +2      1000.0042 1997.9939 1997.9766 0.02 76 6
                 KLVIIEGDLER   +2      642.8832 1283.7519 1283.7448 0.01 46    12
                 ALKDEEKMELQEIQLK      +2      973.0300 1944.0455 1944.0237 0.02 120  18
                 AREQAEAEVASLNR +2     772.4009 1542.7873 1542.7750 0.01 100   8
                 ILTDKLKEAETR  +2      708.9112 1415.8078 1415.7984 0.01 77    4
                 AREQAEAEVASLNRR       +3      567.3033 1698.8880 1698.8761 0.01 56 22
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Identified Human Platelet Proteins

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
329.	IPI00197579		Y	Y	1.12	5	12	15	55	189		
*Des:	Tubulin beta-5 chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)					12	11	33.62%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ISVYYNEATGGK		+2	3.733	0.538	1.0000	10				
		EVDEQMLNVQNK		+2	4.547	0.261	0.9992	15				
		IMNTFSVVPSPK		+2	4.308	0.460	0.9999	2				
		PDNFVFGQSGAGNNWAK			+2	3.938	0.499	0.9996	1			
		AILVDLEPGTMDSVR			+2	3.407	0.544	0.9999	5			
		ISEQFTAMFR		+2	4.035	0.550	1.0000	6				
		YLTVAAVFR		+2	3.168	0.395	0.9995	6				
		ALTVPELTQQVFDAK			+2	4.392	0.502	1.0000	3			
		SGPFGQIFRPDNFVFGQSGAGNNWAK				+3	8.076	0.644	1.0000	5		
		LHFFMPGFAPLTSR		+2	2.638	0.599	0.9998	6				
		MAVTFIGNSTAIQELFK			+2	6.138	0.556	1.0000	6			
		MAVTFIGNSTAIQELFKRISEQFTAMFR				+3	4.506	0.568	1.0000	3		
	MASCOT:(PepMatched Observed.Hits Coverage)					15	13	46.46%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ISVYYNEATGGK		+2	651.32	1300.63	1300.63	0	75	9		
		EVDEQMLNVQNK		+2	723.85	1445.69	1445.68	0.01	86	58		
		FPGQLNADLRK		+3	420.24	1257.69	1257.68	0.01	44	35		
		IMNTFSVVPSPK		+2	660.36	1318.70	1318.70	0	89	6		
		FPGQLNADLR		+2	565.80	1129.59	1129.59	0	58	63		
		KLAVNMVPFPR		+2	635.99	1269.97	1270.72	-0.74	51	10		
		YLTVAAVFR		+2	521.28	1040.55	1038.59	1.96	63	12		
		ALTVPELTQQVFDAK			+2	830.46	1658.90	1658.89	0.01	83	2	
		SGPFGQIFRPDNFVFGQSGAGNNWAK				+3	933.46	2797.35	2797.34	0.01	94	8
		ISEQFTAMFR		+2	615.30	1228.59	1228.59	0	73	30		
		AILVDLEPGTMDSVR			+2	808.42	1614.83	1614.83	0	46	23	
		NSSYFVEWIPNNVK		+2	848.92	1695.83	1695.83	0	72	30		
		LHFFMPGFAPLTSR		+3	540.95	1619.83	1619.83	0	52	12		
		MAVTFIGNSTAIQELFK			+2	935.50	1868.98	1868.97	0.01	109	6	
		GHYTEGAELVDSVLDVVR			+2	979.99	1957.97	1957.97	0	125	15	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
330.	IPI00207038		Y	Y	0.11	2	2	3	5	42		
*Des:	Type II keratin Kb15											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	4.8%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		SRAEAESWYQTK		+2	3.309	0.379	0.9972	1				
		SLDLDSIIAEVK		+2	4.329	0.469	1.0000	5				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	5	7.02%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		FLEQQNKVLETK		+2	739.8685	1477.7225	1475.7983	1.92	60	6		
		LALDIEIATYR		+2	639.3679	1276.7213	1276.7027	0.02	58	17		

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                SLDLDSIIAEVK    +2          651.8712    1301.7279   1301.7078   0.02        48          5

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
331.        IPI00361908             N           Y           0.24        1           0           2           0           16
*Des:       26 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           11.25%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        LEGFQTQISK              +2          575.81      1149.61     1149.60     0.01        50          4
                        IEDGNNFGVAVQEK          +2          760.38      1518.74     1518.73     0.01        82          14

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
332.        IPI00190020             Y           Y           0.02        1           2           2           2           4
*Des:       Splice Isoform SERCA2B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           3.1%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        VDQSILTGESVSVIK         +2          3.767       0.442       0.9990      2
                        AFTGREFDELSPSAQR                    +3          3.353       0.277       0.9841      2
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           2.35%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        IGIFGQDEDVTSK           +2          704.8573    1407.7000   1407.6881   0.01        48          2
                        EWGSGSDTLR              +2          554.2618    1106.5090   1106.4992   0.01        43          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
333.        IPI00557102             N           Y           0.43        1           0           3           0           13
*Des:       45 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      3           1           13.71%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        DNSDRPPLQEGALPQMLPGHSGPSGTNR                    +3          976.81      2927.41     2927.39     0.02        50          5
                        TSYFIEFSVR              +2          625.35      1248.69     1247.62     1.07        47          8
                        FPQVSNFFEHTPPK          +2          837.92      1673.82     1673.82     0           64          8

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
334.        IPI00191761             N           Y           0.87        1           0           3           0           6
*Des:       PREDICTED: similar to Rab5c protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      3           1           19.54%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        GVDLQESNPASR            +2          636.8572    1271.6998   1271.6106   0.09        64          2
                        QASPNIVIALAGNK          +2          698.4429    1394.8712   1394.7881   0.08        53          2
                        TAMNVNEIFMAIAK          +2          776.9560    1551.8974   1551.7789   0.12        79          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
335.        IPI00212655             Y           Y           0.41        4           2           2           3           56
*Des:       Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           6.93%
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		Seq	Charge	Xcor	Delta	Probility	PepHits		
		IYAMHWGTDSR	+2	3.518	0.495	0.9999	4		
		LIIWDSYTTNK	+2	2.969	0.335	0.9961	1		
	MASCOT:(PepMatched Observed.Hits Coverage)	2	5	6.64%					
		Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
		AGVLAGHDNR	+2	505.26	1008.51	1008.51	0	44	3
		IYAMHWGTDSR	+2	668.82	1335.62	1335.60	0.02	41	4

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
336.	IPI00361693	Y	Y	1	3	7	8	22	19
*Des:	Protein tyrosine kinase 9								
	SEQUEST:(PepMatched Observed.Hits Coverage)	7	5	32.02%					
		Seq	Charge	Xcor	Delta	Probility	PepHits		
		ISEVQTDVSVDTK	+2	4.758	0.502	1.0000	8		
		EFGGGHIKDEVFGTVK	+2	4.313	0.485	1.0000	5		
		NETIILANTENTELK	+2	5.007	0.414	0.9998	2		
		HQTLQGVAFPISR	+2	3.668	0.544	1.0000	4		
		SPLLDIVER	+2	3.282	0.351	0.9991	3		
		YLLSQSSPAPLTAAEEELR	+2	5.423	0.578	1.0000	6		
		KIEIDNGDELTADFLYDEVHPK	+3	6.246	0.592	1.0000	3		
	MASCOT:(PepMatched Observed.Hits Coverage)	8	2	35.67%					
		Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
		ISEVQTDVSVDTK	+2	710.87	1419.72	1419.71	0.01	111	5
		HQTLQGVAFPISR	+2	727.40	1452.80	1452.78	0.02	60	4
		NETIILANTENTELK	+2	851.95	1701.89	1701.88	0.01	91	2
		EFGGGHIKDEVFGTVK	+2	860.45	1718.88	1718.86	0.02	59	5
		SPLLDIVER	+2	521.30	1040.59	1040.59	0	51	2
		QLNYVQLEIDIK	+2	738.72	1475.42	1474.80	0.62	53	1
		YLLSQSSPAPLTAAEEELR	+3	692.70	2075.08	2074.06	1.02	48	3
		KIEIDNGDELTADFLYDEVHPK	+3	854.42	2560.25	2560.23	0.02	88	6

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
337.	IPI00339167	Y	Y	1.04	4	3	13	56	643
*Des:	PREDICTED: similar to Tubulin alpha-2 chain (Alpha-tubulin 2)								
	SEQUEST:(PepMatched Observed.Hits Coverage)	3	2	6.5%					
		Seq	Charge	Xcor	Delta	Probility	PepHits		
		SIQFVDWCPTGFK	+2	4.812	0.588	0.9542	7		
		LISQIVSSITASLR	+3	5.122	0.352	1.0000	66		
		RSIQFVDWCPTGFK	+2	3.004	0.260	0.9818	8		
	MASCOT:(PepMatched Observed.Hits Coverage)	13	6	31.88%					
		Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
		DVNAAIATIK	+2	508.2954	1014.5763	1014.5709	0.01	76	66
		EIIDLVLDR	+2	542.7372	1083.4598	1084.6128	-1.14	53	42
		AVFVDLEPTVIDEVR	+2	851.4640	1700.9134	1700.8984	0.01	93	136
		NLDIERPTYTNLNR	+2	859.9511	1717.8877	1717.8747	0.01	58	63
		AVCMLSNTTAIAEAWAR	+2	904.4519	1806.8893	1806.8756	0.01	70	9
		SIQFVDWCPTGFK	+2	764.3749	1526.7352	1526.7227	0.01	78	10

GHYTIGKEIIDLVLDR	+3	614.6802	1841.0187	1841.0046	0.01	76	6
RSIQFVDWCPTGFK	+2	842.4284	1682.8423	1682.8239	0.02	61	23
VGINYQPPTVVPGGDLAK	+2	913.0029	1823.9912	1823.9781	0.01	90	109
LISQIVSSITASLR	+2	744.4479	1486.8812	1486.8719	0.01	95	181
DVNAAIATIKTKR	+2	700.8766	1399.7387	1399.8147	-0.07	45	6
RNLDIERPTYTNLNR	+2	938.0027	1873.9909	1873.9758	0.02	51	16
IHFPLATYAPVISAEK	+2	878.9921	1755.9696	1755.9559	0.01	94	272

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
338.	IPI00210115	Y	Y	0.44	1	5	2	7	4

*Des: SNAP-29 protein

SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 32.06%

Seq	Charge	Xcor	Delta	Probility	PepHits
DLPDGPDAPIDR	+2	2.962	0.398	0.9970	3
IGVASSEELVR	+2	3.533	0.446	0.9995	3
LHDAELDSVPASTVNTEVYPK	+2	4.874	0.599	1.0000	1
IDSNLDELSVGLGR	+2	3.874	0.492	0.9997	1
SKPVEPPPEQNGSIVPQPSSR	+3	4.578	0.419	0.9997	2

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 10.3%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
IGVASSEELVR	+2	580.32	1158.63	1158.62	0.01	70	3
IDSNLDELSVGLGR	+2	744.39	1486.77	1486.76	0.01	74	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
339.	IPI00203690	Y	Y	0.18	1	2	2	4	2

*Des: 4-trimethylaminobutyraldehyde dehydrogenase

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.11%

Seq	Charge	Xcor	Delta	Probility	PepHits
VSFTGSVPTGMK	+2	2.934	0.517	0.9998	2
EEIFGPVMSILTFETEAEVLER	+2	5.590	0.687	1.0000	4

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 4.74%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VSFTGSVPTGMK	+2	605.81	1209.61	1209.61	0	47	2
VTIEYYSQLK	+2	622.34	1242.66	1242.65	0.01	41	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
340.	IPI00192639	Y	N	0.27	2	3	0	3	0

*Des: 63 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 10.63%

Seq	Charge	Xcor	Delta	Probility	PepHits
IDQLQEELLHTQLK	+3	3.119	0.314	0.9980	1
SIVTDLVSQMDPHGR	+3	3.414	0.423	0.9998	1
SLIDMYSEVLDVLSDYDASYNTQDHLPR	+3	4.318	0.461	0.9999	1

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
341.	IPI00421560	Y	Y	0.14	1	3	13	5	19

*Des:	Actn4 protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	6.36%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		MLDAEDIVNTARPDEK			+2	3.916	0.381	0.9994	2			
		ETTDTDTADQVIASFK			+2	4.500	0.589	1.0000	1			
		IMSVVDPNHSGLVTFQAFIDFMSR				+3	4.301	0.564	1.0000	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					13	1	25.67%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MAPYQGPDAAPGALDYK			+2	882.92	1763.83	1763.82	0.01	56	2	
		NVNVQNFHISWK		+2	743.39	1484.76	1484.75	0.01	62	1		
		LVSIGAEEIVDGNAK		+2	757.91	1513.81	1513.80	0.01	93	1		
		QLETIDQLHLEYAK		+2	850.95	1699.89	1699.88	0.01	66	2		
		ETTDTDTADQVIASFK			+2	871.41	1740.81	1740.81	0	56	1	
		MLDAEDIVNTARPDEK			+2	908.95	1815.88	1815.87	0.01	66	2	
		KDDPVTNLNNAFEVAEK			+2	952.48	1902.94	1902.93	0.01	93	2	
		LSGSNPYTSVTPQIINSK			+2	953.51	1905.01	1904.98	0.03	62	2	
		AGTQIENIDEDFRDGLK			+2	960.97	1919.93	1919.92	0.01	70	1	
		QFASQANMVGPWIQTK			+2	903.46	1804.91	1804.89	0.02	51	2	
		LMLLLEVISGERLPKPER			+3	698.41	2092.21	2092.21	0	42	1	
		IMSVVDPNHSGLVTFQAFIDFMSR				+3	904.46	2710.36	2710.32	0.04	54	2
		VEQIAAIAQELNELDYYDSHNVNTR				+3	969.14	2904.39	2904.39	0	52	2
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
342.	IPI00200425		Y	Y	0.64	4	4	5	7	17		
*Des:	Ras-related protein Rab-27B											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	4	30.63%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VVYDTQGADGSSGK			+2	3.930	0.630	1.0000	4			
		YGIPYFETSAATGQNVEK			+2	3.627	0.357	0.9955	1			
		SVETLLDLIMK		+2	2.934	0.490	0.9990	6				
		DAMGFLLMFDLTSQQSFLNVR			+3	4.421	0.331	0.9993	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					5	3	25.67%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LLALGDSGVGK		+2	515.3329	1028.6512	1028.5865	0.06	54	2		
		TQVPDTVNGVNSGK		+2	708.4145	1414.8144	1414.7052	0.11	60	1		
		LLALGDSGVGKTTFLYR			+3	604.3787	1810.1143	1809.9988	0.12	40	1	
		YGIPYFETSAATGQNVEK			+2	988.0485	1974.0824	1973.9370	0.15	51	1	
		ELAEKYGIPYFETSAATGQNVEK				+3	849.1462	2544.4168	2544.2383	0.18	78	1
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
343.	IPI00326135		N	Y	0.02	1	0	2	0	4		
*Des:	Apoptosis-inducing factor											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	4.68%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TGGLEIDSDFGGFR		+2	735.8578	1469.7011	1469.6786	0.02	64	2		
		DGEQHEDLNEVAK		+2	742.3489	1482.6833	1482.6586	0.02	59	2		

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
344. IPI00325260 N Y 0.24 1 0 2 0 2
*Des: Small glutamine-rich tetratricopeptide repeat-containing protein A
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 8.09%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
MGLALSSLNK +2 517.29 1032.57 1032.56 0.01 44 1
LAYAIIQFLHGQLR +3 548.32 1641.93 1641.94 0 43 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
345. IPI00470301 Y Y 0.27 2 5 5 14 16
*Des: Chaperonin containing TCP1, subunit 5
SEQUEST:(PepMatched Observed.Hits Coverage) 5 2 13.61%
Seq Charge Xcor Delta Probility PepHits
IADGYEQAAR +2 3.655 0.494 1.0000 5
WVGGPEIELIAIATGGR +2 4.123 0.551 1.0000 4
FSELTSEKLGFAGVVR +3 3.216 0.471 1.0000 1
KQQISLATQMVR +2 2.783 0.327 0.9919 1
GVIVDKDFSHPQMPK +2 4.717 0.464 1.0000 7
MASCOT:(PepMatched Observed.Hits Coverage) 5 5 12.15%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
IADGYEQAAR +2 547.2702 1092.5259 1092.5199 0.01 90 7
WVGGPEIELIAIATGGR +2 869.9867 1737.9588 1737.9413 0.02 74 8
LGFAGVVR +2 409.7500 817.4855 817.4810 0 50 1
KQQISLATQMVR +2 701.8990 1401.7834 1401.7762 0.01 57 1
GVIVDKDFSHPQMPK +2 849.4361 1696.8576 1696.8606 0 70 6

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
346. IPI00421565 N Y 0.22 1 0 5 0 17
*Des: GDP dissociation inhibitor 2
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 5 1 20.3%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
YIAIVSTTVETK +2 662.87 1323.73 1323.73 0 48 3
DLGTDSQIFISR +2 676.35 1350.68 1350.68 0 63 6
VLHMDQNPYYGGESASITPLEDLYK +3 947.46 2839.35 2839.34 0.01 53 2
VPSTEAEALASSLMGLFEK +2 990.51 1979.00 1978.99 0.01 87 4
FDLGQDVIDFTGHSLALYR +3 723.03 2166.08 2166.07 0.01 66 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
347. IPI00198520 N Y 0.24 1 0 2 0 7
*Des: Cortactin isoform B
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 6.17%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VDQSAVGFEYQGK +2 714.34 1426.67 1426.67 0 65 3

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                        NASTFEEVVQVPSAYQK           +2          948.97      1895.93     1895.93     0           67          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
348.        IPI00364311             Y           Y           0.52        2           8           7           32          28
*Des:       Glucose phosphate isomerase
            SEQUEST:(PepMatched Observed.Hits Coverage)     8           3           24.29%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        TFTTQETITNAETAK +2      5.026       0.544       1.0000      1
                        FAAYFQQGDMESNGK         +2          4.548       0.585       1.0000      1
                        EVLHMLVDLAK +2          2.881       0.418       0.9990      2
                        TLANLNPESSLFIIASK       +2          4.045       0.464       0.9999      2
                        AITDIINIGIGGSDLGPLMVTEALKPYSK       +3          4.680       0.589       1.0000      1
                        NMFEFWDWVGGR +2         3.762       0.525       1.0000      1
                        ILLANFLAQTEALMK+2       5.208       0.535       1.0000      4
                        LTPFILGALIAMYEHK        +2          4.579       0.560       1.0000      3
            MASCOT:(PepMatched Observed.Hits Coverage)      7           4           22.18%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        TFTTQETITNAETAK +2      828.41      1654.81     1654.80     0.01        90          1
                        FAAYFQQGDMESNGK         +2          846.87      1691.73     1691.72     0.01        90          1
                        TLANLNPESSLFIIASK       +2          909.51      1817.00     1816.99     0.01        50          2
                        NMFEFWDWVGGR +2         772.35      1542.68     1542.67     0.01        44          1
                        ILLANFLAQTEALMK+2       838.48      1674.95     1674.94     0.01        99          4
                        LTPFILGALIAMYEHK        +2          909.01      1816.00     1816.00     0           70          3
                        AITDIINIGIGGSDLGPLMVTEALKPYSK       +3          996.22      2985.63     2985.61     0.02        83          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
349.        IPI00373134             Y           N           0.32        1           3           0           4           0
*Des:       PREDICTED: similar to RIKEN cDNA B430104H02
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           1           13.22%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        VNGEIVQSSNTNQMVFK       +2          4.977       0.519       1.0000      1
                        ALAAQLPLIPR +2          2.766       0.423       0.9974      2
                        FSSSIVGPYDSIILPPESK     +2          3.577       0.507       0.9996      2
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
350.        IPI00372407             Y           Y           0.17        1           2           2           6           5
*Des:       PREDICTED: similar to apoA-I binding protein
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           4.27%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LFGYQPTIYYPK +2         3.693       0.419       0.9999      4
                        GNPSGIQPDLLISLTAPK      +2          4.556       0.646       1.0000      4
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           4.27%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        LFGYQPTIYYPK +2         745.40      1488.78     1488.77     0.01        53          3
                        GNPSGIQPDLLISLTAPK      +2          911.02      1820.02     1820.00     0.02        85          4
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No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
351.        IPI00197727             Y           N           0.94        1           2           0           2           0
*Des:       Protein phosphatase 1 regulatory subunit 14A
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           9.33%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        GPGGSPSGLQK +2          2.819       0.386       0.9964      4
                        ARGPGGSPSGLQK +2        3.031       0.320       0.9714      6
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
352.        IPI00366856             Y           N           1.01        2           4           0           8           0
*Des:       18 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)     4           4           33.12%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        YALYDASFETK +2          2.902       0.720       0.9984      2
                        LGGSLIVAFEGSP +2        3.624       0.633       0.9948      2
                        ESRKEELMFFLWAPEQAPLK    +3          5.496       0.741       1.0000      2
                        TSIAEKLGGSLIVAFEGSP     +2          4.700       0.706       1.0000      4
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
353.        IPI00365118             Y           Y           0.79        1           3           2           6           4
*Des:       PREDICTED: similar to transmembrane emp24 protein transport domain containing 7
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           1           19.56%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        TVYFDFQVGEDPPLFPSENR    +2          4.484       0.583       1.0000      1
                        SVIDYQTHFR  +2          3.070       0.422       0.9997      6
                        KQYDSFTFTASK +2         3.380       0.427       0.9998      3
            MASCOT:(PepMatched Observed.Hits Coverage)     2           1           10.43%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        SVIDYQTHFR  +2          633.32      1264.63     1264.62     0.01        56          4
                        KQYDSFTFTASK +2         711.85      1421.69     1421.68     0.01        46          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
354.        IPI00358691             Y           Y           0.17        1           2           3           2           3
*Des:       Epidermal growth factor receptor pathway substrate 15 isoform B
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           3.84%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LQQETAQLEESVESGK        +2          4.927       0.596       1.0000      1
                        DQFALAFHLINQK +2        4.219       0.385       0.9996      1
            MASCOT:(PepMatched Observed.Hits Coverage)     3           1           4.96%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        LQQETAQLEESVESGK        +2          888.44      1774.86     1774.86     0           79          1
                        LPVEILGR    +2          448.78      895.55      895.55      0           56          1
                        DQFALAFHLINQK +2        772.92      1543.83     1543.81     0.02        81          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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355.	IPI00371462		Y	Y	1.02	1	5	6	8	13		
*Des:	PREDICTED: similar to HSPC263											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	1	24.84%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IQQEIAVQNPLVSER		+2	4.507	0.469	0.9999	2				
		FFEHFIEGGR		+2	3.244	0.416	0.9995	3				
		AFGFSHLEALLDDSK			+2	4.394	0.505	1.0000	2			
		QTSVADLLASFNDQSTSDYLVVYLR				+3	4.152	0.531	1.0000	1		
		EYAEDDNIYQQK		+2	3.628	0.477	0.9998	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					6	1	25.75%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		EYAEDDNIYQQK		+2	758.34	1514.66	1514.65	0.01	58	1		
		GEGGTTNPHVFPEGSEPK			+2	920.43	1838.85	1838.84	0.01	61	2	
		LLTSGYLQR		+2	525.80	1049.59	1049.59	0	54	9		
		FFEHFIEGGR		+2	619.80	1237.58	1237.59	0	48	2		
		IQQEIAVQNPLVSER		+2	862.47	1722.93	1722.93	0	91	2		
		AFGFSHLEALLDDSK			+2	825.42	1648.82	1648.81	0.01	62	2	
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
356.	IPI00231247		Y	Y	0.26	2	2	2	3	4		
*Des:	Dual specificity mitogen-activated protein kinase kinase 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	2	6.26%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VGELKDDDFEK		+2	2.798	0.301	0.9620	2				
		KLEELELDEQQR		+2	3.846	0.426	0.9998	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					2	2	6.26%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VGELKDDDFEK		+2	647.8221	1293.6297	1293.6088	0.02	36	2		
		KLEELELDEQQR		+2	765.4079	1528.8012	1528.7733	0.03	88	2		
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
357.	IPI00365985		Y	Y	0.39	5	23	21	49	48		
*Des:	PREDICTED: tumor rejection antigen gp96 (predicted)											
	SEQUEST:(PepMatched Observed.Hits Coverage)					23	8	40.83%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ELISNASDALDK		+2	3.914	0.495	0.9999	4				
		SGYLLPDTK		+2	2.714	0.426	0.9991	4				
		FAFQAEVNR		+2	3.193	0.465	0.9998	6				
		NLLHVTDTGVGMTR		+3	4.475	0.515	1.0000	6				
		IYFMAGSSR		+2	3.074	0.385	0.9993	4				
		FQSSHHSTDITSLDQYVER			+2	5.530	0.675	1.0000	5			
		GVVDSDDLPLNVSR		+2	4.414	0.425	0.9999	4				
		ELISNASDALDKIR		+2	3.513	0.386	0.9770	1				
		EEEAIQLDGLNASQIR			+2	4.901	0.429	0.9999	1			
		EEASDYLELDTIK		+2	3.358	0.445	0.9996	3				
		SILFVPTSAPR		+2	3.315	0.321	0.9980	4				
		RVFITDDFHDMMPK		+3	2.779	0.403	0.9994	4				

Seq	Charge	Xcor	Delta	Probility	PepHits
LISLTDENALAGNEELTVK	+2	6.702	0.546	1.0000	3
TDDEVVQREEEAIQLDGLNASQIR	+3	5.324	0.441	0.9994	2
ESDDPMAYIHFTAEGEVTFK	+3	3.158	0.499	0.9999	2
EATEKEFEPLLNWMK	+2	4.271	0.436	0.9955	2
TVWDWELMNDIKPIWQRPSK	+3	3.776	0.460	0.9999	2
YSQFINFPIYVWSSK	+2	5.422	0.617	1.0000	3
TVWDWELMNDIKPIWQR	+2	5.024	0.443	0.9996	1
MTEAQEDGQSTSELIGQFGVGFYSAFLVADK	+3	6.962	0.670	1.0000	1
VKEDEDDKTVMDLAVVLFETATLR	+2	6.538	0.600	1.0000	6
DISTNYYASQK	+2	3.706	0.545	1.0000	3
SGTSEFLNK	+2	2.824	0.270	0.9923	2

MASCOT:(PepMatched Observed.Hits Coverage) 21 8 33.25%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SGTSEFLNK	+2	491.75	981.48	981.48	0	41	1
LGVIEDHSNR	+2	570.30	1138.58	1138.57	0.01	41	2
ELISNASDALDK	+2	638.33	1274.64	1274.64	0	83	12
DISTNYYASQK	+2	645.09	1288.17	1288.59	-0.41	63	3
SGYLLPDTK	+2	497.27	992.53	992.52	0.01	42	4
IYFMAGSSR	+2	516.25	1030.49	1030.49	0	63	4
FAFQAEVNR	+2	541.28	1080.54	1080.54	0	64	7
NLLHVTDTGVGMTR	+2	757.40	1512.78	1512.77	0.01	74	6
SILFVPTSAPR	+2	594.34	1186.67	1186.67	0	43	4
GVVDSDDLPLNVSR	+2	743.38	1484.75	1484.75	0	92	4
EEASDYLELDTIK	+2	763.37	1524.73	1524.72	0.01	59	3
ELISNASDALDKIR	+2	772.92	1543.83	1543.82	0.01	86	2
EEEAIQLDGLNASQIR	+2	893.46	1784.90	1784.89	0.01	85	2
FQSSHHSTDITSLDQYVER	+3	750.69	2249.05	2249.03	0.02	60	3
VFITDDFHDMMPK	+2	798.37	1594.72	1594.72	0	49	2
RVFITDDFHDMMPK	+2	876.42	1750.82	1750.82	0	52	2
TDDEVVQREEEAIQLDGLNASQIR	+3	910.12	2727.35	2727.33	0.02	60	1
EATEKEFEPLLNWMK	+2	932.97	1863.92	1863.91	0.01	58	2
YSQFINFPIYVWSSK	+2	939.98	1877.95	1877.94	0.01	84	3
TVWDWELMNDIKPIWQRPSK	+3	848.11	2541.30	2541.28	0.02	57	1
VKEDEDDKTVMDLAVVLFETATLR	+3	913.14	2736.40	2736.39	0.01	64	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
358.	IPI00357893	Y	N	0.5	1	3	0	9	0

*Des: 3-hydroxyisobutyryl-Coenzyme A hydrolase

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 13.24%

Seq	Charge	Xcor	Delta	Probility	PepHits
AGIATHFVDSEK	+2	3.507	0.368	0.9990	6
SPSAEDVAGVLESYHAK	+2	4.446	0.463	1.0000	2
DPDTFLIIIK	+2	3.723	0.406	0.9997	4

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
359.	IPI00364249	Y	Y	0.11	1	2	2	2	2

*Des:	PREDICTED: similar to mKIAA1458 protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	5.33%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AGVSTPSSGAASPR		+2	3.427	0.466	0.9995	2				
		SGAVQSAGLLGPGSPAR			+2	4.338	0.540	1.0000	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	5.33%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AGVSTPSSGAASPR		+2	622.8181	1243.6217	1243.6156	0.01	66	1		
		SGAVQSAGLLGPGSPAR			+2	762.9166	1523.8186	1523.8055	0.01	61	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
360.	IPI00566940		N	Y	0.15	2	0	4	0	26		
*Des:	68 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	3	8.51%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		APDFVFYAPR		+2	591.8043	1181.5941	1181.5869	0.01	52	16		
		SEEERTTEAEKNER		+3	569.9315	1706.7727	1706.7707	0	51	8		
		ILALCMGNHELYMR		+2	832.4280	1662.8415	1662.8044	0.04	42	12		
		ISQLEMAR		+2	474.2526	946.4906	946.4906	0	62	8		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
361.	IPI00213536		Y	Y	0.81	3	5	6	23	24		
*Des:	PREDICTED: calpain, small subunit 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	2	29.91%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ILGGVISAISEAAAQYNPEPPPPR				+3	6.324	0.651	1.0000	10		
		SGTIGSNELPGAFEAAGFHLNQHIYSMIIR				+4	3.554	0.506	1.0000	3		
		KLFVQLAGDDMEVSATELMNILNK				+3	4.019	0.358	0.9994	2		
		SMVAVMDSDTTGK		+2	4.921	0.599	1.0000	9				
		SHYSNIEANESEEER			+3	5.682	0.437	1.0000	5			
	MASCOT:(PepMatched Observed.Hits Coverage)					6	3	23.71%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		SHYSNIEANESEEER			+2	897.39	1792.77	1792.75	0.02	94	5	
		SMVAVMDSDTTGK		+2	671.31	1340.60	1340.60	0	113	9		
		LGFEEFK	+2	435.23	868.44	868.43	0.01	53	9			
		ILGGVISAISEAAAQYNPEPPPPR				+3	816.44	2446.30	2446.29	0.01	101	7
		LFVQLAGDDMEVSATELMNILNK				+3	851.10	2550.29	2550.27	0.02	110	2
		KLFVQLAGDDMEVSATELMNILNK				+3	893.81	2678.40	2678.37	0.03	56	2

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
362.	IPI00213463		Y	N	0.16	2	11	0	16	0		
*Des:	Alpha-actinin 4											
	SEQUEST:(PepMatched Observed.Hits Coverage)					11	2	22.33%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		MAPYQGPDAAPGALDYK			+2	4.096	0.487	0.9999	1			
		VLAVNQENEHLMEDYER			+2	5.636	0.582	1.0000	3			

LSGSNPYTSVTPQIINSK +2 4.880 0.493 1.0000 2
LVSIGAEEIVDGNAK +2 4.143 0.518 0.9999 1
QLETIDQLHLEYAK +2 3.738 0.492 0.9999 2
KDDPVTNLNNAFEVAEK +2 4.811 0.582 1.0000 2
AGTQIENIDEDFRDGLK +2 4.309 0.478 0.9976 2
NVNVQNFHISWK +2 3.190 0.509 0.9998 1
QFASQANMVGPWIQTK +2 3.680 0.509 0.9999 2
VEQIAAIAQELNELDYYDSHNVNTR +3 4.930 0.384 0.9998 3
SIVDYKPNLDLLEQQHQLIQEALIFDNK +3 5.152 0.645 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
363. IPI00205519 Y Y 0.17 2 7 9 10 13
*Des: UDP-glucose glycoprotein:glucosyltransferase
SEQUEST:(PepMatched Observed.Hits Coverage) 7 1 7.21%
Seq Charge Xcor Delta Probility PepHits
ILETTTFFQR +2 2.787 0.384 0.9974 2
VWQLQDLSFQTAAR +2 5.019 0.553 1.0000 1
FLFVDADQIVR +2 3.748 0.538 0.9999 2
SYYDAILEAAFR +2 3.588 0.467 0.9998 2
ILAAPVELALVVMK +2 3.593 0.621 1.0000 2
IIGPLEDSELFNQDDFHLLENIILK +3 4.215 0.497 1.0000 1
WFSAPLLLEASEFLAEDSQEK +3 5.435 0.587 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 9 2 8.67%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
SGYWASHLAGR +2 603.35 1204.68 1203.58 1.1 68 1
QLQTLFQEEK +2 632.34 1262.66 1262.65 0.01 42 1
ILETTTFFQR +2 628.34 1254.66 1254.66 0 43 2
FLFVDADQIVR +2 661.86 1321.71 1321.70 0.01 58 2
VWQLQDLSFQTAAR +2 831.94 1661.86 1661.85 0.01 57 1
SYYDAILEAAFR +2 709.85 1417.69 1417.69 0 48 2
ILAAPVELALVVMK +2 733.96 1465.90 1465.89 0.01 70 2
WFSAPLLLEASEFLAEDSQEK +3 804.07 2409.19 2409.17 0.02 53 1
IIGPLEDSELFNQDDFHLLENIILK +3 975.85 2924.53 2924.52 0.01 67 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
364. IPI00212666 Y Y 0.13 1 7 13 8 91
*Des: Rat alpha(1)-inhibitor 3, variant I precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 7 1 7.67%
Seq Charge Xcor Delta Probility PepHits
ESVVFVQTDKPVYKPGQSVK +3 4.536 0.394 0.9999 2
SSGSLFNNAMK +2 2.713 0.313 0.9851 1
TPLVTIQSSGSFSQK +2 4.592 0.574 1.0000 1
GGEFEMMPLGVNK +2 3.998 0.413 0.9997 1
FSIDTSSISGYSLNIK +2 3.499 0.527 0.9998 1
DMGLTAFTNLK +2 3.504 0.482 0.9998 1
MLIYTILPDGEVIADSVTFQVEK +3 5.147 0.474 1.0000 1

MASCOT:(PepMatched Observed.Hits Coverage) 13 3 16.07%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
TPLVTIQSSGSFSQK	+2	790.43	1578.84	1578.83	0.01	57	1
VHLSFSPSQSLPASQTHMR	+3	704.03	2109.06	2109.04	0.02	43	2
LPSSEEEESLDINIEGAK	+2	980.48	1958.95	1958.93	0.02	117	6
FSIDTSSISGYSLNIK	+2	866.45	1730.89	1730.87	0.02	88	3
YMVLVPSQLYTETPEK	+2	949.49	1896.97	1896.95	0.02	85	8
SEGYLYTPQASSAEVEMSAYVVLAR	+3	907.78	2720.31	2720.30	0.01	50	6
MLSGFIPLKPTVK	+2	715.93	1429.85	1429.84	0.01	48	5
AHFSVMGDILSSAIK	+2	788.42	1574.83	1574.81	0.02	77	15
EEHSFTVMEFVLPR	+3	574.29	1719.84	1719.83	0.01	66	35
QLSFSLSAEPIQGPYK	+2	882.97	1763.92	1763.91	0.01	84	15
AFIFIDESHITDAFTWLSK	+3	747.72	2240.13	2240.12	0.01	57	6
DGSYSAFGDHNGQGQGNTWLTAFVLK	+3	924.11	2769.30	2769.28	0.02	73	4
NLHPLNELFPLAYIEDPK	+3	708.38	2122.12	2122.11	0.01	50	27

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
365.	IPI00326140	Y	Y	0.22	2	26	21	57	46

*Des: Alpha-1-macroglobulin

SEQUEST:(PepMatched Observed.Hits Coverage) 26 6 28.39%

Seq	Charge	Xcor	Delta	Probility	PepHits
AEDITHNGIVYTPK	+3	3.699	0.481	0.9998	6
QLNYQHSDGSYSTFGDR	+3	3.997	0.546	1.0000	4
DAVNEEESVHWQR	+2	3.542	0.384	0.9928	1
VAEVPALVQK	+2	2.826	0.458	0.9992	6
AESPVFVQTDKPIYKPGQTVK	+2	5.144	0.558	1.0000	4
DTVVKPVIVEPEGIEK	+2	3.711	0.468	0.9997	2
AFAQAQSYIYIEK	+2	3.780	0.478	0.9998	1
AISYLISGYQR	+2	3.197	0.388	0.9988	2
GSIFNSGSHVLPLEQGK	+2	3.499	0.526	0.9998	2
IHFLLNEDALK	+2	2.817	0.468	0.9992	2
TSSMMMMGASEVAQEVEVR	+2	4.731	0.617	1.0000	2
LSPQSIYNLLPQK	+3	3.831	0.370	0.9999	1
PLSPSALIAVEIK	+3	3.562	0.440	0.9998	3
YVVLVPSELYAGVPEK	+2	3.126	0.406	0.9979	1
THITNAFNWLSMK	+2	3.737	0.646	1.0000	2
QDLNDNDAYSVFQSIGLK	+2	5.664	0.597	1.0000	4
HSQGNTWLTAFVLK	+2	5.332	0.565	1.0000	2
LIVYTILPNEELIADVQK	+3	5.143	0.599	1.0000	3
ALLAYAFALAGNR	+2	2.950	0.361	0.9956	2
ANTFYRPGLPFFGQVLLVDEK	+3	5.809	0.557	1.0000	3
IFQWQNVDLPGGLHQLSFPLSVEPALGIYK	+3	6.449	0.640	1.0000	2
KYFPETWIWDMVPLDLSGDGELPVK	+3	4.024	0.342	0.9995	1
VFQPFFLELTLPYSVVR	+2	4.437	0.574	1.0000	3
APSAEVEMTAYVLLAYLTSASSR	+3	3.988	0.566	1.0000	1
DAVNEEESVHWQRPK	+2	3.645	0.473	0.9997	3
RSEVLESLNK	+2	3.065	0.167	0.9614	2

MASCOT:(PepMatched Observed.Hits Coverage) 21 4 21.11%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VAEVPALVQK	+2	527.28	1052.54	1052.62	-0.07	51	5
RSEVLESLNK	+2	587.82	1173.63	1173.64	0	50	3
AEDITHNGIVYTPK	+2	779.40	1556.79	1556.78	0.01	58	7
DAVNEEESVHWQRPK	+2	912.44	1822.87	1822.86	0.01	67	2
QLNYQHSDGSYSTFGDR	+2	987.94	1973.86	1973.85	0.01	68	4
TVSWAVTPK	+2	494.78	987.55	987.54	0.01	66	1
AISYLISGYQR	+2	635.84	1269.67	1269.67	0	76	4
AFAQAQSYIYIEK	+2	766.40	1530.78	1530.77	0.01	71	1
DTVVKPVIVEPEGIEK	+2	876.50	1750.98	1750.97	0.01	76	3
GSIFNSGSHVLPLEQGK	+2	885.46	1768.92	1768.91	0.01	72	2
IHFLLNEDALK	+2	656.87	1311.73	1311.72	0.01	52	2
ALLAYAFALAGNR	+2	675.88	1349.75	1349.75	0	84	1
LSPQSIYNLLPQK	+3	500.95	1499.84	1499.83	0.01	49	2
THITNAFNWLSMK	+2	781.90	1561.78	1561.77	0.01	80	1
HSQGNTWLTAFVLK	+2	801.43	1600.85	1600.84	0.01	100	4
QDLNDNDAYSVFQSIGLK	+3	676.66	2026.97	2025.96	1.01	59	3
LIVYTILPNEELIADVQK	+3	691.07	2070.18	2070.16	0.02	69	2
TSSMMMMGASEVAQEVEVR	+3	691.64	2071.91	2071.90	0.01	44	1
ANTFYRPGLPFFGQVLLVDEK	+3	804.43	2410.27	2410.27	0	70	3
AEQGAYLGPLPYK	+2	703.87	1405.72	1405.72	0	48	2
YVVLVPSELYAGVPEK	+2	881.99	1761.96	1761.96	0	53	3

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
366.	IPI00200504	Y	Y	0.06	1	4	3	4	8

*Des: Kalirin-12a

SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 2.32%

Seq	Charge	Xcor	Delta	Probility	PepHits
LQGFEGTLTAQGK	+2	2.885	0.372	0.9959	1
MFVLNELVQTEK	+2	4.063	0.351	0.9995	1
VILQAANSDIQQAWVQDINQVLETQR	+3	4.313	0.486	1.0000	1
VFLFEQIVIFSELLR	+3	3.948	0.371	0.9998	1

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 1.42%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LQGFEGTLTAQGK	+2	675.36	1348.70	1348.70	0	55	2
MFVLNELVQTEK	+2	725.89	1449.76	1449.75	0.01	72	1
VFLFEQIVIFSELLR	+3	618.36	1852.06	1852.05	0.01	65	5

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
367.	IPI00205378	Y	Y	1.6	3	7	6	12	13

*Des: PREDICTED: similar to Syntaxin-11

SEQUEST:(PepMatched Observed.Hits Coverage) 7 2 36.64%

Seq	Charge	Xcor	Delta	Probility	PepHits
LAELQELSR	+2	3.387	0.361	0.9993	4
AFQQAMYEYNQAEMK	+2	4.795	0.503	1.0000	3
QADTLNVIELNVQK	+2	3.566	0.507	0.9998	1

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                    DVSGEQIEDMFEQGK               +2        4.382     0.517     1.0000    2
                    VIQDIQDENQLLLIDVR             +2        4.920     0.460     1.0000    2
                    WDVFSENLLADVK       +2        2.901     0.211     0.9570    1
                    IRDVHELFLQMAVLVEK             +3        5.056     0.566     1.0000    3
          MASCOT:(PepMatched Observed.Hits Coverage)        6         3         27.05%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    LAELQELSR           +2        529.80    1057.58   1057.58   0         65        4
                    MKDRLAELQELSR       +3        529.80    1586.37   1587.84   -1.46     45        4
                    AFQQAMYEYNQAEMK               +2        926.41    1850.80   1850.80   0         74        3
                    QADTLNVIELNVQK      +2        792.93    1583.85   1583.85   0         62        1
                    DVSGEQIEDMFEQGK               +2        856.38    1710.75   1710.74   0.01      59        2
                    IRDVHELFLQMAVLVEK             +3        680.71    2039.12   2039.12   0         72        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
368.      IPI00201307         Y         Y         1.15      2         3         3         8         9
*Des:     PREDICTED: similar to ubiquinol-cytochrome c reductase binding protein
          SEQUEST:(PepMatched Observed.Hits Coverage)       3         1         26.54%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    DDTMHETEDVKEAIR               +2        4.334     0.358     0.9994    4
                    YEEDKFYLEPYLK       +2        4.817     0.436     1.0000    3
                    DDTMHETEDVK         +2        2.921     0.334     0.9983    2
          MASCOT:(PepMatched Observed.Hits Coverage)        3         2         26.54%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    DDTMHETEDVK         +2        660.2853  1318.5560 1318.5347 0.02      56        3
                    YEEDKFYLEPYLK       +2        868.9398  1735.8650 1735.8344 0.03      74        3
                    DDTMHETEDVKEAIR               +2        894.9232  1787.8319 1787.7996 0.03      73        4

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
369.      IPI00564409         N         Y         0.32      2         0         3         0         19
*Des:     PREDICTED: similar to Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A)
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)        3         2         8.45%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    LNGTDPEDVIR         +2        615.7902  1229.5658 1227.6095 1.96      47        44
                    EAFNMIDQNR          +2        619.2893  1236.5641 1236.5557 0.01      54        10
                    GNFNYIEFTR          +2        630.8066  1259.5987 1259.5934 0.01      46        5

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
370.      IPI00324618         Y         Y         0.29      2         6         5         6         5
*Des:     General vesicular transport factor p115
          SEQUEST:(PepMatched Observed.Hits Coverage)       6         2         10.25%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    SVPVEGESELVTAAK               +2        3.797     0.523     0.9999    1
                    IVAFENAFER          +2        2.715     0.343     0.9959    2
                    QLGPPVQQIILVSPMGVSK           +2        4.088     0.453     0.9998    1
                    EQDDLLVLLADQDQK               +2        3.127     0.185     0.9533    1
                    QSEDLGSQFTEIFIK +2            3.943     0.503     0.9999    1
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          QPENVTLLLSLLEEFDFHVR    +3       3.932    0.431    0.9999   1
MASCOT:(PepMatched Observed.Hits Coverage) 5        2        7.79%
          Seq       Charge   ObservedMS        ExpectedMS        CalculatedMS                Pepscore PepHits
          SVPVEGESELVTAAK           +2       758.40   1514.78  1514.78  0        59       1
          IVAFENAFER     +2       598.31   1194.61  1194.60  0.01     43       2
          QSEDLGSQFTEIFIK +2      871.44   1740.87  1740.86  0.01     73       1
          QLGPPVQQIILVSPMGVSK     +2       996.08   1990.14  1990.13  0.01     56       2
          NDGVLLLQALTR   +2       656.88   1311.75  1311.75  0        43       1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
371.      IPI00369190         Y        Y        0.28     2        6        5        8        6
*Des:     PREDICTED: similar to RIKEN cDNA 6330406L22
          SEQUEST:(PepMatched Observed.Hits Coverage) 6        3        9.31%
          Seq       Charge   Xcor     Delta    Probility PepHits
          ELVELSQASPHDISNVLK      +2       5.857    0.571    1.0000   1
          PTDATVSLSSLVDYPHQAR     +3       4.564    0.456    0.9999   1
          YDFEPYVSTNAWSPIMR       +2       3.418    0.457    0.9994   1
          LQLFGQDFSQAAHSTPDGVPFIIK         +3       4.122    0.476    1.0000   1
          YPLLNTVETLTAAGTLIAK     +2       5.806    0.527    1.0000   3
          LYDPGQQYASHVR  +2       3.804    0.410    0.9995   1
MASCOT:(PepMatched Observed.Hits Coverage) 5        1        6.34%
          Seq       Charge   ObservedMS        ExpectedMS        CalculatedMS                Pepscore PepHits
          LYDPGQQYASHVR  +2       767.38   1532.75  1532.74  0.01     51       1
          QDGSESEAATLAMVGR        +2       811.38   1620.75  1620.74  0.01     45       1
          ELVELSQASPHDISNVLK      +2       990.03   1978.05  1978.04  0.01     114      2
          LCQAFENGKELVELSQASPHDISNVLK      +3       990.03   2967.08  2968.50  -1.41    65       1
          YPLLNTVETLTAAGTLIAK     +2       995.08   1988.14  1988.12  0.02     175      3

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
372.      IPI00373140         Y        Y        0.89     3        2        6        2        34
*Des:     PREDICTED: similar to sid23p
          SEQUEST:(PepMatched Observed.Hits Coverage) 2        1        11.3%
          Seq       Charge   Xcor     Delta    Probility PepHits
          HEYQANGPEDLNR  +2       4.284    0.579    1.0000   1
          FPGIKHEYQANGPEDLNR      +3       5.737    0.524    1.0000   1
MASCOT:(PepMatched Observed.Hits Coverage) 6        6        44.64%
          Seq       Charge   ObservedMS        ExpectedMS        CalculatedMS                Pepscore PepHits
          HEYQANGPEDLNR  +2       771.86   1541.70  1541.69  0.01     67       6
          KFPGIKHEYQANGPEDLNR     +3       738.38   2212.11  2212.10  0.01     41       4
          MIYASSKDAIKK   +2       677.87   1353.73  1353.73  0        54       3
          LGGSLIVAFEGSPV +2       673.37   1344.73  1344.73  0        49       8
          TSIAEKLGGSLIVAFEGSPV    +2       988.04   1974.07  1974.07  0        97       20
          ESRKEELMFFLWAPEQAPLK    +3       817.10   2448.26  2448.25  0.01     43       3

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
373.      IPI00470317         Y        Y        0.19     2        6        8        12       16
*Des:     PREDICTED: eukaryotic translation elongation factor 1 gamma
```

	SEQUEST:(PepMatched Observed.Hits Coverage)					6	3	15.34%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		KLDPGSEETQTLVR		+2	3.828	0.433	0.9998	4				
		ALIAAQYSGAQIR		+2	2.780	0.401	0.9976	3				
		VLSAPPHFHFGQTNR			+2	3.137	0.465	0.9994	3			
		DGWSLWYAEYR		+2	2.877	0.444	0.9993	2				
		GQDLAFPLSPDWQVDYESYTWR					+2	4.844	0.550	1.0000	4	
		YSNEDTLSVALPYFWEHFDK			+3	4.740	0.367	0.9996	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					8	4	19.6%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		KLDPGSEETQTLVR		+2	786.92	1571.82	1571.82	0	74	4		
		ALIAAQYSGAQIR		+2	681.38	1360.75	1360.75	0	54	2		
		VLSAPPHFHFGQTNR			+2	854.44	1706.87	1706.86	0.01	53	1	
		ILGLLDTHLK		+2	561.85	1121.68	1121.68	0	57	1		
		DGWSLWYAEYR		+2	723.33	1444.64	1444.64	0	49	2		
		EYFSWEGAFQHVGK			+2	842.89	1683.76	1683.77	0	48	2	
		YSNEDTLSVALPYFWEHFDK			+3	821.05	2460.13	2460.13	0	45	2	
		NAFASVILFGTNNSSSISGVWVFR				+3	858.45	2572.32	2572.31	0.01	59	1

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
374.	IPI00364321		Y	Y	1.57	1	3	7	5	19		
*Des:	Electron-transfer-flavoprotein, beta polypeptide											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	17.3%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VETTEDLVAK		+2	3.174	0.410	0.9997	3				
		AGDLGVDLTSK		+2	3.309	0.379	0.9995	3				
		GIHVEVPGAEAENLGPLQVAR			+3	5.177	0.415	0.9999	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					7	1	34.23%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VETTEDLVAK		+2	552.80	1103.58	1103.57	0.01	68	3		
		AGDLGVDLTSK		+2	538.29	1074.56	1074.56	0	74	4		
		EIDGGLETIR		+2	551.79	1101.57	1101.57	0	76	6		
		VSVISVEEPPQR		+2	670.37	1338.72	1338.71	0.01	68	5		
		LPAVVTADLR		+2	527.82	1053.62	1053.62	0	67	3		
		GIHVEVPGAEAENLGPLQVAR			+3	719.39	2155.15	2155.14	0.01	51	2	
		VDLLFLGK		+2	452.78	903.55	903.54	0.01	50	8		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
375.	IPI00607153		N	Y	0.15	1	0	2	0	13		
*Des:	Hypothetical protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	4.65%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YTATSQVLLSAK		+2	641.36	1280.70	1280.70	0	82	12		
		GFSPADIFVQWLQR		+2	832.43	1662.85	1662.85	0	45	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		

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376.      IPI00373218         N         Y         0.25      1         0         2         0         4
*Des:     40 kDa peptidyl-prolyl cis-trans isomerase
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)  2         1         7.18%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    MLENVEVNGEKPAK+2              779.41    1556.81   1556.79   0.02      41        2
                    VFFDVDIGGER         +2        627.31    1252.61   1252.61   0         48        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
377.      IPI00358845         Y         Y         0.96      1         3         4         5         5
*Des:     PREDICTED: similar to Proline synthetase associated
          SEQUEST:(PepMatched Observed.Hits Coverage)  3         1         16.07%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    VMVQINTSGEDSK  +2        3.463     0.546     1.0000    2
                    HGLLPSETVAVVEHIK              +3        4.220     0.524     1.0000    2
                    TFGENYVQELLEK  +2        2.999     0.487     0.9998    2
          MASCOT:(PepMatched Observed.Hits Coverage)  4         1         19.64%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    VMVQINTSGEDSK  +2        704.35    1406.68   1406.67   0.01      69        2
                    VGSTIFGER           +2        483.26    964.50    964.50    0         53        1
                    HGLLPSETVAVVEHIK              +3        577.00    1727.97   1727.96   0.01      51        3
                    TFGENYVQELLEK  +2        785.40    1568.78   1568.77   0.01      47        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
378.      IPI00195123         N         Y         0.87      1         0         3         0         4
*Des:     ATP synthase oligomycin sensitivity conferral protein, mitochondrial precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)  3         1         15.66%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    TVLNSFLSK           +2        504.8226  1007.6306 1007.5651 0.07      34        1
                    YATALYSAASK         +2        573.3322  1144.6498 1144.5764 0.07      75        2
                    VSLAVLNPYIK         +2        608.9124  1215.8102 1215.7227 0.09      44        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
379.      IPI00231253         Y         Y         2.44      1         8         7         29        40
*Des:     3-hydroxyacyl-CoA dehydrogenase type II
          SEQUEST:(PepMatched Observed.Hits Coverage)  8         1         56.22%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    VINVNLIGTFNVIR  +2       4.489     0.440     1.0000    4
                    VVTIAPGLFATPLLTTLPDK          +2        4.317     0.614     1.0000    4
                    LVAGVMGQNEPDQGGQR             +2        5.382     0.474     1.0000    6
                    NQVHTLEDFQR    +2        3.320     0.529     1.0000    3
                    LVGQGATAVLLDVPNSEGETEAK                 +2        5.900     0.627     1.0000    2
                    GGIVGMTLPIAR   +2        3.437     0.299     0.9980    4
                    GLVAVITGGASGLGLSTAK           +3        4.596     0.602     1.0000    18
                    GVIINTASVAAFEGQVGQAAYSASK               +3        3.017     0.401     0.9985    4
          MASCOT:(PepMatched Observed.Hits Coverage)  7         1         41.5%
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Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LVAGVMGQNEPDQGGQR	+2	878.43	1754.85	1754.84	0.01	114	14
EVQAALTLAK	+2	522.31	1042.61	1042.60	0.01	58	14
NQVHTLEDFQR	+2	693.85	1385.68	1385.67	0.01	51	6
GGIVGMTLPIAR	+2	592.85	1183.68	1183.67	0.01	64	6
GLVAVITGGASGLGLSTAK	+2	836.49	1670.97	1670.96	0.01	91	17
VINVNLIGTFNVIR	+2	786.47	1570.93	1570.92	0.01	53	5
VVTIAPGLFATPLLTTLPDK	+3	689.74	2066.21	2066.20	0.01	51	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
380.	IPI00198467	Y	Y	0.28	1	3	3	4	6

*Des: Trifunctional enzyme beta subunit, mitochondrial precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 7.86%

Seq	Charge	Xcor	Delta	Probility	PepHits
LAAAFAVSR	+2	2.705	0.400	0.9987	3
DFIYVSQDPK	+2	2.710	0.247	0.9798	1
DVVDYIIFGTVIQEVK	+2	3.959	0.532	0.9999	3

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 7.66%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LAAAFAVSR	+2	453.27	904.52	904.51	0.01	51	3
AALSGLLYR	+2	482.29	962.56	962.55	0.01	57	1
DVVDYIIFGTVIQEVK	+2	919.51	1837.00	1836.99	0.01	90	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
381.	IPI00370815	Y	Y	0.21	3	3	7	5	11

*Des: PREDICTED: similar to mKIAA0002 protein

SEQUEST:(PepMatched Observed.Hits Coverage) 3 3 6.09%

Seq	Charge	Xcor	Delta	Probility	PepHits
AVDDGVNTFK	+2	2.986	0.373	0.9954	2
FAEAFEAIPR	+2	2.865	0.463	0.9985	2
HFSGLEEAVYR	+3	3.215	0.391	0.9997	4

MASCOT:(PepMatched Observed.Hits Coverage) 7 3 15.77%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LATNAAVTVLR	+2	564.84	1127.66	1127.67	0	92	2
DVDEVSSLLR	+2	566.79	1131.58	1131.58	0	60	1
FAEAFEAIPR	+2	575.80	1149.58	1149.58	0	71	2
QYGSEEFLAK	+2	586.29	1170.56	1170.56	0	43	2
HFSGLEEAVYR	+2	654.32	1306.63	1306.63	0	61	1
AIAGTGANVIVTGGK	+2	664.88	1327.75	1327.75	0	99	2
LVPGGGATEIELAK	+2	677.88	1353.75	1353.75	0	78	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
382.	IPI00365056	Y	Y	0.04	1	2	2	3	2

*Des: PREDICTED: similar to Cleavage stimulation factor, 3 pre-RNA, subunit 1

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 1.79%

Seq	Charge	Xcor	Delta	Probility	PepHits
IGAVTLSPQLGNAVQK	+2	4.033	0.473	0.9999	1

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                    VASSVAGLLLFVSR  +2          3.734       0.524       0.9999      2
          MASCOT:(PepMatched Observed.Hits Coverage)        2           1           1.79%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore  PepHits
                    IGAVTLSPQLGNAVQK            +2          798.46      1594.92     1594.90     0.02        84          1
                    VASSVAGLLLFVSR  +2          709.92      1417.83     1417.83     0           66          2

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
383.      IPI00194324       Y           N           0.45        1           8           0           17          0
*Des:     Pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)       8           2           38.9%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    EAINQGMDEELERDEK            +2          4.260       0.504       0.9977      3
                    ILEDNSIPQVK     +2          3.186       0.264       0.9889      1
                    VTGADVPMPYAK    +2          3.101       0.447       0.9988      3
                    TIRPMDIEAIEASVMK            +2          4.118       0.576       1.0000      3
                    VFLLGEEVAQYDGAYK            +3          3.901       0.400       0.9995      3
                    TYYMSAGLQPVPIVFR            +2          4.241       0.595       1.0000      3
                    IMEGPAFNFLDAPAVR            +2          3.641       0.546       0.9998      3
                    SAIRDDNPVVMLENELMYGVAFELPTEAQSK             +3          4.002       0.479       0.9978      2
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
384.      IPI00361924       Y           Y           0.15        1           2           2           5           8
*Des:     Annexin A7
          SEQUEST:(PepMatched Observed.Hits Coverage)       2           3           4.45%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    SDTSGHFER   +2          2.725       0.333       0.9989      2
                    AIQGAGTQER  +2          2.812       0.314       0.9984      6
          MASCOT:(PepMatched Observed.Hits Coverage)        2           1           6.15%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore  PepHits
                    GFGTDEQAIVDVVSNR            +2          853.9214    1705.8283 1705.8271 0           105         4
                    GAGTDDSTLVR +2          546.2679    1090.5213 1090.5254 0           59          4

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
385.      IPI00212741       Y           Y           0.15        2           2           2           3           3
*Des:     Phosphofructokinase, liver, B-type
          SEQUEST:(PepMatched Observed.Hits Coverage)       2           1           3.78%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    AIGVLTSGGDAQGMNAAVR         +2          5.758       0.705       1.0000      2
                    TFVLEVMGR   +2          2.712       0.383       0.9976      2
          MASCOT:(PepMatched Observed.Hits Coverage)        2           2           3.78%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore  PepHits
                    AIGVLTSGGDAQGMNAAVR         +2          894.4647    1786.9148 1786.8995 0.02        124         2
                    TFVLEVMGR   +2          526.2908    1050.5671 1050.5531 0.01        45          1

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
386.      IPI00196794       N           Y           0.3         1           0           2           0           2
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Identified Human Platelet Proteins

*Des: Ras-related protein Rab-14
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 13.69%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
TGENVEDAFLEAAK		+2	747.4178	1492.8210	1492.7045	0.12	44	1		
STYNHLSSWLTDAR		+3	550.9732	1649.8978	1649.7798	0.12	36	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)
387.	IPI00558930		N	Y	0.24	1	0	2	0	7

*Des: Regulator of G-protein signaling 19 interacting protein 1
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 9.14%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
APPLVENEEAEPSR		+2	769.38	1536.75	1536.74	0.01	50	6		
GPATVEDLPSAFEEK			+2	795.40	1588.78	1588.76	0.02	85	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)
388.	IPI00213618		N	Y	0.02	1	0	2	0	3

*Des: Sarcoplasmic/endoplasmic reticulum calcium ATPase 1
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 2.57%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
VDQSILTGESVSVIK		+2	787.9436	1573.8727	1573.8562	0.02	60	2		
GAPEGVIDR		+2	457.2468	912.4791	912.4664	0.01	42	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)
389.	IPI00565213		N	Y	0.5	1	0	10	0	32

*Des: 101 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 10 1 17.71%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
LTQYDIVIK		+2	546.82	1091.63	1091.62	0.01	44	6		
EVAFDVEIPK		+2	573.81	1145.61	1145.60	0.01	44	4		
NMEQFTIHITVGAQSK			+2	902.47	1802.92	1802.90	0.02	84	8	
GSLVPASHANLQAAQDFVR			+2	991.02	1980.03	1980.02	0.01	100	6	
ATFQLTYEEVLK		+2	721.39	1440.76	1440.75	0.01	47	2		
FSLAGATNLNGGLLR			+2	752.92	1503.82	1502.82	1	62	4	
NLVFVIDISGSMEGQK			+2	868.95	1735.89	1735.88	0.01	79	4	
QLVHHFEIDVDIFEPQGISR			+3	793.75	2378.22	2378.20	0.02	63	4	
LWAYLTIQELLAK		+2	781.46	1560.90	1560.89	0.01	85	3		
ILGDMKPVDNFDLVLFGSQVQSWK				+3	912.81	2735.42	2735.40	0.02	52	5

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)
390.	IPI00567681		N	Y	0.23	1	0	2	0	5

*Des: 36 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 3.89%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LEKPAKYDDLK	+2	660.3704	1318.7262	1318.7132	0.01	44	1
LEKPAKYDDLKK	+2	724.4151	1446.8156	1446.8082	0.01	52	10

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
391.	IPI00389806	Y	Y	0.22	2	3	11	5	21

*Des: PREDICTED: similar to inter-alpha-inhibitor H2 chain

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 3.55%

Seq	Charge	Xcor	Delta	Probility	PepHits
IQPSGGTNINEALLR	+2	3.197	0.457	0.9991	2
KFYNQVSTPLLR	+2	3.112	0.458	0.9993	1
AHVSFKPTVAQQR	+2	3.381	0.522	0.9998	5

MASCOT:(PepMatched Observed.Hits Coverage) 11 3 14.69%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
FYNQVSTPLLR	+2	669.37	1336.73	1336.71	0.02	48	2
VQFELHYQEVK	+2	710.37	1418.73	1418.72	0.01	85	2
IQPSGGTNINEALLR	+2	791.94	1581.86	1581.85	0.01	102	4
TEDQFSVVDFNHNVR	+2	904.44	1806.86	1805.83	1.03	69	4
HLEVNVWIIEPQGMR	+2	910.99	1819.96	1819.94	0.02	89	3
LVNHSPLPQNVVFDVQIPK	+3	715.41	2143.20	2143.18	0.02	59	2
FLHVPDTFEGHFQGVPVISK	+3	752.07	2253.17	2253.16	0.01	51	2
TILDDLRTEDQFSVVDFNHNVR	+3	878.44	2632.31	2632.29	0.02	65	3
LWAYLTVNQLLTER	+2	860.48	1718.95	1718.94	0.01	81	5
NILFVIDVSGSMWGIK	+2	889.98	1777.95	1777.94	0.01	89	2
AGELEVFNGYFVHFFAPENLDPIPK	+3	950.82	2849.43	2849.41	0.02	69	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
392.	IPI00205389	Y	Y	1.13	4	16	14	56	91

*Des: Fibrinogen beta chain precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 16 16 40.65%

Seq	Charge	Xcor	Delta	Probility	PepHits
GFGNIATNEDTK	+2	3.360	0.366	0.9984	3
TENGGWTVIQNR	+2	3.879	0.358	0.9992	6
LYIDETVNDNIPLNLR	+2	3.888	0.443	0.9996	4
DNENVINEYSSILEDQK	+2	3.868	0.404	0.9993	1
YYWGGLYSWDMSK	+2	4.309	0.554	1.0000	4
IGPTELLIEMEDWK	+2	3.520	0.523	1.0000	3
IGPTELLIEMEDWKGDKVK	+3	3.713	0.517	1.0000	19
GFGNIATNEDTKK	+2	3.260	0.422	0.9990	3
SILEDLRSK	+2	2.705	0.301	0.9653	3
KGFGNIATNEDTKK	+3	3.755	0.427	1.0000	6
AHYGGFTVQTEANKYQVSVNK	+2	6.564	0.639	1.0000	10
KGGETSEMYLIQPDTSSKPYR	+3	3.678	0.493	1.0000	4
YCGLPGEYWLGNDKISQLTR	+2	4.620	0.626	1.0000	5
ARPAKVDAGQK	+2	2.736	0.422	0.9911	21
AHYGGFTVQTEANKYQVSVNKYK	+3	4.473	0.608	1.0000	8
QTLLNHERPIK	+2	2.711	0.422	0.9921	4

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	MASCOT:(PepMatched Observed.Hits Coverage)					14	12	31.82%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IGPTELLIEMEDWK		+2	837.4345	1672.8545	1672.8382	0.02	65	8		
		GFGNIATNEDTK		+2	633.8066	1265.5986	1265.5887	0.01	56	7		
		TENGGWTVIQNR		+2	688.3417	1374.6688	1373.6687	1	66	21		
		LYIDETVNDNIPLNLR			+2	951.5082	1901.0019	1900.9894	0.01	72	12	
		YYWGGLYSWDMSK		+2	828.3695	1654.7245	1654.7126	0.01	67	10		
		QDGSVDFGR		+2	490.7284	979.4422	979.4359	0.01	42	4		
		GFGNIATNEDTKK		+2	697.8550	1393.6954	1393.6837	0.01	52	6		
		ARPAKVDAGQK		+2	570.8322	1139.6499	1139.6411	0.01	57	38		
		KGFGNIATNEDTKK		+2	761.9014	1521.7883	1521.7787	0.01	65	12		
		KGGETSEMYLIQPDTSSKPYR			+3	796.3968	2386.1685	2386.1474	0.02	52	2	
		AHYGGFTVQTEANKYQVSVNK			+3	781.0657	2340.1752	2340.1498	0.03	56	5	
		AHYGGFTVQTEANKYQVSVNKYK				+4	658.8386	2631.3251	2631.3080	0.02	56	7
		ARPAKVDAGQKK		+3	423.5887	1267.7443	1267.7360	0.01	47	4		
		QTLLNHERPIK		+2	674.8934	1347.7722	1347.7623	0.01	53	8		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
393.	IPI00200519		Y	Y	0.17	3	2	3	4	3		
*Des:	Putative SKAP55											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	3	8.24%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DHSFLGFEWQK		+2	2.794	0.419	0.9992	1				
		YGWWVGEMQGAIGLVPK			+2	4.574	0.513	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	10.16%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IYQFTAASPK		+2	563.3057	1124.5968	1124.5866	0.01	42	1		
		AGYLEKR	+2	418.7381	835.4616	835.4552	0.01	44	1			
		YGWWVGEMQGAIGLVPK			+2	945.9921	1889.9696	1889.9497	0.02	47	1	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
394.	IPI00421659		N	Y	0.06	1	0	2	0	4		
*Des:	Optic atrophy 1-like protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	2.45%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ALGYFAVVTGK		+2	563.32	1124.62	1124.62	0	46	2		
		TSVLEMIAQAR		+2	609.83	1217.65	1217.64	0.01	51	2		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
395.	IPI00331919		Y	N	0.28	1	3	0	3	0		
*Des:	Phosphoserine aminotransferase 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	10.07%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IISNTENLVR		+2	2.772	0.259	0.9873	1				
		ASLYNAVTTEDVEK		+2	3.107	0.401	0.9984	1				
		LPYSVLLEIQK		+2	2.729	0.471	0.9992	2				

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          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
396.      IPI00369419       N          Y          0.3        1          0          2          0          4
*Des:     PREDICTED: similar to cofilin
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)     2          1          19.52%
                      Seq         Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      YALYDATYETK            +2         669.85     1337.68    1336.62    1.06       51         2
                      ESKKEDLVFIFWAPESAPLK   +3         778.75     2333.23    2333.23    0          60         3

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
397.      IPI00365202       Y          Y          0.38       1          2          2          3          3
*Des:     PREDICTED: similar to RIKEN cDNA 2700067E09
          SEQUEST:(PepMatched Observed.Hits Coverage)    2          1          10.71%
                      Seq         Charge     Xcor       Delta      Probility  PepHits
                      AYAEELASHGLNIILISQEEEK +3         4.701      0.451      0.9999     2
                      VETLVLVADFSR           +2         3.518      0.448      0.9997     1
          MASCOT:(PepMatched Observed.Hits Coverage)     2          1          10.71%
                      Seq         Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      VETLVLVADFSR           +2         674.88     1347.74    1347.74    0          46         1
                      AYAEELASHGLNIILISQEEEK +3         819.76     2456.26    2456.24    0.02       63         2

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
398.      IPI00199272       Y          Y          0.3        1          3          2          3          2
*Des:     Tyrosine-protein phosphatase, non-receptor type 1
          SEQUEST:(PepMatched Observed.Hits Coverage)    3          1          12.5%
                      Seq         Charge     Xcor       Delta      Probility  PepHits
                      FIMGDSSVQDQWK          +2         3.731      0.333      0.9989     1
                      FSYLAVIEGAK            +2         2.969      0.446      0.9995     1
                      EILHFHYTTWPDFGVPESPASFLNFLFK      +3         4.277      0.283      0.9966     1
          MASCOT:(PepMatched Observed.Hits Coverage)     2          1          5.9%
                      Seq         Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      FIMGDSSVQDQWK          +2         770.86     1539.71    1539.70    0.01       59         1
                      FSYLAVIEGAK            +2         599.33     1196.65    1196.64    0.01       51         1

No.       Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
399.      IPI00373151       N          Y          0.05       2          0          4          0          5
*Des:     PREDICTED: similar to hypothetical protein FLJ40243
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)     4          2          3.57%
                      Seq         Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      GMGGAMDLVSSSK          +2         620.86     1239.71    1238.56    1.15       65         2
                      GGHVNLTMLGAMQVSK                  +3         548.29     1641.83    1641.83    0          55         1
                      DLTAVSNNAGVDNFGLGLLLR  +3         720.39     2158.15    2158.14    0.01       62         1
                      AAGTTVVEVEEIVDIGSFAPEDIHIPK                  +3         946.16     2835.47    2835.45    0.02       50         1
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No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
400.	IPI00231331		Y	Y	0.72	1	4	2	4	2		
*Des:	Dual specificity mitogen-activated protein kinase kinase 2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	1	18.38%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ISELGAGNGGVVTK		+2	2.848	0.452	0.9901	1				
		KLEELDLDEQQR		+2	3.670	0.330	0.9989	1				
		PAMAIFELLDYIVNEPPPK			+3	3.905	0.524	0.9991	1			
		LQGTHYSVQSDIWSMGLSLVELAIGR				+3	4.223	0.387	0.9994	1		
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	9.8%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		KLEELDLDEQQR		+2	758.39	1514.76	1514.76	0	63	1		
		LQGTHYSVQSDIWSMGLSLVELAIGR				+3	954.17	2859.48	2859.46	0.02	62	1

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
401.	IPI00207202		Y	Y	0.23	1	2	2	2	4		
*Des:	Dynein light intermediate chain 2, cytosolic											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	8.49%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		NNAASEGVLASFFNSLLSK			+2	5.532	0.588	1.0000	1			
		ETLVIFVADMSRPWTIMESLQK			+3	4.162	0.526	0.9999	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	8.49%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NNAASEGVLASFFNSLLSK			+2	985.01	1968.01	1968.00	0.01	78	2	
		ETLVIFVADMSRPWTIMESLQK			+3	865.45	2593.33	2593.33	0	46	2	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
402.	IPI00194404		Y	N	0.43	1	3	0	6	0		
*Des:	Nucleoside diphosphate kinase A											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	34.19%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VMLGETNPADSKPGTIR			+2	4.187	0.641	0.9986	6			
		NIIHGSDSVESAEK		+3	2.363	0.604	0.9988	2				
		YMHSGPVVAMVWEGLNVVK			+2	4.888	0.667	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
403.	IPI00364262		N	Y	0.38	1	0	5	0	6		
*Des:	PREDICTED: similar to Glycyl-tRNA synthetase											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					5	1	8.9%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GEFTIETEGK		+2	555.77	1109.53	1109.52	0.01	45	1		
		AEVSELPSVVR		+2	593.33	1184.64	1184.64	0	46	3		
		TVNVVQFEPNK		+2	637.84	1273.67	1273.67	0	50	1		
		LPFAAAQIGNSFR		+2	696.38	1390.74	1390.74	0	50	3		
		LGDAVEQGVINNSVLGYFIGR			+3	741.06	2220.15	2220.15	0	43	2	

Identified Human Platelet Proteins

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
404.	IPI00231264	Y	Y	0.98	1	5	7	5	16

*Des: Serum paraoxonase/arylesterase 1

SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 23.88%

Seq	Charge	Xcor	Delta	Probility	PepHits
IFFYDSENPPGSEVLR	+2	5.394	0.456	1.0000	1
YVYIAELLAHK	+2	3.104	0.445	0.9996	2
VVADGFDFANGIGISLDGK	+2	4.516	0.573	1.0000	1
LLGLTLVGLVLALYKNHR	+3	4.545	0.563	1.0000	3
AKLLGLTLVGLVLALYK	+3	4.280	0.421	0.9972	1

MASCOT:(PepMatched Observed.Hits Coverage) 7 1 26.94%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
IQSILSEDPK	+2	565.31	1128.60	1128.60	0	53	2
YVYIAELLAHK	+2	660.37	1318.74	1318.73	0.01	50	4
IFFYDSENPPGSEVLR	+2	935.46	1868.91	1868.89	0.02	91	2
VVADGFDFANGIGISLDGK	+2	947.99	1893.96	1893.95	0.01	59	2
LLGLTLVGLVLALYK	+2	793.52	1585.03	1585.02	0.01	92	6
AKLLGLTLVGLVLALYK	+3	595.72	1784.15	1784.15	0	50	2
LLGLTLVGLVLALYKNHR	+3	665.09	1992.23	1992.22	0.01	50	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
405.	IPI00370752	Y	Y	1.1	1	5	5	10	11

*Des: PREDICTED: similar to Nit protein 2

SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 22.04%

Seq	Charge	Xcor	Delta	Probility	PepHits
AVDNQVYVATASPAR	+2	4.572	0.559	1.0000	4
FAELAQIYAR	+2	3.096	0.287	0.9967	1
KIHLFDIDVPGK	+3	4.103	0.442	1.0000	1
AGTEETILYSDIDLK	+2	4.656	0.459	1.0000	1
LALIQLQVSSIK	+2	3.704	0.422	0.9999	9

MASCOT:(PepMatched Observed.Hits Coverage) 5 2 22.04%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
AVDNQVYVATASPAR	+2	781.41	1560.80	1560.79	0.01	76	3
FAELAQIYAR	+2	591.32	1180.63	1180.62	0.01	55	1
KIHLFDIDVPGK	+3	461.27	1380.79	1380.78	0.01	44	1
AGTEETILYSDIDLK	+2	834.43	1666.85	1666.83	0.02	84	1
LALIQLQVSSIK	+2	656.92	1311.82	1311.81	0.01	71	11

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
406.	IPI00231192	N	Y	0.73	1	0	6	0	37

*Des: Hemoglobin beta chain, minor-form

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 6 1 51.67%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VINAFNDGLK	+2	545.8022	1089.5898	1089.5818	0.01	42	4
KVINAFNDGLK	+2	609.8498	1217.6850	1217.6768	0.01	63	6

FGDLSSASAIMGNPQVK +2 861.4402 1720.8659 1720.8454 0.02 64 1
LLVVYPWTQR +2 637.8699 1273.7252 1273.7183 0.01 55 19
GTFAHLSELHCDKLHVDPENFR +3 855.7529 2564.2368 2564.2230 0.01 66 2
VVAGVASALAHK +2 561.8383 1121.6621 1121.6556 0.01 71 12

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
407. IPI00568706 N Y 0.16 1 0 3 0 8
*Des: 69 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 6.33%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
DGTLVSGGGR +2 459.7373 917.4601 917.4566 0 53 4
QITSADTVR +2 495.7660 989.5174 989.5142 0 50 4
SAGFHPSGSVLAVGTVTGR +2 900.4777 1798.9409 1798.9325 0.01 78 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
408. IPI00370681 Y Y 0.67 2 5 3 9 5
*Des: Capping protein (aCtin filament) musCle Z-line, alpha 2
SEQUEST:(PepMatched Observed.Hits Coverage) 5 2 35.73%
Seq Charge Xcor Delta Probility PepHits
DIQDSLTVSNEVQTAK +2 4.092 0.345 0.9990 3
IEGYEDQVLITEHGDLGNGK +3 3.388 0.323 0.9974 2
EGAAHAFAQYNLDQFTPVK +2 5.103 0.639 1.0000 2
IVEAAENEYQTAISENYQTMSDTTFK +3 6.324 0.537 1.0000 1
FIIHAPPGEFNEVFNDVR +3 4.253 0.396 0.9997 3
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 21.99%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
DIQDSLTVSNEVQTAK +2 874.44 1746.87 1746.86 0.01 72 3
EGAAHAFAQYNLDQFTPVK +3 703.01 2106.02 2106.02 0 45 1
IVEAAENEYQTAISENYQTMSDTTFK +3 995.13 2982.36 2982.34 0.02 86 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
409. IPI00193607 Y Y 0.29 1 4 2 11 9
*Des: PREDICTED: similar to triggering receptor expressed on myeloid cells-like 1
SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 15.83%
Seq Charge Xcor Delta Probility PepHits
KPPAPPPEPPLPPK +2 3.627 0.508 0.9999 13
PVTYATVVFPGR +2 3.474 0.538 0.9997 1
LDSPPSFDSIYTDPSLDPPSR +2 4.712 0.550 1.0000 1
IFLTDMGGGLLQVEMVSLQEEDTGK +2 6.103 0.630 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 8.54%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
KPPAPPPEPPLPPK +2 731.43 1460.85 1460.84 0.01 63 12
IFLTDMGGGLLQVEMVSLQEEDTGK +3 904.12 2709.33 2709.32 0.01 51 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
410. IPI00363395 Y Y 2.3 5 2 8 4 44

*Des:	Ras-related protein Rap-1b											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	12.23%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VKDTDDVPMILVGNK			+2	4.719	0.498	1.0000	4			
		VKDTDDVPMILVGNKCDLEDER				+3	5.214	0.498	1.0000	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					8	13	55.85%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VVGKEQGQNLAR		+2	649.86	1297.71	1297.71	0	48	6		
		EYKLVVLGSGGVGK		+2	703.40	1404.79	1404.80	0	65	4		
		VKDTDDVPMILVGNK			+2	822.44	1642.87	1642.86	0.01	64	3	
		MREYKLVVLGSGGVGK			+2	846.98	1691.94	1691.94	0	114	6	
		SALTVQFVQGIFVEK			+2	833.47	1664.92	1664.91	0.01	66	10	
		SKINVNEIFYDLVR		+2	855.47	1708.92	1708.91	0.01	80	10		
		SALTVQFVQGIFVEKYDPTIEDSYR				+3	969.16	2904.46	2904.45	0.01	73	4
		INVNEIFYDLVRQINRK			+3	712.07	2133.17	2133.17	0	42	2	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
411.	IPI00210071		Y	Y	0.42	4	7	6	17	16		
*Des:	CORO1A protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					7	6	20.46%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ADQCYEDVR		+2	3.005	0.339	0.9976	3				
		VSQTTWDSGFCAVNPK			+2	3.930	0.508	1.0000	3			
		KSDLFQEDLYPPTAGPDPALTAEEWLSGR					+3	6.484	0.654	1.0000	2	
		HVFGQPAKADQCYEDVR			+3	3.402	0.521	1.0000	1			
		RGLEVNKCEIAR		+3	3.494	0.461	1.0000	7				
		HVFGQPAK		+2	2.490	0.426	0.9982	24				
		DAGPLLISLKDGYVPPK			+2	3.823	0.416	0.9971	9			
	MASCOT:(PepMatched Observed.Hits Coverage)					6	5	14.49%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NLNAIVQK		+2	450.2719	898.5292	898.5236	0.01	42	2		
		DGALICTSCR		+2	519.7416	1037.4687	1037.4634	0.01	58	2		
		VSQTTWDSGFCAVNPK			+2	870.4139	1738.8132	1738.7984	0.01	77	3	
		DAGPLLISLK		+2	513.8167	1025.6189	1025.6121	0.01	60	3		
		RGLEVNKCEIAR		+3	463.2560	1386.7460	1386.7401	0.01	53	7		
		DAGPLLISLKDGYVPPK			+2	892.0103	1782.0061	1781.9927	0.01	64	9	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
412.	IPI00564353		N	Y	1.89	1	0	6	0	28		
*Des:	47 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					6	1	20.09%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TLLLQDNTLR		+2	593.84	1185.67	1185.67	0	62	8		
		TLSLAENSLTR		+2	602.83	1203.65	1203.65	0	55	4		
		LAAGMALNSGGLGR			+2	644.35	1286.68	1286.68	0	81	16	
		AVSLEVLDLR		+2	557.83	1113.64	1113.64	0	57	4		

ELPPYTFAGLASLQR +2 831.95 1661.88 1661.88 0 43 8
LPLVVSLDLSGNSLHGSLVER +3 735.75 2204.21 2204.22 0 65 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
413. IPI00339197 N Y 1.08 1 0 9 0 35
*Des: 58 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 9 1 22.87%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
FDEILEASDGIMVAR +2 833.4252 1664.8359 1664.8079 0.03 105 1
EAEAAIYHLQLFEELRR +3 696.7125 2087.1156 2087.0799 0.04 41 3
AEGSDVANAVLDGADCIMLSGETAK +3 813.0612 2436.1618 2436.1148 0.05 41 2
GDLGIEIPAEK +2 571.3184 1140.6223 1140.6026 0.02 38 3
DAVLDAWAEDVDLR +2 794.4008 1586.7870 1586.7576 0.03 107 7
GADYLVTEVENGGSLGSK +2 898.9482 1795.8818 1794.8635 1.02 94 3
RFDEILEASDGIMVAR +2 911.4796 1820.9447 1820.9090 0.04 75 7
FGVEQDVDMVFASFIR +2 930.4693 1858.9240 1858.8923 0.03 124 7
EAEAAIYHLQLFEELR +2 966.5156 1931.0166 1930.9788 0.04 91 5

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
414. IPI00421806 N Y 0.02 1 0 2 0 3
*Des: Type I keratin KA10
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 3.92%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LENEIQTYR +2 583.2969 1164.5793 1164.5775 0 44 1
LKYENEVALR +2 617.8419 1233.6692 1233.6717 0 47 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
415. IPI00389749 N Y 0.11 3 0 5 0 13
*Des: Splice Isoform IIAA of Dynamin-2
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 5 3 9.83%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
QEIEAETDR +2 545.7634 1089.5122 1089.4938 0.02 39 2
ALLQMVQQFGVDFEK +2 876.9711 1751.9276 1751.8916 0.04 94 4
IEGSGDQVDTLELSGGAR +2 902.4549 1802.8952 1802.8646 0.03 86 2
AGVYPEKDQAENEDGAQENTFSMDPQLER +3 1090.1699 3267.4879 3267.4261 0.06 48 1
LDLMDEGTDAR +2 618.2918 1234.5691 1234.5499 0.02 66 5

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
416. IPI00324633 Y Y 0.22 2 4 4 6 12
*Des: Glutamate dehydrogenase 1, mitochondrial precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 4 2 12.5%
Seq Charge Xcor Delta Probility PepHits
IIAEGANGPTTPEADKIFLER +3 4.041 0.569 1.0000 1
GFIGPGIDVPAPDMSTGER +2 4.764 0.572 1.0000 2

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                        GVFHGIENFINEASYMSILGMTPGLGDK            +3          3.326       0.411       0.9990      1
                        IIAEGANGPTTPEADK                        +2          4.877       0.541       1.0000      2
            MASCOT:(PepMatched Observed.Hits Coverage)          4           2           9.5%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        YSTDVSVDEVK             +2          621.30      1240.59     1240.58     0.01        41          4
                        IIAEGANGPTTPEADK                    +2          792.40      1582.78     1582.78     0           73          4
                        IIAEGANGPTTPEADKIFLER               +3          748.07      2241.18     2241.16     0.02        64          2
                        GFIGPGIDVPAPDMSTGER                 +2          958.46      1914.91     1914.91     0           72          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
417.        IPI00324561             Y           Y           0.27        3           5           8           9           30
*Des:       Tyrosine-protein phosphatase, non-receptor type 11
            SEQUEST:(PepMatched Observed.Hits Coverage)         5           3           12.27%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        SGMVQTEAQYR             +2          3.118       0.422       0.9991      3
                        QGFWEEFETLQQQECK                    +2          4.150       0.617       1.0000      1
                        GVDGSFLARPSK            +2          2.863       0.433       0.9985      4
                        FIYMAVQHYIETLQR         +2          4.805       0.417       1.0000      4
                        KNPMVETLGTVLQLK                     +2          4.122       0.332       0.9986      2
            MASCOT:(PepMatched Observed.Hits Coverage)          8           5           15.58%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        SGMVQTEAQYR             +2          635.3027    1268.5908   1268.5819   0.01        53          8
                        INAAEIESR               +2          501.7675    1001.5204   1001.5141   0.01        50          4
                        NGAVTHIK                +2          420.2433    838.4720    838.4661    0.01        46          6
                        VTHVMIR     +2          428.1931    854.3716    854.4796    -0.1        44          4
                        GVDGSFLARPSK            +2          617.3375    1232.6604   1232.6513   0.01        61          4
                        FIYMAVQHYIETLQR         +2          956.4997    1910.9848   1910.9712   0.01        95          6
                        KNPMVETLGTVLQLK                     +2          835.9850    1669.9555   1669.9436   0.01        61          4
                        WFHGHLSGK               +2          534.7769    1067.5393   1067.5301   0.01        42          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
418.        IPI00368550             N           Y           0.07        1           0           3           0           5
*Des:       PREDICTED: complement component 5
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)          3           1           4.42%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        VTYSSGYVNLSPENK                     +2          829.41      1656.81     1656.80     0.01        69          2
                        DENPVSHVYLEVVSMHFSK                 +3          739.69      2216.06     2216.06     0           50          2
                        SITHSADGVASFVVNLPSEVTSLK                        +3          820.10      2457.28     2457.28     0           43          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
419.        IPI00198620             Y           Y           5.07        2           3           2           5           5
*Des:       ATP synthase delta chain, mitochondrial precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)         3           1           17.54%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        AEIQIRIEANEALVK         +3          3.726       0.439       0.9944      3
                        AQSELSGAADEAARAEIQIRIEANEALVK           +3          4.078       0.630       0.9995      1
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                    AQSELSGAADEAAR+2        4.117       0.668       1.0000      1
          MASCOT:(PepMatched Observed.Hits Coverage)    2           1           14.61%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                    AQSELSGAADEAAR+2        688.3344    1374.6543 1374.6375 0.02        69          1
                    IEANEALVK   +2          493.7853    985.5561    985.5444    0.01        56          6

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
420.      IPI00390070           Y           N           0.1         1           2           0           3           0
*Des:     81 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)   2           1           3.76%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    IDIIPNPQER  +2          3.055       0.329       0.9977      2
                    NPDDITQEEYGEFYK         +2          4.986       0.527       1.0000      3
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
421.      IPI00199425           N           Y           0.3         2           0           4           0           69
*Des:     61 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)    4           2           8.68%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                    LVINSGNGTVEDR +2        687.85      1373.69     1372.69     1           56          12
                    EPTETPDQFMTADETR        +2          934.41      1866.80     1866.79     0.01        60          18
                    GFETCRYGFIEGHVVIPR      +3          693.88      2078.63     2079.04     -0.4        48          9
                    YGFIEGHVVIPR +2         693.88      1385.75     1385.75     0           64          30

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
422.      IPI00331856           Y           Y           0.28        1           3           4           11          11
*Des:     Carbonyl reductase [NADPH] 1
          SEQUEST:(PepMatched Observed.Hits Coverage)   3           2           18.14%
                    Seq         Charge      Xcor        Delta       Probility   PepHits
                    VVNVSSSVSLR +2          2.784       0.257       0.9727      2
                    SETITEEELVGLMNK+2       4.087       0.389       0.9991      1
                    DFLLQEYGGLNVLVNNAGIAFK              +3          4.311       0.432       0.9997      1
          MASCOT:(PepMatched Observed.Hits Coverage)    4           1           17.43%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                    EGWPNSAYGVTK +2         654.82      1307.62     1307.61     0.01        41          4
                    IGVTVLSR    +2          422.77      843.52      843.52      0           42          3
                    FLGDVVLTAR  +2          545.82      1089.62     1089.62     0           53          3
                    SETITEEELVGLMNK+2       846.92      1691.83     1691.83     0           92          3

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
423.      IPI00560148           N           Y           0.06        1           0           2           0           2
*Des:     PREDICTED: similar to Testis derived transcript
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)    2           1           3.14%
                    Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
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                      EKQPVAGSEGAQYR              +3          507.2584    1518.7534 1518.7426 0.01        46          1
                      NVMILTNPVAAK      +2        635.8687    1269.7229 1269.7114 0.01        46          1

No.         Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
424.        IPI00359734         Y         Y         0.64      1           7           7           29          40
*Des:       PREDICTED: similar to predominantly fetal expressed T1 domain
            SEQUEST:(PepMatched Observed.Hits Coverage)  7           2           27.32%
                      Seq       Charge    Xcor      Delta     Probility   PepHits
                      MFTQQQPQELAR      +2        4.730     0.506       1.0000      7
                      SPSGGAAGPLLTPSQSLDGSR +2              5.552       0.663       1.0000      2
                      SGYITIGYR         +2        3.354     0.521       1.0000      2
                      YILDYLR  +2       2.901     0.253     0.9958      3
                      EAEYFELPELVR      +2        4.286     0.474       1.0000      13
                      FNFLEQAFDK        +2        2.481     0.332       0.9914      13
                      DLQLVLPDYFPER     +2        3.397     0.304       0.9967      5
            MASCOT:(PepMatched Observed.Hits Coverage)   7           1           28.52%
                      Seq       Charge    ObservedMS          ExpectedMS              CalculatedMS                        Pepscore PepHits
                      MFTQQQPQELAR      +2        738.87      1475.73     1475.72     0.01        91          7
                      EVFGDTLNESR       +2        633.81      1265.60     1265.59     0.01        61          16
                      SGYITIGYR         +2        515.28      1028.54     1028.53     0.01        68          3
                      SPSGGAAGPLLTPSQSLDGSR +2              978.01      1954.00     1953.98     0.02        116         2
                      FNFLEQAFDK        +2        629.81      1257.61     1257.60     0.01        77          14
                      EAEYFELPELVR      +2        747.88      1493.75     1493.74     0.01        70          13
                      DLQLVLPDYFPER     +2        802.93      1603.84     1603.82     0.02        55          3

No.         Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
425.        IPI00215302         Y         Y         0.72      2           2           2           3           3
*Des:       Metalloproteinase inhibitor 3 precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)  2           1           14.41%
                      Seq       Charge    Xcor      Delta     Probility   PepHits
                      GWAPPDKSISNATD +2             3.507     0.535       0.9599      1
                      EGPFGTLVYTIKQMK               +2        3.975       0.599       0.9936      3
            MASCOT:(PepMatched Observed.Hits Coverage)   2           2           14.88%
                      Seq       Charge    ObservedMS          ExpectedMS              CalculatedMS                        Pepscore PepHits
                      GWAPPDKSISNATDP               +2          778.37      1554.73     1554.73     0           48          1
                      EGPFGTLVYTIKQMK               +2          856.46      1710.91     1710.90     0.01        59          2

No.         Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
426.        IPI00400615         Y         Y         1.09      1           4           3           5           4
*Des:       ATPase, H+ transporting, V1 subunit E isoform 1
            SEQUEST:(PepMatched Observed.Hits Coverage)  4           1           26.95%
                      Seq       Charge    Xcor      Delta     Probility   PepHits
                      IQMSNLMNQAR       +2        2.860     0.330       0.9919      1
                      LDLIAQQMMPEVR     +2        2.796     0.446       0.9976      1
                      ARDDLITDLLNEAK    +2        3.817     0.394       0.9858      2
                      YQVLLDGLVLQGLYQLLEPR          +2        4.559       0.383       0.9994      2
            MASCOT:(PepMatched Observed.Hits Coverage)   3           1           17.82%
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		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IQMSNLMNQAR		+2	653.32	1304.63	1304.63	0	50	1		
		LDLIAQQMMPEVR		+2	772.41	1542.80	1542.79	0.01	52	1		
		ARDDLITDLLNEAK		+2	793.93	1585.84	1585.83	0.01	72	2		

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
427.	IPI00464786		Y	N	0.27	1	2	0	2	0		
*Des:	Caspase 6											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	8.15%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		FFWHLALPER		+3	3.305	0.331	0.9978	2				
		IEIQTLTGLFK		+2	3.599	0.490	0.9998	3				
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
428.	IPI00365216		Y	Y	0.38	1	2	2	5	4		
*Des:	30 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	11.61%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GPDSALLPSTPGPR		+2	3.104	0.391	0.9966	2				
		VFNAGDDPSVPLHVLSR			+2	5.667	0.554	1.0000	4			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	11.61%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GPDSALLPSTPGPR		+2	682.86	1363.71	1363.71	0	55	2		
		VFNAGDDPSVPLHVLSR			+2	911.98	1821.95	1821.94	0.01	87	4	

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
429.	IPI00365217		N	Y	0.24	1	0	2	0	5		
*Des:	PREDICTED: similar to RIKEN cDNA 0610011D08											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	11.68%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		EMDQTMAANAQK		+2	669.3000	1336.5854	1336.5751	0.01	75	4		
		IVPVEITISLLKR		+2	740.9792	1479.9439	1479.9388	0.01	49	2		

No.	Protein	Matched	(SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)		
430.	IPI00214430		Y	Y	0.8	3	7	4	16	7		
*Des:	CGMP-binding cGMP specific phosphodiesterase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					7	8	33.19%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DSEGTVSFLSDSGKK			+2	3.405	0.362	0.9982	2			
		DSEGTVSFLSDSGK		+2	3.950	0.508	0.9999	2				
		AGPSSVQSQQQR		+2	3.054	0.360	0.9978	1				
		GIVGHVAAFGEPLNIK			+2	4.299	0.536	1.0000	4			
		DMVNAWFSER		+2	3.048	0.603	1.0000	1				
		DQDWVEAWLDDHR		+3	3.239	0.405	0.9997	2				
		DQDWVEAWLDDHRDFTFSYFVR				+3	4.263	0.528	1.0000	2		

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          MASCOT:(PepMatched Observed.Hits Coverage)   4          3          21.16%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                      Pepscore   PepHits
                    AGPSSVQSQQQR +2       636.8293   1271.6441  1271.6218  0.02       46         2
                    DSEGTVSFLSDSGK +2     714.8395   1427.6644  1427.6416  0.02       70         3
                    DQDWVEAWLDDHR +2      842.8869   1683.7593  1683.7277  0.03       55         1
                    DQDWVEAWLDDHRDFTFSYFVR           +3         949.7815   2846.3227  2846.2724  0.05       46         2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
431.      IPI00209828          Y          Y          2.29       4          9          3          19         18
*Des:     Myosin regulatory light chain 2, smooth muscle isoform
          SEQUEST:(PepMatched Observed.Hits Coverage)  9          5          57.22%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    LNGTDPEDVIR           +2         3.305      0.633      0.9980     10
                    EAFNMIDQNR            +2         2.823      0.682      0.9979     2
                    FTDEEVDEMYR           +2         3.472      0.797      1.0000     1
                    KGNFNYVEFTR           +2         3.563      0.682      1.0000     3
                    EAPIDKKGNFNYVEFTR                +3         3.198      0.499      0.9954     4
                    ELLTTMGDRFTDEEVDEMYR             +3         4.798      0.744      1.0000     2
                    DGFIDKEDLHDMLASLGK               +2         5.488      0.659      1.0000     3
                    ATSNVFAMFDQSQIQEFK               +2         5.735      0.739      1.0000     1
                    ATSNVFAMFDQSQIQEFKEAFNMIDQNR                +3         5.730      0.749      1.0000     3
          MASCOT:(PepMatched Observed.Hits Coverage)   3          5          19.07%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                      Pepscore   PepHits
                    LNGTDPEDVIR           +2         615.3099   1228.6053  1227.6095  1          54         2
                    ELLTTMGDR             +2         518.2649   1034.5152  1034.5066  0.01       49         12
                    EAFNMIDQNR            +2         619.2900   1236.5655  1236.5557  0.01       60         5

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
432.      IPI00371634          Y          N          0.23       1          2          0          3          0
*Des:     B-cell receptor-associated protein 31
          SEQUEST:(PepMatched Observed.Hits Coverage)  2          1          11.6%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    GTAEDGGKLDVGSPEMK                +3         3.604      0.383      0.9989     1
                    AENEALAMQK            +2         3.991      0.416      0.9996     2
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
433.      IPI00207070          Y          Y          1.37       1          3          3          5          5
*Des:     GTP-binding protein Rheb
          SEQUEST:(PepMatched Observed.Hits Coverage)  3          1          33.51%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    RIILEAEKIDGAASQGK                +2         4.737      0.706      1.0000     4
                    LLDMVGKVQIPIMLVGNKK              +3         4.107      0.732      1.0000     1
                    VISYEEGKALAESWNAAFLESSAK                    +3         3.433      0.589      0.9987     1
          MASCOT:(PepMatched Observed.Hits Coverage)   3          1          26.06%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                      Pepscore   PepHits
                    RIILEAEKIDGAASQGK                +2         900.01     1798.00    1797.99    0.01       68         3
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Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
ENQTAVDVFR	+2	589.79	1177.57	1177.57	0	41	2
LLDMVGKVQIPIMLVGNKK	+3	699.42	2095.23	2095.23	0	48	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
434.	IPI00207217	Y	Y	0.72	1	2	4	10	6

*Des: Enoyl-CoA hydratase, mitochondrial precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 12.2%

Seq	Charge	Xcor	Delta	Probility	PepHits
NSSVGLIQLNRPK	+2	3.032	0.392	0.9989	3
AQFGQPEILLGTIPGAGGTQR	+2	5.620	0.551	1.0000	10

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 20%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EGMSAFVEK	+2	499.24	996.46	996.46	0	45	3
NSSVGLIQLNRPK	+2	713.42	1424.82	1424.81	0.01	54	3
SLAMEMVLTGDR	+2	661.83	1321.65	1321.64	0.01	51	2
AQFGQPEILLGTIPGAGGTQR	+3	704.38	2110.13	2110.12	0.01	52	7

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
435.	IPI00214434	N	Y	0.67	2	0	4	0	16

*Des: Ras-related protein Rab-11A

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 4 2 22.27%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VVLIGDSGVGK	+2	522.3424	1042.6702	1042.6022	0.07	53	1
STIGVEFATR	+2	540.8239	1079.6332	1079.5611	0.07	56	3
AQIWDTAGQER	+2	637.8571	1273.6996	1273.6051	0.09	44	2
GAVGALLVYDIAK	+2	645.4185	1288.8224	1288.7390	0.08	43	3

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
436.	IPI00207146	Y	N	0.34	2	4	0	17	0

*Des: Zero beta-1 globin

SEQUEST:(PepMatched Observed.Hits Coverage) 4 2 22%

Seq	Charge	Xcor	Delta	Probility	PepHits
FGDLSSVSAIMGNPQVK	+2	3.059	0.485	0.9992	1
VVAGVASALAHK	+2	3.758	0.538	1.0000	7
VVAGVASALAHKY	+2	3.709	0.573	1.0000	12
VVAGVASALAHKYH	+2	3.868	0.565	1.0000	16

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
437.	IPI00363619	N	Y	0.55	1	0	2	0	3

*Des: PREDICTED: similar to clathrin-associated protein 19 - mouse

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 16.77%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
AIEQADLLQEEDESPR	+2	921.95	1841.88	1841.86	0.02	93	1
ELMQVVLAR	+2	529.81	1057.60	1057.60	0	49	3

Identified Human Platelet Proteins

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
438.	IPI00363547	Y	Y	0.15	3	5	4	6	6

*Des: PREDICTED: similar to Formin homology 2 domain containing 1

SEQUEST:(PepMatched Observed.Hits Coverage) 5 3 6.05%

Seq	Charge	Xcor	Delta	Probility	PepHits
GDGDPVSVVTVR	+2	3.082	0.329	0.9953	1
FLENVAAAETEK	+2	3.752	0.370	0.9992	2
TQLTLYESALR	+2	2.713	0.384	0.9665	1
AALLNFDEFAVSK	+2	4.095	0.591	1.0000	2
SGLGDDLVQALGLSK	+2	4.321	0.548	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 4 4 4.54%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
FLENVAAAETEK	+2	661.34	1320.66	1320.66	0	78	2
LQLWAFK	+2	453.27	904.52	904.52	0	49	1
AALLNFDEFAVSK	+2	712.88	1423.75	1423.73	0.02	71	2
SGLGDDLVQALGLSK	+2	736.91	1471.80	1471.79	0.01	110	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
439.	IPI00607179	N	Y	3.5	2	0	3	0	36

*Des: Platelet glycoprotein Ib beta

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 3 2 11.42%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VHLGANPWR	+2	525.3197	1048.6248	1048.5566	0.07	42	8
LLPYVAEDELR	+2	659.4041	1316.7936	1316.6976	0.1	52	52
GRLLPYVAEDELR	+2	765.9707	1529.9268	1529.8201	0.11	61	6

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
440.	IPI00361871	Y	Y	0.13	1	2	3	2	6

*Des: PREDICTED: similar to Smoothelin

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 2.6%

Seq	Charge	Xcor	Delta	Probility	PepHits
SNMATTETTTR	+2	3.527	0.398	0.9994	3
LVHSNDGTQTAR	+2	3.159	0.573	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 3.53%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SNMATTETTTR	+2	606.7838	1211.5530	1211.5452	0.01	53	3
SLSVLSPR	+2	429.7426	857.4706	857.4970	-0.02	42	1
LVHSNDGTQTAR	+2	649.8323	1297.6501	1297.6375	0.01	51	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
441.	IPI00389750	N	Y	0.26	1	0	7	0	23

*Des: Splice Isoform IIBA of Dynamin-2

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 7 1 10.43%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits

		TIMHLMINNTK		+2	658.35	1314.68	1314.68	0	44	2		
		VPVGDQPPDIEYQIK		+2	849.44	1696.87	1696.87	0	67	4		
		IEGSGDQVDTLELSGGAR			+2	902.45	1802.88	1802.86	0.02	83	1	
		FFLSHPAYR		+2	569.30	1136.58	1136.58	0	42	8		
		LDLMDEGTDAR		+2	618.28	1234.55	1234.55	0	53	12		
		GWLTINNISLMK		+2	695.38	1388.75	1388.75	0	49	3		
		DMILQFISR		+2	561.80	1121.59	1121.59	0	49	8		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
442.	IPI00200601		N	Y	0.3	1	0	2	0	3		
*Des:	Thioredoxin-related protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	13.26%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IDQYQGADAVGLEEK			+2	818.40	1634.79	1634.78	0.01	81	2	
		VGVKPVGSDPDFQPELSGAGSR				+3	733.71	2198.10	2198.10	0	53	1
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
443.	IPI00210224		Y	Y	0.14	4	18	23	64	90		
*Des:	PREDICTED: von Willebrand factor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					18	6	7.45%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ILVGNEGCTYPSVK		+2	3.951	0.508	1.0000	4				
		YVGSQLASTSEVLK		+2	3.966	0.561	1.0000	5				
		LSEAEFEVLK		+2	3.661	0.412	0.9997	5				
		AFLLSGVDELEQR		+2	4.587	0.520	1.0000	5				
		VEDAVFVQQR		+2	3.043	0.430	0.9992	1				
		LSYGEDLQMEWDGR			+2	3.460	0.399	0.9988	1			
		LLDLVFLLDGSYR		+2	4.071	0.494	1.0000	5				
		VAVFPIGVGDRYDEAQLR			+3	2.582	0.502	0.9999	2			
		LVCPADNPR		+2	2.619	0.451	0.9988	5				
		HAGLSVELR		+2	2.975	0.443	0.9994	6				
		HIVTFDGQNFK		+2	3.397	0.483	0.9998	4				
		VILLLTASQEPQR		+3	3.458	0.465	1.0000	8				
		ILAGPGASSNVVK		+2	3.948	0.527	1.0000	24				
		ANIGPHLTQVSVIQYGSINTIDVPWNVAQEK					+3	5.927	0.639	1.0000	5	
		LQQVEDLLTMVTPGNSFFHR			+2	4.700	0.531	1.0000	5			
		LSALHNSLMK		+2	3.304	0.423	0.9995	7				
		YVTSQIHGARPGASK			+2	4.255	0.573	1.0000	14			
		KLSLDVSLAACHNNIMK			+3	3.680	0.450	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					23	9	8.33%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VSPQCADTR		+2	488.7328	975.4510	975.4444	0.01	52	6		
		QTMVDSSCR		+2	513.7238	1025.4331	1025.4270	0.01	54	8		
		DGTVTTDWKR		+2	589.7975	1177.5804	1177.5727	0.01	55	6		
		ANLQELER		+2	486.7618	971.5090	971.5036	0.01	48	3		
		VEDAVFVQQR		+2	595.8202	1189.6258	1189.6091	0.02	52	2		

LSEAEFEVLK	+2	582.8140	1163.6135	1163.6073	0.01	71	6
LSYGEDLQMEWDGR	+2	849.8787	1697.7428	1697.7355	0.01	49	2
AFLLSGVDELEQR	+2	738.8941	1475.7737	1475.7619	0.01	85	8
LVCPADNPR	+2	492.7535	983.4925	983.4858	0.01	44	3
AFVVGTMER	+2	505.2633	1008.5120	1008.5062	0.01	45	1
ILVGNEGCTYPSVK	+2	740.3849	1478.7553	1478.7439	0.01	88	4
YVGSQLASTSEVLK	+2	741.4030	1480.7914	1480.7773	0.01	89	3
LLDLVFLLDGSYR	+2	762.4340	1522.8534	1522.8395	0.01	74	5
HIVTFDGQNFK	+2	653.3375	1304.6605	1304.6513	0.01	50	3
VILLLTASQEPQR	+2	734.4352	1466.8558	1466.8456	0.01	82	7
HAGLSVELR	+2	491.2803	980.5461	980.5403	0.01	67	7
ANIGPHLTQVSVIQYGSINTIDVPWNVAQEK	+3	1131.2720	3390.7941	3390.7571	0.04	99	5
LQQVEDLLTMVTPGNSFFHR	+2	1166.5995	2331.1844	2331.1681	0.02	121	5
IQHTVMASVR	+2	571.3148	1140.6151	1140.6073	0.01	51	1
ILAGPGASSNVVK	+2	606.8542	1211.6938	1211.6873	0.01	86	20
LSALHNSLMK	+2	557.3112	1112.6079	1112.6012	0.01	60	4
LHISQKR	+2	441.2723	880.5301	880.5243	0.01	41	3
YVTSQIHGARPGASK	+2	786.4245	1570.8344	1570.8215	0.01	80	13

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
444.	IPI00211891	Y	N	0.2	1	2	0	2	0

*Des: PREDICTED: similar to SH2/SH3 adaptor protein

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 10.33%

Seq	Charge	Xcor	Delta	Probility	PepHits
FAYVAEREDELSLVK	+3	2.857	0.443	0.9921	3
VLHVVQTLYPFSSVTEEELSFEK	+3	4.504	0.529	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
445.	IPI00388015	Y	Y	0.27	2	3	3	9	9

*Des: PREDICTED: similar to Coronin, actin binding protein 1C

SEQUEST:(PepMatched Observed.Hits Coverage) 3 3 9.76%

Seq	Charge	Xcor	Delta	Probility	PepHits
ISKLEQQLAK	+2	3.428	0.315	0.9966	9
KSDLFQDDLYPDTAGPEAALEAEEWFEGK	+3	5.997	0.519	1.0000	2
FVAIIIEASGGGAFLVLPLHK	+3	3.957	0.454	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 3 3 9.76%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
ISKLEQQLAK	+2	579.3560	1156.6974	1156.6815	0.02	50	7
FVAIIIEASGGGAFLVLPLHK	+3	718.1025	2151.2856	2151.2455	0.04	52	1
KSDLFQDDLYPDTAGPEAALEAEEWFEGK	+3	1091.1924	3270.5553	3270.4880	0.07	76	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
446.	IPI00204748	N	Y	0.64	1	0	3	0	6

*Des: S100 calcium-binding protein A4

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 22.33%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
LNKTELK	+2	423.2609	844.5072	844.5018	0.01	42	2			
RTDEAAFQK		+2	533.2725	1064.5304	1064.5250	0.01	41	1		
LNKTELKELLTR		+2	729.4365	1456.8584	1456.8613	0	52	6		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)
447.	IPI00212767		N	Y	2.42	1	0	2	0	4

*Des: Anionic trypsin I precursor

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 2 9.96%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
LGEHNINVLEGDEQFINAAK			+3	737.71	2210.11	2210.10	0.01	74	4	
IQVRLGEHNINVLEGDEQFINAAK				+3	903.52	2707.55	2706.41	1.14	43	1

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)
448.	IPI00201333		Y	Y	0.13	2	3	2	3	4

*Des: PREDICTED: similar to alpha glucosidase II, alpha subunit

SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 4.67%

Seq	Charge	Xcor	Delta	Probility	PepHits		
KPGVNVASDWSIHL	+3		4.050	0.525	1.0000	1	
LSFQHDPETSVLTLR			+3	4.228	0.412	0.9999	1
FPQPLNMLEHLASK	+3		4.342	0.277	0.9992	1	

MASCOT:(PepMatched Observed.Hits Coverage) 2 2 3.15%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
VLLVLELQGLQK		+2	676.9344	1351.8542	1351.8438	0.01	50	2		
VVIMGAGKPAAVVLQTK			+2	841.5132	1681.0119	1680.9960	0.02	80	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)
449.	IPI00201262		Y	Y	0.24	3	18	14	29	100

*Des: Alpha-1-inhibitor III precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 18 5 20.7%

Seq	Charge	Xcor	Delta	Probility	PepHits			
PASNMVIADVK		+2	3.475	0.500	0.9990	2		
ESVVFVQTDKPMYKPGQSVK			+3	3.800	0.484	1.0000	3	
VHLSFSPSQSLPASQTHMR			+3	3.534	0.458	0.9999	3	
LPSSEEEESLDINIEGAK			+2	6.672	0.607	1.0000	2	
KLFDELVVDK		+2	2.840	0.242	0.9731	2		
GMYESLPVVAVK		+2	2.944	0.335	0.9943	2		
MLSGFIPLKPTVK		+2	3.504	0.335	0.9969	1		
FSIDTNGISDYSLNIK		+2	5.202	0.345	0.9997	2		
YMVLVPSQLYTETPEK			+2	4.601	0.642	1.0000	1	
QQNSYGGFSSTQDTVVALDALSK				+2	4.686	0.659	1.0000	1
LTAQPAPSPEDLALSMGTIK			+2	4.255	0.565	1.0000	3	
MLIYTILPDGEVIADSVK			+2	5.131	0.489	1.0000	3	
AHFSVMGDILSSAIK		+2	4.305	0.563	1.0000	2		
EEHSFTVMEFVLPR		+2	4.099	0.574	1.0000	4		
NLHPLNELFPLAYIEDPK			+2	4.912	0.610	1.0000	2	

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                    AFIFIDESHITDAFTWLSK       +2        4.880     0.607     1.0000    2
                    TPSVTVQSSGSFSQK           +2        4.380     0.504     0.9999    1
                    HAEAHHTAYAVYSLSK          +3        3.996     0.565     1.0000    1
          MASCOT:(PepMatched Observed.Hits Coverage)    14        4         15.37%
                    Seq       Charge    ObservedMS      ExpectedMS          CalculatedMS                  Pepscore PepHits
                    TPSVTVQSSGSFSQK           +2        770.39    1538.77   1538.76   0.01      80        4
                    GMYESLPVVAVK    +2        646.85    1291.69   1291.68   0.01      43        2
                    VHLSFSPSQSLPASQTHMR       +3        704.03    2109.06   2109.04   0.02      45        5
                    ESVVFVQTDKPMYKPGQSVK +3             756.40    2266.18   2266.17   0.01      46        4
                    LPSSEEEESLDINIEGAK        +2        980.48    1958.95   1958.93   0.02      112       6
                    FSIDTNGISDYSLNIK+2        893.95    1785.89   1785.88   0.01      111       2
                    LTAQPAPSPEDLALSMGTIK      +3        680.70    2039.07   2039.06   0.01      45        5
                    YMVLVPSQLYTETPEK          +2        949.48    1896.95   1896.95   0         86        9
                    MLSGFIPLKPTVK   +2        715.93    1429.84   1429.84   0         44        7
                    AHFSVMGDILSSAIK +2        788.42    1574.82   1574.81   0.01      85        18
                    EEHSFTVMEFVLPR  +2        860.93    1719.84   1719.83   0.01      71        32
                    MLIYTILPDGEVIADSVK        +2        989.04    1976.06   1976.05   0.01      82        24
                    ETGLMAFTNLK     +2        612.82    1223.62   1223.62   0         44        1
                    KLFDELVVDK      +2        603.34    1204.67   1204.67   0         68        6

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
450.      IPI00202139         Y         Y         0.41      1         3         3         5         6
*Des:     Copper chaperone for superoxide dismutase
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         1         17.56%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    SLVVDEGEDDLGR   +2        4.026     0.589     1.0000    4
                    NLGAAVAIMEGSGTVQGVVR      +2        4.066     0.517     0.9998    2
                    GDLGNVHAEASGR   +2        3.429     0.580     0.9999    2
          MASCOT:(PepMatched Observed.Hits Coverage)    3         1         17.56%
                    Seq       Charge    ObservedMS      ExpectedMS          CalculatedMS                  Pepscore PepHits
                    GDLGNVHAEASGR   +2        641.81    1281.61   1281.61   0         71        1
                    SLVVDEGEDDLGR   +2        702.34    1402.66   1402.66   0         74        4
                    NLGAAVAIMEGSGTVQGVVR      +2        965.02    1928.02   1928.01   0.01      78        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
451.      IPI00210158         Y         N         0.3       1         3         0         6         0
*Des:     26S protease regulatory subunit 6B
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         1         14.11%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    LQQELEFLEVQEEYIKDEQK      +3        3.933     0.394     0.9929    1
                    ILLELLNQMDGFDQNVNVK       +2        5.711     0.687     1.0000    1
                    ENAPAIIFIDEIDAIATK        +2        4.875     0.354     0.9998    4
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
452.      IPI00476086         Y         Y         0.93      1         4         4         9         20
*Des:     ATPase, H+ transporting, V0 subunit D isoform 1
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Identified Human Platelet Proteins

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          SEQUEST:(PepMatched Observed.Hits Coverage) 4         1         19.32%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    NVADYYPEYK          +2        2.878     0.404     0.9988    3
                    LLFEGAGSNPGDK       +2        3.933     0.383     0.9995    2
                    LHLQSTDYGNFLANEASPLTVSVIDDK           +3        6.030     0.465     1.0000    1
                    AFIITINSFGTELSK     +2        4.866     0.499     1.0000    5
          MASCOT:(PepMatched Observed.Hits Coverage)  4         1         19.32%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    NVADYYPEYK          +2        631.29    1260.58   1260.57   0.01      50        6
                    LLFEGAGSNPGDK       +2        652.83    1303.65   1303.64   0.01      87        4
                    LHLQSTDYGNFLANEASPLTVSVIDDK           +3        983.17    2946.49   2946.46   0.03      79        2
                    AFIITINSFGTELSK     +2        820.96    1639.90   1639.88   0.02      113       10

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
453.      IPI00197900         Y         N         0.42      2         6         0         21        0
*Des:     29 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage) 6         3         32.06%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    FYEQMNGPVTAGSR                +2        4.943     0.500     1.0000    9
                    IASLEVENQNLR        +2        4.323     0.467     1.0000    5
                    FEEHVQSVDIAAFNK               +2        5.177     0.586     1.0000    3
                    VGTDLLEEEITK        +2        3.424     0.327     0.9981    1
                    GVVQDLQQAISK        +2        3.752     0.467     0.9998    9
                    SIQLDGLVWGASK       +2        4.452     0.572     1.0000    3
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
454.      IPI00200466         Y         Y         0.35      2         6         3         17        32
*Des:     ADP,ATP carrier protein 2
          SEQUEST:(PepMatched Observed.Hits Coverage) 6         4         22.84%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    YFPTQALNFAFK        +2        3.882     0.531     1.0000    9
                    GMGGAFVLVLYDEIKK              +2        4.895     0.486     1.0000    3
                    LLLQVQHASK          +2        2.927     0.390     0.9992    9
                    VKLLLQVQHASK        +2        4.094     0.375     0.9943    5
                    AAYFGIYDTAK         +2        3.987     0.584     1.0000    5
                    DFLAGGVAAAISK       +2        4.923     0.514     0.9569    11
          MASCOT:(PepMatched Observed.Hits Coverage)  3         3         8.6%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    GMGGAFVLVLYDEIK               +2        806.4425  1610.8705 1610.8377 0.03      90        4
                    GMGGAFVLVLYDEIKK              +2        870.4880  1738.9615 1738.9327 0.03      72        4
                    GAWSNVLR            +2        451.7527  901.4909  901.4770  0.01      44        5

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
455.      IPI00382131         N         Y         0.12      1         0         2         0         2
*Des:     Ab1-018
          SEQUEST:(PepMatched Observed.Hits Coverage)
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MASCOT:(PepMatched Observed.Hits Coverage) 2 1 2.6%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
YFQGLMNR +2 514.7798 1027.5450 1027.4909 0.05 56 1
DHGLESLQSTQK +2 671.8796 1341.7446 1341.6524 0.09 36 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
456. IPI00331865 Y Y 0.24 1 3 2 4 10
*Des: Splice Isoform 2 of Drebrin-like protein
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 9.97%
Seq Charge Xcor Delta Probility PepHits
TGELEQEVVSR +2 2.889 0.298 0.9916 1
AMSTTSVSSSQPGK +2 3.127 0.401 0.9980 1
SRQEWESAGQQAPHPR +3 4.747 0.603 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 6.57%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
TGELEQEVVSR +2 623.8169 1245.6192 1245.6200 0 48 8
SRQEWESAGQQAPHPR +3 621.9666 1862.8780 1862.8772 0 48 12

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
457. IPI00358003 Y Y 0.64 1 11 9 17 12
*Des: PREDICTED: similar to 5-nucleotidase, cytosolic III
SEQUEST:(PepMatched Observed.Hits Coverage) 11 4 48.07%
Seq Charge Xcor Delta Probility PepHits
GELIHVFNK +2 2.842 0.308 0.9925 1
SHGLLIEQGIPK +2 2.986 0.441 0.9984 2
NTDYFSQLK +2 2.720 0.360 0.9953 2
MADGVANVEHILK +2 3.547 0.464 0.9995 3
DNSNIILLGDSQGDLR +2 4.337 0.428 0.9996 1
EESLEVVNSILQK +2 4.149 0.449 0.9997 2
EQYYAIEVDPVLTVEEK +2 5.859 0.582 1.0000 2
VVSNFMDFDENGVLK +2 4.552 0.503 0.9999 1
FPYMVEWYTK +2 2.806 0.369 0.9957 1
LQIITDFDMTLSR +2 2.984 0.451 0.9984 1
LQQHGIPVFIFSAGIGDVLEEVIR +2 6.131 0.681 1.0000 4
MASCOT:(PepMatched Observed.Hits Coverage) 9 4 39.76%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
SHGLLIEQGIPK +2 646.37 1290.73 1290.73 0 49 1
NTDYFSQLK +2 558.27 1114.53 1114.53 0 47 2
MADGVANVEHILK +2 698.87 1395.72 1395.72 0 85 3
DNSNIILLGDSQGDLR +2 865.44 1728.87 1728.86 0.01 61 1
FPYMVEWYTK +2 682.33 1362.64 1362.63 0.01 42 1
EESLEVVNSILQK +2 744.40 1486.79 1486.79 0 87 2
LQIITDFDMTLSR +2 776.91 1551.80 1551.80 0 56 3
VVSNFMDFDENGVLK +2 857.41 1712.81 1712.81 0 88 1
LQQHGIPVFIFSAGIGDVLEEVIR +3 879.82 2636.44 2636.43 0.01 50 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

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458.      IPI00382134    Y          Y          0.2        3          2          10         3          113
*Des:     Ac1-581
          SEQUEST:(PepMatched Observed.Hits Coverage)     2          1          6.64%
                         Seq        Charge     Xcor       Delta      Probility  PepHits
                         IQKLESDISAQTEYCHTPCTVNCNIPVVSGK                          +3         7.192      0.651      1.0000     4
                         SKIQKLESDISAQTEYCHTPCTVNCNIPVVSGK                        +3         7.445      0.644      1.0000     2
          MASCOT:(PepMatched Observed.Hits Coverage)      10         6          28.32%
                         Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore   PepHits
                         TENGGWTVIQNR          +2         688.3461   1374.6776  1373.6687  1.01       41         3
                         IGPTELLIEMEDWKGDK     +3         658.6782   1973.0128  1972.9815  0.03       44         3
                         NSIAELNSNINSVSETSSVTFQYLTLLK     +3         1024.8793  3071.6160  3071.5662  0.05       44         1
                         QDGSVDFGR  +2         491.7203   981.4261   979.4359   1.99       40         3
                         DNDGWVTTDPR           +2         637.8853   1273.7561  1274.5527  -0.79      74         9
                         HGTDDGVVWMNWK         +2         772.8647   1543.7149  1543.6878  0.03       96         7
                         YYWGGLYSWDMSK +2      828.3782   1654.7419  1654.7126  0.03       85         3
                         IGPTELLIEMEDWK  +2    837.4401   1672.8656  1672.8382  0.03       72         25
                         LYIDETVNDNIPLNLR      +2         951.5185   1901.0224  1900.9894  0.03       84         3
                         DNENVINEYSSILEDQK     +2         1005.4880  2008.9614  2008.9225  0.04       106        5

No.       Protein        Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
459.      IPI00189813    Y          Y          1.2        4          16         3          618        32
*Des:     Actin, alpha skeletal muscle
          SEQUEST:(PepMatched Observed.Hits Coverage)     16         26         35.41%
                         Seq        Charge     Xcor       Delta      Probility  PepHits
                         SYELPDGQVITIGNER      +3         5.152      0.473      1.0000     211
                         DSYVGDEAQSKR +2       3.831      0.552      1.0000     73
                         DSYVGDEAQSK  +2       3.432      0.490      0.9998     11
                         AGFAGDDAPR +2         3.817      0.395      0.9997     176
                         EITALAPSTMK  +2       3.082      0.471      0.9995     131
                         YPIEHGIITNWDDMEK      +2         4.752      0.492      1.0000     21
                         LDLAGRDLTDYLMK +3     3.398      0.465      1.0000     59
                         LDLAGRDLTDYLMKILTER   +3         4.211      0.483      1.0000     2
                         HQGVMVGMGQKDSYVGDEAQSK           +2         5.849      0.699      1.0000     8
                         GILTLKYPIEHGIITNWDDMEK +3        3.778      0.403      0.9999     6
                         MQKEITALAPSTMK +2     5.024      0.465      1.0000     47
                         HQGVMVGMGQK  +2       3.478      0.387      0.9992     210
                         HQGVMVGMGQKDSYVGDEAQSKR          +4         6.515      0.596      1.0000     88
                         IWHHTFYNELR  +3       3.149      0.444      1.0000     6
                         AVFPSIVGRPR  +2       3.415      0.346      0.9984     302
                         MQKEITALAPSTMKIK      +2         3.419      0.325      0.9817     2
          MASCOT:(PepMatched Observed.Hits Coverage)      3          6          11.97%
                         Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore   PepHits
                         SYELPDGQVITIGNER      +2         895.9525   1789.8905  1789.8846  0.01       52         2
                         YPIEHGIITNWDDMEK      +3         654.3091   1959.9054  1959.9036  0          40         4
                         IWHHTFYNELR  +2       758.3783   1514.7420  1514.7419  0          54         41

No.       Protein        Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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460.	IPI00231423		N	Y	0.9	1	0	7	0	15		
*Des:	C9 protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					7	1	17.5%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DGNTLTYYR		+2	551.76	1101.51	1101.51	0	42	2		
		SIEVFGQFQGK		+2	620.32	1238.63	1238.63	0	46	2		
		AIEDYVNEFSAR		+2	707.34	1412.66	1412.66	0	51	3		
		TENYEEQFEMFK		+2	797.84	1593.66	1593.67	0	42	1		
		GVMLTTTFLDDVK		+2	720.88	1439.74	1438.74	1	74	4		
		KPWNVAFLAYETK		+2	783.92	1565.82	1565.82	0	43	2		
		TIDVNDFINWASSLDDAPALISQK				+3	878.44	2632.31	2632.30	0.01	62	2

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
461.	IPI00231426		Y	Y	0.4	2	11	5	40	46		
*Des:	Phosphoglycerate kinase 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					11	5	46.09%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		NNQITNNQR		+2	3.384	0.340	0.9989	8				
		LGDVYYVNDAFGTAHR			+3	3.331	0.548	1.0000	6			
		VLNNMEIGTSLYDEEGAK			+2	5.983	0.599	1.0000	5			
		DCVGSEVENACANPAAGTVILLENLR				+3	4.496	0.498	1.0000	1		
		QIVWNGPVGVFEWEAFAR			+2	5.048	0.548	1.0000	4			
		WNTEDKVSHVSTGGGASLELLEGK				+3	4.418	0.522	1.0000	1		
		TGQATVASGIPAGWMGLDCGTESSKK				+3	3.729	0.331	0.9995	2		
		VDFNVPMKNNQITNNQR			+3	4.206	0.453	1.0000	7			
		AHSSMVGVNLPQK		+3	4.151	0.338	1.0000	13				
		SLLGKDVLFLK		+3	2.328	0.287	0.9830	5				
		ALESPERPFLAILGGAK			+3	4.891	0.566	1.0000	7			
	MASCOT:(PepMatched Observed.Hits Coverage)					5	5	16.78%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VLNNMEIGTSLYDEEGAK			+2	991.9769	1981.9392	1981.9302	0.01	97	4	
		SLMDEVVKATSR		+2	668.3510	1334.6875	1334.6864	0	74	24		
		AEPAKIDAFR		+2	559.3041	1116.5937	1116.5927	0	47	12		
		ALESPERPFLAILGGAK			+2	885.0027	1767.9908	1767.9882	0	61	17	
		NNQITNNQR		+2	551.2719	1100.5292	1100.5323	0	56	20		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
462.	IPI00189819		Y	Y	0.74	4	14	10	601	98		
*Des:	Actin, cytoplasmic 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					14	20	65.18%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GYSFTTTAER		+2	2.905	0.581	1.0000	189				
		GYSFTTTAEREIVR		+2	3.425	0.415	0.9995	45				
		KDLYANTVLSGGTTMYPGIADR				+2	6.578	0.630	1.0000	34		
		TTGIVMDSGDGVTHTVPIYEGYALPHAILR				+3	6.949	0.646	1.0000	56		
		LCYVALDFEQEMATAASSSSLEK				+3	6.886	0.642	1.0000	479		

EKLCYVALDFEQEMATAASSSSLEK +2 5.473 0.675 1.0000 19
QEYDESGPSIVHR +3 3.308 0.384 1.0000 86
LCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNER +3 6.463 0.746 1.0000 30
DIKEKLCYVALDFEQEMATAASSSSLEK +3 6.358 0.644 1.0000 28
ILTERGYSFTTTAER +2 3.931 0.453 0.9999 16
FRCPEALFQPSFLGMESCGIHETTFNSIMK +3 8.137 0.682 1.0000 55
DLTDYLMKILTERGYSFTTTAER +3 3.310 0.420 0.9999 2
VAPEEHPVLLTEAPLNPK +2 4.425 0.607 0.9627 64
YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR +3 5.628 0.568 1.0000 5

MASCOT:(PepMatched Observed.Hits Coverage) 10 9 29.58%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
IIAPPERK +2 462.2867 922.5589 922.5600 0 41 7
DSYVGDEAQSKR +2 677.8155 1353.6164 1353.6160 0 42 3
QEYDESGPSIVHR +3 506.2381 1515.6926 1515.6953 0 42 12
AGFAGDDAPR +2 488.7270 975.4394 975.4410 0 57 7
DSYVGDEAQSK +2 599.7647 1197.5149 1197.5149 0 72 7
GYSFTTTAER +2 566.7662 1131.5178 1131.5196 0 61 14
VAPEEHPVLLTEAPLNPK +2 977.5364 1953.0583 1953.0571 0 69 11
EITALAPSTMK +2 581.3112 1160.6078 1160.6111 0 48 9
IWHHTFYNELR +2 758.3791 1514.7436 1514.7419 0 39 15
HQGVMVGMGQK +2 586.2888 1170.5631 1170.5637 0 66 44

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
463. IPI00198567 Y Y 0.52 2 4 4 7 8
*Des: LIM and SH3 domain protein 1

SEQUEST:(PepMatched Observed.Hits Coverage) 4 4 19.77%

Seq Charge Xcor Delta Probility PepHits
TGDTGMLPANYVEA +2 2.760 0.431 0.9658 1
QSFTMVADTPENLR +2 3.290 0.400 0.9985 1
YKEEFEKNK +2 2.881 0.255 0.9554 2
LKQQSELQSQVR +2 3.643 0.196 0.9507 4

MASCOT:(PepMatched Observed.Hits Coverage) 4 3 20.14%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
EPAAPVSIQR +2 534.30 1066.58 1066.58 0 46 3
MGPSGGEGIEPER +2 658.31 1314.60 1314.59 0.01 66 3
GFSVVADTPELQR +2 709.87 1417.73 1417.72 0.01 60 2
QSFTMVADTPENLR +2 804.89 1607.77 1607.76 0.01 78 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
464. IPI00215243 Y Y 0.6 2 3 3 5 12
*Des: Splice Isoform RC6-IL of Proteasome subunit alpha type 7

SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 19.69%

Seq Charge Xcor Delta Probility PepHits
ALLEVVQSGGK +2 2.879 0.514 0.9999 1
NYTDDAIETDDLTIK +2 4.997 0.519 1.0000 2
AITVFSPDGHLFQVEYAQEAVK +3 3.657 0.391 0.9996 2

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 16.6%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
LYQTDPSGTYHAWK			+2	833.39	1664.77	1665.78	-1	48	4	
ALLEVVQSGGK		+2	550.82	1099.63	1099.62	0.01	48	4		
NYTDDAIETDDLTIK		+2	863.92	1725.82	1725.79	0.03	116	4		

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
465.	IPI00214442	N	Y	0.05	1	0	2	0	2

*Des: Nck-associated protein 1

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 1.91%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
IGQETDKTTTR		+2	625.3284	1248.6422	1248.6310	0.01	58	1		
TISQAVNKK		+2	494.7959	987.5772	987.5713	0.01	46	2		

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
466.	IPI00371718	Y	Y	0.47	5	57	74	316	1243

*Des: PREDICTED: similar to Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin)

SEQUEST:(PepMatched Observed.Hits Coverage) 57 23 28.59%

Seq	Charge	Xcor	Delta	Probility	PepHits				
SGQSAAGASPAGGIDTR			+2	5.195	0.588	1.0000	6		
VTAQGPGLEPSGNIANK			+2	5.455	0.637	1.0000	6		
AYGPGIEPTGNMVK		+2	3.982	0.489	1.0000	7			
TGVAINKPAEFTVDAK			+2	4.500	0.571	1.0000	13		
ANLPQSFQVDTSK		+2	4.382	0.545	1.0000	7			
GAGTGGLGLAVEGPSEAK			+2	5.084	0.601	1.0000	5		
VSGLVDKVDVGKDQEFTVK			+2	6.097	0.610	1.0000	7		
DGSCGVAYVVQEPGDYEVSVK			+2	4.335	0.553	1.0000	5		
AWGPGLEGGIVGK		+2	3.667	0.509	1.0000	14			
IANLQTDLSDGLR		+2	4.077	0.430	0.9997	7			
GLVEPVDVVDNADGTQTVNYVPSR				+2	6.434	0.679	1.0000	11	
EGSYSISVLYGEEEVPR			+2	4.533	0.625	1.0000	2		
GTVEPQLEAR		+2	3.014	0.329	0.9966	4			
VEPGLGADNSVVR		+2	2.703	0.459	0.9983	1			
TPCEEILVK		+2	2.708	0.255	0.9850	2			
DAEMPATEKDLAEDAPWK			+2	4.917	0.477	1.0000	3		
QMQLENVSVALEFLDR			+2	4.015	0.447	0.9997	1		
VKVEPSHDASK		+2	3.304	0.466	0.9983	6			
VPVHDVTDASK		+2	2.890	0.357	0.9964	2			
WGDEHIPGSPYR		+3	2.828	0.306	0.9986	4			
DAEMPATEKDLAEDAPWKK			+2	4.219	0.555	1.0000	3		
EAGAGGLAIAVEGPSKAEISFEDRK				+3	5.621	0.491	1.0000	4	
VHSPSGALEECYVTEIDQDKYAVR				+3	3.974	0.467	1.0000	1	
EGSYSISVLYGEEEVPRSPFK			+2	4.359	0.616	1.0000	2		
ALGALVDSCAPGLCPDWDSWDASKPVNNAR					+3	4.722	0.606	1.0000	3
QMQLENVSVALEFLDRESIK			+3	3.474	0.323	0.9986	6		
VNVGAGSHPNK		+2	2.809	0.521	0.9996	4			

AGVAPLQVK	+2	3.116	0.509	1.0000	19				
VAQPSITDNKDGTVTVR		+2	3.860	0.470	0.9987	2			
GKLDVQFSGLAK	+2	3.863	0.494	1.0000	15				
LVSNHSLHETSSVFVDSLTK		+2	5.941	0.594	1.0000	11			
SPFSVGVSPSLDLSK		+2	4.067	0.426	0.9996	4			
DKGEYTLVVKWGDEHIPGSPYR			+3	3.988	0.532	1.0000	1		
TFSVWYVPEVTGTHK		+3	2.570	0.444	0.9999	4			
RLTVSSLQESGLK	+2	3.522	0.373	0.9987	1				
VTVLFAGQHIAK	+2	3.932	0.465	1.0000	14				
VKVEPSHDASKVK	+2	3.538	0.539	1.0000	7				
ALTQTGGPHVK	+2	3.280	0.463	0.9996	32				
AYGPGIEPTGNMVKK		+2	3.790	0.353	0.9984	5			
AFGPGLQGGNAGSPAR		+2	4.477	0.538	1.0000	18			
VNVGAGSHPNKVK	+2	4.143	0.453	1.0000	18				
VRVHGPGIQSGTTNKPNK		+3	4.680	0.438	1.0000	6			
VHGPGIQSGTTNKPNKFTVETR			+2	5.314	0.605	1.0000	22		
VATVPQHATSGPGPADVSKVVAK			+3	4.333	0.612	1.0000	4		
TAGKGKLDVQFSGLAK		+3	4.610	0.514	1.0000	18			
YGGPYHIGGSPFK	+2	4.036	0.464	1.0000	4				
VATVPQHATSGPGPADVSK		+2	4.842	0.577	1.0000	45			
TGVELGKPTHFTVNAK		+3	3.321	0.471	1.0000	11			
FNGTHIPGSPFK	+2	2.990	0.326	0.9945	5				
LIALLEVLSQKK	+2	4.043	0.494	1.0000	41				
NGHVGISFVPKETGEHLVHVKK			+3	3.367	0.501	1.0000	2		
AEGPGLNRTGVELGKPTHFTVNAK			+3	3.210	0.393	0.9995	1		
IVSPSGAAVPCKVEPGLGADNSVVR			+3	4.981	0.434	1.0000	17		
AGNNMLLVGVHGPR		+3	3.436	0.447	1.0000	8			
VRAWGPGLEGGIVGK		+2	3.215	0.385	0.9891	1			
HTAMVSWGGVSIPNSPFR		+2	5.094	0.614	1.0000	4			
TFSVWYVPEVTGTHKVTVLFAGQHIAK			+3	4.351	0.522	1.0000	1		
MASCOT:(PepMatched Observed.Hits Coverage)			74	30	41.87%				
Seq Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
AEFTVETR	+2	476.74	951.47	951.47	0	57	16		
GTVEPQLEAR	+2	550.29	1098.57	1098.57	0	59	35		
VPVHDVTDASK	+2	584.31	1166.60	1166.59	0.01	50	1		
VSGLVDKVDVGK	+2	608.99	1215.96	1214.69	1.27	44	2		
VEPGLGADNSVVR	+2	656.85	1311.69	1311.68	0.01	80	50		
VDVGKDQEFTVK	+2	682.86	1363.71	1363.70	0.01	71	27		
AFGPGLQGGNAGSPAR		+2	728.87	1455.73	1455.72	0.01	92	89	
SGQSAAGASPAGGIDTR		+2	751.87	1501.72	1501.71	0.01	96	3	
VTAQGPGLEPSGNIANK		+2	826.94	1651.86	1651.85	0.01	92	62	
TGVELGKPTHFTVNAK		+2	849.97	1697.92	1697.91	0.01	82	26	
VQVQDNEGHSVETTVK		+2	885.44	1768.87	1768.86	0.01	95	22	
VAQPSITDNKDGTVTVR		+2	900.98	1799.95	1799.94	0.01	86	12	
VATVPQHATSGPGPADVSK		+2	909.98	1817.94	1817.93	0.01	77	96	
LPQLPITNFSR	+2	643.37	1284.73	1284.72	0.01	64	18		
AEAGVPAEFGIWTR	+2	752.39	1502.76	1502.75	0.01	64	7		

VTYTPMAPGSYLISIK	+2	870.97	1739.93	1739.92	0.01	65	14
TFSVWYVPEVTGTHK	+2	875.95	1749.89	1749.87	0.02	57	26
QMQLENVSVALEFLDR	+2	946.49	1890.96	1890.95	0.01	118	24
HTAMVSWGGVSIPNSPFR	+2	971.99	1941.97	1941.95	0.02	116	9
SADFVVEAIGDDVGTLGFSVEGPSQAK	+3	899.11	2694.31	2694.30	0.01	109	26
TTYFEIFTAGAGIGEVEVVIQDPTGQK	+3	957.49	2869.46	2869.44	0.02	61	12
VGSAADIPINISETDLSLLTATVVPPSGR	+3	965.20	2892.57	2892.54	0.03	60	10
LIALLEVLSQK	+2	613.89	1225.77	1225.76	0.01	92	177
AGVAPLQVK	+2	442.74	883.47	881.53	1.94	55	16
AEISFEDR	+2	483.73	965.45	965.45	0	42	22
DKGEYTLVVK	+2	576.32	1150.63	1150.62	0.01	66	87
EATTEFSVDAR	+2	613.29	1224.57	1224.56	0.01	72	98
YGGQPVPNFPSK	+2	645.83	1289.65	1289.64	0.01	81	46
DVDIIDHHDNTYTVK	+2	892.93	1783.85	1783.84	0.01	80	22
WGDEHIPGSPYR	+2	707.34	1412.66	1412.65	0.01	61	77
AYGPGIEPTGNMVK	+2	717.36	1432.71	1432.70	0.01	56	22
ANLPQSFQVDTSK	+2	717.87	1433.73	1433.72	0.01	72	55
YNDQHIPGSPFTAR	+2	801.89	1601.77	1601.76	0.01	65	69
TGVAINKPAEFTVDAK	+2	830.96	1659.90	1659.88	0.02	98	83
SPYTVTVGQACNPTACR	+2	883.41	1764.81	1766.81	-1.99	49	4
TGVAINKPAEFTVDAKHAGKAPLR	+3	830.96	2489.85	2490.37	-0.51	52	30
KTHIQDNHDGTYTVAYVPDVTGR	+3	863.10	2586.27	2586.25	0.02	89	21
DLAEDAPWKK	+2	586.81	1171.60	1171.59	0.01	48	21
LTVSSLQESGLK	+2	631.36	1260.70	1260.69	0.01	91	35
GAGTGGLGLAVEGPSEAK	+2	785.91	1569.81	1569.80	0.01	122	68
YSPSEAGLHEMDIR	+2	802.88	1603.74	1603.73	0.01	65	30
FNGTHIPGSPFK	+2	651.34	1300.67	1300.66	0.01	58	61
EAGAGGLAIAVEGPSK	+2	713.89	1425.76	1425.75	0.01	126	58
NGHVGISFVPK	+2	578.32	1154.62	1153.62	1	44	48
FADQHVPGSPFSVK	+2	758.39	1514.77	1514.75	0.02	61	56
VSGLVDKVDVGKDQEFTVK	+3	688.38	2062.11	2062.09	0.02	65	37
YTPVQQGPVGVSVTYGGDHIPK	+3	767.07	2298.18	2298.16	0.02	48	20
GKLDVQFSGLAK	+2	631.86	1261.72	1261.70	0.02	75	32
VTVLFAGQHIAK	+2	642.38	1282.75	1282.74	0.01	87	59
YGGPYHIGGSPFK	+2	690.35	1378.68	1378.67	0.01	79	41
AGNNMLLVGVHGPR	+3	478.93	1433.76	1433.76	0	73	37
VNQPASFAVSLNGAK	+2	751.91	1501.80	1501.79	0.01	87	13
FVPAEMGMHTVSVK	+2	766.89	1531.77	1531.75	0.02	76	9
SPFEVYVDK	+2	542.27	1082.53	1082.53	0	66	14
ENGVYLIDVK	+2	575.81	1149.60	1148.61	0.99	50	11
DAGEGGLSLAIEGPSK	+2	750.88	1499.75	1499.75	0	105	12
LVSNHSLHETSSVFVDSLTK	+3	734.05	2199.14	2199.12	0.02	105	11
SAGQGEVLVYVEDPAGHQEEAK	+3	771.71	2312.11	2312.09	0.02	68	11
KNGQHVASSPIPVVISQSEIGDASR	+3	859.78	2576.33	2575.34	0.99	56	2
DLAEDAPWK	+2	522.76	1043.50	1043.49	0.01	49	18
LYSVSYLLK	+2	542.84	1083.67	1084.62	-0.94	50	5
AWGPGLEGGIVGK	+2	620.84	1239.67	1239.66	0.01	71	18

		YGGDEIPFSPYR		+2	700.83	1399.65	1399.64	0.01	70	8		
		IANLQTDLSDGLR		+2	708.38	1414.75	1414.74	0.01	97	16		
		SPFSVGVSPSLDLSK			+2	760.41	1518.80	1518.79	0.01	92	7	
		DAGYGGLSLSIEGPSK			+2	775.89	1549.77	1549.76	0.01	96	7	
		EGSYSISVLYGEEEVPR			+2	957.46	1912.91	1912.91	0	107	13	
		DAGEGLLAVQITDPEGKPK			+2	969.52	1937.02	1937.01	0.01	109	15	
		ASGPGLNTTGVPASLPVEFTIDAK				+3	781.42	2341.24	2341.22	0.02	46	3
		VSGQGLHEGHTFEPAEFIIDTR			+3	814.07	2439.20	2439.18	0.02	59	5	
		FNEEHIPDSPFVVPVASPSGDAR				+3	823.07	2466.20	2466.18	0.02	53	12
		GLVEPVDVVDNADGTQTVNYVPSR				+3	848.76	2543.27	2543.25	0.02	69	7
		LLGWIQNK		+2	486.29	970.56	970.56	0	64	16		
		GQHVPGSPFQFTVGPLGEGGAHK				+3	768.73	2303.17	2303.14	0.03	50	8

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
467.	IPI00231356		Y	Y	0.09	2	2	3	3	9		
*Des:	C-1-tetrahydrofolate synthase, cytoplasmic											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	4.94%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		YSGLQPHVVVLVATVR			+3	4.404	0.517	1.0000	2			
		ASFITPVPGGVGPMTVAMLMQSTVESAQR					+3	3.676	0.506	0.9999	1	
	MASCOT:(PepMatched Observed.Hits Coverage)					3	2	4.62%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AYTEEDLDLVEK		+2	712.8553	1423.6960	1423.6718	0.02	48	1		
		TDPAALTDDEINR		+2	715.8549	1429.6952	1429.6685	0.03	70	4		
		EIGLLTEEVELYGETK			+2	911.9865	1821.9585	1821.9247	0.03	62	4	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
468.	IPI00568723		N	Y	0.77	1	0	2	0	8		
*Des:	PREDICTED: similar to immunoglobulin light chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	13.81%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		FSGSGSGTDFTLK		+2	652.31	1302.61	1302.61	0	88	6		
		FSGVPDRFSGSGSGTDFTLK			+3	688.00	2060.99	2060.98	0.01	47	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
469.	IPI00370844		Y	Y	0.17	2	4	4	5	7		
*Des:	PREDICTED: similar to PLS1 protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	3	10.92%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		MINLSEPDTIDER		+2	4.669	0.432	1.0000	2				
		EHLTDEDKLNNAK		+2	3.959	0.592	1.0000	1				
		SISTSLPVLDLIDAIAPNAVRPEMIK				+3	3.424	0.443	1.0000	4		
		AGFMLQEADKLGCR			+2	3.266	0.384	0.9910	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					4	2	9.2%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MINLSEPDTIDER		+2	766.8737	1531.7329	1531.7188	0.01	65	4		

		KIENCNYAVELGKNEAK			+3	641.6632	1921.9678	1921.9567	0.01	50	1	
		EHLTDEDKLNNAK		+2	763.8821	1525.7497	1525.7372	0.01	63	1		
		AYFHLLNQIAPK		+2	707.9074	1413.8003	1413.7768	0.02	41	1		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
470.	IPI00195156		N	Y	0.31	1	0	6	0	8		
*Des:	Dipeptidyl-peptidase III											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					6	1	16.24%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LASVLNTEPALDSELTSK			+2	944.50	1886.99	1886.98	0.01	49	1	
		LAQDFLDSQNLSAYNTR			+2	978.48	1954.94	1954.94	0	92	1	
		VLLEAGEGLVTVTPTTGSDGRPDAR				+3	837.77	2510.29	2510.30	0	47	2
		NVSLGNVLAVAYATK			+2	760.43	1518.84	1518.84	0	61	2	
		AGLLALEFYTPETANWR			+2	976.50	1950.99	1950.98	0.01	69	1	
		FPEDGPELEEVLTQLATADAQFWR				+3	921.45	2761.32	2761.32	0	85	1
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
471.	IPI00197696		Y	Y	0.46	2	7	2	22	6		
*Des:	Malate dehydrogenase, mitochondrial precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					7	3	31.68%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VNVPVIGGHAGK		+2	3.396	0.570	0.9999	7				
		AGAGSATLSMAYAGAR			+2	5.124	0.573	1.0000	7			
		MIAEAIPELK		+2	2.777	0.269	0.9808	3				
		LTLYDIAHTPGVAADLSHIETR			+3	5.411	0.627	1.0000	4			
		IFGVTTLDIVR		+2	3.730	0.395	0.9993	5				
		FVFSLVDAMNGK		+2	4.654	0.605	1.0000	5				
		VAVLGASGGIGQPLSLLLK			+2	6.295	0.619	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	8.72%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VNVPVIGGHAGK		+2	574.3422	1146.6698	1146.6509	0.02	38	2		
		AGAGSATLSMAYAGAR			+2	727.8687	1453.7229	1453.6983	0.02	90	4	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
472.	IPI00198498		Y	Y	0.78	1	6	3	22	33		
*Des:	Cortactin isoform C											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	2	12.73%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TEKHESQKDYVK		+3	3.871	0.366	1.0000	14				
		HCSQVDSVR		+2	2.771	0.443	0.9998	17				
		YGVQADRVDK		+2	3.054	0.335	0.9982	9				
		TEKHESQKDYSK		+3	2.683	0.341	0.9991	9				
		SAVGHEYQSK		+2	2.871	0.462	0.9999	17				
		MDKSAVGHEYQSK		+3	3.114	0.384	0.9999	6				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	6.68%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits

		HCSQVDSVR		+2	515.7419	1029.4692	1029.4662	0	51	37		
		SAVGHEYQSK		+2	553.2659	1104.5172	1104.5199	0	52	37		
		YGVQADRVDK		+2	575.7953	1149.5760	1149.5778	0	41	12		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)					
473.	IPI00231358		Y	Y	3.26	5	10	11	164	190		
*Des:	Profilin-1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					10	10	62.67%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TFVSITPAEVGVLVGKDR			+2	4.760	0.494	1.0000	46			
		DSLLQDGEFTMDLR		+2	5.382	0.553	1.0000	27				
		TFVSITPAEVGVLVGK			+3	5.777	0.550	1.0000	22			
		STGGAPTFNVTVTMTAK			+2	5.011	0.639	1.0000	71			
		SSFFVNGLTLGGQK		+2	4.912	0.526	1.0000	26				
		TLVLLMGK		+2	2.937	0.352	0.9983	32				
		TKSTGGAPTFNVTVTMTAK			+2	5.218	0.599	1.0000	9			
		EGVHGGLINKK		+2	3.020	0.273	0.9908	35				
		TLVLLMGKEGVHGGLINKK			+3	4.724	0.443	1.0000	13			
		TLVLLMGKEGVHGGLINK			+2	4.699	0.580	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					11	13	62.67%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		SSFFVNGLTLGGQK		+2	727.8906	1453.7666	1453.7565	0.01	94	28		
		DSLLQDGEFTMDLR		+2	820.3915	1638.7685	1638.7559	0.01	94	40		
		TFVSITPAEVGVLVGK			+2	808.9737	1615.9328	1615.9184	0.01	89	20	
		TFVSITPAEVGVLVGKDR			+2	944.5361	1887.0576	1887.0465	0.01	104	47	
		STGGAPTFNVTVTMTAK			+2	841.9318	1681.8490	1681.8345	0.01	93	70	
		TLVLLMGK		+2	437.7779	873.5412	873.5357	0.01	63	35		
		EGVHGGLINK		+2	512.2857	1022.5569	1022.5508	0.01	51	4		
		TKSTGGAPTFNVTVTMTAK			+2	956.5057	1910.9969	1910.9771	0.02	97	9	
		EGVHGGLINKK		+2	575.7300	1149.4455	1150.6458	-1.19	53	28		
		TLVLLMGKEGVHGGLINKK			+2	1004.1013	2006.1880	2006.1709	0.02	80	14	
		TLVLLMGKEGVHGGLINK			+2	940.0510	1878.0874	1878.0760	0.01	80	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)					
474.	IPI00213644		Y	Y	2.18	5	6	8	6	17		
*Des:	Peptidyl-prolyl cis-trans isomerase B precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	2	40.45%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		HYGPGWVSMANAGK			+2	3.839	0.782	1.0000	1			
		SIYGERFPDENFK		+2	3.171	0.624	0.9911	2				
		SIYGERFPDENFKLK			+2	3.442	0.461	0.9661	1			
		VIKDFMIQGGDFTRGDGTGGK			+2	4.891	0.561	0.9952	3			
		HYGPGWVSMANAGKDTNGSQFFITTVK				+3	4.774	0.535	0.9989	2		
		TSWLDGKHVVFGKVLEGMDVVR				+3	4.493	0.706	1.0000	3		
	MASCOT:(PepMatched Observed.Hits Coverage)					8	5	50.45%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VLEGMDVVR		+2	509.27	1016.53	1016.53	0	49	1		

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                    HYGPGWVSMANAGK              +2        737.85    1473.69   1473.68   0.01      66        1
                    TVDNFVALATGEK     +2        683.58    1365.14   1363.70   1.44      61        2
                    VIKDFMIQGGDFTR    +2        813.92    1625.83   1625.82   0.01      76        2
                    SIYGERFPDENFKLK             +2        921.98    1841.94   1841.93   0.01      54        1
                    HYGPGWVSMANAGKDTNGSQFFITTVK +3        971.81    2912.40   2912.39   0.01      72        1
                    VYFDFQIGDEPVGR    +2        821.40    1640.79   1640.78   0.01      56        1
                    TSWLDGKHVVFGKVLEGMDVVR      +3        824.78    2471.31   2471.30   0.01      48        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
475.      IPI00364286         Y         Y         0.13      3         3         4         9         9
*Des:     PREDICTED: similar to CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT)
          SEQUEST:(PepMatched Observed.Hits Coverage)   3         3         7.82%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    INALTAASEAACLIVSVDETIKNPR             +3        4.773     0.536     1.0000    1
                    MVVDAVMMLDELLQLK            +3        3.351     0.386     0.9999    7
                    KVQGGALEESR       +2        3.187     0.336     0.9972    2
          MASCOT:(PepMatched Observed.Hits Coverage)    4         3         7.11%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    TATQLAVNK           +2        473.2740  944.5335  944.5291  0         54        4
                    MVVDAVMMLDELLQLK              +3        616.6647  1846.9722 1846.9606 0.01      75        5
                    KVQGGALEESR       +2        587.3221  1172.6297 1172.6149 0.01      64        2
                    LLDVVHPAAK        +2        531.8219  1061.6292 1061.6233 0.01      44        6

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
476.      IPI00211970         Y         Y         1.33      1         5         6         7         12
*Des:     Proteasome activator complex subunit 2
          SEQUEST:(PepMatched Observed.Hits Coverage)   5         2         35.68%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    TKVEAFQTAISK      +2        3.189     0.526     0.9954    1
                    IEDGNDFGVAIQEK    +2        4.278     0.516     0.9999    1
                    AFYAELHHIISSNLEK            +3        3.755     0.563     1.0000    2
                    KIISLSQLLQEDSLNVADLSSLR               +3        4.431     0.540     0.9999    1
                    LLALLALVKPEVWTLK            +2        4.535     0.494     0.9999    2
          MASCOT:(PepMatched Observed.Hits Coverage)    6         2         26.14%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    DEAAYGALR           +2        483.24    964.47    964.46    0.01      58        2
                    VEAFQTAISK          +2        547.30    1092.59   1092.58   0.01      49        4
                    TKVEAFQTAISK        +2        661.87    1321.74   1321.72   0.02      54        6
                    AMVLDLR+2           409.24    816.46    816.45    0.01      55        1
                    IEDGNDFGVAIQEK    +2        767.88    1533.74   1533.73   0.01      97        5
                    AFYAELHHIISSNLEK            +3        624.66    1870.97   1870.96   0.01      43        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
477.      IPI00192755         Y         Y         3.71      1         4         4         6         4
*Des:     PREDICTED: similar to ARP2/3 complex 21 kDa subunit (p21-ARC) (Actin-related protein 2/3 complex subunit 3)
          SEQUEST:(PepMatched Observed.Hits Coverage)   4         1         57.8%
                    Seq       Charge    Xcor      Delta     Probility PepHits
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		ETKDTDIVDEAIYYFK			+2	4.048	0.535	0.9897	1			
		SQGEKEMYTLGITNFPIPGEPGFPLNAIYAK					+3	5.861	0.630	1.0000	2	
		EMYTLGITNFPIPGEPGFPLNAIYAKPASK				+3	5.219	0.686	1.0000	2		
		DTDIVDEAIYYFKANVFFK			+2	4.663	0.636	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	17.91%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AYLQQLR	+2	446.26	890.50	890.50	0	41	1			
		AYLQQLRQETGLR		+2	788.43	1574.85	1574.85	0	41	1		
		DTDIVDEAIYYFK		+2	796.38	1590.75	1590.75	0	75	1		
		ETKDTDIVDEAIYYFK			+2	975.48	1948.94	1948.93	0.01	49	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
478.	IPI00563715		N	Y	0.24	1	0	2	0	7		
*Des:	Protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	5.32%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NEISELNR		+2	487.27	972.52	973.48	-0.95	41	2		
		LALDVEIATYR		+2	632.35	1262.69	1262.69	0	63	5		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
479.	IPI00475433		N	Y	0.06	2	0	3	0	6		
*Des:	106 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	2	6.92%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		EVLEDFAEDGEK		+2	690.8223	1379.6300	1379.6092	0.02	62	2		
		GNSSESIEAIREYEEEFFQNSK			+3	865.0737	2592.1994	2592.1615	0.04	36	2	
		SLIDMYSEVLDVLSDYDASYNTQDHLPR				+3	1087.1979	3258.5718	3258.5026	0.07	102	2

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
480.	IPI00210091		Y	Y	0.3	1	2	3	4	3		
*Des:	PREDICTED: similar to serine protease inhibitor 2.4											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	6.8%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GNTLEEILEVLR		+2	3.180	0.331	0.9964	3				
		MQQVEASLQPETLKK			+3	3.370	0.409	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	9.62%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GNTLEEILEVLR		+2	693.3901	1384.7656	1384.7561	0.01	46	1		
		IQELVSGLKER		+2	636.3744	1270.7342	1270.7244	0.01	57	1		
		MQQVEASLQPETLKK			+2	865.4678	1728.9210	1728.9080	0.01	74	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
481.	IPI00562915		N	Y	2.24	1	0	2	0	6		
*Des:	PREDICTED: bridging integrator 2 (predicted)											
	SEQUEST:(PepMatched Observed.Hits Coverage)											

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         MASCOT:(PepMatched Observed.Hits Coverage)   2        1        6.61%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
                  ASSDASSDPEPPETGEK          +2       852.3667 1702.7188 1702.7169 0      77       4
                  AIVGNNDLLWEDYEEK           +2       954.4547 1906.8949 1906.8948 0      108      2

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
482.     IPI00557083       N        Y        0.1      2        0        2        0        19
*Des:    PREDICTED: similar to keratin 6 alpha
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)   2        4        3.93%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
                  YEELQITAGR        +2       590.30   1178.59  1178.59  0        53       2
                  SLDLDSIIAEVK      +2       651.86   1301.71  1301.71  0        61       4

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
483.     IPI00366104       Y        N        0.72     1        3        0        3        0
*Des:    PREDICTED: similar to TOLLIP protein
         SEQUEST:(PepMatched Observed.Hits Coverage)  3        1        13.97%
                  Seq      Charge   Xcor     Delta    Probility PepHits
                  LSITVVQAK         +2       2.437    0.340    0.9939   2
                  IAWTHITIPESLK     +3       3.121    0.373    0.9994   1
                  GPVYIGELPQDFLR    +2       3.728    0.142    0.9706   1
         MASCOT:(PepMatched Observed.Hits Coverage)

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
484.     IPI00231502       Y        N        0.1      1        3        0        4        0
*Des:    Splice Isoform 2 of Adapter-related protein complex 2 beta 1 subunit
         SEQUEST:(PepMatched Observed.Hits Coverage)  3        1        6.92%
                  Seq      Charge   Xcor     Delta    Probility PepHits
                  KPSETQELVQQVLSLATQDSDNPDLR        +3       4.188    0.445    0.9999   2
                  APEVSQYIYQVYDSILK          +3       3.367    0.352    0.9991   1
                  LAPPLVTLLSGEPEVQYVALR      +3       3.645    0.481    0.9999   1
         MASCOT:(PepMatched Observed.Hits Coverage)

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
485.     IPI00198717       Y        Y        0.55     3        6        4        7        5
*Des:    Cytosolic malate dehydrogenase
         SEQUEST:(PepMatched Observed.Hits Coverage)  6        2        30%
                  Seq      Charge   Xcor     Delta    Probility PepHits
                  GEFITTVQQR        +2       3.401    0.397    0.9995   2
                  NVIIWGNHSSTQYPDVNHAK       +3       4.325    0.553    1.0000   1
                  FVEGLPINDFSR      +2       2.880    0.401    0.9979   1
                  EVGVYEALKDDSWLK            +2       3.708    0.367    0.9750   1
                  DLDVAVLVGSMPR     +2       2.988    0.389    0.9976   1
                  VLVTGAAGQIAYSLLYSIGNGSVFGK        +3       5.489    0.629    1.0000   1
         MASCOT:(PepMatched Observed.Hits Coverage)   4        3        18.82%
                  Seq      Charge   ObservedMS        ExpectedMS        CalculatedMS               Pepscore PepHits
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		LGVTADDVK		+2	459.25	916.49	916.49	0	44	1		
		GEFITTVQQR		+2	589.81	1177.61	1177.61	0	52	2		
		EVGVYEALKDDSWLK			+2	876.45	1750.89	1750.88	0.01	50	1	
		VLVTGAAGQIAYSLLYSIGNGSVFGK				+3	862.47	2584.40	2584.39	0.01	73	1

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
486.	IPI00470282		Y	Y	0.66	4	9	9	16	53		
*Des:	Serine (Or cysteine) proteinase inhibitor, clade B (Ovalbumin), member 10											
	SEQUEST:(PepMatched Observed.Hits Coverage)					9	9	31.43%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ANFSNMTSER		+2	3.064	0.380	0.9985	4				
		EINSWVGSQTGGK		+2	4.230	0.547	1.0000	5				
		DMGMTDAFNQGK		+2	3.877	0.570	1.0000	4				
		MEESYDLQSALR		+2	3.851	0.400	0.9995	3				
		TFLEINEEGTEAAAGTGSEVNFR				+3	4.244	0.601	1.0000	1		
		KEINSWVGSQTGGK		+2	3.831	0.327	0.9981	1				
		GTTAAQMSQVLHFGSIQDFK			+2	4.750	0.598	1.0000	4			
		GTWEHQFSVQNTTERPFR			+2	3.339	0.527	0.9997	3			
		NLFLSNVFHK		+2	3.225	0.282	0.9942	13				
	MASCOT:(PepMatched Observed.Hits Coverage)					9	9	28.71%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DMGMTDAFNQGK		+2	657.7801	1313.5456	1313.5380	0.01	75	17		
		MEESYDLQSALR		+2	721.3415	1440.6684	1440.6555	0.01	67	9		
		EINSWVGSQTGGK		+2	681.8415	1361.6684	1361.6575	0.01	87	10		
		ANFSNMTSER		+2	578.8120	1155.6093	1155.4978	0.11	49	9		
		KEINSWVGSQTGGK		+2	745.8889	1489.7633	1489.7524	0.01	50	2		
		GTTAAQMSQVLHFGSIQDFK			+2	1083.5420	2165.0694	2165.0575	0.01	74	12	
		TTSKPVQMMSMK		+2	684.8411	1367.6677	1367.6611	0.01	44	3		
		GTWEHQFSVQNTTERPFR			+2	1110.5386	2219.0626	2219.0508	0.01	44	9	
		NLFLSNVFHK		+2	609.8381	1217.6617	1217.6556	0.01	48	12		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
487.	IPI00197770		Y	Y	0.48	1	8	5	12	9		
*Des:	Aldehyde dehydrogenase, mitochondrial precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					8	3	24.43%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TEQGPQVDETQFK		+2	4.243	0.499	1.0000	2				
		ELGEYGLQAYTEVK		+2	2.998	0.315	0.9929	1				
		YGLAAAVFTK		+2	2.789	0.376	0.9980	4				
		AAQAAFQLGSPWR		+2	2.918	0.340	0.9952	1				
		TFVQEDVYDEFVER		+2	3.991	0.563	1.0000	4				
		EEIFGPVMQILK		+2	3.198	0.201	0.9707	2				
		VAEQTPLTALYVANLIK			+2	4.273	0.568	1.0000	3			
		TYLAALETLDNGKPYVISYLVDLDMVLK				+3	5.260	0.398	0.9997	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					5	3	13.63%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TEQGPQVDETQFK		+2	753.86	1505.71	1505.70	0.01	63	2		

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                YGLAAAVFTK          +2          520.79      1039.57     1039.57     0           51          4
                AAQAAFQLGSPWR       +2          701.87      1401.72     1401.72     0           51          1
                TFVQEDVYDEFVER      +2          888.41      1774.80     1774.80     0           86          4
                VAEQTPLTALYVANLIK               +2          922.53      1843.05     1843.05     0           70          6

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
488.        IPI00188950         Y           Y           0.18        1           4           4           6           6
*Des:       Tyrosine-protein kinase CSK
            SEQUEST:(PepMatched Observed.Hits Coverage)   4           1           12.22%
                Seq             Charge      Xcor        Delta       Probility   PepHits
                VMEGTVAAQDEFYR+2            3.829       0.552       1.0000      1
                GDVLTIVAVTK         +2          3.272       0.519       0.9999      2
                GGLYIVTEYMAK        +2          2.930       0.351       0.9967      1
                HSNLVQLLGVIVEEK                 +2          4.851       0.440       0.9999      2
            MASCOT:(PepMatched Observed.Hits Coverage)    4           1           11.57%
                Seq             Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore  PepHits
                IPLKDVVPR           +2          518.83      1035.64     1035.64     0           48          3
                VMEGTVAAQDEFYR+2            808.38      1614.74     1614.73     0.01        81          1
                GDVLTIVAVTK         +2          558.34      1114.66     1114.66     0           66          2
                HSNLVQLLGVIVEEK                 +2          839.48      1676.95     1676.95     0           92          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
489.        IPI00199448         Y           Y           0.15        1           2           2           5           3
*Des:       Mama
            SEQUEST:(PepMatched Observed.Hits Coverage)   2           1           6.67%
                Seq             Charge      Xcor        Delta       Probility   PepHits
                TNPEAQALWQVVGSSVIMR         +3          4.547       0.550       1.0000      1
                AVDQWSTATGASHGDVER          +2          5.149       0.571       1.0000      4
            MASCOT:(PepMatched Observed.Hits Coverage)    2           1           6.67%
                Seq             Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore  PepHits
                AVDQWSTATGASHGDVER          +2          943.94      1885.87     1885.86     0.01        97          4
                TNPEAQALWQVVGSSVIMR         +3          696.03      2085.07     2085.07     0           50          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
490.        IPI00231506         Y           Y           0.47        1           4           4           13          18
*Des:       Phosphoglycerate mutase 2
            SEQUEST:(PepMatched Observed.Hits Coverage)   4           1           16.34%
                Seq             Charge      Xcor        Delta       Probility   PepHits
                KAMEAVAAQGK         +2          3.543       0.442       0.9997      3
                HYGGLTGLNKAETAAK                +2          4.553       0.555       1.0000      8
                VLIAAHGNSLR         +2          2.889       0.461       0.9992      10
                RVLIAAHGNSLR        +2          2.950       0.332       0.9946      1
            MASCOT:(PepMatched Observed.Hits Coverage)    4           1           15.95%
                Seq             Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore  PepHits
                AMEAVAAQGK          +2          488.2533    974.4921    974.4855    0.01        41          2
                KAMEAVAAQGK         +2          552.3008    1102.5871 1102.5804 0.01          79          3
                VLIAAHGNSLR         +2          575.5364    1149.0583 1149.6618 -0.59         64          22
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		HYGGLTGLNKAETAAK			+2	815.9390	1629.8634	1629.8474	0.02	95	14	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
491.	IPI00470288		Y	Y	0.75	3	9	8	20	14		
*Des:	Creatine kinase, B chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)					9	8	39.69%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		FPAEDEFPDLSSHNNHMAK			+2	4.693	0.473	0.9999	4			
		LEQGQPIDDLMPAQ		+2	4.343	0.499	0.9998	2				
		RGTGGVDTAAVGGVFDVSNADR				+3	5.050	0.580	1.0000	2		
		TDLNPDNLQGGDDLDPNYVLSSR				+2	5.341	0.648	1.0000	3		
		LAVEALSSLDGDLSGR			+2	4.866	0.643	1.0000	2			
		DLFDPIIEDR		+2	3.111	0.320	0.9976	2				
		HGGYQPSDEHK		+2	3.092	0.370	0.9986	1				
		TFLVWINEEDHLR		+2	3.979	0.544	1.0000	4				
		LGFSEVELVQMVVDGVK			+2	5.581	0.370	0.9999	6			
	MASCOT:(PepMatched Observed.Hits Coverage)					8	8	30.67%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		PFSNSHNTQK		+2	580.28	1158.55	1158.54	0.01	41	1		
		LEQGQPIDDLMPAQK			+2	841.93	1681.84	1681.83	0.01	64	2	
		GTGGVDTAAVGGVFDVSNADR				+2	982.97	1963.93	1963.92	0.01	87	2
		RGTGGVDTAAVGGVFDVSNADR				+3	707.68	2120.03	2120.02	0.01	61	1
		FPAEDEFPDLSSHNNHMAK			+3	729.33	2184.96	2184.95	0.01	48	1	
		LAVEALSSLDGDLSGR			+2	801.92	1601.83	1601.83	0	97	2	
		TFLVWINEEDHLR		+2	836.43	1670.85	1670.84	0.01	56	4		
		LGFSEVELVQMVVDGVK			+2	925.00	1847.98	1847.97	0.01	113	6	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
492.	IPI00372458		Y	Y	0.17	1	6	5	8	6		
*Des:	PREDICTED: similar to Coatomer protein complex subunit alpha											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	1	6.98%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LLELGPKPEVAQQTR			+3	3.670	0.532	1.0000	2			
		LLHDQVGVVQFGPYK			+3	3.490	0.339	0.9995	1			
		LVGQSIIAYLQK		+2	3.752	0.431	0.9997	1				
		SILLSVPLLVVDNK		+2	2.709	0.457	0.9974	1				
		LSFLYLITGNLEK		+2	4.598	0.556	1.0000	1				
		YAVTTGDHGIIR		+2	3.297	0.383	0.9986	3				
	MASCOT:(PepMatched Observed.Hits Coverage)					5	1	5.22%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YAVTTGDHGIIR		+2	651.85	1301.68	1301.67	0.01	57	3		
		LLELGPKPEVAQQTR			+3	560.32	1677.94	1677.94	0	42	2	
		TALNLFFK		+2	477.28	952.54	952.54	0	66	1		
		LVGQSIIAYLQK		+2	666.90	1331.79	1331.78	0.01	61	1		
		LSFLYLITGNLEK		+2	755.93	1509.85	1509.84	0.01	88	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		

493.	IPI00189759		Y	Y	0.37	1	3	2	4	12		
*Des:	NADH dehydrogenase 1 alpha subcomplex 10-like protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	13.29%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VVEDIEYLNYNK		+2	4.038	0.510	1.0000	2				
		YGLLASILGDK		+2	2.674	0.482	0.9992	3				
		LLQYSDALEHLLSTGQGVVLER				+3	3.610	0.337	0.9984	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	6.92%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VVEDIEYLNYNK		+2	749.88	1497.74	1497.74	0	79	6		
		YGLLASILGDK		+2	575.33	1148.65	1148.64	0.01	66	6		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
494.	IPI00358887		Y	N	0.02	1	2	0	4	0		
*Des:	PREDICTED: similar to hypothetical protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	1%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		NDMAALTAAGK		+2	3.191	0.398	0.9995	4				
		HLIIGVSSDR		+2	2.524	0.337	0.9936	4				
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
495.	IPI00363493		N	Y	0.25	1	0	6	0	10		
*Des:	PREDICTED: maternal embryonic message 3											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					6	1	11.23%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LSQLEGVNVER		+2	622.34	1242.66	1242.66	0	56	2		
		SEDPDQQYLILNTAR			+2	881.93	1761.85	1761.85	0	70	1	
		IPVDTYNNILTVLK		+2	801.96	1601.91	1601.90	0.01	82	2		
		HFHPLFEYFDYESR		+3	629.62	1885.84	1885.84	0	54	2		
		AQLAAITLIIGTFER		+2	808.98	1615.94	1615.93	0.01	51	3		
		FTLPPLVFAAYQLAFR			+2	927.52	1853.03	1853.02	0.01	67	3	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
496.	IPI00372388		Y	Y	0.14	1	2	6	5	10		
*Des:	Chaperonin containing TCP1, subunit 3											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	4.5%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		KVQSGNINAAK		+2	3.304	0.386	0.9989	3				
		GVMINKDVTHPR		+2	3.456	0.444	0.9979	4				
	MASCOT:(PepMatched Observed.Hits Coverage)					6	1	12.97%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AVAQALEVIPR		+2	583.8547	1165.6949	1165.6819	0.01	59	2		
		IVLLDSSLEYK		+2	640.3636	1278.7126	1278.7071	0.01	42	1		
		TAVETAVLLLR		+2	593.8602	1185.7059	1184.7128	0.99	50	1		
		KVQSGNINAAK		+2	565.3233	1128.6321	1128.6251	0.01	75	3		

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                EIQVQHPAAK          +2        560.8130  1119.6114 1119.6036 0.01      55        3
                GVMINKDVTHPR        +2        683.8702  1365.7259 1365.7187 0.01      66        3

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
497.      IPI00231298         Y         Y         0.39      2         2         4         4         4
*Des:     Platelet-activating factor acetylhydrolase IB alpha subunit
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         2         6.25%
                Seq           Charge    Xcor      Delta     Probility PepHits
                EAELDMNEELDKK +2        3.744     0.370     0.9997    2
                VWDYETGDFER   +2        3.825     0.537     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    4         2         16.58%
                Seq           Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                TAPYVVTGSVDQTVK         +2        782.92    1563.82   1563.81   0.01      61        1
                LNEAKEEFTSGGPLGQK       +2        902.96    1803.91   1803.90   0.01      65        2
                TMHGHDHNVSSVAIMPNGDHIVSASR        +3        923.44    2767.28   2768.29   -1        62        1
                AIADYLR  +2   411.23    820.45    820.44    0.01      41        2

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
498.      IPI00193568         Y         Y         0.1       2         5         3         6         30
*Des:     Splice Isoform 4 of Dynamin 1-like protein
          SEQUEST:(PepMatched Observed.Hits Coverage)   5         3         10.51%
                Seq           Charge    Xcor      Delta     Probility PepHits
                SSLLDDLLTESEDMAQR       +2        4.426     0.462     1.0000    2
                LDLMDAGTDAMDVLMGR       +2        4.083     0.530     1.0000    1
                IGDGGQEPTTGNWR          +2        4.505     0.458     1.0000    1
                RLEEPSLR      +2        2.924     0.184     0.9751    1
                VFSPNVVNLTLVDLPGMTK     +2        5.372     0.599     1.0000    1
          MASCOT:(PepMatched Observed.Hits Coverage)    3         1         7.22%
                Seq           Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                LDLMDAGTDAMDVLMGR       +2        912.4384  1822.8622 1822.8263 0.04      104       6
                SSLLDDLLTESEDMAQR       +2        961.9700  1921.9254 1921.8939 0.03      75        24
                LYTDFDEIRQEIENETER      +3        767.3761  2299.1065 2299.0604 0.05      39        18

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
499.      IPI00205568         Y         Y         0.26      1         2         2         2         2
*Des:     Kallistatin
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         7.19%
                Seq           Charge    Xcor      Delta     Probility PepHits
                VSTSDFYVDENTVVK         +2        3.544     0.438     0.9996    1
                MVLVNYIFFQGLWK +2       3.964     0.536     1.0000    1
          MASCOT:(PepMatched Observed.Hits Coverage)    2         1         7.19%
                Seq           Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                VSTSDFYVDENTVVK         +2        851.91    1701.81   1701.81   0         49        1
                MVLVNYIFFQGLWK +2       879.48    1756.95   1756.94   0.01      86        1

No.       Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
500.      IPI00213587         Y         Y         0.1       1         2         2         3         3
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*Des:     26S protease regulatory subunit 8
          SEQUEST:(PepMatched Observed.Hits Coverage)  2          1          8.95%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    EHAPSIIFMDEIDSIGSSR              +3         3.549      0.351      0.9998     1
                    TMLELLNQLDGFEATK                 +2         4.410      0.499      1.0000     3
          MASCOT:(PepMatched Observed.Hits Coverage)   2          1          8.95%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                    TMLELLNQLDGFEATK                 +2         911.9831   1821.9516 1821.9182 0.03       62         2
                    EHAPSIIFMDEIDSIGSSR              +3         702.0168   2103.0287 2102.9942 0.03       57         1

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
501.      IPI00210319           Y          Y          0.16       2          10         2          16         10
*Des:     98 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)  10         2          21.44%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    IEGSGDQVDTLELSGGAR               +2         4.819      0.538      1.0000     1
                    VPVGDQPPDIEYQIK +2    4.140      0.581      1.0000     3
                    AGVYPEKDQAENEDGAQENTFSMDPQLER               +3         5.867      0.599      1.0000     1
                    AFIHHELLAYLYSSADQSSLMEESAEQAQR              +3         7.267      0.692      1.0000     1
                    ESSLILAVTPANMDLANSDALK +2        4.899      0.614      1.0000     1
                    DMILQFISR             +2         3.291      0.268      0.9972     1
                    GWLTINNISLMK          +2         3.046      0.439      0.9993     1
                    VYSPHVLNLTLIDLPGITK              +2         5.069      0.643      1.0000     4
                    ALLQMVQQFGVDFEK                  +2         5.045      0.584      1.0000     3
                    RPLILQLIFSK           +3         3.892      0.431      0.9999     1
          MASCOT:(PepMatched Observed.Hits Coverage)   2          1          2.48%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                    QEIEAETDR             +2         545.7620   1089.5094 1089.4938 0.02       35         5
                    LDLMDEGTDAR           +2         618.2916   1234.5686 1234.5499 0.02       69         8

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
502.      IPI00561114           N          Y          0.51       1          0          2          0          8
*Des:     PREDICTED: similar to Serine/threonine protein kinase 24
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)   2          1          9.56%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                    VLFLIPK    +2         415.28     828.55     828.55     0          43         6
                    ADIWSLGITAIELAK +2    800.95     1599.89    1599.89    0          46         2

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
503.      IPI00557167           Y          Y          0.87       2          2          2          2          6
*Des:     13 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)  2          1          35.13%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    IEINFPAEYPFKPPK +3    3.181      0.600      0.9995     1
                    TDQVIQSLIALVNDPQPEHPLR +3        5.243      0.533      0.9996     1
          MASCOT:(PepMatched Observed.Hits Coverage)   2          1          10.81%
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                            Seq           Charge        ObservedMS                  ExpectedMS                  CalculatedMS                              Pepscore      PepHits
                            ADLAEEYSK                   +2            513.2504      1024.4863     1024.4713     0.02          40            4
                            ADLAEEYSKDR                 +2            648.8171      1295.6197     1295.5993     0.02          41            2

No.           Protein       Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
504.          IPI00198720                 Y             Y             1.15          1             6             6             17            16
*Des:         NAD+-specific isocitrate dehydrogenase a-subunit
              SEQUEST:(PepMatched Observed.Hits Coverage)               6             1             22.25%
                            Seq           Charge        Xcor          Delta         Probility     PepHits
                            APIQWEER                    +2            3.030         0.366         0.9991        7
                            MSDGLFLQK                   +2            2.709         0.371         0.9978        1
                            TPYTDVNIVTIR                +2            3.151         0.492         0.9997        2
                            TPIAAGHPSMNLLLR                           +3            3.933         0.516         1.0000        3
                            IAEFAFEYAR                  +2            3.988         0.503         1.0000        2
                            ENTEGEYSGIEHVIVDGVVQSIK                                 +3            4.605         0.469         1.0000        7
              MASCOT:(PepMatched Observed.Hits Coverage)                6             1             22.25%
                            Seq           Charge        ObservedMS                  ExpectedMS                  CalculatedMS                              Pepscore      PepHits
                            APIQWEER                    +2            514.76        1027.51       1027.51       0             70            8
                            MSDGLFLQK                   +2            519.77        1037.53       1037.52       0.01          45            1
                            TPYTDVNIVTIR                +2            696.38        1390.75       1390.75       0             67            2
                            IAEFAFEYAR                  +2            608.81        1215.60       1215.59       0.01          75            2
                            TPIAAGHPSMNLLLR                           +3            530.97        1589.88       1589.87       0.01          51            3
                            ENTEGEYSGIEHVIVDGVVQSIK                                 +3            834.76        2501.25       2501.23       0.02          64            7

No.           Protein       Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
505.          IPI00366110                 Y             N             0.5           1             3             0             3             0
*Des:         Nucleosome assembly protein 1-like 4
              SEQUEST:(PepMatched Observed.Hits Coverage)               3             1             10.72%
                            Seq           Charge        Xcor          Delta         Probility     PepHits
                            LDNVSHTPSSYIETLPK                         +3            3.130         0.472         0.9997        1
                            QVPNESFFNFFSPLK                           +2            2.948         0.374         0.9965        1
                            GIPEFWFTIFR                 +2            3.582         0.478         0.9999        1
              MASCOT:(PepMatched Observed.Hits Coverage)

No.           Protein       Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
506.          IPI00560245                 N             Y             0.35          1             0             2             0             5
*Des:         39 kDa protein
              SEQUEST:(PepMatched Observed.Hits Coverage)
              MASCOT:(PepMatched Observed.Hits Coverage)                2             1             8.15%
                            Seq           Charge        ObservedMS                  ExpectedMS                  CalculatedMS                              Pepscore      PepHits
                            LGSQHSPGR                   +2            469.7465      937.4785      937.4729      0.01          54            3
                            RMESSINHISQTVDIHKEK                       +3            751.3903      2251.1489     2251.1379     0.01          46            2

No.           Protein       Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
507.          IPI00331955                 Y             Y             0.85          1             5             6             12            11
*Des:         Guanine nucleotide-binding protein G(z), alpha subunit
              SEQUEST:(PepMatched Observed.Hits Coverage)               5             1             21.94%
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Seq	Charge	Xcor	Delta	Probility	PepHits
GQNTYEEAAVYIQR	+3	3.427	0.442	0.9999	4
GEITPELLGVMR	+2	2.848	0.359	0.9965	1
AYDAVQLFALTGPAESK	+2	4.750	0.506	1.0000	7
EYKPLIIYNAIDSLTR	+2	3.010	0.370	0.9967	2
IAAPDYIPTVEDILR	+2	3.045	0.409	0.9982	3

MASCOT:(PepMatched Observed.Hits Coverage) 6 1 23.61%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
DMTTGIVENK	+2	554.27	1106.53	1106.53	0	42	3
LLLLGTSNSGK	+2	551.83	1101.65	1101.64	0.01	51	1
GQNTYEEAAVYIQR	+2	821.40	1640.79	1640.78	0.01	63	4
GEITPELLGVMR	+2	657.86	1313.71	1313.70	0.01	56	1
AYDAVQLFALTGPAESK	+2	890.97	1779.92	1779.90	0.02	106	8
IAAPDYIPTVEDILR	+2	843.47	1684.92	1684.90	0.02	44	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
508.	IPI00198723	Y	Y	0.31	3	5	3	11	10

*Des: Solute carrier family 2, facilitated glucose transporter, member 3

SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 7.96%

Seq	Charge	Xcor	Delta	Probility	PepHits
EEDQATEILQR	+2	3.020	0.298	0.9808	2
KEEDQATEILQR	+2	4.155	0.402	0.9994	5
GSAGVELNSMQPVKETPGNA	+2	4.678	0.506	1.0000	2
GSAGVELNSMQPVKETPGN	+2	5.204	0.532	1.0000	1
FLLINRKEEDQATEILQR	+3	5.502	0.445	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 3 5 4.18%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EEDQATEILQR	+2	666.3331	1330.6517	1330.6364	0.02	50	4
TFEDITR	+2	441.2256	880.4367	880.4290	0.01	44	7
KEEDQATEILQR	+2	730.3812	1458.7479	1458.7314	0.02	70	5

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
509.	IPI00382226	N	Y	0.08	2	0	4	0	46

*Des: Ab2-162

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 4 4 3.67%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
MGNHLTNLR	+2	528.2744	1054.5342	1054.5342	0	48	4
QNYSTEVEAAVNR	+2	740.8553	1479.6961	1479.6953	0	95	17
LVNLHLR	+2	432.7741	863.5337	863.5341	0	52	17
NLNQALLDLHALGSAR	+2	853.4705	1704.9265	1704.9271	0	102	9

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
510.	IPI00382153	Y	Y	0.08	1	5	10	6	20

*Des: Keratin 5

SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 8.87%

Seq	Charge	Xcor	Delta	Probility	PepHits

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                        YEELQQTAGR  +2          3.285       0.441       1.0000      1
                        SRTEAESWYQTK +2         3.220       0.366       0.9961      1
                        TTAENEFVMLKK +2         3.242       0.293       0.9964      1
                        SRTEAESWYQTKYEELQQTAGR              +3          6.013       0.529       1.0000      3
                        VLDTKWTLLQEQGTK         +2          3.667       0.501       1.0000      2
            MASCOT:(PepMatched Observed.Hits Coverage)      10          1           17.57%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        NKYEDEINKR              +3          436.8886    1307.6441 1307.6469 0          43          5
                        YEELQQTAGR              +2          597.7906    1193.5666 1193.5676 0          39          1
                        SRTEAESWYQTK            +2          743.3524    1484.6903 1484.6895 0          39          1
                        WTLLQEQGTK              +2          602.3184    1202.6222 1202.6295 0          34          1
                        LALDVEIATYRK            +2          696.3994    1390.7843 1390.7820 0          55          6
                        TLNNKFASFIDK            +2          699.3791    1396.7437 1396.7350 0.01       38          1
                        TTAENEFVMLKK            +2          705.8680    1409.7215 1409.7224 0          49          1
                        VLDTKWTLLQEQGTK                     +2          880.4855    1758.9565 1758.9516 0          70          2
                        LALDVEIATYR             +2          632.3504    1262.6863 1262.6870 0          67          2
                        SLDLDSIIAEVK            +2          651.8602    1301.7058 1301.7078 0          96          16

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
511.        IPI00373332             N           Y           0.13        1           0           2           0           4
*Des:       PREDICTED: similar to coronin, actin binding protein, 2B
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           2.08%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        QLQLELK +2              436.2636    870.5127    870.5174    0           50          2
                        KLRVIEPR                +2          505.2683    1008.5220 1009.6396 -1.11      43          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
512.        IPI00367853             Y           Y           0.15        2           3           3           3           8
*Des:       Guanylyl cyclase alpha 1 subunit
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           1           6%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        DVVLIGEQAR              +2          3.056       0.240       0.9888      1
                        ATLEHAHQALEEEKKK                    +3          3.164       0.191       0.9515      1
                        GLYLSDIPIHNALR          +2          3.383       0.389       0.9985      1
            MASCOT:(PepMatched Observed.Hits Coverage)      3           2           6.14%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        DVVLIGEQAR              +2          550.3119    1098.6092 1098.6033 0.01       45          4
                        IIAEEAIAAGVPVEALK                   +4          423.7500    1690.9709 1692.9661 -1.99      44          4
                        GLYLSDIPIHNALR          +2          791.4465    1580.8784 1580.8674 0.01       48          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
513.        IPI00197780             Y           Y           6.98        1           5           4           27          23
*Des:       CXC chemokine RTCK1
            SEQUEST:(PepMatched Observed.Hits Coverage)     5           2           33.62%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        EVCLDPTAPMIK            +2          3.147       0.271       0.9910      3
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                        EVCLDPTAPMIKK           +2          3.781       0.366       0.9990      8
                        NGKEVCLDPTAPMIK                     +2          3.932       0.484       0.9990      4
                        NGKEVCLDPTAPMIKK                    +2          4.760       0.505       1.0000      9
                        VNVFRPGAHCDNVEVIATLK                +3          5.815       0.545       1.0000      18
            MASCOT:(PepMatched Observed.Hits Coverage)                  4           2           33.62%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                            Pepscore    PepHits
                        NGKEVCLDPTAPMIK                     +2          808.4218    1614.8290   1614.8109   0.02        46          4
                        EVCLDPTAPMIKK           +2          722.8870    1443.7595   1443.7465   0.01        59          2
                        NGKEVCLDPTAPMIKK                    +2          872.4653    1742.9160   1742.9059   0.01        72          10
                        VNVFRPGAHCDNVEVIATLK                +2          1091.5842   2181.1539   2181.1364   0.02        91          23

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
514.        IPI00189690             N           Y           0.93        2           0           5           0           33
*Des:       Ras-related protein Rab-8B
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)                  5           2           34.12%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                            Pepscore    PepHits
                        NIEEHASSDVER            +2          693.3734    1384.7322   1384.6218   0.11        48          2
                        SSTNVEEAFFTLAR          +2          786.4533    1570.8920   1570.7627   0.13        62          1
                        MNDSNSSGAGGPVKITESR                 +3          636.3443    1906.0111   1905.8850   0.13        45          1
                        LQIWDTAGQER             +2          658.8831    1315.7516   1315.6520   0.1         67          21
                        LLLIGDSGVGK             +2          536.3587    1070.7028   1070.6335   0.07        63          9

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
515.        IPI00400573             Y           Y           0.59        3           3           14          15          136
*Des:       Tubulin, beta2-like
            SEQUEST:(PepMatched Observed.Hits Coverage)                 3           4           12.58%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        INVYYNEATGGK            +2          3.258       0.463       0.9996      2
                        AVLVDLEPGTMDSVR                     +2          4.525       0.430       0.9998      1
                        FWEVISDEHGIDPTGTYHGDSDLQLER                     +3          6.225       0.568       1.0000      3
            MASCOT:(PepMatched Observed.Hits Coverage)                  14          7           45.91%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                            Pepscore    PepHits
                        INVYYNEATGGK            +2          664.83      1327.64     1327.64     0           70          1
                        EVDEQMLNVQNK            +2          723.85      1445.68     1445.68     0           71          18
                        AVLVDLEPGTMDSVR                     +2          801.42      1600.82     1600.81     0.01        65          1
                        FPGQLNADLR              +2          565.80      1129.59     1129.59     0           55          24
                        IMNTFSVVPSPK            +2          660.36      1318.70     1318.70     0           81          6
                        MSATFIGNSTAIQELFK                   +2          929.48      1856.94     1856.93     0.01        93          6
                        YLTVAAVFR               +2          520.30      1038.59     1038.59     0           52          2
                        LHFFMPGFAPLTSR          +3          540.95      1619.83     1619.83     0           62          12
                        SGPFGQIFRPDNFVFGQSGAGNNWAK                      +3          933.46      2797.35     2797.34     0.01        94          8
                        ISEQFTAMFR              +2          615.30      1228.59     1228.59     0           58          10
                        LAVNMVPFPR              +2          572.79      1143.57     1142.63     0.94        70          24
                        ALTVPELTQQMFDAK                     +3          564.63      1690.85     1690.86     0           60          9
                        NSSYFVEWIPNNVK          +2          849.42      1696.82     1695.83     0.99        58          36
                        GHYTEGAELVDSVLDVVR                  +2          980.00      1957.98     1957.97     0.01        125         18
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Identified Human Platelet Proteins

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
516.	IPI00371661	Y	Y	0.2	1	4	4	8	6

*Des: PREDICTED: similar to Rho GTPase activating protein 18

SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 9.74%

Seq	Charge	Xcor	Delta	Probility	PepHits
FLSQESGVAQTLK	+2	3.052	0.388	0.9983	4
DSGLFGIPLTILLEQDQR	+3	5.193	0.540	1.0000	3
EQLQALNLLVILLPDANR	+3	3.588	0.406	0.9998	1
AANGADVPQGVIR	+2	2.755	0.339	0.9932	3

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 9.3%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
GNDASLPSFR	+2	532.26	1062.51	1062.51	0	47	1
FLSQESGVAQTLK	+2	704.38	1406.74	1406.74	0	57	4
DSGLFGIPLTILLEQDQR	+3	672.37	2014.08	2014.07	0.01	70	2
EQLQALNLLVILLPDANR	+3	678.40	2032.17	2032.17	0	51	1

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
517.	IPI00569541	N	Y	1.07	4	0	12	0	70

*Des: 67 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 12 4 25.38%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
ISQLEMAR	+2	474.25	946.49	946.49	0	63	4
ESEAEEWQQK	+2	632.28	1262.54	1262.54	0	51	2
ALTSELANAR	+2	523.28	1044.55	1044.56	0	59	20
AQMVQEDLEK	+2	595.79	1189.56	1189.56	0	61	12
TQEQLASEMAELTAR	+2	839.41	1676.80	1676.80	0	82	2
KTQEQLASEMAELTAR	+2	903.46	1804.91	1804.90	0.01	116	2
GMLREDAVLEYLK	+2	768.91	1535.80	1535.80	0	50	4
IAQDLEMYGVNYFSIK	+2	945.97	1889.92	1889.92	0	95	8
IGFPWSEIR	+2	552.79	1103.57	1103.58	0	42	20
APDFVFYAPR	+2	591.80	1181.59	1181.59	0	62	32
EVWFFGLQYQDTK	+2	830.90	1659.79	1659.79	0	77	8
KGSELWLGVDALGLNIYEQNDR	+3	830.76	2489.26	2489.25	0.01	44	8

No.	Protein	Matched (SEQUEST MASCOT)		emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)	
518.	IPI00372391	Y	Y	0.25	4	11	14	26	57

*Des: Ac2-120

SEQUEST:(PepMatched Observed.Hits Coverage) 11 10 7.29%

Seq	Charge	Xcor	Delta	Probility	PepHits
ITNNNLNDSQR	+2	3.494	0.417	0.9995	4
MYEQEWVR	+2	3.164	0.428	0.9996	3
MPMGLSTGAISDSQIK	+2	5.046	0.521	1.0000	5
FAPSEMDNEETDNTPK	+2	5.094	0.556	1.0000	1
AEVDDVIQVR	+2	3.669	0.291	0.9707	4
SWWGSYWEPSLAR	+2	2.838	0.298	0.9834	2

Seq	Charge	Xcor	Delta	Probility	PepHits
SSMVDKIFEGNSNTK	+2	4.154	0.537	1.0000	2
ANNNKQWLQIDLLK	+3	3.155	0.345	0.9993	4
TFNPLVVVGLSR	+2	4.117	0.557	1.0000	6
INTTGKPSNLPTFSR	+2	4.413	0.590	1.0000	4
NKADKPLSIHPQGIR	+3	3.339	0.442	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 14 16 9.77%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SWYIEDNINK	+2	641.31	1280.61	1280.60	0.01	58	1
AWVYYSAVDVER	+2	729.36	1456.71	1456.70	0.01	82	2
MPMGLSTGAISDSQIK	+2	818.41	1634.82	1634.80	0.02	100	2
NFFNPPIISR	+2	602.83	1203.65	1203.64	0.01	43	5
TFNPLVVVGLSR	+2	651.39	1300.76	1300.75	0.01	70	5
NPDTIAAWYLR	+2	660.35	1318.68	1318.67	0.01	77	2
QHVLLFAVFDESK	+3	511.61	1531.81	1531.80	0.01	68	2
TSPDLGQVLLSLDDK	+2	800.94	1599.86	1599.84	0.02	65	2
SWWGSYWEPSLAR	+2	812.89	1623.76	1623.75	0.01	73	2
DPQGEYEEHLGILGPVIR	+3	674.69	2021.04	2021.02	0.02	56	3
SYSILYSDQGVSWKPYR	+3	683.68	2048.02	2048.00	0.02	62	1
NSHEFYAINGMIYNLPGLR	+3	737.04	2208.09	2208.08	0.01	69	2
EFVLLFMVFDEK	+2	758.90	1515.78	1515.77	0.01	98	3
VADMEQEVVFAMFDENK	+3	667.97	2000.90	2000.89	0.01	51	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
519.	IPI00208118	Y	Y	0.79	4	14	14	27	28

*Des: Non-muscle caldesmon

SEQUEST:(PepMatched Observed.Hits Coverage) 14 7 29.62%

Seq	Charge	Xcor	Delta	Probility	PepHits
VLEEEEQR	+2	2.871	0.279	0.9944	1
LEQYTNAIEGTK	+2	3.726	0.475	0.9998	3
ASKPMKPAASDLPVPAEGVR	+3	4.083	0.234	0.9976	3
MQNNSAENETAEGEEKGESR	+3	3.946	0.390	0.9999	3
GETESEEFEKLK	+2	3.097	0.402	0.9931	1
STHQAAVVSK	+2	3.210	0.550	1.0000	5
RKVLEEEEQR	+3	3.467	0.325	0.9997	2
ASGDKEAEGAPQVEAGKR	+2	5.361	0.377	1.0000	4
RMQNNSAENETAEGEEKGESR	+3	5.565	0.499	1.0000	2
ASGDKEAEGAPQVEAGK	+3	3.394	0.398	0.9998	3
GGNLGENQIKDEK	+2	3.149	0.302	0.9702	1
RGETESEEFEKLK	+3	4.127	0.407	1.0000	2
LKQTENAFSPSR	+3	3.255	0.390	0.9999	3
GSVFSSPSASGTPNKETAGLK	+2	4.755	0.610	1.0000	7

MASCOT:(PepMatched Observed.Hits Coverage) 14 8 29.07%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
KVLEEEEQR	+2	580.3056	1158.5967	1158.5880	0.01	47	2
QTENAFSPSR	+2	568.7731	1135.5317	1135.5258	0.01	78	4
GETESEEFEKLK	+2	713.3454	1424.6762	1424.6670	0.01	48	2
LEQYTNAIEGTK	+2	683.8501	1365.6856	1365.6776	0.01	57	4

STHQAAVVSK		+2	514.2839	1026.5533	1026.5458	0.01	51	3		
RKVLEEEEQR		+3	439.2401	1314.6984	1314.6891	0.01	57	1		
ASGDKEAEGAPQVEAGK			+2	822.3995	1642.7844	1642.7798	0	71	3	
ASGDKEAEGAPQVEAGKR			+2	900.4596	1798.9046	1798.8809	0.02	92	5	
GSSLKIEER		+2	509.7830	1017.5515	1017.5454	0.01	46	1		
RGETESEEFEKLK		+3	527.9337	1580.7791	1580.7681	0.01	43	2		
LKQTENAFSPSR		+2	689.3645	1376.7145	1376.7048	0.01	57	3		
GSVFSSPSASGTPNKETAGLK			+2	1011.5184	2021.0223	2021.0065	0.02	108	5	
QKEFDPTITDGSLSVPSRR			+3	711.7090	2132.1053	2132.0862	0.02	60	2	
SPDGNKSPAPKPSDLRPGDVSGK				+3	769.4000	2305.1782	2305.1662	0.01	47	1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

520. IPI00206443 N Y 0.17 2 0 3 0 6

*Des: PREDICTED: similar to hypothetical protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 3 2 8.36%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
TSGQTSANAHSSR		+2	652.3098	1302.6051	1302.5912	0.01	101	6		
FTARPLVETIFER		+2	789.9408	1577.8670	1577.8565	0.01	47	2		
ARPSQLPEQSSSAQQNAR			+3	652.3326	1953.9759	1953.9616	0.01	79	2	

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

521. IPI00192914 Y Y 0.05 2 7 6 9 11

*Des: Sarcoplasmic/endoplasmic reticulum calcium ATPase 3

SEQUEST:(PepMatched Observed.Hits Coverage) 7 6 8.83%

Seq	Charge	Xcor	Delta	Probility	PepHits		
LGIFGDTEDVLGK		+2	2.850	0.424	0.9950	3	
AYTGREFDDLSPEQQR			+2	4.708	0.403	0.9977	4
MNVFDTDLK		+2	2.790	0.391	0.9957	2	
SQMAAVEPER		+2	3.464	0.325	0.9964	1	
RLGIFGDTEDVLGK		+2	4.044	0.299	0.9950	2	
QWGVVLQMSLPVILLDEALK			+2	2.911	0.500	0.9983	2
LHEFTISGTTYTPEGEVR			+3	3.863	0.511	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 6 4 5.98%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
LGIFGDTEDVLGK		+2	682.3611	1362.7077	1362.7030	0	51	3		
MNVFDTDLK		+2	541.7687	1081.5228	1081.5114	0.01	44	2		
AYTGREFDDLSPEQQR			+2	956.4557	1910.8968	1910.8758	0.02	48	3	
GAPESVIER		+2	479.2596	956.5047	956.4927	0.01	52	4		
SQMAAVEPER		+2	559.2761	1116.5377	1116.5233	0.01	54	1		
RLGIFGDTEDVLGK		+2	760.4230	1518.8315	1518.8041	0.03	75	3		

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

522. IPI00213735 Y Y 0.52 2 6 6 9 17

*Des: Sideroflexin 1

SEQUEST:(PepMatched Observed.Hits Coverage) 6 1 36.58%

Seq	Charge	Xcor	Delta	Probility	PepHits

```
                    YAYDSAFHPDTGEK +2         3.503     0.387     0.9989    2
                    NILLTNEQLENAR  +2         4.378     0.483     1.0000    2
                    QGIVPAGLTENELWR           +2        3.068     0.248     0.9768    1
                    SSMSVTSLEDDLQASIQK        +2        4.791     0.537     1.0000    2
                    ILMAAPGMAIPPFIMNTLEK      +2        3.288     0.495     0.9996    3
                    SGDAPLTVNELGTAYVSATTGAVATALGLNALTK  +3        4.801     0.643     1.0000    1
          MASCOT:(PepMatched Observed.Hits Coverage)    6         2         29.26%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore PepHits
                    QAITQVVISR          +2        557.83    1113.65   1113.65   0         51        6
                    YAYDSAFHPDTGEK +2   800.85    1599.69   1599.68   0.01      53        4
                    NILLTNEQLENAR  +2   764.41    1526.81   1526.81   0         82        4
                    QGIVPAGLTENELWR           +2        841.95    1681.89   1681.88   0.01      43        1
                    SSMSVTSLEDDLQASIQK        +2        969.98    1937.94   1937.93   0.01      72        2
                    ILMAAPGMAIPPFIMNTLEK      +3        720.06    2157.16   2157.14   0.02      48        4

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
523.      IPI00214538         Y         Y         0.45      1         5         4         18        9
*Des:     Transforming growth factor beta 1 precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)   5         1         20.9%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    STVEQHVELYQK   +2        4.288     0.456     1.0000    7
                    VAGESADPEPEPEADYYAK      +2        5.953     0.622     1.0000    6
                    DNVLHVEINGISPK +2        3.433     0.351     0.9981    5
                    QWLNQGDGIQGFR  +2        2.884     0.535     0.9997    2
                    LLTPTDTPEWLSFDVTGVVR     +2        5.333     0.583     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    4         1         15.86%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore PepHits
                    STVEQHVELYQK   +2   730.88    1459.74   1459.73   0.01      58        4
                    DNVLHVEINGISPK +2   768.41    1534.81   1533.82   0.99      75        5
                    QWLNQGDGIQGFR  +2   759.88    1517.75   1517.74   0.01      54        2
                    LLTPTDTPEWLSFDVTGVVR     +3        749.40    2245.19   2245.16   0.03      41        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
524.      IPI00204843         Y         N         0.22      1         2         0         4         0
*Des:     Guanine nucleotide-binding protein G(o), alpha subunit 2
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         7.52%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    TTGIVETHFTFK   +2        3.595     0.447     0.9997    3
                    WFTDTSIILFLNK  +2        2.886     0.400     0.9955    2
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
525.      IPI00566208         N         Y         0.62      2         0         2         0         4
*Des:     14 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)    2         2         21.64%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore PepHits
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GPSYGLSAEVK +2 554.29 1106.56 1106.56 0 49 8
SMQNWHQLENLSNFIK +2 994.99 1987.96 1987.96 0 64 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
526. IPI00211128 Y N 1.04 1 2 0 2 0
*Des: Peripheral-type benzodiazepine receptor
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 27.9%
Seq Charge Xcor Delta Probility PepHits
QMGWALVDLMLVSGVATATTLAWHR +3 5.545 0.709 1.0000 1
LLYPYLAWLAFATMLNYYVWR +3 4.288 0.602 0.9998 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
527. IPI00212794 N Y 0.33 1 0 2 0 6
*Des: Ras-related protein Rab-27A
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 10.22%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
TSVLYQYTDGK +2 637.82 1273.63 1273.62 0.01 70 2
FITTVGIDFR +2 584.83 1167.64 1167.63 0.01 54 8

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
528. IPI00326412 Y N 0.14 1 2 0 12 0
*Des: Gamma enolase
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.7%
Seq Charge Xcor Delta Probility PepHits
LGAEVYHTLK +2 2.996 0.426 0.9998 10
SGETEDTFIADLVVGLCTGQIK +2 3.267 0.417 0.9997 13
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
529. IPI00202235 N Y 0.28 1 0 2 0 9
*Des: Hypertrophied skeletal muscle protein FHL1c
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 11.68%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
QVIGTGSFFPK +2 590.8633 1179.7120 1179.6288 0.08 34 3
AIVAGDQNVEYK +2 653.8860 1305.7574 1305.6564 0.1 58 6

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
530. IPI00327144 Y Y 1.7 4 6 6 40 29
*Des: Cofilin-1
SEQUEST:(PepMatched Observed.Hits Coverage) 6 9 38.52%
Seq Charge Xcor Delta Probility PepHits
YALYDATYETK +2 3.688 0.728 1.0000 5
LGGSAVISLEGKP +3 3.861 0.514 0.9981 6
EILVGDVGQTVDDPYTTFVK +2 6.275 0.508 1.0000 2

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                MIYASSKDAIKK    +2      3.501   0.521   0.9861  1
                NIILEEGKEILVGDVGQTVDDPYTTFVK    +3      6.928   0.774   1.0000  3
                ESKKEDLVFIFWAPESAPLK    +2      5.762   0.642   1.0000  4
        MASCOT:(PepMatched Observed.Hits Coverage)      6       7       32.03%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                YALYDATYETK     +2      669.3281 1336.6417 1336.6187 0.02       39      3
                HELQANCYEEVKDR+3        578.6116 1732.8129 1732.7838 0.03       56      2
                EDLVFIFWAPESAPLK        +2      931.5083 1861.0021 1860.9661 0.04       70      3
                EILVGDVGQTVDDPYTTFVK    +2      1098.5762 2195.1378 2195.0997 0.04      133     2
                NIILEEGKEILVGDVGQTVDDPYTTFVK    +3      1031.5618 3091.6635 3091.5964 0.07      96      3
                KEDLVFIFWAPESAPLK       +2      995.5567 1989.0989 1989.0611 0.04       88      7

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
531.    IPI00324741     Y       Y       0.41    3       11      9       22      25
*Des:   Protein disulfide-isomerase A3 precursor
        SEQUEST:(PepMatched Observed.Hits Coverage)     11      8       30.82%
                Seq     Charge  Xcor    Delta   Probility PepHits
                VDCTANTNTCNK    +2      4.156   0.470   1.0000  4
                LAPEYEAAATR     +2      3.383   0.358   0.9986  5
                DLLTAYYDVDYEKNTK        +2      4.635   0.585   1.0000  2
                FVMQEEFSR       +2      2.903   0.460   0.9995  2
                DLFSDGHSEFLK    +2      2.766   0.248   0.9743  3
                FLQEYFDGNLKR    +2      3.935   0.452   0.9998  4
                KTFSHELSDFGLESTTGEIPVVAIR       +3      4.155   0.514   1.0000  1
                LSKDPNIVIAK     +3      3.942   0.262   0.9871  4
                FISDKDASVVGFFR  +2      4.285   0.589   1.0000  3
                TADGIVSHLKK     +2      3.314   0.454   0.9996  3
                TFLDAGHKLNFAVASR        +2      3.948   0.547   1.0000  1
        MASCOT:(PepMatched Observed.Hits Coverage)      9       8       24.27%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                LNFAVASR        +2      439.2564 876.4983 876.4817 0.02 55      2
                YGVSGYPTLK      +2      542.7959 1083.5772 1083.5600 0.02      39      1
                LSKDPNIVIAK     +2      599.3733 1196.7320 1196.7128 0.02      58      2
                DGEEAGAYDGPR    +2      618.7710 1235.5274 1235.5054 0.02      52      4
                SEPIPETNEGPVK   +2      698.8635 1395.7124 1395.6881 0.02      36      1
                ELNDFISYLQR     +2      699.3677 1396.7209 1396.6986 0.02      66      2
                DLLTAYYDVDYEK   +2      804.3920 1606.7695 1606.7402 0.03      72      4
                MDATANDVPSPYEVK +2      818.8954 1635.7762 1635.7450 0.03      59      2
                EYDDNGEGITIFRPLHLANKFEDK        +3      941.1477 2820.4213 2820.3718 0.05      54      2

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
532.    IPI00367930     N       Y       0.14    1       0       2       0       3
*Des:   PREDICTED: similar to Erbb2 interacting protein isoform 2
        SEQUEST:(PepMatched Observed.Hits Coverage)
        MASCOT:(PepMatched Observed.Hits Coverage)      2       1       4.59%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                MVLTNYMFPQQPR   +2      812.91  1623.80 1623.79 0.01    41      2
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          IDENQLMYLPDSIGGLR          +2        967.49    1932.96   1932.96   0         66        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
533.      IPI00392935         Y         Y         3.06      5         5         8         59        173
*Des:     17 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)        5         4         45.75%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    NKDQGTYEDYVEGLR               +2        4.458     0.493     1.0000    2
                    VLGNPKSDEMNVK  +2             3.814     0.463     1.0000    16
                    VLDFEHFLPMLQTVAK              +2        4.965     0.475     1.0000    65
                    ALGQNPTNAEVLKVLGNPKSDEMNVK              +3        4.699     0.567     1.0000    4
                    HVLVTLGEK           +2        2.568     0.453     0.9998    26
          MASCOT:(PepMatched Observed.Hits Coverage)         8         10        60.13%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    ALGQNPTNAEVLK  +2             677.87    1353.73   1353.73   0         64        36
                    VFDKEGNGTVMGAEIR              +2        861.93    1721.84   1721.84   0         65        6
                    NKDQGTYEDYVEGLR               +2        893.92    1785.82   1785.82   0         90        8
                    NKDQGTYEDYVEGLRVFDK           +3        759.37    2275.07   2275.08   0         44        2
                    ALGQNPTNAEVLKVLGNPK           +2        982.05    1962.09   1962.09   0         98        9
                    EAFQLFDR            +2        513.25    1024.50   1024.50   0         45        3
                    VLDFEHFLPMLQTVAK              +2        944.51    1887.00   1887.00   0         73        6
                    VFDKEGNGTVMGAEIRHVLVTLGEK               +3        900.48    2698.41   2698.41   0         57        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
534.      IPI00394395         Y         Y         0.19      2         2         3         3         4
*Des:     64 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)        2         2         7.84%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    ILEVVNQVQDEER  +2             4.666     0.500     1.0000    2
                    GLLEPQIDDPDSNLEEVIDEADAVSVNNLGSK                  +3        4.574     0.488     1.0000    1
          MASCOT:(PepMatched Observed.Hits Coverage)         3         1         6.51%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    SLQSQENMSPLASTR               +2        824.91    1647.81   1647.79   0.02      50        2
                    ILEVVNQVQDEER  +2             785.92    1569.82   1569.80   0.02      44        2
                    IPVFSAFR            +2        468.77    935.53    935.52    0.01      45        3

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
535.      IPI00199607         Y         N         0.71      1         4         0         4         0
*Des:     Carcinoembryonic antigen-related cell adhesion molecule, secreted isoform CEACAM1a-4C2 precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)        4         1         16.27%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    RPTSASSSPTETVYSVVK            +2        4.109     0.462     0.9998    1
                    WLFNSQSLQLTDR  +2             4.094     0.290     0.9981    1
                    AYTLSVFDQQFNPIQTSVQFR  +2     4.986     0.606     1.0000    1
                    SVLLLAHNLPQEFQVFYWYK  +3      3.641     0.518     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)
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No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
536.       IPI00366051          Y          N          0.16       2          3          0          3          0
*Des:      PREDICTED: transforming growth factor beta 1 induced transcript 1
           SEQUEST:(PepMatched Observed.Hits Coverage)  3          2          5.49%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      DFLQLFAPR             +2         2.767      0.323      0.9950     5
                      GSLDTMLGLLQSDLSRR                +3         3.137      0.291      0.9962     1
                      RDFLQLFAPR            +2         2.901      0.298      0.9933     6
           MASCOT:(PepMatched Observed.Hits Coverage)

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
537.       IPI00365323          Y          Y          0.9        4          4          7          19         48
*Des:      PREDICTED: similar to Chain A, Solution Structure Of Coactosin-Like Protein (Cofilin Family) From Mus Musculus
           SEQUEST:(PepMatched Observed.Hits Coverage)  4          5          26.82%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      SKFALITWIGEDVSGLQR               +2         6.698      0.562      1.0000     22
                      ELEEDFIRSELK          +2         3.234      0.254      0.9572     1
                      AKTGTDKTLVK           +2         3.481      0.337      0.9927     6
                      FTTGDAMSKR            +2         2.788      0.480      0.9993     4
           MASCOT:(PepMatched Observed.Hits Coverage)   7          6          31.21%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      FALITWIGEDVSGLQR                 +2         902.9915   1803.9685  1803.9519  0.02       99         18
                      TGTDKTLVK             +2         481.7826   961.5506   961.5444   0.01       64         16
                      EVVQNFAK              +2         467.7562   933.4978   933.4919   0.01       50         7
                      ELEEDFIRSELK          +2         754.3921   1506.7696  1506.7565  0.01       51         2
                      AKTGTDKTLVK           +2         581.3494   1160.6843  1160.6765  0.01       75         7
                      FTTGDAMSKR            +2         557.2753   1112.5361  1112.5284  0.01       66         3
                      SKFALITWIGEDVSGLQR               +2         1010.5564  2019.0982  2019.0789  0.02       115        3

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
538.       IPI00358033          N          Y          0.14       1          0          2          0          2
*Des:      NADH dehydrogenase (Ubiquinone) Fe-S protein 1, 75kDa
           SEQUEST:(PepMatched Observed.Hits Coverage)
           MASCOT:(PepMatched Observed.Hits Coverage)   2          1          4.32%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore PepHits
                      FASEIAGVDDLGTTGR                 +2         804.90     1607.78    1607.78    0          83         1
                      GLLTYTSWEDALSR +2                806.40     1610.79    1610.79    0          65         1

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
539.       IPI00372470          Y          Y          0.13       2          4          2          12         11
*Des:      PREDICTED: similar to calcium and DAG-regulated guanine nucleotide exchange factor I
           SEQUEST:(PepMatched Observed.Hits Coverage)  4          3          12.12%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      NFDVDGDGHISQEEFQIIR              +3         5.061      0.515      1.0000     2
                      EEEVQTVEDGVFDIH                  +2         5.319      0.586      1.0000     2
                      YWVSAFPAEFDLNPELAEQIK +2         4.732      0.545      1.0000     4
                      DLVALQLALPDWLDPGR                +2         3.228      0.380      0.9984     2
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MASCOT:(PepMatched Observed.Hits Coverage) 2 2 6.69%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
NFDVDGDGHISQEEFQIIR	+3	740.3625	2218.0658	2218.0290	0.04	53	2
YWVSAFPAEFDLNPELAEQIK	+2	1234.1340	2466.2535	2466.2106	0.04	93	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
540.	IPI00367939	Y	Y	0.28	1	5	4	7	5

*Des: PREDICTED: integrin, alpha 2

SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 7.48%

Seq	Charge	Xcor	Delta	Probility	PepHits
GVLNQHQFLEGPEGTGNAR	+3	4.130	0.343	0.9997	1
VDISLEKPGTSPALEAYSETVK	+3	5.244	0.546	1.0000	2
YFFNVADEAALLEK	+2	4.183	0.547	1.0000	2
FGIAVLGYLNR	+2	3.176	0.450	0.9995	2
ADNSVSLIVPLLYDAELHLTR	+3	3.562	0.454	0.9999	1

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 5.61%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
FVQGLDIGPK	+2	537.30	1072.59	1072.59	0	47	1
GVLNQHQFLEGPEGTGNAR	+3	675.34	2022.99	2022.99	0	51	1
VDISLEKPGTSPALEAYSETVK	+3	778.75	2333.22	2333.20	0.02	62	2
YFFNVADEAALLEK	+2	815.41	1628.81	1628.81	0	62	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
541.	IPI00199394	Y	Y	0.2	1	2	2	2	2

*Des: 2',3'-cyclic-nucleotide 3'-phosphodiesterase

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 6.79%

Seq	Charge	Xcor	Delta	Probility	PepHits
ATGAEEYAQQDVVR	+2	4.471	0.498	1.0000	1
DFLPLYFGWFLTK	+2	3.461	0.457	0.9997	1

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 6.79%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
ATGAEEYAQQDVVR	+2	768.87	1535.73	1535.72	0.01	82	1
DFLPLYFGWFLTK	+2	823.94	1645.86	1645.85	0.01	61	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
542.	IPI00464897	Y	Y	0.02	1	2	2	2	6

*Des: Hypothetical LOC361596

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 5.65%

Seq	Charge	Xcor	Delta	Probility	PepHits
ATDFVVDR	+2	2.833	0.389	0.9971	2
LNEHFLNTTDFLDTIK	+2	3.941	0.435	0.9992	1

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 5.65%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
ATDFVVDR	+2	461.7392	921.4638	921.4556	0.01	60	4
LNEHFLNTTDFLDTIK	+2	961.0001	1919.9857	1919.9629	0.02	54	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)

543.	IPI00391997	N	Y	0.25	1	0	2	0	14

*Des: Splice Isoform 5 of Tropomyosin 1 alpha chain

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 12%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SLQEQADAAEER	+2	673.8185	1345.6224	1345.6109	0.01	54	12
AQKDEEKMEIQEIQLK	+3	654.0146	1959.0221	1958.9982	0.02	50	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
544.	IPI00373419	Y	Y	0.06	4	9	10	13	30

*Des: 251 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 9 7 6.2%

Seq	Charge	Xcor	Delta	Probility	PepHits
EGEDMIAEEHFGSEK	+2	3.714	0.536	0.9999	1
TQTAIASEDMPNTLTEAEK	+2	5.419	0.588	1.0000	1
LAEISDVWEEMK	+2	3.251	0.385	0.9991	2
DVEDEILWVGER	+2	2.901	0.458	0.9994	2
EVDDLEQWIAER	+2	3.383	0.410	0.9995	2
DLDDFQSWLSR	+2	3.301	0.403	0.9995	2
FFWEMAEEEGWIR	+2	4.762	0.550	1.0000	2
DGLNEAWADLLELIDTR	+2	3.552	0.417	0.9995	1
IFQEMLYIMDWMDEMK	+2	3.938	0.552	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 10 7 6.66%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VAVVNQIAR	+2	485.3029	968.5912	968.5767	0.01	47	2
DLDDFQSWLSR	+2	691.3327	1380.6509	1380.6310	0.02	68	4
LAEISDVWEEMK	+2	725.3636	1448.7127	1448.6857	0.03	82	4
DVEDEILWVGER	+2	730.3693	1458.7240	1458.6990	0.02	77	4
EVDDLEQWIAER	+2	751.8717	1501.7289	1501.7048	0.02	67	4
EGEDMIAEEHFGSEK	+2	854.3799	1706.7452	1706.7093	0.04	60	2
FFWEMAEEEGWIR	+2	865.4026	1728.7907	1728.7606	0.03	68	4
DGLNEAWADLLELIDTR	+2	972.5115	1943.0085	1942.9636	0.04	47	2
TQTAIASEDMPNTLTEAEK	+2	1025.5027	2048.9908	2048.9572	0.03	111	2
IFQEMLYIMDWMDEMK	+2	1061.9949	2121.9752	2121.9283	0.05	60	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
545.	IPI00364452	Y	N	0.2	2	2	0	2	0

*Des: PREDICTED: similar to Serine/threonine protein kinase 24

SEQUEST:(PepMatched Observed.Hits Coverage) 2 3 7.63%

Seq	Charge	Xcor	Delta	Probility	PepHits
LADFGVAGQLTDTQIK	+2	4.878	0.476	1.0000	1
ADIWSLGITAIELAK	+2	3.793	0.450	0.9997	1

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
546.	IPI00198667	Y	Y	0.32	2	4	5	11	11

*Des: Clusterin precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 4 4 11.64%

Seq	Charge	Xcor	Delta	Probility	PepHits
ASGIIDTLFQDR	+2	2.908	0.390	0.9974	1
VSTVTTHSSDSEVPSR	+3	3.574	0.365	0.9999	1
VSTVTTHSSDSEVPSRVTEVVVK	+3	3.420	0.356	0.9991	1
LTQQYNELLHSLQSK	+2	4.195	0.492	1.0000	3

MASCOT:(PepMatched Observed.Hits Coverage) 5 4 12.08%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LTQQYNELLHSLQSK	+2	901.49	1800.96	1800.94	0.02	58	3
LFDSDPITVVLPEEVSK	+2	944.51	1887.00	1886.99	0.01	104	6
EGALDDTR	+2	438.71	875.40	875.40	0	52	2
SLLNSLEEAK	+2	552.30	1102.59	1102.59	0	49	2
KSLLNSLEEAK	+2	616.35	1230.69	1230.68	0.01	44	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
547.	IPI00231381	Y	N	0.12	1	3	0	3	0

*Des: Major vault protein

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 6.88%

Seq	Charge	Xcor	Delta	Probility	PepHits
GIQDVYVLSEQQGLLLK	+2	3.597	0.416	0.9959	1
LAQDPFPLYPGEVLEK	+2	3.675	0.368	0.9989	1
SVGAYLPAVFEEVLDLVDAVILTEK	+3	4.909	0.496	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
548.	IPI00194525	Y	Y	0.99	4	21	17	63	57

*Des: Coagulation factor XIII A chain precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 21 16 34.76%

Seq	Charge	Xcor	Delta	Probility	PepHits
DGTHVVENVDATHIGK	+3	4.544	0.545	1.0000	6
LIASMTSDSLR	+2	3.545	0.585	1.0000	2
LSVQSSPECIVGK	+2	3.857	0.446	0.9997	2
EIGGDGMQDITDTYK	+2	3.509	0.524	0.9998	2
GTYIPVPVVTELQSGK	+2	3.615	0.551	1.0000	11
SDVDMNFDVENAVLGK	+2	4.797	0.504	1.0000	3
SDVDMNFDVENAVLGKDFR	+2	5.048	0.527	1.0000	4
TESFEVTLDPLSLEK	+2	4.816	0.487	1.0000	2
VGSAMVNAK	+2	3.016	0.495	0.9997	5
WDSNKIDHHTDKYDNNK	+3	4.795	0.415	1.0000	2
HVYGELDLQIR	+2	2.754	0.413	0.9978	4
RAIPPNNSNAAEVDLPTEDLQGLVPR	+3	4.215	0.509	1.0000	1
TESFEVTLDPLSLEKK	+2	3.977	0.438	0.9996	3
KDGTHVVENVDATHIGK	+3	5.700	0.569	1.0000	6
KLIASMTSDSLR	+2	3.917	0.527	1.0000	7
DYLNVTAVHLFK	+2	3.565	0.465	0.9962	3
AGEYMSYLLEQGLLHFFVTAR	+3	5.161	0.588	1.0000	2
GTYIPVPVVTELQSGKWGAK	+2	3.311	0.474	0.9973	3

GVSLKDYLNVTAVHLFK	+2	5.694	0.642	1.0000	21
IDHHTDKYDNNKLIVR	+3	3.177	0.471	1.0000	1
NVWLHLEGPGVMRPK	+3	3.127	0.427	1.0000	7

MASCOT:(PepMatched Observed.Hits Coverage) 17 18 25.23%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LIASMTSDSLR	+2	597.3173	1192.6200	1192.6122	0.01	97	4
EIGGDGMQDITDTYK	+2	821.8745	1641.7345	1641.7192	0.02	62	3
SDVDMNFDVENAVLGK	+2	876.9194	1751.8242	1751.8035	0.02	90	5
TESFEVTLDPLSLEK	+2	854.4453	1706.8761	1706.8614	0.01	88	4
LSVQSSPECIVGK	+2	673.8581	1345.7016	1345.6911	0.01	62	2
GTYIPVPVVTELQSGK	+2	844.4738	1686.9331	1686.9192	0.01	101	10
TESFEVTLDPLSLEKK	+2	918.4932	1834.9718	1834.9564	0.02	43	4
IDHHTDKYDNNK	+2	750.3547	1498.6948	1498.6801	0.01	53	2
VGSAMVNAK	+2	438.7373	875.4601	875.4534	0.01	70	5
DGTHVVENVDATHIGK	+2	846.4302	1690.8459	1690.8274	0.02	65	5
KLIASMTSDSLR	+2	661.3658	1320.7170	1320.7071	0.01	91	6
DYLNVTAVHLFK	+2	711.3621	1420.7097	1418.7558	1.95	56	1
GNPIKVSR	+2	435.7645	869.5145	869.5083	0.01	41	3
KDGTHVVENVDATHIGK	+2	910.4752	1818.9358	1818.9224	0.01	61	7
AGEYMSYLLEQGLLHFFVTAR	+3	815.7532	2444.2379	2444.2198	0.02	75	2
GTYIPVPVVTELQSGKWGAK	+2	1065.5925	2129.1705	2129.1520	0.02	67	3
GVSLKDYLNVTAVHLFK	+2	952.5452	1903.0759	1903.0567	0.02	106	16

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
549.	IPI00207254	Y	Y	0.1	1	2	2	2	2

*Des: Splice Isoform 2 of Synaptotagmin-like protein 4

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 8.62%

Seq	Charge	Xcor	Delta	Probility	PepHits
SALEAESESLDSYTADSDSTSR	+2	5.736	0.593	1.0000	1
SVIDLRPEDVAQESGILGDR	+3	3.823	0.421	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 8.62%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SVIDLRPEDVAQESGILGDR	+3	723.7225	2168.1456	2168.1073	0.04	67	1
SALEAESESLDSYTADSDSTSR	+2	1161.0204	2320.0262	2319.9826	0.04	90	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
550.	IPI00382098	Y	N	0.22	1	2	0	2	0

*Des: RT1 class I histocompatibility antigen, AA alpha chain precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.67%

Seq	Charge	Xcor	Delta	Probility	PepHits
FIAVGYVDDTEFVR	+2	4.067	0.397	0.9997	2
TWTAADFAAQITR	+2	2.931	0.196	0.9515	1

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
551.	IPI00196994	Y	Y	2.55	3	8	4	29	21

*Des: Rho GDP dissociation inhibitor (GDI) alpha

SEQUEST:(PepMatched Observed.Hits Coverage) 8 4 50%

Seq	Charge	Xcor	Delta	Probility	PepHits
IDKTDYMVGSYGPR	+2	3.937	0.515	1.0000	9
VAVSADPNVPNVIVTR	+2	4.655	0.541	1.0000	9
LTLVCSTAPGPLELDLTGDLESFKK	+3	2.786	0.367	0.9986	4
SIQEIQELDKDDESLR	+2	5.731	0.493	1.0000	4
AEEYEFLTPMEEAPK	+2	4.700	0.521	1.0000	5
SIQEIQELDKDDESLRK	+3	4.046	0.488	1.0000	2
YKEALLGR	+2	2.706	0.287	0.9675	2
GVKIDKTDYMVGSYGPR	+2	5.500	0.595	1.0000	5

MASCOT:(PepMatched Observed.Hits Coverage) 4 4 25%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SIQEIQELDKDDESLR	+2	959.4800	1916.9455	1916.9327	0.01	85	8
IDKTDYMVGSYGPR	+2	801.3906	1600.7666	1600.7555	0.01	98	9
VAVSADPNVPNVIVTR	+2	825.9686	1649.9226	1649.9100	0.01	97	9
GVKIDKTDYMVGSYGPR	+2	943.4833	1884.9521	1884.9403	0.01	99	5

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
552.	IPI00362927	Y	Y	1.09	4	3	11	41	118

*Des: Similar to Tubulin alpha-4 chain

SEQUEST:(PepMatched Observed.Hits Coverage) 3 7 8.33%

Seq	Charge	Xcor	Delta	Probility	PepHits
AVFVDLEPTVIDEIR	+2	3.656	0.344	0.9996	4
AVFVDLEPTVIDEIRNGPYR	+2	3.184	0.353	0.9973	14
GHYTIGKEIIDPVLDR	+3	4.875	0.440	1.0000	31

MASCOT:(PepMatched Observed.Hits Coverage) 11 13 30.04%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
NLDIERPTYTNLNR	+2	859.95	1717.88	1717.87	0.01	64	48
DVNAAIAAIK	+2	493.29	984.56	984.56	0	72	6
EIIDPVLDR	+2	535.30	1068.58	1068.58	0	47	4
VGINYQPPTVVPGGDLAK	+2	913.00	1823.99	1823.98	0.01	65	10
FDLMYAK	+2	444.22	886.43	886.43	0	51	12
LDHKFDLMYAK	+2	690.85	1379.69	1379.69	0	44	4
QLFHPEQLITGK	+2	705.89	1409.77	1409.77	0	46	16
QLFHPEQLITGKEDAANNYAR	+3	805.74	2414.20	2414.20	0	79	4
AVFVDLEPTVIDEIR	+2	858.47	1714.92	1714.91	0.01	95	4
IHFPLATYAPVISAEK	+2	878.99	1755.96	1755.96	0	90	42
LISQIVSSITASLR	+2	744.45	1486.88	1486.87	0.01	84	28

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
553.	IPI00207184	Y	Y	0.83	3	4	4	11	8

*Des: Endoplasmic reticulum protein ERp29 precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 4 2 20%

Seq	Charge	Xcor	Delta	Probility	PepHits
FDTQYPYGEK	+2	3.233	0.456	0.9999	5
DGDFENPVPYSGAVK	+2	4.569	0.473	1.0000	3
ILDQGEDFPASELAR	+2	4.878	0.595	1.0000	2

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                    SLNILTAFR           +2        3.489     0.456     0.9996    6
          MASCOT:(PepMatched Observed.Hits Coverage)        4         4         20%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    FDTQYPYGEK          +2        624.29    1246.56   1246.55   0.01      42        5
                    DGDFENPVPYSGAVK               +2        797.88    1593.75   1593.73   0.02      62        3
                    ILDQGEDFPASELAR               +2        830.92    1659.83   1659.81   0.02      114       2
                    SLNILTAFR           +2        518.77    1035.52   1033.59   1.93      56        6

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
554.      IPI00215349         Y         Y         0.91      4         15        15        70        51
*Des:     Hypothetical LOC360950
          SEQUEST:(PepMatched Observed.Hits Coverage)       15        6         42.3%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    VFASLPQVER          +2        3.181     0.368     0.9986    6
                    MTVDESGQLVSCSMDDTVR           +2        5.891     0.670     1.0000    2
                    YAPSGFYIASGDISGK              +2        3.665     0.481     0.9997    1
                    FATASADGQIFIYDGK              +2        4.015     0.513     1.0000    1
                    FGAVFLWDTGSSVGEITGHNK         +3        4.475     0.505     1.0000    2
                    IKDIAWTEDSKR        +3        3.813     0.420     1.0000    5
                    NIDNPAVADIYTEHAHQVVVAK        +2        4.912     0.508     1.0000    6
                    SYIYSGSHDGHINYWDSETGENDSFSGK            +3        7.511     0.634     1.0000    1
                    VYSILGATLKDEGK      +3        2.795     0.393     0.9995    9
                    GPVTDLAYSHDGAFLAVCDASK                  +2        5.783     0.695     1.0000    2
                    LATGSDDNCAAFFEGPPFK           +2        3.991     0.337     0.9985    2
                    IWDTTQKEHILK        +2        3.853     0.375     0.9970    5
                    LHHVSSLAWLDEHTLVTTSHDASVK               +3        5.254     0.540     1.0000    7
                    KVFASLPQVER         +2        3.656     0.478     1.0000    15
                    FKFTIGDHSR          +2        2.763     0.323     0.9720    5
          MASCOT:(PepMatched Observed.Hits Coverage)        15        8         29.33%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    DYSGQGVVK           +2        476.7431  951.4717  951.4661  0.01      46        4
                    FTIGDHSR            +2        466.7351  931.4557  931.4512  0         41        2
                    FATASADGQIFIYDGK              +2        852.4224  1702.8302 1702.8202 0.01      75        2
                    IAVVGEGR            +2        400.7375  799.4604  799.4551  0.01      41        6
                    VINSVDIK +2         444.2656  886.5167  886.5123  0         43        3
                    VYSILGATLKDEGK      +2        747.4201  1492.8257 1492.8136 0.01      92        8
                    YAPSGFYIASGDISGK              +2        816.9069  1631.7993 1631.7831 0.02      57        1
                    LATGSDDNCAAFFEGPPFK           +2        993.9537  1985.8928 1985.8829 0.01      75        2
                    IKDIAWTEDSKR        +2        731.3898  1460.7651 1460.7623 0         44        3
                    VKIQDAHR            +2        483.7810  965.5474  965.5406  0.01      46        2
                    IWDTTQKEHILK        +2        756.4193  1510.8239 1510.8144 0.01      47        5
                    VFASLPQVER          +2        573.3232  1144.6318 1144.6240 0.01      41        3
                    LHHVSSLAWLDEHTLVTTSHDASVK               +3        928.4814  2782.4223 2782.4038 0.02      73        3
                    FKFTIGDHSR          +2        604.3174  1206.6203 1206.6145 0.01      46        3
                    KVFASLPQVER         +3        425.2492  1272.7257 1272.7190 0.01      75        9

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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555.	IPI00211206		Y	Y	0.93	3	11	9	36	34		
*Des:	PDZ and LIM domain protein 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					11	6	53.61%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GCVDNMTLTVSR		+2	3.902	0.448	0.9998	2				
		AAIANLCIGDLITAIDGEDTSSMTHLEAQNK					+3	5.081	0.600	1.0000	4	
		VAASVGNAQK		+2	3.204	0.405	0.9992	4				
		TSASGEEANSRPSAQPHPSGGLIIDKESEVYK					+3	5.124	0.559	1.0000	3	
		GHFFVGDQIYCEK		+2	3.166	0.393	0.9982	1				
		ERVTPPEGYDVVTVFP			+3	3.786	0.515	1.0000	2			
		ERVTPPEGYDVVTVFPK			+2	3.934	0.362	0.9948	1			
		VAASVGNAQKLPICDK			+2	4.856	0.533	1.0000	11			
		SAMPFTASPAPGTR		+2	3.551	0.488	0.9997	5				
		MNLASEPQEVLHIGSAHNR			+2	5.803	0.563	1.0000	17			
		LVGGKDFEQPLAISR			+2	4.859	0.513	1.0000	17			
	MASCOT:(PepMatched Observed.Hits Coverage)					9	7	35.24%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GCVDNMTLTVSR		+2	648.3126	1294.6106	1294.6009	0.01	80	2		
		GHFFVGDQIYCEK		+2	771.8634	1541.7123	1541.6972	0.02	45	1		
		VAASVGNAQK		+2	472.7646	943.5146	943.5086	0.01	62	4		
		IWSPLVTEEGKR		+2	707.8950	1413.7755	1413.7616	0.01	57	2		
		SVKAPVTK		+2	415.2633	828.5121	828.5069	0.01	49	3		
		MNLASEPQEVLHIGSAHNR			+2	1052.0321	2102.0497	2102.0327	0.02	118	11	
		VAASVGNAQKLPICDK			+2	807.4447	1612.8749	1612.8606	0.01	88	10	
		SAMPFTASPAPGTR		+2	695.8477	1389.6809	1389.6711	0.01	61	5		
		LVGGKDFEQPLAISR			+2	815.4589	1628.9033	1628.8885	0.01	85	14	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
556.	IPI00213677		Y	N	0.59	3	4	0	7	0		
*Des:	ADP-ribosylation factor 2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	3	30.81%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ILMVGLDAAGK		+2	3.338	0.493	0.9998	6				
		LGEIVTTIPTIGFNVETVEYK			+2	3.753	0.616	1.0000	1			
		LKLGEIVTTIPTIGFNVETVEYK			+3	3.436	0.392	0.9997	2			
		HYFQNTQGLIFVVDSNDRER			+3	4.189	0.548	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
557.	IPI00192859		Y	Y	0.14	2	7	6	15	16		
*Des:	PREDICTED: similar to mKIAA1631 protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					7	4	9.03%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IQVHYYEDGNVQLVSHK			+3	5.774	0.453	1.0000	7			
		IEGYDDQVLITEHGDLGNSR			+2	4.934	0.627	1.0000	2			
		EGAAHAFAQYNMDQFTPVK			+2	5.241	0.567	1.0000	2			
		LLLNNDNLLR		+2	2.840	0.217	0.9741	4				

		FITHAPPGEFNEVFNDVR			+3	4.210	0.519	1.0000	3			
		EASDPQPEDVDGGLK			+2	3.505	0.436	0.9994	1			
		DVQDSVTVSNEVQTAK			+2	4.785	0.406	0.9998	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					6	3	7.32%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		EASDPQPEDVDGGLK			+2	778.86	1555.71	1555.70	0.01	52	2	
		DVQDSVTVSNEVQTAK			+2	860.43	1718.85	1718.83	0.02	96	3	
		IQVHYYEDGNVQLVSHK			+3	677.02	2028.03	2028.01	0.02	49	6	
		IEGYDDQVLITEHGDLGNSR			+3	744.36	2230.07	2230.05	0.02	61	1	
		LLLNNDNLLR		+2	599.35	1196.70	1196.69	0.01	55	2		
		FTITPPTAQVVGVLK		+2	785.97	1569.93	1569.91	0.02	53	2		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
558.	IPI00557328		Y	Y	0.27	1	2	2	2	2		
*Des:	31 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	13.87%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TSSGPGASSGPGGDHSDLIVR			+3	3.549	0.582	1.0000	2			
		VMLPNSPETLGQATPR			+2	3.502	0.472	0.9996	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	13.87%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TSSGPGASSGPGGDHSDLIVR			+3	651.98	1952.93	1952.92	0.01	42	2	
		VMLPNSPETLGQATPR			+2	855.96	1709.90	1709.88	0.02	77	1	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
559.	IPI00476338		N	Y	0.16	1	0	2	0	2		
*Des:	PREDICTED: striatin, calmodulin binding protein 3											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	3.46%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AYIASAGADALAK		+2	611.33	1220.64	1220.64	0	48	2		
		SASLDVEPIYTFR		+2	749.39	1496.76	1496.75	0.01	44	1		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
560.	IPI00476266		N	Y	0.02	1	0	2	0	4		
*Des:	Protein tyrosine PhosPhatase, recePtor tyPe, Q isoform 2 Precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	0.93%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TLGEGLSER		+2	480.7304	959.4462	960.4876	-1.03	42	2		
		DWQSVSVR		+2	488.7317	975.4488	975.4774	-0.02	38	4		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
561.	IPI00421782		Y	Y	0.1	2	2	2	2	5		
*Des:	Type II keratin Kb18											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	3.94%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					

YEELQVTAGR +2 2.783 0.373 0.9981 1
SRAEAESWYQTKYEELQVTAGR +3 5.936 0.537 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 2 2 4.45%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LVELEDALQKAK +2 679.36 1356.70 1355.77 0.93 54 2
SLDLDSIIAEVK +2 651.86 1301.71 1301.71 0 67 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
562. IPI00190179 Y Y 0.52 4 13 10 20 12
*Des: Glycogen phosphorylase, liver form
SEQUEST:(PepMatched Observed.Hits Coverage) 13 6 26.93%
Seq Charge Xcor Delta Probility PepHits
GIVGVENVAELKK +2 3.476 0.480 0.9998 2
HLQIIYEINQK +2 3.208 0.390 0.9991 2
VIPATDLSEQISTAGTEASGTGNMK +2 6.440 0.680 1.0000 2
TFAYTNHTVLPEALER +2 4.519 0.448 0.9999 3
AWNTMVLR +2 3.049 0.252 0.9957 2
LVTSVAEVVNNDPMVGSK +2 5.098 0.546 1.0000 3
ARPEFMLPVHFYGR +3 3.878 0.358 0.9997 2
EGWQVEEADDWLR +2 3.673 0.447 0.9998 1
DIINMLFYHDR +2 3.011 0.462 0.9996 2
LVIDQIDNGFFSPNQPDLFK +2 5.433 0.713 1.0000 3
LKQEYFVVAATLQDVIR +2 5.869 0.582 1.0000 2
DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR +4 5.483 0.533 1.0000 2
APNDFNLQDFNVGDYIQAVLDR +2 5.840 0.592 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 10 5 17.57%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
GIVGVENVAELKK +2 678.40 1354.79 1354.78 0.01 46 2
DFSELEPDKFQNK +2 798.88 1595.75 1595.75 0 60 1
AWNTMVLR +2 495.76 989.51 989.51 0 46 1
HLQIIYEINQK +2 699.33 1396.64 1397.77 -1.12 55 2
LVTSVAEVVNNDPMVGSK +2 929.99 1857.96 1857.95 0.01 88 2
TFAYTNHTVLPEALER +2 931.48 1860.94 1860.94 0 104 3
EGWQVEEADDWLR +2 816.87 1631.73 1631.72 0.01 74 1
DIINMLFYHDR +2 718.86 1435.70 1435.69 0.01 49 2
LKQEYFVVAATLQDVIR +2 997.06 1992.11 1992.10 0.01 103 2
APNDFNLQDFNVGDYIQAVLDR +3 842.08 2523.22 2523.20 0.02 63 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
563. IPI00421857 Y Y 0.1 2 3 5 5 22
*Des: Type II keratin Kb1
SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 6.13%
Seq Charge Xcor Delta Probility PepHits
TNAENEFVTIKK +2 3.057 0.384 0.9986 3
LLRDYQELMNTK +2 3.419 0.216 0.9757 2
WELLQQVDTSTR +2 2.898 0.371 0.9978 3
MASCOT:(PepMatched Observed.Hits Coverage) 5 12 8.33%

Identified Human Platelet Proteins

		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TNAENEFVTIKK		+2	697.3812	1392.7478	1392.7248	0.02	48	2		
		SLNDKFASFIDKVR		+3	546.9663	1637.8771	1638.8729	-0.99	47	3		
		FLEQQNQVLQTKWELLQQVDTSTR				+3	978.1982	2931.5727	2931.5090	0.06	58	1
		FLEQQNQVLQTK		+2	738.4095	1474.8044	1474.7780	0.03	69	3		
		FASFIDKVR		+2	541.8123	1081.6100	1081.5920	0.02	47	14		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
564.	IPI00369618		Y	Y	0.59	2	9	10	13	31		
*Des:	Eukaryotic translation initiation factor 4A, isoform 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					9	2	34.86%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		KGVAINMVTEEDKR		+3	4.088	0.320	0.9990	2				
		DFTVSAMHGDMDQK			+2	3.898	0.485	0.9999	1			
		KEELTLEGIR		+2	2.734	0.293	0.9910	2				
		LQMEAPHIIVGTPGR		+3	3.968	0.468	0.9999	3				
		GFKDQIYDIFQK		+2	2.992	0.489	0.9952	2				
		LNSNTQVVLLSATMPSDVLEVTK				+2	5.012	0.582	1.0000	3		
		DIETFYNTSIEEMPLNVADL			+2	4.218	0.623	1.0000	1			
		TATFAISILQQIELDLK			+2	4.767	0.481	1.0000	3			
		TATFAISILQQIELDLKATQALVLAPTR				+3	6.818	0.647	1.0000	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					10	3	36.8%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GYDVIAQAQSGTGK		+2	697.85	1393.69	1393.68	0.01	75	6		
		KGVAINMVTEEDKR		+3	530.62	1588.83	1588.82	0.01	41	6		
		DFTVSAMHGDMDQK			+2	791.34	1580.67	1580.66	0.01	67	2	
		KEELTLEGIR		+2	594.28	1186.54	1186.66	-0.11	43	4		
		LQMEAPHIIVGTPGR		+2	809.94	1617.87	1617.87	0	65	6		
		GIYAYGFEKPSAIQQR			+2	914.48	1826.94	1826.93	0.01	74	4	
		VLITTDLLAR		+2	557.85	1113.68	1113.68	0	46	3		
		MFVLDEADEMLSR		+2	778.36	1554.71	1554.71	0	55	3		
		GIDVQQVSLVINYDLPTNR			+3	715.39	2143.13	2143.13	0	43	6	
		TATFAISILQQIELDLK			+2	952.54	1903.06	1903.07	0	82	6	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
565.	IPI00382317		N	Y	0.94	3	0	26	0	182		
*Des:	Ac1873											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					26	5	34.17%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VTSTGTSTTR		+2	505.7622	1009.5099	1009.5040	0.01	70	24		
		NNKDSNSLTR		+2	574.7904	1147.5663	1147.5581	0.01	61	24		
		TVLGNDGHR		+2	484.7518	967.4891	967.4835	0.01	58	40		
		GDLPGDSRGDSATR			+2	702.3346	1402.6546	1402.6436	0.01	44	8	
		MADEAASEAHQEGDTR			+2	859.3647	1716.7149	1716.7009	0.01	94	42	
		EINLKDYEGQQK		+2	732.8768	1463.7390	1463.7256	0.01	76	10		
		GLIDEANQDFTNR		+2	746.8607	1491.7069	1491.6953	0.01	79	6		

SQLQEGPPEWK	+2	649.8266	1297.6386	1297.6302	0.01	59	20
FGSLTSNFK	+2	500.7615	999.5085	999.5025	0.01	49	8
GLIDEANQDFTNRINK	+2	924.4745	1846.9344	1846.9173	0.02	72	6
AQQIQVLQK	+2	528.3175	1054.6205	1054.6135	0.01	72	22
MSPVPDLVPGSFK	+2	687.3657	1372.7168	1372.7060	0.01	61	29
IVERQPSQCK	+2	594.3190	1186.6234	1186.6128	0.01	57	3
TVLGNDGHREVVK	+2	712.3924	1422.7702	1422.7579	0.01	65	4
MELERPGKDGASR	+2	723.3685	1444.7224	1444.7092	0.01	58	8
AQQIQVLQKDVR	+2	713.4180	1424.8215	1424.8099	0.01	65	2
LVTSKGDKELLIGNEK	+2	872.5020	1742.9895	1742.9777	0.01	91	26
RLEVDIDIKIR	+2	685.4185	1368.8225	1368.8089	0.01	51	13
FGSLTSNFKEFGSK	+2	774.8947	1547.7748	1547.7619	0.01	93	11
MKGLIDEANQDFTNRINK	+2	1054.0426	2106.0707	2106.0527	0.02	86	9
VIEKAQQIQVLQK	+2	762.9645	1523.9145	1523.9035	0.01	84	19
QLEQVIAKELLPAKDR	+3	617.6980	1850.0722	1850.0625	0.01	50	3
GDLPGDSRGDSATRGPGSK	+3	610.6337	1828.8794	1828.8663	0.01	48	12
KVIEKAQQIQVLQK	+2	827.0121	1652.0096	1651.9984	0.01	104	16
GLIDEANQDFTNRINKLK	+2	1045.0616	2088.1087	2088.0963	0.01	48	4
RIEILKR	+2	464.3116	926.6086	926.6025	0.01	41	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
566.	IPI00188111	Y	N	0.13	1	2	0	8	0

*Des: PREDICTED: similar to CCT (chaperonin containing TCP-1) zeta subunit

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 5.55%

Seq	Charge	Xcor	Delta	Probility	PepHits
HKSETDTSLIR	+2	2.876	0.371	0.9863	1
AQLGVQAFADALLIIPK	+2	4.205	0.508	1.0000	7

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
567.	IPI00208203	Y	Y	0.33	1	2	2	4	4

*Des: Similar to Peci protein

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.03%

Seq	Charge	Xcor	Delta	Probility	PepHits
GILVTSEGGITK	+2	3.636	0.547	1.0000	4
ATQQDFENAMNQVK	+2	4.208	0.451	0.9998	1

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 7.03%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
GILVTSEGGITK	+2	587.84	1173.67	1173.66	0.01	66	4
ATQQDFENAMNQVK	+2	812.38	1622.75	1622.74	0.01	85	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
568.	IPI00359927	N	Y	0.05	1	0	2	0	3

*Des: PREDICTED: similar to stabilin-2

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 1.46%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits

		VTSGSAGVR		+2	416.7420	831.4695	832.4402	-0.96	35	3		
		CPDGYIKVTSGSAGVR			+4	403.2113	1608.8161	1608.7929	0.02	37	3	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
569.	IPI00189925		Y	Y	1.15	3	10	9	17	11		
*Des:	Alpha-soluble NSF attachment protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					10	3	49.66%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LLEAHEEQNVDSYTESVK			+2	6.034	0.661	1.0000	3			
		VAGYAAQLEQYQK		+2	4.616	0.538	1.0000	3				
		AIEIYTDMGR		+2	2.902	0.400	0.9986	2				
		QAEAMALLAEAER		+2	4.017	0.353	0.9993	1				
		HHISIAEIYETELVDVEK			+4	5.293	0.484	1.0000	3			
		AIDIYEQVGTSAMDSPLLK			+2	6.032	0.603	1.0000	3			
		NSQSFFSGLFGGSSK			+2	4.128	0.526	1.0000	1			
		LDQWLTTMLLR		+2	3.804	0.369	0.9995	1				
		AIAHYEQSADYYKGEESNSSANK				+2	5.888	0.614	1.0000	4		
		AIAHYEQSADYYK		+2	3.799	0.502	0.9999	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					9	4	42.66%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TIQGDEEDLR		+2	587.83	1173.64	1174.55	-0.9	43	1		
		AIAHYEQSADYYK		+2	779.87	1557.72	1557.71	0.01	44	2		
		LLEAHEEQNVDSYTESVK			+3	697.67	2089.99	2089.98	0.01	49	2	
		AIAHYEQSADYYKGEESNSSANK				+3	854.72	2561.15	2561.13	0.02	53	1
		VAGYAAQLEQYQK		+2	734.88	1467.74	1467.74	0	60	3		
		AIEIYTDMGR		+2	584.79	1167.56	1167.56	0	47	2		
		QAEAMALLAEAER		+2	701.86	1401.70	1401.69	0.01	60	3		
		NSQSFFSGLFGGSSK			+2	775.37	1548.72	1548.72	0	103	1	
		HHISIAEIYETELVDVEK			+3	709.03	2124.08	2124.07	0.01	62	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
570.	IPI00208205		Y	Y	1.06	3	13	20	42	96		
*Des:	Heat shock cognate 71 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					13	4	20.85%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		MKEIAEAYLGK		+3	3.528	0.432	1.0000	7				
		TVTNAVVTVPAYFNDSQR			+3	3.515	0.384	0.9999	4			
		DAGTIAGLNVLR		+2	3.640	0.298	0.9973	7				
		SFYPEEVSSMVLTK		+2	3.828	0.348	0.9986	4				
		RFDDAVVQSDMK		+2	3.413	0.522	1.0000	4				
		NQVAMNPTNTVFDAK			+2	4.411	0.484	1.0000	1			
		NQVAMNPTNTVFDAKR			+2	4.444	0.505	1.0000	7			
		SQIHDIVLVGGSTR		+2	4.396	0.597	1.0000	5				
		MVNHFIAEFK		+3	3.670	0.452	1.0000	12				
		LDKSQIHDIVLVGGSTR			+3	3.505	0.284	0.9972	11			
		DAKLDKSQIHDIVLVGGSTR			+2	6.142	0.575	1.0000	10			
		MVNHFIAEFKR		+3	3.353	0.463	1.0000	1				

HWPFMVVNDAGRPK	+3	4.202	0.558	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 20 6 33.78%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
STAGDTHLGGEDFDNR	+2	846.3734	1690.7323	1690.7183	0.01	70	34
RFDDAVVQSDMK	+2	705.8436	1409.6727	1409.6609	0.01	69	9
DAGTIAGLNVLR	+2	600.3447	1198.6749	1198.6669	0.01	82	10
FEELNADLFR	+2	627.3157	1252.6169	1252.6087	0.01	71	6
SFYPEEVSSMVLTK	+2	808.8900	1615.7654	1615.7803	0	52	1
VEIIANDQGNR	+2	614.8228	1227.6310	1227.6207	0.01	66	23
MKEIAEAYLGK	+2	626.8386	1251.6627	1251.6532	0.01	66	8
TVTNAVVTVPAYFNDSQR	+3	661.3420	1981.0041	1980.9904	0.01	41	4
TTPSYVAFTDTER	+2	744.3618	1486.7091	1486.6940	0.02	77	11
NQVAMNPTNTVFDAK	+2	825.4089	1648.8033	1648.7879	0.02	65	1
ARFEELNADLFR	+2	740.8877	1479.7608	1479.7470	0.01	68	8
LSKEDIER	+2	495.2702	988.5259	988.5189	0.01	53	1
VQVEYKGETK	+2	590.8182	1179.6218	1179.6135	0.01	42	2
NQVAMNPTNTVFDAKR	+2	903.4634	1804.9123	1804.8890	0.02	96	8
MVNHFIAEFK	+2	618.3203	1234.6261	1234.6168	0.01	56	8
SQIHDIVLVGGSTR	+2	741.4141	1480.8136	1480.7997	0.01	69	7
ITITNDKGR	+2	509.2917	1016.5688	1016.5614	0.01	51	11
LDKSQIHDIVLVGGSTR	+2	919.5170	1837.0195	1837.0057	0.01	103	8
DAKLDKSQIHDIVLVGGSTR	+2	1076.6019	2151.1893	2151.1647	0.02	117	8
HWPFMVVNDAGRPK	+3	551.9536	1652.8388	1652.8245	0.01	51	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
571.	IPI00358046	Y	Y	0.64	3	11	10	27	18

*Des: PREDICTED: similar to actin related protein 2/3 complex subunit 2

SEQUEST:(PepMatched Observed.Hits Coverage) 11 3 44.13%

Seq	Charge	Xcor	Delta	Probility	PepHits
ASHTAPQVLFSHR	+2	2.953	0.509	0.9992	2
DSIVHQAGMLK	+2	3.047	0.388	0.9976	5
ELQAHGADELLK	+2	3.778	0.419	0.9994	7
YFQFQEEGKEGENR	+2	4.689	0.471	0.9981	4
IIEETLALK	+2	3.150	0.367	0.9983	2
DNTINLIHTFR	+2	3.432	0.360	0.9982	3
VTVVFSTVFK	+2	3.259	0.535	0.9998	1
VTVVFSTVFKDDDDVVIGK	+2	5.974	0.558	1.0000	3
RVYGSFLVNPESGYNVSLLYDLENLPASK	+3	5.529	0.546	1.0000	1
DTDAAVGDNIGYITFVLFPR	+2	6.091	0.645	1.0000	6
DDETMYVESK	+2	3.003	0.484	0.9806	3

MASCOT:(PepMatched Observed.Hits Coverage) 10 3 34.07%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
DSIVHQAGMLK	+2	599.82	1197.62	1197.62	0	74	4
DDETMYVESK	+2	607.82	1213.62	1215.50	-1.87	55	3
ELQAHGADELLK	+2	662.35	1322.69	1322.68	0.01	67	6
YFQFQEEGKEGENR	+2	880.90	1759.79	1759.78	0.01	67	4
VMVSISLK	+2	438.77	875.52	875.51	0.01	43	1

		VFMQEFK+2		464.78	927.54	927.45	0.09	41	7			
		IIEETLALK		+2	515.31	1028.61	1028.61	0	67	2		
		DNTINLIHTFR		+2	672.36	1342.70	1342.70	0	54	3		
		VTVVFSTVFK		+2	563.83	1125.65	1125.64	0.01	55	1		
		DTDAAVGDNIGYITFVLFPR			+3	728.71	2183.10	2183.09	0.01	82	4	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
572.	IPI00365192		Y	Y	0.27	2	6	3	8	10		
*Des:	PREDICTED: adaptor-related protein complex 1, gamma 1 subunit											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	1	12.75%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		SPDMLAHFR		+2	2.722	0.303	0.9941	1				
		NLIMSGYSPEHDVSGISDPFLQVR				+3	4.538	0.499	1.0000	1		
		TFQLQLLSPSSSVVPAFNTGTITQVIK				+3	4.649	0.428	0.9999	1		
		IGYLGAMLLLDER		+2	3.255	0.315	0.9964	1				
		NVGNAILYETVLTIMDIK			+2	5.534	0.569	1.0000	3			
		VLTTAGSYVR		+2	2.524	0.402	0.9973	3				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	2	7.62%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VLTTAGSYVR		+2	533.80	1065.58	1065.58	0	72	6		
		NLIMSGYSPEHDVSGISDPFLQVR				+3	887.78	2660.31	2660.29	0.02	75	2
		TFQLQLLSPSSSVVPAFNTGTITQVIK				+3	959.54	2875.60	2875.57	0.03	41	2

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
573.	IPI00207335		Y	N	0.55	1	2	0	4	0		
*Des:	Platelet-activating factor acetylhydrolase IB beta subunit											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	12.87%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IIVLGLLPR		+2	3.307	0.371	0.9997	3				
		ELFSPLHALNFGIGGDTTR			+2	4.330	0.486	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
574.	IPI00193662		N	Y	0.13	1	0	2	0	2		
*Des:	PREDICTED: similar to ELMO1											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	2.83%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MDPQDQAQR		+2	544.7440	1087.4734	1087.4716	0	50	1		
		QEMANILAQK		+2	572.6348	1143.2550	1144.5910	-1.33	48	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
575.	IPI00212014		Y	Y	0.76	3	15	12	25	24		
*Des:	Transitional endoplasmic reticulum ATPase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					15	4	32.11%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AHVIVMAATNRPNSIDPALR			+2	3.329	0.430	0.9993	3			

EVDIGIPDATGR	+2	2.928	0.404	0.9985	3
WALSQSNPSALR	+2	3.375	0.443	0.9996	1
KYEMFAQTLQQSR	+2	4.490	0.393	0.9998	3
ELQELVQYPVEHPDK	+2	4.209	0.519	0.9999	3
QTNPSAMEVEEDDPVPEIR	+2	5.207	0.581	1.0000	1
LIVDEAINEDNSVVSLSQPK	+2	6.282	0.595	1.0000	2
MDELQLFR	+2	2.969	0.427	0.9996	1
VINQILTEMDGMSTK	+2	5.000	0.571	1.0000	2
NVFIIGATNRPDIIDPAILRPGR	+3	4.045	0.501	1.0000	2
LDQLIYIPLPDEK	+2	3.786	0.370	0.9994	2
IVSQLLTLMDGLK	+2	3.545	0.495	0.9998	2
AVANETGAFFFLINGPEIMSK	+2	5.754	0.614	1.0000	3
NAPAIIFIDELDAIAPK	+2	4.633	0.554	1.0000	4
KMDLIDLEDETIDAEVMNSLAVTMDDFR	+3	5.349	0.487	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 12 5 20.31%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EVDIGIPDATGR	+2	622.32	1242.63	1241.63	1	55	4
WALSQSNPSALR	+2	665.35	1328.69	1328.68	0.01	72	1
KYEMFAQTLQQSR	+2	815.41	1628.80	1628.80	0	80	3
GDIFLVR	+2	410.24	818.47	818.46	0.01	44	1
LEILQIHTK	+2	547.84	1093.66	1093.65	0.01	46	1
ELQELVQYPVEHPDK	+2	912.47	1822.93	1822.91	0.02	75	2
MDELQLFR	+2	526.27	1050.52	1050.52	0	60	1
LDQLIYIPLPDEK	+2	778.94	1555.86	1555.85	0.01	73	2
VINQILTEMDGMSTK	+2	840.42	1678.83	1678.83	0	85	2
IVSQLLTLMDGLK	+2	715.92	1429.83	1429.82	0.01	64	2
NAPAIIFIDELDAIAPK	+2	906.01	1810.01	1809.99	0.02	94	4
AVANETGAFFFLINGPEIMSK	+3	752.72	2255.12	2255.13	0	54	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
576.	IPI00566223	N	Y	0.28	1	0	2	0	2

*Des: 51 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 5.05%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
TTPIEAASSGAR	+2	580.7562	1159.4979	1159.5833	-0.08	41	1
TEHINIHQLR	+2	630.8500	1259.6855	1259.6734	0.01	41	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
577.	IPI00211216	Y	Y	1.23	2	3	4	12	8

*Des: PREDICTED: similar to eukaryotic translation initiation factor 5A

SEQUEST:(PepMatched Observed.Hits Coverage) 3 3 24.84%

Seq	Charge	Xcor	Delta	Probility	PepHits
VHLVGIDIFTGKK	+3	3.831	0.867	1.0000	2
VHLVGIDIFTGK	+2	2.651	0.806	1.0000	3
RNDFQLIGIQDGYLSLLQDSGEVR	+3	6.298	0.709	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 4 3 24.84%

		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VHLVGIDIFTGKK		+3	476.29	1425.84	1425.83	0.01	45	4		
		VHLVGIDIFTGK		+2	649.88	1297.74	1297.74	0	56	2		
		NDFQLIGIQDGYLSLLQDSGEVR				+3	860.77	2579.29	2579.29	0	67	1
		RNDFQLIGIQDGYLSLLQDSGEVR				+3	912.81	2735.40	2735.39	0.01	95	2

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
578.	IPI00194396		Y	N	0.3	1	2	0	4	0		
*Des:	PREDICTED: similar to Cops7b protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	10.06%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ELEDLIIEAVYTDIIQGK			+3	4.282	0.303	0.9991	1			
		ESLPELSAAQQNK		+2	3.223	0.403	0.9994	3				
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
579.	IPI00193595		Y	N	0.29	2	5	0	8	0		
*Des:	Eukaryotic translation initiation factor 4A2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	4	18.55%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GYDVIAQAQSGTGK		+2	3.748	0.553	1.0000	3				
		GIYAYGFEKPSAIQQR			+2	4.730	0.515	1.0000	2			
		VLITTDLLAR		+2	3.298	0.419	0.9997	1				
		GIDVQQVSLVINYDLPTNR			+3	3.810	0.442	0.9997	3			
		MFVLDEADEMLSR		+2	3.483	0.346	0.9986	1				
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
580.	IPI00211075		Y	Y	0.55	4	11	9	18	13		
*Des:	Contrapsin-like protease inhibitor 6 precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					11	6	48.94%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		MQQVEASLQPETLR		+2	4.839	0.497	1.0000	2				
		DTFQSEFYSGK		+2	2.762	0.485	0.9995	1				
		AVLDVAETGTEAAAATGVK			+2	5.276	0.687	1.0000	2			
		ALYQAEAFTADFQQSR			+3	4.867	0.507	1.0000	3			
		EVFSTQADLSGITGDKDLMVSQVVHK				+3	4.515	0.447	0.9974	2		
		DEIQISTGNALFIEK		+2	3.986	0.354	0.9992	1				
		DSLRPSMIDELYLPK			+3	4.889	0.508	1.0000	1			
		TSMVLVNYIYFK		+2	3.431	0.457	0.9998	2				
		FSISADYNLEDVLPELGIK			+2	5.420	0.586	1.0000	1			
		NVVFSPLSISAALAVVSLGAK			+2	7.263	0.668	1.0000	5			
		LDPLIIAFDRPFLMIISDTETAIAPFLAK				+3	5.793	0.560	1.0000	3		
	MASCOT:(PepMatched Observed.Hits Coverage)					9	4	36.94%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MQQVEASLQPETLR		+2	815.42	1628.82	1628.82	0	94	2		
		LQVLAEFQEK		+2	603.08	1204.15	1203.65	0.5	43	2		

AVLDVAETGTEAAAATGVK +2 887.47 1772.93 1772.92 0.01 81 4
TSMVLVNYIYFK +2 739.40 1476.78 1476.77 0.01 47 2
DEIQISTGNALFIEK +2 839.44 1676.87 1676.86 0.01 54 1
DSLRPSMIDELYLPK +3 592.98 1775.92 1775.91 0.01 47 2
ALYQAEAFTADFQQSR +2 923.45 1844.88 1844.87 0.01 105 3
EVFSTQADLSGITGDKDLMVSQVVHK +3 935.48 2803.42 2803.41 0.01 58 2
NVVFSPLSISAALAVVSLGAK +3 681.74 2042.18 2042.18 0 70 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
581. IPI00200651 Y Y 0.78 1 4 3 5 4
*Des: PREDICTED: similar to N-acetylneuraminic acid synthase (sialic acid synthase)
SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 18.58%
Seq Charge Xcor Delta Probility PepHits
VGSGDTNNFPYLEK +2 3.609 0.402 0.9993 2
GSDHLASLEPGELAELVR +2 4.572 0.592 1.0000 3
IPAGTILTLDMLTVK +2 4.738 0.550 1.0000 1
LFPDIPIGYSGHETGIAISVAAVALGAK +3 3.132 0.267 0.9856 1
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 11.76%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VGSGDTNNFPYLEK +2 770.88 1539.74 1539.72 0.02 60 2
GSDHLASLEPGELAELVR +2 947.00 1891.98 1891.96 0.02 68 2
IPAGTILTLDMLTVK +2 793.47 1584.92 1584.92 0 71 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
582. IPI00326433 N Y 1 1 0 3 0 6
*Des: 10 kDa heat shock protein, mitochondrial
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 37.86%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VLLPEYGGTK +2 538.8362 1075.6578 1075.5913 0.07 51 4
VLQATVVAVGSGGK +2 643.4171 1284.8196 1284.7401 0.08 65 3
VVLDDKDYFLFR +2 765.4527 1528.8908 1528.7925 0.1 46 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
583. IPI00388209 Y N 0.21 1 2 0 2 0
*Des: PREDICTED: similar to alpha glucosidase II, beta subunit
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 5.8%
Seq Charge Xcor Delta Probility PepHits
SLEDQVETLR +2 2.840 0.303 0.9943 1
MPPYDEETQAIIDAAQEAR +3 3.908 0.265 0.9972 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
584. IPI00200653 Y Y 0.3 2 4 3 7 16
*Des: SLP-76 adaptor ptotein
SEQUEST:(PepMatched Observed.Hits Coverage) 4 2 11.61%
Seq Charge Xcor Delta Probility PepHits

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          SEVLAWNPDNLADYFR     +2       4.720      0.568      1.0000     4
          GKEDFLSVSDIIDYFR     +2       4.475      0.647      1.0000     1
          LSQDINKNEERR  +3     3.715    0.210      0.9900     2
          FLNLTENDIQKFPK  +2   4.283    0.431      0.9989     3
MASCOT:(PepMatched Observed.Hits Coverage)      3          2          9.17%
          Seq        Charge    ObservedMS       ExpectedMS            CalculatedMS                        Pepscore  PepHits
          SEVLAWNPDNLADYFR     +2       955.4639   1908.9133  1908.9006  0.01       71         10
          GKEDFLSVSDIIDYFR     +2       952.9867   1903.9588  1902.9363  1.02       83         2
          FLNLTENDIQKFPK  +2   853.9680 1705.9214  1705.9039  0.02       66         8

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
585.      IPI00561215           N         Y        0.22     2          0          7          0          49
*Des:     50 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)      7          2          20.61%
          Seq        Charge    ObservedMS       ExpectedMS            CalculatedMS                        Pepscore  PepHits
          DVNAAIATIK           +2       508.2916   1014.5686  1014.5709  0          47         6
          NLDIERPTYTNLNR       +2       859.9444   1717.8742  1717.8747  0          38         6
          FDLMYAK+2  444.2191  886.4236   886.4258   0          41         3
          EIIDLVLDR            +2       543.3129   1084.6112  1084.6128  0          38         4
          IHFPLATYAPVISAEK              +2         878.9840   1755.9535  1755.9559  0          37         9
          AVCMLSNTTAIAEAWAR             +2         904.4464   1806.8783  1806.8756  0          75         29
          LISQIVSSITASLR       +3       496.6295   1486.8668  1486.8719  0          46         18

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
586.      IPI00561142           N         Y        0.2      1          0          2          0          2
*Des:     46 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)      2          1          6.06%
          Seq        Charge    ObservedMS       ExpectedMS            CalculatedMS                        Pepscore  PepHits
          ISFDLSLAR            +2       511.29     1020.57    1020.56    0.01       46         1
          LLFEYLTLFGIDDK       +2       843.96     1685.90    1685.89    0.01       67         1

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
587.      IPI00369550           Y         N        0.02     1          2          0          7          0
*Des:     PREDICTED: similar to Ab2-162
          SEQUEST:(PepMatched Observed.Hits Coverage)     2          1          12.5%
          Seq        Charge    Xcor     Delta      Probility  PepHits
          QNYSTEVEAAVNR        +2       4.111      0.489      1.0000     2
          NLNQALLDLHALGSAR     +2       4.759      0.536      1.0000     5
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
588.      IPI00421791           Y         N        0.02     1          2          0          2          0
*Des:     Type I keratin KA22
          SEQUEST:(PepMatched Observed.Hits Coverage)     2          1          5.21%
          Seq        Charge    Xcor     Delta      Probility  PepHits
```

TKYETELNLR	+2	2.621	0.371	0.9916	2
NRKDAEEWFFTK	+3	3.191	0.229	0.9956	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
589.	IPI00561146	N	Y	0.3	1	0	2	0	3

*Des: PREDICTED: similar to Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor interacting protein 1) (TRIP-1)

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 12.3%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
DPSQIDSNEPYMK	+2	762.35	1522.68	1522.66	0.02	60	2
QINDIQLSR	+2	543.80	1085.59	1085.58	0.01	45	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
590.	IPI00369480	Y	N	0.51	1	2	0	2	0

*Des: PREDICTED: similar to HSPC263

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 10.35%

Seq	Charge	Xcor	Delta	Probility	PepHits
LLTSGYLQR	+2	2.591	0.342	0.9945	3
GEGGTTNPHVFPEGSEPK	+2	3.978	0.464	0.9998	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
591.	IPI00372700	Y	N	0.08	1	2	0	2	0

*Des: PREDICTED: aminopeptidase puromycin sensitive

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 4.48%

Seq	Charge	Xcor	Delta	Probility	PepHits
VTLSFPSTLQTGTGTLK	+2	2.909	0.403	0.9976	1
IDLIAIADFAAGAMENWGLVTYR	+3	4.306	0.496	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
592.	IPI00369628	Y	Y	0.37	4	11	7	20	12

*Des: PREDICTED: similar to arachidonate 12-lipoxygenase

SEQUEST:(PepMatched Observed.Hits Coverage) 11 8 24.85%

Seq	Charge	Xcor	Delta	Probility	PepHits
LEDFDQIFWGQK	+2	3.777	0.530	1.0000	1
SWNRLEDFDQIFWGQK	+2	4.784	0.552	1.0000	2
GKEEEFDFDVAEDLGPLQFVK	+3	3.312	0.216	0.9676	1
TKAVLSQFQADLENLEKEITAR	+3	5.477	0.619	1.0000	1
EITEVGLCHAQDR	+2	3.725	0.372	0.9990	1
LVLPPGTEELQAQLEK	+2	3.482	0.494	0.9996	2
MPPPTSKDDVTMETIMGSLPDVQK	+3	3.607	0.458	1.0000	3
TQLISDGGIFDQVVSTGGGGHVQLLTR	+3	4.395	0.526	1.0000	4
AGVLEMGLKR	+2	2.961	0.294	0.9937	7
LWLVGAHR	+2	2.821	0.340	0.9974	5

		SRTQLISDGGIFDQVVSTGGGGHVQLLTR				+3	7.821	0.670	1.0000	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					7	7	12.86%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LEDFDQIFWGQK		+2	763.3755	1524.7364	1524.7249	0.01	67	2		
		EITEVGLCHAQDR		+2	735.8590	1469.7035	1469.6932	0.01	70	1		
		TQLISDGGIFDQVVSTGGGGHVQLLTR				+3	919.1568	2754.4486	2754.4300	0.02	77	1
		LWLVGAHR		+2	476.2825	950.5504	950.5450	0.01	44	4		
		SALAEKVHR		+2	505.7947	1009.5749	1009.5668	0.01	44	1		
		AGVLEMGLKR		+2	537.3131	1072.6117	1072.6062	0.01	64	6		
		SRTQLISDGGIFDQVVSTGGGGHVQLLTR				+4	750.4052	2997.5917	2997.5631	0.03	91	3

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
593.	IPI00196210		N	Y	0.04	1	0	2	0	6		
*Des:	PREDICTED: similar to probable ATP-dependent RNA helicase - mouse											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	2.18%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DFLDEYIFLAVGR		+2	779.4175	1556.8205	1556.7874	0.03	43	1		
		DLLDLLVEAK		+2	564.8375	1127.6605	1127.6438	0.02	50	5		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
594.	IPI00231610		Y	Y	0.32	2	2	10	2	11		
*Des:	Calpain-1 catalytic subunit											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	3.72%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DKELGLGRHENAIK		+2	3.333	0.407	0.9924	1				
		ELAGQPVHLKR		+2	2.943	0.407	0.9976	4				
	MASCOT:(PepMatched Observed.Hits Coverage)					10	2	21.93%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LAGDDMEISVK		+2	589.29	1176.57	1176.57	0	47	2		
		VLSEEEIDDNFK		+2	719.34	1436.67	1436.67	0	57	1		
		GPWSDNSYEWNK		+2	741.82	1481.62	1481.62	0	57	1		
		AGTQELDDQIQANLPDEK			+2	992.98	1983.95	1983.94	0.01	107	1	
		APSDLYQIILK		+2	630.86	1259.71	1259.71	0	42	2		
		NWNTTFYEGTWR		+2	788.76	1575.51	1573.69	1.82	57	1		
		DMETIGFAVYQVPR		+2	813.40	1624.79	1624.79	0	41	3		
		LPPGEYIVVPSTFEPNKEGDFLLR				+3	906.48	2716.42	2716.41	0.01	48	1
		ILDTDLDGVVTFDLFK			+2	905.98	1809.94	1809.94	0	105	1	
		LVFVHSAQGNEFWSALLEK			+3	725.71	2174.11	2174.12	0	64	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
595.	IPI00287835		N	Y	1.6	1	0	2	0	4		
*Des:	Hemoglobin alpha-1 and alpha-2 chains											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	27.08%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IGGHGGEYGEEALQR			+2	786.8735	1571.7324	1571.7327	0	62	3	

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                    AADHVEDLPGALSTLSDLHAHK              +3        766.3866  2296.1380 2296.1447 0         43        2

No.        Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
596.       IPI00373505        Y         Y         0.32      1         3         3         6         7
*Des:      Tropomodulin 3
           SEQUEST:(PepMatched Observed.Hits Coverage)     3         1         14.24%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    SNDPVAAAFADMLK +2   3.253     0.576     1.0000    4
                    DLGDYKDLDEDELLGKLSESELK                 +3        4.938     0.503     1.0000    1
                    LGYQFTQQGPR    +2   3.065     0.418     0.9989    5
           MASCOT:(PepMatched Observed.Hits Coverage)      3         1         10.05%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    SNDPVAAAFADMLK +2   725.3569  1448.6993 1448.6969 0         63        2
                    LGYQFTQQGPR    +2   647.8353  1293.6561 1293.6465 0.01      57        4
                    HFSLAATR       +2   451.7489  901.4833  901.4770  0.01      49        1

No.        Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
597.       IPI00373432        N         Y         0.32      1         0         3         0         8
*Des:      PREDICTED: small inducible cytokine subfamily E, member 1
           SEQUEST:(PepMatched Observed.Hits Coverage)
           MASCOT:(PepMatched Observed.Hits Coverage)      3         1         14.33%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    AILQATLR            +2        443.28    884.55    884.54    0.01      46        4
                    TVVSGLVNHVPLEQMQNR  +3        674.36    2020.06   2020.05   0.01      58        4
                    ITFDAFPGEPDKELNPK   +2        959.99    1917.97   1916.95   1.02      45        5

No.        Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
598.       IPI00560349        N         Y         0.22      1         0         2         0         8
*Des:      Protein
           SEQUEST:(PepMatched Observed.Hits Coverage)
           MASCOT:(PepMatched Observed.Hits Coverage)      2         1         6.64%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    FRHENIIGINDIIR +2   855.4830  1708.9514 1708.9372 0.01      47        7
                    MLTFNPHKR      +2   572.3125  1142.6104 1142.6019 0.01      44        2

No.        Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
599.       IPI00208213        Y         Y         1.47      1         2         4         5         8
*Des:      ZW10 interactor
           SEQUEST:(PepMatched Observed.Hits Coverage)     2         1         10.33%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    AFEQLEAK       +2   2.973     0.262     0.9955    2
                    NAVAEENAVAEENAVADK  +2        6.647     0.610     1.0000    4
           MASCOT:(PepMatched Observed.Hits Coverage)      4         1         19.55%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    AFEQLEAK       +2   468.25    934.49    934.48    0.01      50        1
                    LDGSHQELETLK   +2   685.36    1368.70   1368.69   0.01      43        2
                    NAVAEENAVAEENAVADK  +2        922.45    1842.89   1842.86   0.03      139       4
```

		ATYMDHVDVIK		+2	646.31	1290.60	1290.63	-0.02	47	2		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
600.	IPI00358052		Y	Y	0.94	1	4	5	17	28		
*Des:	30 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	2	26.88%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		EVAEAYEVLSDK		+2	3.115	0.493	0.9997	1				
		SVSINGVPDDLALGLELSR			+2	4.806	0.537	1.0000	2			
		EFFGSGDPFSELFDDLGAFSELQNQGSR				+3	5.080	0.550	1.0000	1		
		SVSTSTTFVQGR		+2	3.455	0.584	1.0000	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					5	2	26.88%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VEVEEDGQLK		+2	573.29	1144.57	1144.56	0.01	49	3		
		SVSTSTTFVQGR		+2	635.33	1268.64	1268.64	0	71	6		
		FKEVAEAYEVLSDK		+2	814.42	1626.83	1626.81	0.02	117	2		
		SVSINGVPDDLALGLELSR			+2	978.04	1954.06	1954.04	0.02	66	9	
		SETGGMEPGFTFTFR			+2	832.38	1662.75	1662.73	0.02	98	14	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
601.	IPI00366218		Y	Y	0.35	2	10	9	11	15		
*Des:	Chaperonin containing TCP1, subunit 2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					10	3	33.82%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		EALLSSAVDHGSDEVK			+2	4.345	0.516	1.0000	1			
		GATQQILDEAER		+2	3.928	0.354	0.9995	2				
		ILIANTGMDTDKIK		+2	3.945	0.452	0.9977	2				
		LIEEVMIGEDK		+2	3.172	0.420	0.9995	2				
		LGGSLADSYLDEGFLLDK			+2	3.270	0.249	0.9859	1			
		MLPTIIADNAGYDSADLVAQLR			+3	5.030	0.394	0.9997	1			
		QVLLSAAEAAEVILR		+2	3.378	0.478	0.9997	2				
		LSSFIGAIAIGDLVK		+2	4.654	0.453	0.9999	1				
		VQDDEVGDGTTSVTVLAAELLR				+3	4.928	0.475	0.9999	1		
		QLIYNYPEQLFGAAGVMAIEHADFAGVER				+3	5.488	0.544	1.0000	1		
	MASCOT:(PepMatched Observed.Hits Coverage)					9	3	26.47%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GATQQILDEAER		+2	665.83	1329.66	1329.65	0.01	60	2		
		ILIANTGMDTDKIK		+2	766.93	1531.84	1531.83	0.01	63	2		
		EALLSSAVDHGSDEVK			+2	828.91	1655.80	1655.80	0	64	1	
		LAVEAVLR		+2	435.77	869.53	869.53	0	46	1		
		LIEEVMIGEDK		+2	638.33	1274.65	1274.64	0.01	60	2		
		MLPTIIADNAGYDSADLVAQLR			+3	783.07	2346.19	2346.19	0	50	1	
		LSSFIGAIAIGDLVK		+2	752.44	1502.87	1502.87	0	62	1		
		QVLLSAAEAAEVILR		+2	791.96	1581.91	1581.91	0	57	2		
		VQDDEVGDGTTSVTVLAAELLR				+3	763.39	2287.16	2287.15	0.01	51	1

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										

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602.     IPI00373436     Y       Y       0.25    1       2       3       3       4
*Des:    PREDICTED: similar to adaptor protein DAPP1
         SEQUEST:(PepMatched Observed.Hits Coverage)     2       2       6.48%
                 Seq     Charge  Xcor    Delta   Probility       PepHits
                 HAAEALLLSNGR    +2      3.396   0.538   1.0000  3
                 TENDLVPTAPSLGTK         +2      3.470   0.352   0.9987  1
         MASCOT:(PepMatched Observed.Hits Coverage)      3       2       11.18%
                 Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 HAAEALLLSNGR    +2      626.35  1250.69 1250.67 0.02    66      3
                 TENDLVPTAPSLGTK         +2      771.91  1541.81 1541.79 0.02    44      1
                 ADGGSDLFQDLGWYHSNLTR +3         751.93  2252.76 2251.03 1.73    41      1

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
603.     IPI00208215     N       Y       0.32    1       0       2       0       2
*Des:    PRx III
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)      2       1       9.54%
                 Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 HLSVNDLPVGR     +2      603.8700 1205.7254 1205.6516 0.07 51    1
                 GLFIIDPNGVIK    +2      643.4263 1284.8380 1284.7441 0.09 38    1

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
604.     IPI00358127     Y       N       0.18    2       3       0       6       0
*Des:    PREDICTED: similar to actin-related protein 3-beta
         SEQUEST:(PepMatched Observed.Hits Coverage)     3       3       8.94%
                 Seq     Charge  Xcor    Delta   Probility       PepHits
                 NIVLSGGSTMFR    +2      3.765   0.444   0.9998  2
                 HGIVEDWDLMER    +2      3.191   0.608   1.0000  3
                 DITYFIQQLLR     +2      3.642   0.411   0.9997  3
         MASCOT:(PepMatched Observed.Hits Coverage)

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
605.     IPI00363816     N       Y       0.62    1       0       3       0       3
*Des:    PREDICTED: similar to Williams-Beuren syndrome critical region protein 21
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)      3       1       12.46%
                 Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                 AVDIPENIPHSR    +2      674.36  1346.71 1346.69 0.02    44      4
                 LADEQLSSVVK     +2      594.83  1187.65 1187.64 0.01    57      2
                 QFLLTNLVEVNGR   +2      752.41  1502.81 1501.83 0.98    42      1

No.      Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
606.     IPI00365348     Y       Y       0.32    3       13      14      19      33
*Des:    PREDICTED: RAS p21 protein activator 3
         SEQUEST:(PepMatched Observed.Hits Coverage)     13      5       17.2%
                 Seq     Charge  Xcor    Delta   Probility       PepHits
                 QVIAGVGTLEQEHAQYR       +2      4.684   0.570   1.0000  4
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LKDGENLENNMESLR	+2	4.559	0.350	0.9892	2
SHFDFEEEDVDKLEIR	+3	3.742	0.483	0.9993	2
VDLWNASNLK	+2	3.460	0.486	0.9999	2
NMFQVIQPER	+2	2.994	0.403	0.9683	3
DTWFQLQHVDADSEVQGK	+2	4.822	0.625	1.0000	2
SVYDGPEQEEYSTFIIDDPQETYK	+3	4.117	0.318	0.9989	1
LNVVYTEDHVFSSEYYSPLR	+3	4.400	0.625	1.0000	2
FGDEFLGELR	+2	3.375	0.330	0.9988	1
NFLDLISSSGR	+2	3.010	0.331	0.9969	2
YASSYEAWYFLQPR	+3	2.899	0.378	0.9992	2
IYSLFNLYMGK	+2	3.031	0.639	1.0000	1
ESYMATFYEFFNEQK	+2	3.841	0.471	0.9998	2

MASCOT:(PepMatched Observed.Hits Coverage) 14 5 15.76%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
TIQTLGSLSK	+2	524.31	1046.60	1046.60	0	53	2
DGENLENNMESLR	+2	760.84	1519.66	1519.66	0	49	4
LKDGENLENNMESLR	+2	881.43	1760.84	1760.84	0	101	4
QVIAGVGTLEQEHAQYR	+2	950.00	1897.98	1897.96	0.02	111	8
VDLWNASNLK	+2	580.31	1158.61	1158.60	0.01	69	2
NMFQVIQPER	+2	630.37	1258.73	1260.63	-1.89	53	3
SHFDFEEEDVDKLEIR	+3	669.99	2006.95	2006.92	0.03	42	2
DTWFQLQHVDADSEVQGK	+3	701.67	2101.98	2101.97	0.01	54	1
FGDEFLGELR	+2	591.80	1181.58	1181.57	0.01	62	2
NFLDLISSSGR	+2	604.82	1207.62	1207.62	0	56	4
LNVVYTEDHVFSSEYYSPLR	+3	806.73	2417.16	2417.15	0.01	48	2
YTAVSSFIFLR	+2	652.36	1302.70	1302.70	0	42	2
IYSLFNLYMGK	+2	674.86	1347.70	1347.69	0.01	55	2
ESYMATFYEFFNEQK	+2	967.43	1932.84	1932.82	0.02	59	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
607.	IPI00197885	Y	N	0.3	2	5	0	13	0

*Des: Tubulin beta chain

SEQUEST:(PepMatched Observed.Hits Coverage) 5 5 15.01%

Seq	Charge	Xcor	Delta	Probility	PepHits
INVYYNEAAGNK	+2	4.296	0.455	0.9999	8
ALTVPELTQQMFDSK	+2	4.446	0.545	1.0000	6
YLTVAAIFR	+2	3.078	0.383	0.9993	1
MSATFIGNSTAIQELFK	+2	5.384	0.447	0.9609	2
MSATFIGNSTAIQELFKRISEQFTAMFR	+3	3.813	0.425	0.9937	3

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
608.	IPI00189795	Y	Y	1.57	4	19	7	193	60

*Des: Tubulin alpha-1 chain

SEQUEST:(PepMatched Observed.Hits Coverage) 19 14 58.6%

Seq	Charge	Xcor	Delta	Probility	PepHits
DVNAAIATIK	+2	3.417	0.478	0.9998	9

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                    NLDIERPTYTNLNR  +3        2.611     0.440     0.9999    15
                    TIGGGDDSFNTFFSETGAGK      +2        5.918     0.677     1.0000    4
                    AVFVDLEPTVIDEVR +2        5.529     0.460     1.0000    20
                    AYHEQLSVAEITNACFEPANQMVK            +2        5.764     0.609     1.0000    14
                    AVCMLSNTTAIAEAWAR         +2        4.588     0.562     1.0000    7
                    TIQFVDWCPTGFK   +2        4.351     0.463     1.0000    3
                    FDGALNVDLTEFQTNLVPYPR     +2        5.703     0.622     1.0000    10
                    VGINYQPPTVVPGGDLAK        +2        4.644     0.480     1.0000    37
                    EIIDLVLDR       +2        2.604     0.371     0.9963    5
                    GHYTIGKEIIDLVLDR          +3        5.170     0.551     1.0000    2
                    QLFHPEQLITGKEDAANNYAR     +3        4.798     0.547     1.0000    21
                    AFVHWYVGEGMEEGEFSEAR      +3        4.636     0.488     1.0000    2
                    LDHKFDLMYAK     +3        4.587     0.433     1.0000    19
                    LIGQIVSSITASLR  +2        5.077     0.568     1.0000    26
                    RNLDIERPTYTNLNR+3         2.959     0.363     0.9997    7
                    LDHKFDLMYAKR    +2        2.914     0.358     0.9820    2
                    IHFPLATYAPVISAEK          +2        4.664     0.691     1.0000    54
                    GHYTIGKEIIDLVLDRIR        +3        2.475     0.403     0.9988    4
          MASCOT:(PepMatched Observed.Hits Coverage)    7         8         22.44%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore PepHits
                    DVNAAIATIK          +2        508.30    1014.58   1014.57   0.01      45        6
                    NLDIERPTYTNLNR      +2        859.95    1717.89   1717.87   0.02      45        28
                    VGINYQPPTVVPGGDLAK            +2        913.01    1824.00   1823.98   0.02      42        5
                    IHFPLATYAPVISAEK              +2        878.99    1755.97   1755.96   0.01      58        30
                    EIIDLVLDR           +2        543.32    1084.62   1084.61   0.01      44        20
                    AVFVDLEPTVIDEVR     +2        851.46    1700.91   1700.90   0.01      71        20
                    LIGQIVSSITASLR      +2        729.44    1456.87   1456.86   0.01      60        4

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
609.      IPI00197888         Y         N         0.22      1         2         0         6         0
*Des:     Splice Isoform 1 of Tropomyosin 1 alpha chain
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         11.41%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    HIAEDADRKYEEVAR               +2        3.758     0.509     1.0000    13
                    AQKDEEKMEIQEIQLK              +2        5.511     0.462     1.0000    5
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
610.      IPI00188059         Y         N         0.02      1         2         0         5         0
*Des:     Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         6.23%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    MPFSLVGDVFELNFK               +2        5.214     0.556     1.0000    3
                    YHVPVVVVPEGSASDTQEQAILR                 +3        5.843     0.428     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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611. IPI00205745 Y Y 1.03 2 6 4 8 9
*Des: Peroxiredoxin 5, mitochondrial precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 6 2 34.56%
Seq Charge Xcor Delta Probility PepHits
FSMVIDKGVVK +3 2.568 0.558 0.9972 7
KVNLAELFKDK +3 3.487 0.420 0.9936 1
VGDTIPSVEVFEGEPGKK +2 3.221 0.579 0.9950 2
VGDTIPSVEVFEGEPGK +2 3.202 0.688 0.9979 1
VQLLADPTGAFGKETDLLLDDSLVSLFGNRR +3 4.056 0.544 0.9984 2
VQLLADPTGAFGKETDLLLDDSLVSLFGNR +3 4.759 0.609 0.9996 2
MASCOT:(PepMatched Observed.Hits Coverage) 4 2 19.81%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
FSMVIDKGVVK +2 611.85 1221.69 1221.68 0.01 49 8
KVNLAELFKDK +3 435.59 1303.75 1303.75 0 43 1
VGDTIPSVEVFEGEPGK +2 880.44 1758.87 1758.87 0 53 1
VGDTIPSVEVFEGEPGKK +3 630.00 1886.97 1886.96 0.01 41 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
612. IPI00211080 N Y 0.14 1 0 2 0 3
*Des: Guanylate nucleotide binding protein 2
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 3.99%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
IKAETAEAANR +2 587.3207 1172.6269 1172.6149 0.01 47 2
DFSLELEVNGK +2 626.2999 1250.5852 1249.6190 0.97 41 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
613. IPI00200591 Y N 0.14 2 3 0 6 0
*Des: Contrapsin-like protease inhibitor 3 precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 3 4 10.23%
Seq Charge Xcor Delta Probility PepHits
VFSQQADLSR +2 2.726 0.281 0.9876 3
MQQVESSLQPETLKK +3 3.481 0.247 0.9975 1
ITGTKDLYVSQVVHK +3 3.763 0.501 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
614. IPI00389888 N Y 0.3 1 0 3 0 7
*Des: 41 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 9.04%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
EQALADLNSVER +2 672.84 1343.67 1343.67 0 64 4
TAVLTLIR+2 443.79 885.57 885.56 0.01 52 2
TIAQMIEDEQR +2 667.32 1332.63 1332.63 0 42 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

615.	IPI00421874	Y	Y	1.93	3	8	10	15	34

*Des: Voltage-dependent anion-selective channel protein 1

SEQUEST:(PepMatched Observed.Hits Coverage) 8 2 47.84%

Seq	Charge	Xcor	Delta	Probility	PepHits
SENGLEFTSSGSANTETTK	+2	5.676	0.702	1.0000	2
VTQSNFAVGYK	+2	3.341	0.506	0.9997	4
LTFDSSFSPNTGK	+2	3.649	0.506	0.9997	3
KLETAVNLAWTAGNSNTR	+2	6.116	0.651	1.0000	2
TDEFQLHTNVNDGTEFGGSIYQK	+3	5.779	0.506	1.0000	3
WTEYGLTFTEK	+2	2.867	0.468	0.9989	2
WNTDNTLGTEITVEDQLAR	+2	5.753	0.503	1.0000	2
GALVLGYEGWLAGYQMNFETSK	+2	5.836	0.643	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 10 4 51.82%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
VTQSNFAVGYK	+2	607.32	1212.62	1212.61	0.01	74	9
SENGLEFTSSGSANTETTK	+2	980.45	1958.88	1958.87	0.01	121	6
WTEYGLTFTEK	+2	687.84	1373.66	1373.65	0.01	52	3
LTFDSSFSPNTGK	+2	700.84	1399.67	1399.66	0.01	62	8
LETAVNLAWTAGNSNTR	+2	909.47	1816.92	1816.91	0.01	95	6
KLETAVNLAWTAGNSNTR	+2	973.51	1945.01	1945.00	0.01	138	6
VNNSSLIGLGYTQTLKPGIK	+3	701.73	2102.18	2102.17	0.01	52	6
TDEFQLHTNVNDGTEFGGSIYQK	+3	867.40	2599.19	2599.18	0.01	83	4
LTLSALLDGK	+2	515.81	1029.61	1029.61	0	77	2
GALVLGYEGWLAGYQMNFETSK	+3	812.07	2433.17	2433.17	0	46	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
616.	IPI00200593	Y	Y	0.35	3	6	6	11	16

*Des: Contrapsin-like protease inhibitor 1 precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 6 5 17.49%

Seq	Charge	Xcor	Delta	Probility	PepHits
IFSQQADLSR	+2	3.065	0.297	0.9951	3
AVLDVDETGTEGAAATAVTAALK	+2	6.318	0.601	1.0000	3
ALYQAEAFVADFK	+2	3.025	0.490	0.9994	2
DTLPHEDQGKGR	+2	2.834	0.402	0.9886	5
KIFSQQADLSR	+2	3.167	0.349	0.9976	3
NLHVSQVVHK	+2	3.327	0.484	0.9998	7

MASCOT:(PepMatched Observed.Hits Coverage) 6 7 11.82%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
DTLPHEDQGK	+2	570.2745	1138.5344	1138.5255	0.01	51	7
IFSQQADLSR	+2	582.8073	1163.6001	1163.5935	0.01	61	4
ALYQAEAFVADFK	+2	737.6658	1473.3170	1471.7347	1.58	56	2
DTLPHEDQGKGR	+2	676.8358	1351.6570	1351.6480	0.01	64	7
KIFSQQADLSR	+2	646.8557	1291.6968	1291.6884	0.01	62	2
NLHVSQVVHK	+2	580.8342	1159.6538	1159.6461	0.01	53	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
617.	IPI00454431	N	Y	0.4	2	0	33	0	176

Identified Human Platelet Proteins

*Des: Brain-specific alpha actinin 1 isoform
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 33 3 47.74%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
NYITGDELR		+2	540.77	1079.53	1079.52	0.01	41	6		
GISQEQMNEFR		+2	669.81	1337.61	1337.60	0.01	54	7		
RDQALTEEHSR		+3	447.89	1340.65	1340.64	0.01	51	2		
VPENTMQAMQQK		+2	702.84	1403.66	1403.65	0.01	73	2		
QKDYETATLSEIK		+2	763.39	1524.77	1524.77	0	68	4		
LSNRPAFMPSEGR		+3	487.92	1460.72	1460.72	0	46	12		
ASFNHFDR		+2	497.23	992.45	992.45	0	41	4		
HEAFESDLAAHQDR		+3	542.58	1624.73	1624.72	0.01	46	7		
IMSIVDPNR		+2	522.78	1043.55	1043.54	0.01	49	1		
ILAGDKNYITGDELR		+2	839.45	1676.88	1676.87	0.01	102	3		
LAILGIHNEVSK		+2	647.38	1292.75	1292.75	0	61	14		
TINEVENQILTR		+2	715.39	1428.76	1428.76	0	59	6		
ETADTDTADQVMASFK			+2	865.39	1728.77	1728.75	0.02	102	8	
MLDAEDIVGTARPDEK			+2	880.43	1758.85	1758.85	0	55	10	
IVQTYHVNMAGTNPYTTITPQEINGK				+3	964.16	2889.45	2889.43	0.02	66	4
AGTQIENIEEDFR		+2	761.37	1520.72	1520.71	0.01	50	3		
FAIQDISVEETSAK		+2	769.40	1536.78	1536.77	0.01	86	12		
LVSIGAEEIVDGNVK		+2	771.93	1541.84	1541.83	0.01	86	6		
NVNIQNFHISWK		+2	750.40	1498.78	1498.77	0.01	78	4		
QFGAQANVIGPWIQTK			+2	879.47	1756.93	1756.93	0	45	2	
DDPLTNLNTAFDVAER			+2	895.94	1789.86	1789.85	0.01	60	4	
KDDPLTNLNTAFDVAER			+2	959.99	1917.96	1917.94	0.02	107	10	
AGTQIENIEEDFRDGLK			+2	967.98	1933.94	1933.94	0	79	6	
ISIEMHGTLEDQLSHLR			+2	990.01	1978.01	1977.99	0.02	99	8	
IDQLEGDHQLIQEALIFDNK			+3	780.40	2338.19	2338.18	0.01	64	4	
LLETIDQLYLEYAK		+2	856.47	1710.93	1710.91	0.02	83	6		
LGVVTFQAFIDFMSR			+2	865.95	1729.89	1729.89	0	98	12	
IMSIVDPNRLGVVTFQAFIDFMSR				+3	919.49	2755.44	2755.42	0.02	54	8
VEQIAAIAQELNELDYYDSPSVNAR				+3	936.80	2807.38	2807.36	0.02	79	2
LASDLLEWIR		+2	607.37	1212.72	1214.67	-1.94	76	12		
VGWEQLLTTIAR		+2	693.89	1385.77	1385.77	0	77	9		
LMLLLEVISGER		+2	686.90	1371.78	1371.78	0	69	25		
MTLGMIWTIILR		+2	724.41	1446.81	1446.81	0	88	34		

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
618.	IPI00421879	Y	Y	1.16	2	5	6	15	16

*Des: Similar to programmed cell death 10
SEQUEST:(PepMatched Observed.Hits Coverage) 5 2 34.57%

Seq	Charge	Xcor	Delta	Probility	PepHits			
VNLSAAQTLR		+2	3.479	0.440	0.9999	4		
AINVFISANR		+2	3.665	0.389	0.9999	4		
MAADDVEEYMIERPEPEFQDLNEK				+3	5.704	0.537	1.0000	1
LIHQTNLILQTFK		+2	3.534	0.314	0.9984	4		

SVEVNFTESLLR +2 3.776 0.474 1.0000 12

MASCOT:(PepMatched Observed.Hits Coverage) 6 2 38.78%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

IPDEINDR +2 486.25 970.48 970.47 0.01 53 3

VNLSAAQTLR +2 536.81 1071.61 1071.60 0.01 70 5

AINVFISANR +2 552.82 1103.62 1103.61 0.01 52 4

LIHQTNLILQTFK +2 784.97 1567.92 1567.91 0.01 50 5

MAADDVEEYMIERPEPEFQDLNEK +3 966.77 2897.30 2897.27 0.03 77 1

SVEVNFTESLLR +2 697.42 1392.83 1392.72 0.11 72 12

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

619. IPI00199636 Y Y 0.62 2 4 2 6 10

*Des: Calnexin precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 4 3 9.98%

Seq Charge Xcor Delta Probility PepHits

TSELNLDQFHDK +2 3.348 0.425 0.9995 3

APVPTGEVYFADSFDR +2 4.156 0.607 1.0000 1

VVDDWANDGWGLK +2 3.570 0.443 0.9997 3

KIPNPDFFEDLEPFR +2 3.555 0.518 0.9999 2

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 4.15%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

IPNPDFFEDLEPFR +2 868.4345 1734.8545 1734.8253 0.03 80 5

AEEDEILNR +2 544.7733 1087.5321 1087.5145 0.02 54 5

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

620. IPI00365423 Y Y 0.19 1 3 2 3 3

*Des: Alpha isoform of regulatory subunit A, protein phosphatase 2

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 7.51%

Seq Charge Xcor Delta Probility PepHits

VLAMSGDPNYLHR +2 3.451 0.423 0.9993 1

SALASVIMGLSPILGK +2 3.151 0.366 0.9965 2

FGKEWAHATIIPK +2 3.185 0.434 0.9956 1

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 5.17%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

VLAMSGDPNYLHR +2 736.8735 1471.7324 1471.7241 0.01 59 2

SALASVIMGLSPILGK +2 778.9629 1555.9112 1555.9007 0.01 52 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

621. IPI00364621 Y Y 0.12 1 2 3 3 10

*Des: Annexin A11

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 5.27%

Seq Charge Xcor Delta Probility PepHits

DVQELYAAGENR +2 3.705 0.456 0.9999 2

DESTNVDMSLVQR +2 3.814 0.448 0.9999 1

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 7.22%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

SELDLLDIR +2 537.3035 1072.5925 1072.5764 0.02 67 4

		DVQELYAAGENR		+2	682.8368	1363.6590	1363.6367	0.02	72	4		
		DESTNVDMSLVQR		+2	747.3623	1492.7101	1492.6827	0.03	76	2		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
622.	IPI00382191		Y	Y	0.13	1	4	3	6	14		
*Des:	Cc2-27											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	1	6.4%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GILFVGSGVSGGEEGAR			+2	2.884	0.457	0.9990	1			
		LVPLLDTGDIIIDGGNSEYR			+2	5.527	0.552	1.0000	1			
		NPELQNLLLDDFFK		+2	4.952	0.503	1.0000	3				
		TELDSFLIEITANILK		+3	3.223	0.248	0.9889	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	4.51%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GILFVGSGVSGGEEGAR			+2	796.41	1590.80	1590.80	0	60	2	
		NPELQNLLLDDFFK		+2	853.45	1704.89	1704.87	0.02	76	9		
		TELDSFLIEITANILK		+3	607.34	1819.00	1819.00	0	46	3		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
623.	IPI00208224		Y	Y	0.11	1	3	2	5	4		
*Des:	Signal transducer and activator of transcription 3											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	7.64%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GLSIEQLTTLAEK		+2	2.730	0.382	0.9963	2				
		LLQTAATAAQQGGQANHPTAAVVTEK				+3	4.181	0.543	1.0000	1		
		SIVSELAGLLSAMEYVQK			+3	4.413	0.512	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	5.85%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LLQTAATAAQQGGQANHPTAAVVTEK				+3	859.46	2575.35	2575.34	0.01	88	1
		SIVSELAGLLSAMEYVQK			+3	646.68	1937.02	1937.02	0	66	3	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
624.	IPI00358063		Y	Y	0.51	1	3	2	3	6		
*Des:	PREDICTED: similar to chromosome 2 open reading frame 33											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	14.08%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IVVTGNNEDISFSR		+2	3.597	0.470	0.9996	1				
		IQYEMEYTEGISQR		+2	3.419	0.561	1.0000	1				
		PADLDLIQSTPFKPLALK			+3	3.131	0.342	0.9878	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	7.75%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LQLLEEENKER		+2	700.88	1399.74	1399.73	0.01	57	8		
		IQYEMEYTEGISQR		+2	873.91	1745.81	1745.79	0.02	85	2		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
625.	IPI00358138		Y	Y	0.32	1	3	4	5	10		
*Des:	PREDICTED: similar to AP47 protein - mouse											

	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	9.07%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ILQEYITQEGHK		+2	3.769	0.438	0.9998	2				
		SGYQALPWVR		+2	2.745	0.306	0.9930	2				
		KNEVFLDVIEAVNLLVSANGNVLR				+3	5.001	0.445	0.9999	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	9.07%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ILQEYITQEGHK		+2	729.88	1457.75	1457.75	0	50	2		
		SGYQALPWVR		+2	588.81	1175.60	1175.61	0	45	4		
		NEVFLDVIEAVNLLVSANGNVLR				+3	833.46	2497.36	2497.35	0.01	47	2
		KNEVFLDVIEAVNLLVSANGNVLR				+3	876.16	2625.45	2625.45	0	47	4
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
626.	IPI00365283		N	Y	0.6	1	0	7	0	26		
*Des:	F-actin capping protein beta subunit											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					7	2	28.51%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		SGSGTMNLGGSLTR			+2	669.33	1336.65	1336.64	0.01	105	2	
		YDPPLEDGAMPSAR		+2	759.85	1517.69	1517.68	0.01	57	4		
		NDLVEALK		+2	451.25	900.49	900.49	0	42	2		
		LEVEANNAFDQYR		+2	784.88	1567.74	1567.73	0.01	69	3		
		KLEVEANNAFDQYR		+2	848.93	1695.84	1695.82	0.02	109	5		
		STLNEIYFGK		+2	586.31	1170.60	1170.59	0.01	60	5		
		LTSTVMLWLQTNK		+2	767.93	1533.85	1533.82	0.03	62	18		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
627.	IPI00198695		Y	Y	0.44	5	12	11	44	44		
*Des:	Integrin beta3 subunit											
	SEQUEST:(PepMatched Observed.Hits Coverage)					12	14	20.72%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		HVLTLTDQVTR		+2	3.103	0.504	0.9998	13				
		AKWDTANNPLYK		+3	3.756	0.362	0.9965	2				
		EATSTFTNITYR		+2	3.588	0.412	0.9996	5				
		DDLSSIQTLGTK		+2	4.397	0.432	0.9999	7				
		LAGIVLPNDGR		+2	2.945	0.385	0.9984	7				
		IGDTVSFSIEAK		+2	3.976	0.458	0.9999	9				
		EQSFTIKPVGFK		+2	2.743	0.475	0.9993	5				
		NDASHLLVFTTDAK		+2	4.767	0.542	1.0000	6				
		GSGDSAQITQVSPQR			+2	4.245	0.382	0.9996	5			
		PVSPYMFISPPQAIK		+2	4.069	0.570	1.0000	3				
		IGFGAFVDKPVSPYMFISPPQAIK				+3	5.471	0.502	1.0000	3		
		QVEDYPVDIYYLMDLSFSMK			+3	4.447	0.547	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					11	15	20.09%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		HVLTLTDQVTR		+2	641.86	1281.70	1281.70	0	53	13		
		GSGDSAQITQVSPQR			+2	765.88	1529.75	1529.74	0.01	92	4	

DDLSSIQTLGTK	+2	639.34	1276.66	1276.65	0.01	92	7
EATSTFTNITYR	+2	702.35	1402.68	1402.67	0.01	63	5
IFSLQVR	+2	431.76	861.51	861.51	0	42	2
LAGIVLPNDGR	+2	562.83	1123.64	1123.63	0.01	45	8
IGDTVSFSIEAK	+2	633.83	1265.66	1265.65	0.01	84	11
EQSFTIKPVGFK	+2	690.88	1379.75	1379.74	0.01	51	6
NDASHLLVFTTDAK	+2	766.39	1530.77	1530.77	0	95	4
QVEDYPVDIYYLMDLSFSMK	+3	819.39	2455.15	2455.13	0.02	50	2
IGFGAFVDKPVSPYMFISPPQAIK	+3	870.47	2608.39	2608.38	0.01	49	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
628.	IPI00206624	Y	Y	1.29	4	19	20	36	67

*Des: 78 kDa glucose-regulated protein precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 19 7 34.88%

Seq	Charge	Xcor	Delta	Probility	PepHits
TWNDPSVQQDIK	+2	3.253	0.370	0.9982	4
SQIFSTASDNQPTVTIK	+2	5.061	0.597	1.0000	3
DAGTIAGLNVMR	+2	3.382	0.462	0.9996	5
ELEEIVQPIISK	+2	3.312	0.395	0.9988	1
ITITNDQNR	+2	2.976	0.309	0.9961	5
LYGSGGPPPTGEEDTSEKDE	+2	5.350	0.644	1.0000	1
NQLTSNPENTVFDAK	+2	4.362	0.562	1.0000	1
NGRVEIIANDQGNR	+2	3.022	0.395	0.9884	1
AKFEELNMDLFR	+3	3.262	0.442	1.0000	3
IEIESFFEGEDFSETLTR	+2	2.730	0.450	0.9629	1
ALSSQHQAR	+2	3.210	0.399	0.9993	7
MKETAEAYLGKK	+3	3.226	0.309	0.9988	2
TKPYIQVDIGGGQTK	+2	3.995	0.468	0.9998	8
KKELEEIVQPIISK	+2	4.754	0.527	1.0000	5
VTHAVVTVPAYFNDAQR	+2	4.681	0.435	1.0000	3
DNHLLGTFDLTGIPPAPR	+2	4.689	0.589	1.0000	3
RALSSQHQAR	+2	2.845	0.358	0.9968	3
KTKPYIQVDIGGGQTK	+2	4.257	0.516	1.0000	3
KVTHAVVTVPAYFNDAQR	+3	3.293	0.273	0.9974	1

MASCOT:(PepMatched Observed.Hits Coverage) 20 7 41.8%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
MKETAEAYLGK	+2	620.81	1239.61	1239.62	0	74	4
TWNDPSVQQDIK	+2	715.85	1429.68	1429.68	0	67	3
TKPYIQVDIGGGQTK	+2	802.94	1603.86	1603.86	0	62	4
LYGSGGPPPTGEEDTSEKDEL	+3	726.66	2176.97	2176.96	0.01	59	1
VEIIANDQGNR	+2	614.82	1227.62	1227.62	0	43	16
DAGTIAGLNVMR	+2	609.32	1216.62	1216.62	0	71	8
ITPSYVAFTPEGER	+2	783.89	1565.77	1565.77	0	64	4
KSDIDEIVLVGGSTR	+2	794.93	1587.84	1587.85	0	71	3
NQLTSNPENTVFDAK	+2	839.41	1676.81	1676.80	0.01	66	5
SQIFSTASDNQPTVTIK	+2	918.97	1835.94	1835.93	0.01	92	7
VTHAVVTVPAYFNDAQR	+3	629.99	1886.96	1886.96	0	47	6

NELESYAYSLK	+2	658.82	1315.63	1315.63	0	62	4
ELEEIVQPIISK	+2	699.40	1396.79	1396.78	0.01	52	3
IINEPTAAAIAYGLDKR	+2	908.50	1814.99	1814.99	0	71	6
IEWLESHQDADIEDFK	+2	987.96	1973.91	1973.90	0.01	113	5
IINEPTAAAIAYGLDK	+2	830.45	1658.89	1658.89	0	95	20
FEELNMDLFR	+2	658.29	1314.56	1312.61	1.95	47	4
AKFEELNMDLFR	+2	756.88	1511.74	1511.74	0	88	5
TFAPEEISAMVLTK	+2	768.91	1535.80	1535.79	0.01	70	6
DNHLLGTFDLTGIPPAPR	+2	967.51	1933.01	1933.01	0	86	11

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
629.	IPI00362014	Y	Y	1.76	5	115	107	768	896

*Des: PREDICTED: similar to talin

SEQUEST:(PepMatched Observed.Hits Coverage) 115 30 62.46%

Seq	Charge	Xcor	Delta	Probility	PepHits
CTQDLGNSTK	+2	2.806	0.177	0.9553	2
VLVQNAAGSQEK	+2	3.330	0.529	1.0000	17
NGDTMEYR	+2	2.891	0.287	0.9937	5
EVANSTANLVK	+2	3.089	0.464	0.9995	12
STVLQQQYNR	+2	3.433	0.358	0.9990	8
ALSTDPAAPNLK	+2	3.462	0.388	0.9990	19
ALDGAFTEENR	+2	3.636	0.521	1.0000	4
AAAFEDQENETVVVK	+2	4.992	0.490	1.0000	4
QEDVIATANLSR	+2	3.931	0.476	1.0000	5
VLGEAMTGISQNAK	+2	5.051	0.582	1.0000	21
DDILNGSHPVSFDK	+2	4.155	0.500	1.0000	10
IGITNHDEYSLVR	+3	4.594	0.493	1.0000	8
AAMEPIVISAK	+2	3.029	0.390	0.9983	6
LLSDSLPPSTGTFQEAQSR	+2	4.851	0.629	1.0000	13
ALGDLISATK	+2	3.987	0.536	1.0000	5
ASVPTIQDQASAMQLSQCAK	+2	6.431	0.665	1.0000	12
LLGEIAQGNENYAGIAAR	+2	4.732	0.652	1.0000	3
MVAAATNNLCEAANAAVQGHASQEK	+3	4.661	0.455	1.0000	8
AIAVTVQEMVTK	+2	4.604	0.614	1.0000	15
SKDHFGLEGDEESTMLEDSVSPK	+3	5.858	0.525	1.0000	5
VVAPTISSPVCQEQLVEAGR	+2	5.256	0.545	1.0000	2
TMLESAGGLIQTAR	+2	4.608	0.437	1.0000	10
VGDDPAVWQLK	+2	3.519	0.474	0.9998	3
NGNLPEFGDAIATASK	+2	4.518	0.524	1.0000	10
NLGTALAELR	+2	3.215	0.456	0.9996	12
DLDQASLAAVSQQLAPR	+2	4.690	0.436	1.0000	10
SNTSPEELGPLANQLTSDYGR	+2	4.873	0.635	1.0000	5
ILAQATSDLVNAIK	+2	4.719	0.586	1.0000	4
LGAASLGAEDPETQVVLINAVK	+2	5.672	0.567	1.0000	4
AVAEQIPLLVQGVR	+3	5.403	0.458	1.0000	34
LNEAAAGLNQAATELVQASR	+2	6.564	0.545	1.0000	20
TMQFEPSTMVYDACR	+2	4.378	0.469	1.0000	4

VGAIPANALDDGQWSQGLISAAR	+2	6.011	0.684	1.0000	14
GLAGAVSELLR	+2	3.867	0.377	0.9995	20
EADESLNFEEQILEAAK	+2	6.094	0.547	1.0000	11
ILAQATSDLVNAIKADAEGESDLENSRK	+3	5.019	0.495	1.0000	8
ILAQATSDLVNAIKADAEGESDLENSR	+3	6.852	0.591	1.0000	7
VAGSVTELIQAAEAMK	+2	5.396	0.553	1.0000	7
GSQAQPDSPSAQLALIAASQSFLQPGGK	+2	6.610	0.652	1.0000	14
TVTDMLMTICAR	+2	3.733	0.569	1.0000	11
AVTDSINQLITMCTQQAPGQK	+2	5.844	0.563	1.0000	20
VSQMAQYFEPLTLAAVGAASK	+3	6.567	0.585	1.0000	24
DKAPGQLECETAIAALNSCLR	+2	5.116	0.607	1.0000	7
MVGGIAQIIAAQEEMLR	+3	6.647	0.572	1.0000	16
TEDSGLQTQVIAAATQCALSTSQLVACTK	+3	4.433	0.487	1.0000	1
AATAPLLEAVDNLSAFASNPEFSSVPAQISPEGR	+3	6.020	0.601	1.0000	14
GTEWVDPEDPTVIAENELLGAAAAIEAAAK	+3	7.279	0.628	1.0000	14
YDQATDTILTVTENIFSSMGDAGEMVR	+3	6.530	0.657	1.0000	3
AEASQLGHK	+2	2.824	0.313	0.9949	10
AVEDEATKGTR	+2	3.450	0.442	0.9982	14
MATNAAAQNAIK	+2	4.398	0.469	1.0000	10
AAAFEDQENETVVVKEK	+2	5.170	0.461	1.0000	13
SIAAATSALVK	+2	3.673	0.570	1.0000	8
FGQDFSTFLEAGVEMAGQAPSQEDR	+2	6.303	0.661	1.0000	8
AVTDSINQLITMCTQQAPGQKECDNALR	+3	3.515	0.336	0.9986	1
FGQDFSTFLEAGVEMAGQAPSQEDRAQVVSNLK	+3	5.531	0.579	1.0000	1
TIMVDDSKTVTDMLMTICAR	+3	4.190	0.479	0.9999	2
EGISQEALHTQMLTAVQEISHLIEPLASAAR	+3	6.905	0.712	1.0000	23
GAAAHPDSEEQQQR	+3	4.100	0.296	0.9998	4
VKADQDSEAMKR	+2	3.785	0.511	1.0000	13
TVSDSIKK	+2	2.817	0.260	0.9891	12
RASDNLVK	+2	2.611	0.175	0.9554	4
RQFVQSAK	+2	2.626	0.236	0.9760	11
MVEAAKGAAAHPDSEEQQQR	+3	4.962	0.381	1.0000	4
MATNAAAQNAIKK	+2	4.245	0.446	1.0000	11
KSTVLQQQYNR	+2	3.676	0.499	1.0000	7
ALEATTEHIR	+2	3.068	0.310	0.9960	1
ELMEEKKDEGTGTLR	+2	4.825	0.423	1.0000	3
LAQAAQSSVATITR	+2	4.895	0.543	1.0000	14
EAAFHPEVAPDVR	+2	3.108	0.428	0.9988	6
AVAAGNSCRQEDVIATANLSR	+3	4.357	0.426	1.0000	1
TLREQGVEEHETLLLR	+3	4.968	0.449	1.0000	6
VLVEDTKVLVQNAAGSQEK	+3	3.648	0.492	1.0000	2
QKLHTDDELNWLDHGR	+3	3.424	0.301	0.9982	4
SKDHFGLEGDEESTMLEDSVSPKK	+3	7.205	0.461	1.0000	4
AVASAAAALVLK	+2	3.980	0.465	1.0000	11
VMVTNVTSLLK	+2	4.175	0.463	1.0000	44
AKPKEADESLNFEEQILEAAK	+3	3.735	0.524	1.0000	2
LLAALLEDEGGNGRPLLQAAK	+3	5.443	0.591	1.0000	14

LGAASLGAEDPETQVVLINAVKDVAK	+3	3.588	0.481	1.0000	7
LQAAGNAVKR	+2	3.127	0.271	0.9918	29
AGALQCSPSDVYTKK	+3	3.372	0.413	1.0000	3
VQELGHGCSALVTK	+2	4.543	0.472	1.0000	10
LASQAKPAAVAAENEEIGAHIK	+3	6.508	0.488	1.0000	20
QAAASATQTIAAAQHAASAPK	+2	5.631	0.542	1.0000	31
WSVLAGHSR	+2	3.156	0.400	0.9993	3
TLREQGVEEHETLLLRR	+3	3.400	0.450	1.0000	3
AQVVSNLKGISMSSSK	+2	3.551	0.479	0.9982	1
RAIADMLR	+2	3.329	0.264	0.9974	9
QVAASTAQLLVACK	+2	4.286	0.623	1.0000	3
ACEFAGFQCQIQFGPHNEQK	+3	3.805	0.320	0.9930	6
RVAGSVTELIQAAEAMK	+2	4.907	0.565	1.0000	6
ASAGPQPLLVQSCK	+2	3.841	0.526	1.0000	19
RLLSDSLPPSTGTFQEAQSR	+3	5.644	0.562	1.0000	2
AGALQCSPSDVYTKKELIECAR	+3	4.226	0.381	0.9999	2
AGFLDLKDFLPK	+2	4.159	0.254	0.9895	32
VSHVLAALQAGNR	+2	4.712	0.598	1.0000	14
TLSHPQQMALLDQTK	+3	5.126	0.373	1.0000	36
AEHGSVALPAIMR	+2	3.975	0.466	1.0000	12
VLVQNAAGSQEKLAQAAQSSVATITR	+3	6.318	0.538	1.0000	9
ANQAIQMACQSLGEPGCTQAQVLSAATIVAK	+3	7.342	0.634	1.0000	7
MVGGIAQIIAAQEEMLRK	+2	5.841	0.525	1.0000	58
GVGAAATAVTQALNELLQHVK	+2	6.516	0.638	1.0000	53
AHATGAGPAGR	+2	2.687	0.557	0.9997	21
RLQAAGNAVKR	+2	2.860	0.235	0.9602	6
MATNAAAQNAIKKK	+2	3.821	0.428	0.9979	4
VSEKVSHVLAALQAGNR	+3	5.021	0.415	1.0000	5
LAQVAKAVTQALNR	+2	3.632	0.474	0.9985	3
MVAAATNNLCEAANAAVQGHASQEKLISSAK	+3	5.592	0.506	1.0000	4
EKMVGGIAQIIAAQEEMLRK	+3	3.127	0.436	0.9999	2
KLVQRLEHAAK	+2	3.130	0.364	0.9907	4
SGASGPENFQVGSMPPAQQQVTSGQMHR	+3	6.101	0.627	1.0000	24
ALSTDPAAPNLKSQLAAAAR	+2	5.029	0.601	1.0000	8
PAAVAAENEEIGAHIKHR	+3	3.136	0.520	0.9998	1
RVSEKVSHVLAALQAGNR	+3	4.007	0.605	1.0000	1

MASCOT:(PepMatched Observed.Hits Coverage) 107 35 49.45%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SAQPASAEPR	+2	507.2565	1012.4985	1012.4937	0	45	2
CTQDLGNSTK	+2	533.7481	1065.4817	1065.4761	0.01	51	2
TVTDMLMTICAR	+2	677.8356	1353.6567	1353.6454	0.01	83	9
AGFLDLKDFLPK	+2	682.3881	1362.7617	1362.7547	0.01	85	36
VAGSVTELIQAAEAMK	+2	809.4357	1616.8569	1616.8443	0.01	119	9
MVGGIAQIIAAQEEMLR	+2	915.4908	1828.9671	1828.9538	0.01	115	18
TVSDSIKK	+2	439.2557	876.4969	876.4916	0.01	57	13
AEASQLGHK	+2	470.7493	939.4840	939.4774	0.01	70	15
AVEDEATKGTR	+2	588.8005	1175.5864	1175.5782	0.01	93	23

QFVQSAK	+2	403.6350	805.2555	806.4286	-1.16	41	10	
GTPQDLAR	+2	429.2296	856.4447	856.4403	0	43	12	
EGAETFADHR	+2	566.7590	1131.5035	1131.4945	0.01	50	5	
MATNAAAQNAIK	+2	602.3158	1202.6170	1202.6077	0.01	88	13	
VLVQNAAGSQEK	+2	622.3403	1242.6660	1242.6568	0.01	69	21	
ADAEGESDLENSRK	+2	760.8524	1519.6902	1519.6750	0.02	43	3	
STVLQQQYNR	+2	618.8243	1235.6340	1235.6258	0.01	57	10	
EVANSTANLVK	+2	573.3157	1144.6169	1144.6087	0.01	58	37	
NCGQMSEIEAK	+2	605.2707	1208.5268	1208.5165	0.01	85	16	
AAAFEDQENETVVVKEK		+2	953.9852	1905.9558	1905.9319	0.02	90	18
ALDGAFTEENR	+2	611.7925	1221.5705	1221.5625	0.01	63	6	
AAAFEDQENETVVVK		+2	825.4115	1648.8084	1648.7944	0.01	113	6
TSTPEDFIR	+2	533.2676	1064.5206	1064.5138	0.01	54	8	
VLGEAMTGISQNAK	+2	709.8749	1417.7353	1417.7235	0.01	119	20	
DDILNGSHPVSFDK	+2	772.3778	1542.7411	1542.7314	0.01	76	17	
SIAAATSALVK	+2	516.3101	1030.6056	1030.6022	0	59	23	
NGDTMEYR	+2	493.2091	984.4037	984.3971	0.01	54	5	
VGDDPAVWQLK	+2	614.3271	1226.6396	1226.6295	0.01	84	5	
AIAVTVQEMVTK	+2	645.3654	1288.7162	1288.7060	0.01	95	21	
NGNLPEFGDAIATASK		+2	803.3972	1604.7799	1603.7841	1	92	14
DLDQASLAAVSQQLAPR		+2	891.9768	1781.9391	1781.9271	0.01	77	19
EADESLNFEEQILEAAK		+2	968.4700	1934.9255	1934.9108	0.01	107	16
ALSTDPAAPNLK	+2	599.3318	1196.6491	1196.6401	0.01	67	19	
AAMEPIVISAK	+2	565.3215	1128.6285	1128.6212	0.01	57	6	
IGITNHDEYSLVR	+2	758.8995	1515.7844	1515.7681	0.02	70	8	
ALGDLISATK	+2	494.7898	987.5650	987.5600	0.01	76	11	
TMLESAGGLIQTAR	+2	724.3882	1446.7619	1446.7500	0.01	105	14	
LLGEIAQGNENYAGIAAR		+2	930.4915	1858.9685	1858.9536	0.01	103	3
NLGTALAELR	+2	529.3049	1056.5952	1056.5927	0	71	13	
ILAQATSDLVNAIK	+2	728.9280	1455.8414	1455.8297	0.01	106	6	
GLAGAVSELLR	+2	543.3223	1084.6301	1084.6240	0.01	75	20	
AVAEQIPLLVQGVR	+2	746.9517	1491.8888	1491.8772	0.01	91	35	
TMQFEPSTMVYDACR		+2	889.8886	1777.7627	1777.7473	0.02	48	5
QEDVIATANLSR	+2	658.8492	1315.6839	1315.6732	0.01	86	24	
TANPTAKR	+2	429.7465	857.4784	857.4719	0.01	44	1	
EAAFHPEVAPDVR	+2	719.3655	1436.7164	1436.7048	0.01	59	6	
ALDGAFTEENRAQCR		+2	840.8982	1679.7818	1679.7685	0.01	41	5
EQGVEEHETLLLR	+2	776.9105	1551.8064	1551.7892	0.02	51	2	
TLREQGVEEHETLLLR		+2	962.0256	1922.0366	1922.0221	0.01	72	6
QKLHTDDELNWLDHGR		+3	659.6611	1975.9616	1975.9500	0.01	44	5
GIWLEAGK	+2	437.2479	872.4813	872.4756	0.01	45	4	
AVASAAAALVLK	+2	542.8433	1083.6721	1083.6651	0.01	77	15	
GAAAHPDSEEQQQR		+3	508.5698	1522.6876	1522.6760	0.01	52	5
VKADQDSEAMKR	+2	689.3489	1376.6832	1376.6718	0.01	75	51	
RQFVQSAK	+2	482.2749	962.5352	962.5297	0.01	60	8	
LQAAGNAVK	+2	436.2562	870.4978	870.4923	0.01	50	11	
MATNAAAQNAIKK	+2	666.3640	1330.7134	1330.7027	0.01	106	11	

KSTVLQQQYNR	+2	682.8716	1363.7287	1363.7208	0.01	90	7
TVKAVEDEATKGTR	+3	502.2708	1503.7906	1503.7892	0	41	1
ALEATTEHIR	+2	570.8077	1139.6009	1139.5935	0.01	55	1
ELMEEKKDEGTGTLR	+2	868.4362	1734.8578	1734.8457	0.01	79	4
LAQAAQSSVATITR	+2	708.8995	1415.7845	1415.7732	0.01	115	15
RAIADMLR	+2	473.2714	944.5282	944.5225	0.01	54	6
KGIWLEAGK	+2	502.2449	1002.4753	1000.5705	1.9	42	8
WSVLAGHSR	+2	506.7728	1011.5310	1011.5250	0.01	57	3
AQVVSNLKGISMSSSK	+2	818.4430	1634.8714	1634.8661	0.01	64	1
QAAASATQTIAAAQHAASAPK	+2	983.0198	1964.0251	1964.0075	0.02	113	32
QVAASTAQLLVACK	+2	701.8953	1401.7761	1401.7649	0.01	82	3
VMVTNVTSLLK	+2	602.8563	1203.6981	1203.6897	0.01	83	103
RVAGSVTELIQAAEAMK	+2	887.4880	1772.9615	1772.9454	0.02	89	6
LQAAGNAVKR	+2	514.3076	1026.6006	1026.5934	0.01	81	42
VQELGHGCSALVTK	+2	721.3835	1440.7524	1440.7394	0.01	77	8
AHATGAGPAGR	+2	483.2526	964.4906	964.4838	0.01	57	20
RLLSDSLPPSTGTFQEAQSR	+3	730.7144	2189.1214	2189.1076	0.01	83	2
AGALQCSPSDVYTKKELIECAR	+3	794.7372	2381.1897	2381.1718	0.02	55	2
ASVPTIQDQASAMQLSQCAK	+2	1039.0178	2076.0211	2075.9979	0.02	110	2
MVAAATNNLCEAANAAVQGHASQEK	+3	833.7329	2498.1769	2498.1641	0.01	72	1
LLAALLEDEGGNGRPLLQAAK	+2	1075.1118	2148.2091	2148.1902	0.02	91	3
VSQMAQYFEPLTLAAVGAASK	+2	1091.5740	2181.1334	2181.1139	0.02	109	16
AVTDSINQLITMCTQQAPGQK	+2	1124.0692	2246.1239	2246.1035	0.02	108	14
KIFQAHK	+2	436.2639	870.5132	870.5075	0.01	46	2
RLQAAGNAVK	+2	514.3072	1026.5998	1026.5934	0.01	44	4
LEQLKPR	+2	442.2744	882.5342	882.5287	0.01	44	7
LKPLPGETMEK	+3	414.8991	1241.6755	1241.6689	0.01	50	7
LASQAKPAAVAAENEEIGAHIK	+3	740.0710	2217.1913	2217.1752	0.02	94	9
ASAGPQPLLVQSCK	+2	699.8785	1397.7425	1397.7336	0.01	99	20
LEHAAKQAAASATQTIAAAQHAASAPK	+4	654.1256	2612.4733	2613.3622	-0.88	60	2
AEHGSVALPAIMR	+2	676.3657	1350.7169	1350.7077	0.01	78	14
ALGDLISATKAAAGK	+2	694.3734	1386.7322	1385.7878	0.94	44	5
TLSHPQQMALLDQTK	+2	855.9528	1709.8911	1709.8770	0.01	88	36
VLVQNAAGSQEKLAQAAQSSVATITR	+2	1321.2283	2640.4420	2640.4194	0.02	138	9
ANQAIQMACQSLGEPGCTQAQVLSAATIVAK	+3	1034.5215	3100.5426	3101.5307	-0.98	89	6
MVGGIAQIIAAQEEMLRK	+2	979.5388	1957.0630	1957.0488	0.01	117	58
VSHVLAALQAGNR	+2	668.3826	1334.7506	1334.7418	0.01	88	15
VSEKVSHVLAALQAGNR	+2	890.0049	1777.9952	1777.9798	0.02	105	5
AVASAAAALVLKAK	+2	642.3842	1282.7539	1282.7972	-0.03	84	3
LAQVAKAVTQALNR	+2	741.9474	1481.8803	1481.8678	0.01	73	3
MVAAATNNLCEAANAAVQGHASQEKLISSAK	+3	1033.5270	3097.5591	3097.5284	0.03	101	5
GSQAQPDSPSAQLALIAASQSFLQPGGK	+2	1377.7195	2753.4244	2753.3983	0.03	128	13
GVGAAATAVTQALNELLQHVK	+2	1046.0898	2090.1651	2090.1483	0.02	139	51
RLQAAGNAVKR	+2	592.3581	1182.7016	1182.6945	0.01	52	6
LVQRLEHAAK	+2	582.8495	1163.6845	1163.6774	0.01	52	15
MATNAAAQNAIKKK	+2	730.4121	1458.8097	1458.7976	0.01	45	2
KLEQLKPR	+2	506.3217	1010.6289	1010.6236	0.01	63	99

		ALSTDPAAPNLKSQLAAAAR			+2	983.5488	1965.0830	1965.0643	0.02	103	8		
		SGASGPENFQVGSMPPAQQQVTSGQMHR					+3	971.7920	2912.3541	2912.3293	0.02	120	26
		RVSEKVSHVLAALQAGNR			+3	645.7060	1934.0962	1934.0809	0.02	62	2		
		KLVQRLEHAAK		+2	646.8975	1291.7804	1291.7724	0.01	49	4			

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)			
630.	IPI00370107		N	Y	0.27	1	0	3	0	3			
*Des:	PREDICTED: similar to PH domain-containing protein												
	SEQUEST:(PepMatched Observed.Hits Coverage)												
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	8.74%					
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits	
		QATQVLQEMR		+2	602.31	1202.61	1202.61	0	53	2			
		VSWENPSPEEPSVSER			+2	914.92	1827.83	1827.83	0	45	1		
		DLEELNQESPGLVQK			+2	849.93	1697.85	1697.85	0	72	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)			
631.	IPI00207355		Y	Y	0.15	3	4	2	20	3			
*Des:	Heat shock-related 70 kDa protein 2												
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	5	11.18%					
		Seq	Charge	Xcor	Delta	Probility	PepHits						
		STAGDTHLGGEDFDNR			+2	4.504	0.606	1.0000	6				
		LLQDFFNGKELNK		+2	4.310	0.439	1.0000	8					
		ARFEELNADLFR		+2	2.982	0.432	0.9993	10					
		NVLIFDLGGGTFDVSILTIEDGIFEVK				+3	4.880	0.531	1.0000	5			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	6.98%					
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits	
		STAGDTHLGGEDFDNR			+2	846.3823	1690.7501	1690.7183	0.03	63	3		
		NVLIFDLGGGTFDVSILTIEDGIFEVK				+3	971.2007	2910.5802	2910.5265	0.05	65	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)			
632.	IPI00365286		Y	Y	0.44	5	32	30	91	111			
*Des:	PREDICTED: similar to Vinculin (Metavinculin)												
	SEQUEST:(PepMatched Observed.Hits Coverage)					32	17	32.37%					
		Seq	Charge	Xcor	Delta	Probility	PepHits						
		ETVQTTEDQILKR		+2	3.873	0.469	0.9999	2					
		NPGNQAAYEHFETMK			+2	4.985	0.597	1.0000	4				
		QVATALQNLQTK		+2	4.325	0.584	1.0000	3					
		WIDNPTVDDR		+2	3.430	0.364	0.9993	2					
		ETVQTTEDQILK		+2	3.575	0.373	0.9993	2					
		ELTPQVISAAR		+2	2.785	0.405	0.9984	5					
		GWLRDPNASPGDAGEQAIR			+3	4.047	0.407	0.9977	3				
		VMLVNSMNTVK		+2	3.541	0.430	0.9997	2					
		SLLDASEEAIKK		+2	2.984	0.302	0.9937	3					
		ALASQLQDSLK		+2	3.079	0.396	0.9990	5					
		MTGLVDEAIDTK		+2	4.169	0.534	1.0000	2					
		AQQVSQGLDVLTAK		+2	4.867	0.610	1.0000	4					
		LANVMMGPYR		+2	3.101	0.348	0.9984	3					

	LLAVAATAPPDAPNREEVFDER				+2	4.070	0.550	0.9988	3		
	SLGEIAALTSK		+2	3.192	0.478	0.9998	2				
	MSAEINEIIR		+2	3.347	0.357	0.9991	3				
	MLGQMTDQVADLR		+2	4.171	0.575	1.0000	2				
	KIDAAQNWLADPNGGPEGEEQIR				+3	6.028	0.518	1.0000	1		
	LVQAAQMLQSDPYSVPAR			+3	3.580	0.505	1.0000	4			
	EAFQPQEPDFPPPPPDLEQLR			+2	4.032	0.560	1.0000	1			
	MALLMAEMSR		+2	3.390	0.293	0.9979	2				
	VLQLTSWDEDAWASK			+2	4.473	0.589	1.0000	1			
	VAMANIQPQMLVAGATSIAR			+2	4.957	0.533	1.0000	2			
	TQMQEAMTQEVSDVFSDTTTPIK				+2	6.135	0.627	1.0000	3		
	ELLPVLISAMK		+2	2.707	0.290	0.9883	3				
	GILSGTSDLLLTFDEAEVR			+2	6.556	0.609	1.0000	3			
	TIESILEPVAQQISHLVIMHEEGEVDGK				+3	4.052	0.409	0.9998	4		
	AIPDLTAPVAAVQAAVSNLVR			+2	5.233	0.708	1.0000	4			
	STVEGIQASVK		+2	2.664	0.241	0.9719	2				
	VMLVNSMNTVKELLPVLISAMKIFVTTK				+3	5.997	0.641	1.0000	2		
	GILEYLTVAEVVETMEDLVTYTK				+3	5.895	0.385	0.9999	3		
	AVAGNISDPGLQK		+2	2.769	0.386	0.9968	3				
MASCOT:(PepMatched Observed.Hits Coverage)					30	20	21.82%				
	Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
	GNDIIAAAK		+2	436.7483	871.4821	871.4763	0.01	44	7		
	AVAGNISDPGLQK		+2	635.3492	1268.6838	1268.6724	0.01	66	5		
	NQGIEEALK		+2	501.2697	1000.5249	1000.5189	0.01	41	2		
	MSAEINEIIR		+2	588.3124	1174.6103	1174.6016	0.01	89	10		
	VLQLTSWDEDAWASK			+2	874.9302	1747.8458	1747.8417	0	58	4	
	STVEGIQASVK		+2	559.8094	1117.6043	1117.5979	0.01	56	2		
	NQGIEEALKNR		+2	636.3445	1270.6744	1270.6629	0.01	48	3		
	ALASQLQDSLK		+2	587.3344	1172.6542	1172.6401	0.01	42	1		
	TNLLQVCER		+2	538.2853	1074.5561	1074.5491	0.01	69	3		
	MALLMAEMSR		+2	576.7853	1151.5560	1151.5501	0.01	80	9		
	QQELTHQEHR		+2	653.3240	1304.6335	1304.6221	0.01	51	4		
	GLVAEGHR		+2	419.7336	837.4526	837.4456	0.01	52	12		
	AANFENHSGR		+2	551.7597	1101.5049	1101.4951	0.01	74	5		
	GQGASPVAMQK		+2	537.2782	1072.5418	1072.5335	0.01	53	3		
	GNDIIAAAKR		+2	514.7991	1027.5836	1027.5774	0.01	55	6		
	ETVREAEAASIK		+2	652.3516	1302.6886	1302.6779	0.01	43	1		
	IPTISTQLK		+2	500.8083	999.6021	999.5964	0.01	49	7		
	VGKETVQTTEDQILKR			+2	923.0148	1844.0150	1844.0003	0.01	102	11	
	VMLVNSMNTVK		+2	618.3325	1234.6505	1234.6413	0.01	56	3		
	DMPPAFIKVENACTK			+2	832.4196	1662.8247	1662.8109	0.01	71	5	
	NSKNQGIEEALKNR		+3	534.2878	1599.8417	1599.8328	0.01	51	1		
	ALASIDSKLNQAK		+2	679.8907	1357.7668	1357.7565	0.01	46	1		
	ELLPVLISAMK		+2	607.3685	1212.7224	1212.7151	0.01	68	10		
	AAVHLEGKIEQAQR		+2	775.4322	1548.8498	1548.8372	0.01	86	10		
	AIPDLTAPVAAVQAAVSNLVR			+2	1038.6046	2075.1947	2075.1738	0.02	114	25	
	AAAVGAANKSTVEGIQASVKTAR				+3	734.0781	2199.2124	2199.1970	0.02	84	1

VAMANIQPQMLVAGATSIAR +2 1021.5555 2041.0964 2041.0812 0.02 96 5
TNLLQVCERIPTISTQLK +2 1029.0819 2056.1493 2056.1350 0.01 79 7
VMLVNSMNTVKELLPVLISAMK +2 1215.6868 2429.3590 2429.3459 0.01 97 3
ELLPVLISAMKIFVTTK +2 952.0764 1902.1382 1902.1263 0.01 84 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
633. IPI00363828 Y Y 0.22 4 5 5 8 12
*Des: PREDICTED: ARP3 actin-related protein 3 homolog
SEQUEST:(PepMatched Observed.Hits Coverage) 5 4 19.84%
Seq Charge Xcor Delta Probility PepHits
FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR +3 5.008 0.579 1.0000 1
DREVGIPPEQSLETAK +2 3.894 0.483 1.0000 2
GVDDLDFFIGDEAIEKPTYATKWPIR +3 3.825 0.550 1.0000 2
LKLSEELSGGR +2 2.937 0.367 0.9982 3
TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK +3 3.301 0.258 0.9939 1
MASCOT:(PepMatched Observed.Hits Coverage) 5 8 11.74%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LSEELSGGR +2 474.2457 946.4768 946.4719 0 65 5
DREVGIPPEQSLETAK +2 884.9622 1767.9098 1767.9002 0.01 70 1
HGIVEDWDLMER +2 750.3583 1498.7020 1498.6874 0.01 79 2
NIVLSGGSTMFR +2 641.3398 1280.6650 1280.6546 0.01 74 7
LGYAGNTEPQFIIPSCIAIK +2 1068.0750 2134.1354 2134.1132 0.02 99 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
634. IPI00370038 Y Y 0.51 1 2 2 2 4
*Des: Interferon-induced protein 35
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 9.96%
Seq Charge Xcor Delta Probility PepHits
VLVSGFPTGLR +2 2.837 0.344 0.9931 1
LSEEELLDKLEIFFGK +2 4.461 0.603 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 9.96%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VLVSGFPTGLR +2 573.34 1144.66 1144.66 0 41 4
LSEEELLDKLEIFFGK +2 955.52 1909.02 1909.01 0.01 58 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
635. IPI00565513 N Y 0.58 1 0 3 0 18
*Des: 37 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 18.23%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
GAAQNIIPASTGAAK +2 685.28 1368.55 1368.74 -0.18 80 30
RVIISAPSADAPMFVMGVNHEK +3 790.42 2368.22 2368.20 0.02 55 6
VIHDNFGIVEGLMTTVHAITATQK +3 865.79 2594.35 2594.35 0 75 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
636. IPI00203214 Y Y 0.39 3 10 9 14 11

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*Des:       Elongation factor 2
            SEQUEST:(PepMatched Observed.Hits Coverage)   10        4         20.06%
                      Seq       Charge    Xcor      Delta     Probility PepHits
                      VFSGVVSTGLK         +2        3.268     0.507     0.9999    2
                      VNFTVDQIR           +2        3.382     0.364     0.9995    1
                      ARPFPDGLAEDIDKGEVSAR          +3        5.565     0.541     1.0000    4
                      VFDAIMNFR           +2        3.209     0.513     0.9999    1
                      AYLPVNESFGFTADLR              +2        4.498     0.524     1.0000    3
                      ALLELQLEPEELYQTFQR            +2        4.589     0.602     1.0000    1
                      DGSGFLINLIDSPGHVDFSSEVTAALR             +3        5.937     0.665     1.0000    2
                      EGIPALDNFLDK        +2        3.078     0.505     0.9937    1
                      STAISLFYELSENDLNFIK           +2        4.584     0.583     1.0000    2
                      WLPAGDALLQMITIHLPSPVTAQK                +2        5.206     0.528     1.0000    3
            MASCOT:(PepMatched Observed.Hits Coverage)    9         4         16.85%
                      Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                      GVQYLNEIK           +2        533.27    1064.53   1062.57   1.96      41        2
                      VNFTVDQIR           +2        546.30    1090.58   1090.58   0         60        1
                      VFSGVVSTGLK         +2        547.32    1092.62   1092.62   0         65        2
                      ARPFPDGLAEDIDKGEVSAR          +3        715.03    2142.08   2142.07   0.01      64        1
                      VFDAIMNFR           +2        556.78    1111.55   1111.55   0         49        1
                      AYLPVNESFGFTADLR              +2        900.46    1798.91   1798.89   0.02      86        3
                      EGIPALDNFLDKL       +2        722.89    1443.77   1443.76   0.01      53        1
                      WLPAGDALLQMITIHLPSPVTAQK                +3        867.49    2599.44   2599.42   0.02      58        1
                      DGSGFLINLIDSPGHVDFSSEVTAALR             +3        939.81    2816.42   2816.40   0.02      88        2

No.         Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
637.        IPI00204884         Y         N         0.15      1         2         0         4         0
*Des:       57 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         6.22%
                      Seq       Charge    Xcor      Delta     Probility PepHits
                      HSQFIGYPITLFVEK +2        4.866     0.575     1.0000    4
                      YESLTDPSKLDSGK +2         3.326     0.357     0.9523    1
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
638.        IPI00191073         Y         Y         0.48      2         4         3         6         4
*Des:       PREDICTED: similar to Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1)
            SEQUEST:(PepMatched Observed.Hits Coverage)   4         2         22.37%
                      Seq       Charge    Xcor      Delta     Probility PepHits
                      ESTGAQVQVAGDMLPNSTER +2       5.893     0.589     1.0000    3
                      LEEDINSSMTNSTAASRPPVTLR                 +3        3.587     0.272     0.9935    1
                      IITLTGPTNAIFK       +2        3.978     0.477     0.9998    3
                      QVTITGSAASISLAQYLINAR         +3        3.820     0.431     0.9998    2
            MASCOT:(PepMatched Observed.Hits Coverage)    3         2         16.57%
                      Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                      LEEDINSSMTNSTAASRPPVTLR                 +3        830.42    2488.24   2488.22   0.02      56        1
                      IITLTGPTNAIFK       +2        694.92    1387.82   1387.81   0.01      62        3
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		QVTITGSAASISLAQYLINAR			+3	726.41	2176.20	2176.19	0.01	44	1	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
639.	IPI00389890		N	Y	0.24	2	0	7	0	40		
*Des:	Splice Isoform 5 of Dynamin 1-like protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					7	2	16.11%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		RPLILQLVHVSPEDK		+3	582.01	1743.01	1743.00	0.01	46	6		
		SVTDSIRDEYAFLQK		+2	886.45	1770.88	1770.88	0	43	18		
		SATLLQLITK		+2	544.34	1086.66	1086.66	0	78	2		
		DTLQSELVGQLYK		+2	747.40	1492.78	1492.78	0	56	2		
		LDLMDAGTDAMDVLMGR			+2	912.42	1822.83	1822.83	0	56	12	
		SSLLDDLLTESEDMAQR			+2	961.96	1921.90	1921.89	0.01	76	6	
		LQDVFNTVGADIIQLPQIVVVGTQSSGK				+3	976.20	2925.59	2925.58	0.01	81	6

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
640.	IPI00558156		N	Y	0.4	1	0	4	0	23		
*Des:	61 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	8.63%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		SAVGHEYQSK		+2	553.2708	1104.5271	1104.5199	0.01	68	6		
		HCSQVDSVR		+2	515.7438	1029.4730	1029.4662	0.01	68	8		
		YGVQADRVDK		+2	575.8010	1149.5874	1149.5778	0.01	49	1		
		TVQGSGHQEHINIHK			+2	842.9349	1683.8553	1683.8441	0.01	79	20	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
641.	IPI00475634		N	Y	0.4	1	0	2	0	2		
*Des:	Tropomyosin											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	6.34%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LLSNELK	+2	408.7660	815.5175	815.4752	0.04	41	1			
		ILTDKLK	+2	415.7736	829.5327	829.5273	0.01	42	1			

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
642.	IPI00476292		N	Y	0.16	1	0	5	0	17		
*Des:	120 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					5	1	7%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		SSTVAPTLPGEVR		+2	657.36	1312.70	1312.70	0	41	2		
		ALYSEYTDGTFTK		+2	748.35	1494.69	1494.69	0	49	3		
		AGLQAFFQVR		+2	568.81	1135.61	1135.61	0	52	6		
		DIFTGLIGPMK		+2	596.33	1190.64	1190.64	0	42	3		
		GPDEEHLGILGPVIWAEVGDIIR			+3	829.11	2484.31	2484.30	0.01	41	3	

Identified Human Platelet Proteins

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
643. IPI00476439 N Y 0.02 1 0 2 0 4
*Des: 245 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 1.15%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
AMNNSWHPECFR		+2	746.3251	1490.6356	1490.6183	0.02	60	3		
FVEFDMKPVCK		+2	671.8322	1341.6498	1341.6461	0	44	2		

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
644. IPI00327185 Y N 0.46 2 5 0 5 0
*Des: Nap1l1 protein
SEQUEST:(PepMatched Observed.Hits Coverage) 5 2 18.34%

Seq	Charge	Xcor	Delta	Probility	PepHits		
FYEEVHDLER		+2	2.749	0.399	0.9985	4	
LDGLVDTPTGYIESLPK			+2	2.818	0.499	0.9988	1
YAVLYQPLFDK		+2	2.875	0.428	0.9991	1	
QLTVQMMQNPQILAALQER			+2	5.488	0.604	1.0000	1
GIPEFWLTVFK		+2	3.332	0.406	0.9995	1	

MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
645. IPI00475639 N Y 0.35 3 0 19 0 361
*Des: PREDICTED: similar to tubulin, beta 2
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 19 8 27.21%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
AILVDLEPGTMDSVR			+2	808.4290	1614.8435	1614.8287	0.01	68	69	
TAVCDIPPR		+2	486.2559	970.4972	970.4906	0.01	59	78		
EVDEQMLNVQNK		+2	723.8541	1445.6937	1445.6820	0.01	91	11		
MSMKEVDEQMLNVQNK			+2	962.4619	1922.9092	1922.8899	0.02	84	11	
ISEQFTAMFR		+2	615.3072	1228.5998	1228.5910	0.01	63	37		
ALTVPELTQQMFDSK			+2	854.4415	1706.8685	1706.8549	0.01	44	6	
NSSYFVEWIPNNVK		+2	848.9265	1695.8385	1695.8256	0.01	68	40		
GHYTEGAELVDSVLDVVR			+2	980.0010	1957.9875	1957.9744	0.01	123	19	
NMMAACDPR		+2	504.7097	1007.4049	1007.3987	0.01	51	30		
INVYYNEAAGNKYVPR			+2	935.9875	1869.9604	1869.9373	0.02	83	8	
FPGQLNADLR		+2	565.8051	1129.5956	1129.5880	0.01	59	90		
YLTVAAIFR		+2	527.3110	1052.6074	1052.6018	0.01	62	30		
RISEQFTAMFR		+2	693.3569	1384.6992	1384.6921	0.01	63	11		
EIVHIQAGQCGNQIGAK			+2	883.4585	1764.9024	1764.8940	0.01	93	42	
LAVNMVPFPR		+2	571.7278	1141.4410	1142.6270	-1.18	84	232		
MSATFIGNSTAIQELFKR			+2	1007.5355	2013.0564	2013.0353	0.02	52	6	
SGPFGQIFRPDNFVFGQSGAGNNWAK				+3	933.4606	2797.3599	2797.3360	0.02	83	9
LTTPTYGDLNHLVSATMSGVTTCLR				+2	1326.1707	2650.3268	2650.3094	0.02	125	46
FPGQLNADLRK		+2	629.8528	1257.6910	1257.6829	0.01	43	40		

Identified Human Platelet Proteins

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No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
646.    IPI00563778         N         Y         0.65      1         0         9         0         33
*Des:   Apolipoprotein A-I
        SEQUEST:(PepMatched Observed.Hits Coverage)
        MASCOT:(PepMatched Observed.Hits Coverage)        9         1         39.77%
                Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                VVAEEFR   +2        425.2296  848.4447  848.4392  0.01      45        6
                DSGRDYVSQFESSTLGK             +2        938.4471  1874.8796 1874.8646 0.01      102       20
                VKDFATVYVDAVK       +2        728.8663  1455.7180 1453.7816 1.94      67        2
                NEMNKDLENVK         +2        667.3311  1332.6477 1332.6343 0.01      66        2
                NEMNKDLENVKQK       +2        795.4087  1588.8028 1588.7878 0.01      82        6
                AKPALDDLGQGLMPVLEAWK          +2        1076.5842 2151.1539 2151.1397 0.01      115       3
                NHPTLIEYHTK         +3        451.5728  1351.6964 1351.6884 0.01      57        10
                QKLEPLGTELHK        +2        696.9003  1391.7861 1391.7772 0.01      48        2
                LTEIKNHPTLIEYHTK              +2        969.0361  1936.0576 1936.0418 0.02      78        8

No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
647.    IPI00231631         Y         N         0.25      2         3         0         15        0
*Des:   Beta enolase
        SEQUEST:(PepMatched Observed.Hits Coverage)       3         4         11.33%
                Seq       Charge    Xcor      Delta     Probility PepHits
                AAVPSGASTGIYEALELR            +2        5.474     0.578     1.0000    8
                LAQSNGWGVMVSHR                +3        2.811     0.284     0.9966    4
                FGANAILGVSLAVCK               +2        4.918     0.549     1.0000    9
        MASCOT:(PepMatched Observed.Hits Coverage)

No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
648.    IPI00230830         Y         Y         0.53      1         6         5         12        15
*Des:   Eukaryotic translation initiation factor 2 subunit 1
        SEQUEST:(PepMatched Observed.Hits Coverage)       6         1         26.56%
                Seq       Charge    Xcor      Delta     Probility PepHits
                EVLINNINR           +2        2.734     0.253     0.9839    5
                YVMTTTTLER          +2        3.013     0.478     0.9996    5
                HVAEVLEYTKDEQLESLFQR          +3        3.271     0.471     0.9979    1
                FPEVEDVVMVNVR       +2        4.356     0.474     1.0000    5
                TEGLSVLNQAMAVIK               +2        4.341     0.413     0.9997    5
                VVTDTDETELAR        +2        3.611     0.505     1.0000    2
        MASCOT:(PepMatched Observed.Hits Coverage)        5         1         20%
                Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                VVTDTDETELAR        +2        674.84    1347.66   1347.65   0.01      84        2
                EVLINNINR           +2        542.81    1083.61   1083.60   0.01      47        3
                YVMTTTTLER          +2        607.81    1213.61   1213.60   0.01      57        5
                FPEVEDVVMVNVR       +2        766.90    1531.78   1531.77   0.01      82        3
                TEGLSVLNQAMAVIK               +2        787.44    1572.87   1572.85   0.02      84        4

No.     Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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649.	IPI00231633	Y	N	0.19	1	4	0	11	0

*Des: Ras-related protein Rab-1B

SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 39.51%

Seq	Charge	Xcor	Delta	Probility	PepHits
FADDTYTESYISTIGVDFK	+2	4.388	0.626	1.0000	7
NATNVEQAFMTMAAEIK	+3	4.630	0.457	1.0000	2
QWLQEIDRYASENVNK	+2	4.204	0.459	0.9981	2
KVVDNTTAKEFADSLGVPFLETSAK	+3	6.652	0.508	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
650.	IPI00208306	N	Y	1.04	1	0	4	0	15

*Des: Translationally controlled tumor protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 24.57%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
DLISHDELFSDIYK	+2	847.9249	1693.8352	1693.8199	0.02	91	6
GKLEEQKPER	+2	607.3333	1212.6520	1212.6462	0.01	41	4
VKPFMTGAAEQIK	+2	710.3920	1418.7695	1418.7591	0.01	64	5
SLKGKLEEQKPER	+2	771.4437	1540.8728	1540.8572	0.02	43	8

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
651.	IPI00569803	N	Y	2.55	1	0	5	0	35

*Des: PREDICTED: similar to myosin regulatory light chain-like

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 5 1 33.08%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LNGTDPEDVIR	+2	614.81	1227.61	1227.61	0	70	22
GNFNYIEFTR	+2	630.80	1259.59	1259.59	0	65	6
KGNFNYIEFTR	+2	694.85	1387.69	1387.69	0	41	9
FTDEEVDELYR	+2	708.32	1414.63	1414.63	0	59	6
ELLTTMGDRFTDEEVDELYR	+3	811.38	2431.11	2431.12	0	52	10

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
652.	IPI00364707	N	Y	0.37	1	0	2	0	2

*Des: Similar to gp25L2 protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 9.62%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
QLVEQVEQIQK	+2	671.38	1340.74	1340.73	0.01	44	1
FSLFAGGMLR	+2	549.79	1097.57	1097.57	0	46	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
653.	IPI00454375	N	Y	0.1	1	0	2	0	9

*Des: Pkm2 protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 6.45%

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
DAVLDAWAEDVDLR +2 794.4016 1586.7885 1586.7576 0.03 103 6
FGVEQDVDMVFASFIR +3 620.6484 1858.9233 1858.8923 0.03 36 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
654. IPI00400691 Y N 0.26 1 2 0 3 0
*Des: Myeloid differentiation primary response gene 88
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 14.28%
Seq Charge Xcor Delta Probility PepHits
LLELLALLDREDILYELK +3 3.163 0.366 0.9739 1
VGSVSVDSYLFSLPLVALNVGVR +3 4.656 0.413 0.9997 2
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
655. IPI00230835 Y Y 0.92 5 8 7 46 59
*Des: 14-3-3 protein gamma
SEQUEST:(PepMatched Observed.Hits Coverage) 8 6 31.07%
Seq Charge Xcor Delta Probility PepHits
NVTELNEPLSNEER +2 4.966 0.539 1.0000 2
LAEQAERYDDMAAAMK +3 2.968 0.398 0.9996 5
ELEAVCQDVLSLLDNYLIK +3 3.344 0.329 0.9994 1
IEKELEAVCQDVLSLLDNYLIK +3 5.318 0.458 1.0000 1
AYSEAHEISK +2 3.320 0.330 0.9981 2
EKIEKELEAVCQDVLSLLDNYLIK +3 4.189 0.284 0.9665 1
EHMQPTHPIR +2 2.913 0.474 0.9994 29
AYSEAHEISKEHMQPTHPIR +3 5.425 0.540 1.0000 8
MASCOT:(PepMatched Observed.Hits Coverage) 7 7 26.69%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ATVVESSEK +2 475.25 948.48 948.48 0 42 4
YLAEVATGEK +2 540.79 1079.56 1079.55 0.01 54 2
AYSEAHEISK +2 567.78 1133.54 1133.54 0 65 2
YLAEVATGEKR +2 618.84 1235.67 1235.65 0.02 43 2
NVTELNEPLSNEER +2 822.40 1642.79 1642.78 0.01 91 2
YDDMAAAMK +2 508.22 1014.42 1014.42 0 62 24
VISSIEQK +2 451.37 900.73 902.51 -1.77 65 56

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
656. IPI00231637 Y Y 0.15 2 4 6 7 9
*Des: Glucose-6-phosphate 1-dehydrogenase
SEQUEST:(PepMatched Observed.Hits Coverage) 4 4 12.42%
Seq Charge Xcor Delta Probility PepHits
NSYVAGQYDDPASYK +2 4.332 0.561 1.0000 2
DVAGDIFHQQCK +2 3.151 0.365 0.9977 1
DLQSSNQLSNHISSLFR +2 5.251 0.591 1.0000 4
HLNSHMNALHQGMQANR +3 3.865 0.549 1.0000 3
MASCOT:(PepMatched Observed.Hits Coverage) 6 4 14.34%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

		NSYVAGQYDDPASYK			+2	839.3787	1676.7429	1676.7318	0.01	80	3	
		VGFQYEGTYK		+2	596.2936	1190.5726	1190.5607	0.01	43	2		
		DVAGDIFHQQCK		+2	680.8220	1359.6295	1359.6241	0.01	52	1		
		RNELVIR	+2	450.2776	898.5407	898.5348	0.01	41	1			
		DLQSSNQLSNHISSLFR			+2	973.4969	1944.9793	1944.9653	0.01	91	3	
		IFGPIWNR		+2	501.7821	1001.5496	1001.5446	0.01	46	1		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
657.	IPI00206634		Y	Y	1.69	3	2	4	7	22		
*Des:	Platelet factor 4 precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	3	18.69%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AGPHCAVPQLIATLKNGSK			+3	4.497	0.374	0.9968	4			
		AGPHCAVPQLIATLK			+2	4.571	0.469	1.0000	8			
	MASCOT:(PepMatched Observed.Hits Coverage)					4	5	40.18%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ITSLEVIK	+2	452.2513	902.4879	901.5484	0.94	50	7			
		ASPEESDGDLSCVCVK			+2	819.8592	1637.7038	1637.6912	0.01	103	6	
		RITSLEVIK		+2	529.8356	1057.6566	1057.6495	0.01	42	2		
		AGPHCAVPQLIATLK			+2	759.9314	1517.8482	1517.8388	0.01	57	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
658.	IPI00209976		Y	N	1.32	1	2	0	3	0		
*Des:	ATPase inhibitor, mitochondrial precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	15.59%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		HHEDEIDHHSKEIER		+3	3.075	0.431	1.0000	6				
		KHHEDEIDHHSKEIER			+3	3.560	0.399	1.0000	8			
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT)			emPAI Strategy.Hits		PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
659.	IPI00230837		Y	Y	0.86	4	6	5	49	24		
*Des:	14-3-3 protein beta/alpha											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	6	40.4%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TAFDEAIAELDTLNEESYK			+2	6.187	0.670	1.0000	11			
		LGLALNFSVFYYEILNSPEK			+2	6.333	0.574	1.0000	11			
		YLSEVASGDNK		+2	3.642	0.409	0.9999	5				
		YLILNATHAESK		+2	4.171	0.381	0.9999	23				
		AVTEQGHELSNEER		+2	4.452	0.515	1.0000	4				
		QTTVSNSQQAYQEAFEISK			+3	6.755	0.581	1.0000	12			
	MASCOT:(PepMatched Observed.Hits Coverage)					5	7	32%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YLSEVASGDNK		+2	591.79	1181.56	1181.56	0	66	4		
		AVTEQGHELSNEER		+2	799.88	1597.75	1597.73	0.02	117	4		
		YLILNATHAESK		+2	680.37	1358.73	1358.72	0.01	88	20		
		QTTVSNSQQAYQEAFEISK			+3	720.35	2158.04	2158.02	0.02	70	2	

		TAFDEAIAELDTLNEESYK			+3	720.34	2158.01	2158.00	0.01	69	7	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
660.	IPI00231639		Y	Y	0.43	1	2	3	4	9		
*Des:	Glutathione S-transferase Mu 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	13.51%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LGLDFPNLPYLIDGSR			+2	3.412	0.492	0.9999	1			
		ADIVENQVMDNR		+2	3.539	0.389	0.9997	4				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	19.81%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ADIVENQVMDNR		+2	702.34	1402.66	1402.65	0.01	70	4		
		LLLEYTDSSYEEK		+2	795.39	1588.76	1588.75	0.01	64	4		
		LGLDFPNLPYLIDGSR			+2	895.49	1788.96	1788.94	0.02	59	1	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
661.	IPI00230838		Y	Y	0.33	1	2	2	7	7		
*Des:	ATP synthase D chain, mitochondrial											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	3	26.99%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IPVPEDKYTALVDAEEKEDVK			+3	5.173	0.442	1.0000	1			
		NMIPFDQMTIDDLNEVFPETK			+2	5.332	0.478	1.0000	4			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	2	26.99%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IPVPEDKYTALVDAEEKEDVK			+2	1194.6329	2387.2513	2387.2107	0.04	76	3	
		NMIPFDQMTIDDLNEVFPETK			+2	1249.1077	2496.2008	2496.1552	0.05	87	4	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
662.	IPI00231567		N	Y	1.37	1	0	6	0	104		
*Des:	Splice Isoform 7 of Tropomyosin 1 alpha chain											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					6	2	28.85%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ETAEADVASLNR		+2	638.31	1274.61	1274.61	0	50	12		
		SLQEQADAAEER		+2	673.81	1345.62	1345.61	0.01	69	6		
		YSQKEDKYEEEIK		+2	844.91	1687.80	1687.79	0.01	65	27		
		MEIQEIQLK		+2	566.31	1130.60	1130.60	0	74	20		
		IQLVEEELDR		+2	622.33	1242.65	1242.65	0	77	101		
		KLVIIESDLER		+2	657.89	1313.76	1313.76	0	48	5		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
663.	IPI00212115		Y	Y	0.27	1	2	2	3	2		
*Des:	Ubiquitin-activating enzyme E1-domain containing 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	6.09%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		MSDEVVDSNPYSR		+2	3.552	0.540	0.9999	2				
		VEELEQELAR		+2	3.282	0.320	0.9984	1				

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          MASCOT:(PepMatched Observed.Hits Coverage)    2          1          6.09%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                      Pepscore  PepHits
                    MSDEVVDSNPYSR  +2                749.83     1497.65    1497.64    0.01       47         2
                    VEELEQELAR     +2                608.31     1214.61    1214.61    0          55         1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
664.      IPI00388301          N          Y          0.21       1          0          4          0          34
*Des:     81 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)    4          1          9.63%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                      Pepscore  PepHits
                    IGDGGQEPTTGNWR                   +2         744.3525   1486.6904  1486.6800  0.01       86         10
                    LDLMDAGTDAMDVLMGR                +2         912.9783   1823.9420  1822.8263  1.12       70         6
                    SSLLDDLLTESEDMAQR                +2         961.9588   1921.9030  1921.8939  0.01       83         12
                    VFSPNVVNLTLVDLPGMTK              +2         1022.5616  2043.1086  2043.1074  0          105        6

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
665.      IPI00360356          Y          Y          0.17       1          3          2          29         6
*Des:     PREDICTED: similar to RIKEN cDNA 4732495G21 gene
          SEQUEST:(PepMatched Observed.Hits Coverage)   3          1          12.01%
                    Seq        Charge     Xcor       Delta      Probility  PepHits
                    VAPDEHPILLTEAPLNPKINR            +3         3.638      0.391      0.9973     2
                    HQGVMVGMGQKDCYVGDEAQSKR          +3         3.826      0.456      1.0000     109
                    HQGVMVGMGQKDCYVGDEAQSK           +3         3.267      0.527      1.0000     25
          MASCOT:(PepMatched Observed.Hits Coverage)    2          1          6.26%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                      Pepscore  PepHits
                    HQGVMVGMGQKDCYVGDEAQSKR          +3         841.7303   2522.1692  2522.1463  0.02       50         38
                    HQGVMVGMGQKDCYVGDEAQSK           +3         789.6961   2366.0665  2366.0452  0.02       44         15

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
666.      IPI00566258          N          Y          0.39       4          0          7          0          38
*Des:     PREDICTED: stomatin (predicted)
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)    7          10         12.01%
                    Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                      Pepscore  PepHits
                    VIAAEGEMNASR     +2         624.31     1246.61    1246.60    0.01       84         9
                    LPVQLQR+2  427.27     852.52     852.52     0          56         10
                    LLAQTTLR   +2         458.29     914.56     914.55     0.01       55         18
                    YLQTLTTIAAEK     +2         676.38     1350.75    1350.74    0.01       70         3
                    VQNATLAVANITNADSATR              +2         965.51     1929.01    1928.99    0.02       131        4
                    TISFDIPPQEVLTK   +2         794.44     1586.87    1586.86    0.01       43         33
                    EASMVITESPAALQLR                 +2         858.46     1714.91    1714.89    0.02       80         4

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
667.      IPI00204899          Y          Y          0.29       4          5          4          5          5
*Des:     Septin-7
          SEQUEST:(PepMatched Observed.Hits Coverage)   5          4          18.01%
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		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LAAVTYNGVDNNK		+2	3.507	0.566	1.0000	1				
		FEDYLNAESR		+2	3.068	0.412	0.9944	3				
		IYEFPETDDEEENKLVK			+2	4.489	0.556	1.0000	2			
		STLINSLFLTDLYSPEYPGPSHR				+3	4.599	0.554	1.0000	1		
		DVTNNVHYENYR		+2	3.806	0.521	1.0000	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					4	3	13.96%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LAAVTYNGVDNNK		+2	689.85	1377.69	1377.69	0	68	1		
		DVTNNVHYENYR		+2	762.35	1522.69	1522.68	0.01	68	1		
		FEDYLNAESR		+2	622.82	1243.62	1242.55	1.07	53	6		
		STLINSLFLTDLYSPEYPGPSHR				+3	869.78	2606.32	2606.30	0.02	70	1
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
668.	IPI00200757		Y	Y	0.25	3	14	30	37	484		
*Des:	Splice Isoform 1 of Fibronectin precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					14	9	9.32%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		SYTITGLQPGTDYK		+2	4.072	0.629	1.0000	2				
		SSPVVIDASTAIDAPSNLR			+2	4.508	0.511	1.0000	4			
		GLAFTDVDVDSIK		+2	3.309	0.492	0.9996	1				
		HVLQSASAGSGSFTDVR			+2	5.618	0.612	1.0000	9			
		HYQINQQWER		+2	2.573	0.421	0.9976	2				
		NGESQPLVQTAVTNIDRPK			+3	3.204	0.422	0.9999	2			
		TKTETITGFQVDAIPANGQTPVQR				+2	6.032	0.473	1.0000	5		
		WLPSTSPVTGYR		+2	3.160	0.449	0.9993	2				
		FTQVSPTTLTAQWTAPSVK			+2	5.764	0.537	1.0000	4			
		IGDQWDKQHDLGHMMR			+3	5.162	0.469	1.0000	5			
		LGVRPSQGGEAPR		+3	4.525	0.361	1.0000	12				
		WSRPQAPITGYR		+3	3.288	0.302	0.9995	7				
		FLTTTPNSLLVSWQAPR			+2	4.739	0.552	1.0000	6			
		ITGYIIKYEKPGSPPR			+3	3.164	0.486	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					30	11	20%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		QYNVGPMASK		+2	547.77	1093.53	1093.52	0.01	45	8		
		TYHVGEQWQK		+3	425.88	1274.61	1274.60	0.01	49	24		
		HYQINQQWER		+2	701.34	1400.67	1400.66	0.01	52	40		
		HVLQSASAGSGSFTDVR			+2	859.93	1717.85	1717.84	0.01	133	59	
		RPGAAEPSPDGTTGHTYNQYTQR				+3	835.40	2503.17	2503.15	0.02	67	4
		GVTYNIIVEALHNQR		+2	863.97	1725.93	1725.92	0.01	79	29		
		VTWAPPPSIELTNLLVR			+2	953.55	1905.09	1905.07	0.02	61	52	
		FLTTTPNSLLVSWQAPR			+2	966.03	1930.05	1930.03	0.02	89	16	
		NTFAEVTGLSPGVTYLFK			+2	972.52	1943.02	1943.00	0.02	114	32	
		EINLSPDSTSVIVSGLMVATK			+3	721.06	2160.15	2160.13	0.02	57	8	
		NSITLTNLNPGTEYIVTIIAVNGR			+3	858.47	2572.40	2572.39	0.01	71	32	
		DLEVIASTPTSLLISWEPPAVSVR				+3	860.81	2579.41	2579.38	0.03	69	20
		WSRPQAPITGYR		+2	716.38	1430.75	1430.74	0.01	44	47		

IAWESPQGQVSR		+2	679.35	1356.69	1356.68	0.01	62	6		
EATIPGHLNSYTIK		+2	772.42	1542.82	1542.80	0.02	52	47		
IHLYTLNDNAR		+2	665.35	1328.69	1328.68	0.01	72	44		
EESPPLIGQQSTVSDVPR			+2	970.00	1937.99	1937.97	0.02	107	158	
SYTITGLQPGTDYK		+2	772.39	1542.77	1542.76	0.01	77	45		
APITGYIIR		+2	502.30	1002.59	1002.59	0	60	21		
VDVLPVNLPGEHGQR			+2	815.45	1628.88	1628.86	0.02	52	25	
SSPVVIDASTAIDAPSNLR			+2	957.01	1912.00	1911.99	0.01	113	12	
TVLVTWTPPR		+2	585.35	1168.68	1168.66	0.02	57	27		
ATGVFTTLQPLR		+2	652.38	1302.74	1302.73	0.01	63	6		
TFYQIGDSWEK		+2	687.33	1372.64	1372.63	0.01	59	3		
YIVNVYQISEEGK		+2	771.40	1540.79	1540.78	0.01	90	9		
VTDATETTITISWR		+2	797.42	1592.82	1592.80	0.02	62	3		
NLQPGSEYTVTLMAVK			+2	875.96	1749.91	1749.90	0.01	74	12	
VTIMWTPPNSAVTGYR			+2	896.96	1791.91	1791.90	0.01	62	9	
GLTPGVIYEGQLISIQQYGHQEVTR				+3	929.50	2785.46	2785.44	0.02	49	10
TGLDSPTGFDSSDVTANSFTVHWVAPR				+3	955.46	2863.36	2863.34	0.02	76	6

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
669.	IPI00391244		Y	Y	0.75	4	12	13	102	104		
*Des:	PREDICTED: similar to beta-parvin											
	SEQUEST:(PepMatched Observed.Hits Coverage)					12	13	35.7%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		WNVDSIHGK		+2	3.120	0.283	0.9968	24				
		LNVAEVTQSEIGQK		+2	5.274	0.535	1.0000	16				
		ARPEDVVNLDLK		+2	4.059	0.401	0.9997	13				
		QLEEDLYDGQVLQK		+2	5.114	0.445	1.0000	9				
		APIHLPEHVTVQVVVVR			+3	6.054	0.532	1.0000	20			
		SAINSPMAPALVDIHPEDTQLEENEER				+3	4.021	0.394	0.9996	5		
		DAFDTLFDHAPDK		+2	4.371	0.496	1.0000	12				
		DAFDTLFDHAPDKLNLVK			+2	4.572	0.509	1.0000	23			
		EGLLHSSHISEELTTTTEIMMGR				+2	5.774	0.669	1.0000	35		
		VHNVAFAFELMLDGGLK			+2	5.351	0.715	1.0000	11			
		VLLDWINDVLAEER		+2	5.372	0.389	1.0000	10				
		LQTVLEAVQDLLRPHGWPLR			+3	4.628	0.555	1.0000	6			
	MASCOT:(PepMatched Observed.Hits Coverage)					13	11	33.87%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		WNVDSIHGK		+2	528.27	1054.53	1054.52	0.01	56	19		
		SLITFVNK	+2	461.28	920.54	920.53	0.01	55	7			
		ARPEDVVNLDLK		+2	684.88	1367.75	1367.74	0.01	85	14		
		LNVAEVTQSEIGQK		+2	758.41	1514.81	1514.79	0.02	120	20		
		QLEEDLYDGQVLQK		+2	839.43	1676.84	1676.83	0.01	114	9		
		APIHLPEHVTVQVVVVR			+2	947.07	1892.12	1892.10	0.02	80	15	
		VLYTLFTK		+2	492.79	983.58	983.57	0.01	43	2		
		DAFDTLFDHAPDK		+2	746.35	1490.68	1490.67	0.01	84	22		
		DAFDTLFDHAPDKLNLVK			+3	687.03	2058.06	2058.04	0.02	69	18	
		EGLLHSSHISEELTTTTEIMMGR				+3	858.09	2571.25	2571.23	0.02	86	19

		VLLDWINDVLAEER		+2	842.96	1683.90	1683.88	0.02	112	11		
		VHNVAFAFELMLDGGLK			+2	930.99	1859.97	1859.96	0.01	121	10	
		LQTVLEAVQDLLRPHGWPLR			+3	781.11	2340.31	2340.31	0	60	3	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
670.	IPI00201489		Y	Y	1.37	1	5	5	9	8		
*Des:	Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	2	36.66%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VVLELKADVVPK		+3	2.313	0.615	0.9980	4				
		TDWLDGKHVVFGHVK			+3	3.300	0.547	0.9982	2			
		TDWLDGKHVVFGHVKEGMDVVK				+3	4.409	0.625	0.9997	2		
		SIYGSRFPDENFTLK		+3	1.984	0.574	0.9904	4				
		GANSSSQNPLVYLDVGADGGQPLGR				+2	5.298	0.644	1.0000	3		
	MASCOT:(PepMatched Observed.Hits Coverage)					5	2	24.76%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		FPDENFTLK		+2	555.78	1109.54	1109.54	0	42	3		
		VVLELKADVVPK		+2	655.41	1308.80	1308.80	0	73	6		
		TDWLDGKHVVFGHVK			+2	869.46	1736.90	1736.90	0	49	2	
		SIYGSRFPDENFTLK		+2	887.44	1772.87	1772.87	0	67	3		
		TDWLDGKHVVFGHVKEGMDVVK				+3	832.77	2495.28	2495.26	0.02	47	1
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
671.	IPI00421897		N	Y	0.19	1	0	3	0	65		
*Des:	Ras-related protein Rab-1A											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	22.48%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NATNVEQSFMTMAAEIK			+2	942.9573	1883.9001	1883.8757	0.02	120	12	
		QWLQEIDRYASENVNK			+2	997.0054	1991.9962	1991.9700	0.03	69	8	
		LQIWDTAGQER		+2	658.8421	1315.6697	1315.6520	0.02	65	63		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
672.	IPI00209113		Y	Y	1.72	5	88	87	377	585		
*Des:	Myosin heavy chain, nonmuscle type A											
	SEQUEST:(PepMatched Observed.Hits Coverage)					88	22	51.8%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		NTDQASMPDNTAAQK			+2	5.621	0.427	1.0000	12			
		NAEQFKDQADKASTR			+2	4.916	0.598	1.0000	5			
		QLEEAEEEAQR		+2	3.717	0.389	0.9995	3				
		ELEDATETADAMNR		+2	4.646	0.577	1.0000	4				
		ASIAALEAK		+2	3.284	0.343	0.9987	4				
		KVEAQLQELQVK		+2	4.813	0.392	1.0000	10				
		IAQLEEQLDNETK		+2	4.606	0.563	1.0000	3				
		TEMEDLMSSKDDVGK			+2	4.506	0.559	1.0000	6			
		ALELDSNLYR		+2	3.605	0.444	0.9998	8				
		YEILTPNSIPK		+2	2.780	0.438	0.9981	5				

TDLLLEPYNK	+2	3.958	0.471	1.0000	6
KANLQIDQINTDLNLER	+2	6.292	0.553	1.0000	5
LTEMETMQSQLMAEK	+2	5.686	0.473	1.0000	8
MQQNIQELEEQLEEEESAR	+2	6.231	0.608	1.0000	6
LQVELDSVTGLLNQSDSK	+2	4.974	0.503	1.0000	19
NLPIYSEEIVDMYK	+2	4.608	0.551	1.0000	11
ITDVIIGFQACCR	+2	2.863	0.244	0.9741	2
DFSALESQLQDTQELLQEENRQK	+3	5.411	0.606	1.0000	8
IIGLDQVAGMSETALPGAFK	+2	5.908	0.576	1.0000	13
LQQELDDLLVDLDHQR	+2	5.926	0.517	1.0000	13
DFSALESQLQDTQELLQEENR	+3	6.507	0.552	1.0000	5
QLLQANPILEAFGNAK	+3	5.246	0.498	1.0000	30
SMEAEMIQLQEELAAAER	+2	6.433	0.489	1.0000	20
KGTGDCSDEEVDGKADGADAK	+3	5.241	0.406	1.0000	4
NAEQFKDQADK	+2	4.054	0.295	0.9945	5
HEDELLAK	+2	3.355	0.462	1.0000	4
ALEEAMEQK	+2	3.399	0.139	0.9812	5
EMEAELEDERK	+2	3.772	0.330	0.9989	2
VEEEEERCQYLQAEK	+3	3.080	0.372	0.9995	2
ALEQQVEEMK	+2	3.479	0.510	1.0000	2
ALEEAMEQKAELER	+2	5.121	0.509	1.0000	9
KLEEDQIIMEDQNCK	+2	5.780	0.587	1.0000	4
KMEDGVGCLETAEEAK	+2	4.467	0.485	1.0000	3
IAQLEEQLDNETKER	+2	4.882	0.484	1.0000	5
MEDGVGCLETAEEAKR	+2	4.572	0.462	1.0000	3
VAEFTTDLMEEEEKSK	+2	4.569	0.467	1.0000	2
VAEFTTDLMEEEEK	+2	4.451	0.454	1.0000	1
ELEDATETADAMNREVSSLK	+2	4.043	0.517	1.0000	1
ELETQISELQEDLESER	+2	3.395	0.506	0.9997	1
LKSMEAEMIQLQEELAAAER	+3	3.695	0.462	1.0000	1
ALEQQVEEMKTQLEELEDELQATEDAKLR	+4	6.864	0.556	1.0000	4
ALEQQVEEMKTQLEELEDELQATEDAK	+3	4.799	0.412	1.0000	2
NMDPLNDNIATLLHQSSDKFVSELWK	+3	4.143	0.418	0.9999	2
PAGPPGILALLDEECWFPK	+2	4.507	0.515	1.0000	3
SHAQKNENAR	+2	3.253	0.467	0.9986	1
VVQEQGTHPK	+2	3.481	0.362	0.9991	18
VKVNKDDIQK	+2	3.331	0.293	0.9860	5
ATDKSFVEK	+2	2.841	0.321	0.9805	3
RQLEEAEEEAQR	+2	4.346	0.311	0.9992	2
THEAQIQEMR	+2	3.293	0.382	0.9990	3
RQLEEAEEEAQRANASR	+3	3.881	0.348	0.9997	1
DLEAHIDTANKNREEAIK	+3	3.970	0.469	1.0000	1
AKQTLENERGELANEVK	+2	5.258	0.493	1.0000	3
LKNKHEAMITDLEER	+3	5.210	0.556	1.0000	10
KTLEDEAKTHEAQIQEMR	+3	4.317	0.482	1.0000	4
LKKLEEDQIIMEDQNCK	+3	3.248	0.455	1.0000	1
ALEEAMEQKAELERLNK	+3	3.179	0.258	0.9899	1

LQKDLEGLSQRLEEK		+2	3.631	0.374	0.9933	3	
LEVNLQAMK	+2	3.024	0.323	0.9971	4		
TEMEDLMSSKDDVGKSVHELEK			+3	4.709	0.573	1.0000	2
HSQAVEELAEQLEQTKR		+3	6.292	0.616	1.0000	2	
QFRTEMEDLMSSKDDVGK		+3	4.133	0.360	0.9999	2	
HSQAVEELAEQLEQTK		+2	5.258	0.592	1.0000	2	
KQELEEICHDLEAR	+2	4.572	0.486	1.0000	3		
MQQNIQELEEQLEEEESARQK		+3	3.965	0.381	0.9998	1	
KMQQNIQELEEQLEEEESAR		+3	3.646	0.409	1.0000	1	
FLSNGHVTIPGQQDKDMFQETMEAMR			+3	6.257	0.494	1.0000	12
IMGIPEDEQMGLLR	+2	3.747	0.532	1.0000	6		
LTKDFSALESQLQDTQELLQEENRQK			+3	5.149	0.534	1.0000	2
NGFEPASLKEEVGEEAIVELVENGKK			+3	5.941	0.496	1.0000	7
IRELETQISELQEDLESER		+3	3.926	0.421	1.0000	1	
LTKDFSALESQLQDTQELLQEENR			+3	6.067	0.429	1.0000	1
LLEDRVAEFTTDLMEEEEKSK		+3	6.014	0.582	1.0000	1	
ALLQGKGDSEHK	+3	2.408	0.371	0.9982	21		
VRTELADKVSK	+3	3.959	0.371	1.0000	11		
RQQQLTAMK	+2	2.773	0.294	0.9926	9		
TVGQLYKEQLAK	+2	4.445	0.488	1.0000	7		
QIATLHAQVTDMK	+2	4.030	0.555	1.0000	5		
KKVEAQLQELQVK	+2	5.399	0.398	1.0000	12		
HEMPPHIYAITDTAYR		+3	3.905	0.545	1.0000	1	
QRYEILTPNSIPK	+3	3.301	0.342	0.9995	11		
VSHLLGINVTDFTR	+2	4.191	0.539	1.0000	27		
VISGVLQLGNIVFK	+2	4.977	0.558	1.0000	29		
RGDMPFVVTR	+2	2.750	0.344	0.9952	4		
LRLEVNLQAMK	+3	3.146	0.284	0.9978	12		
ALLQGKGDSEHKR	+2	3.735	0.502	1.0000	33		
QIATLHAQVTDMKK	+2	3.353	0.495	0.9996	9		
VISGVLQLGNIVFKK	+2	3.961	0.484	0.9998	16		

MASCOT:(PepMatched Observed.Hits Coverage) 87 27 41.72%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
VNKDDIQK		+2	480.2646	958.5146	958.5083	0.01	51	8		
NAEQFKDQADK		+2	647.3132	1292.6119	1292.5997	0.01	84	6		
ERNTDQASMPDNTAAQK			+3	626.2908	1875.8507	1875.8381	0.01	41	3	
HEDELLAK		+2	477.7512	953.4879	953.4818	0.01	61	3		
LQEMESAVK		+2	517.7664	1033.5182	1033.5114	0.01	43	12		
ALEEAMEQK		+2	524.7562	1047.4979	1047.4906	0.01	56	8		
EMEAELEDERK		+2	689.8168	1377.6191	1377.6082	0.01	80	4		
VEEEEERCQYLQAEK			+2	941.9379	1881.8613	1881.8414	0.02	64	4	
ELEDATETADAMNR		+2	783.3481	1564.6817	1564.6675	0.01	92	8		
ASIAALEAK		+2	437.2586	872.5026	872.4967	0.01	63	5		
ALEQQVEEMK		+2	602.8041	1203.5936	1203.5805	0.01	54	4		
ALEEAMEQKAELER		+2	823.9133	1645.8120	1645.7981	0.01	103	12		
VEAQLQELQVK		+2	642.8647	1283.7148	1283.7085	0.01	48	2		
DVLLQVEDERR		+2	686.3711	1370.7276	1370.7153	0.01	46	7		

MEDGVGCLETAEEAK	+2	791.3479	1580.6812	1580.6698	0.01	69	3
TEMEDLMSSKDDVGK	+2	842.8801	1683.7457	1683.7331	0.01	84	11
KMEDGVGCLETAEEAK	+2	855.3995	1708.7844	1708.7647	0.02	86	6
MEDGVGCLETAEEAKR	+2	869.3965	1736.7784	1736.7709	0.01	110	10
KLEEDQIIMEDQNCK	+2	918.4368	1834.8591	1834.8441	0.01	112	10
VVFQEFR	+2	462.7528	923.4910	923.4864	0	41	7
ALELDSNLYR	+2	597.3155	1192.6164	1192.6088	0.01	78	13
TDLLLEPYNK	+2	603.3282	1204.6419	1204.6339	0.01	76	8
DLEGLSQRLEEK	+2	708.8754	1415.7362	1415.7256	0.01	46	6
VAEFTTDLMEEEEK	+2	835.3928	1668.7711	1669.7392	-0.96	74	2
VAEFTTDLMEEEEKSK	+2	942.9545	1883.8945	1884.8662	-0.96	84	5
ADEWLMK	+2	446.7184	891.4223	891.4160	0.01	44	7
EQADFAIEALAK	+2	653.3419	1304.6693	1304.6612	0.01	69	19
LTEMETMQSQLMAEK	+2	885.4158	1768.8171	1768.8045	0.01	116	14
ANLQIDQINTDLNLER	+2	935.4924	1868.9702	1868.9592	0.01	117	11
LQVELDSVTGLLNQSDSK	+2	973.5149	1945.0152	1945.0004	0.01	139	32
NLPIYSEEIVDMYK	+2	857.4308	1712.8471	1712.8331	0.01	96	16
LQQELDDLLVDLDHQR	+2	975.5079	1949.0013	1948.9854	0.02	127	23
GALALEEKR	+2	494.7636	987.5127	985.5556	1.96	52	4
ASREEILAQAK	+2	608.3420	1214.6694	1214.6619	0.01	56	3
QLEEAEEEAQR	+2	666.3126	1330.6107	1330.6000	0.01	76	5
LEVNLQAMK	+2	523.2928	1044.5710	1044.5637	0.01	47	6
YEILTPNSIPK	+2	637.8576	1273.7007	1273.6918	0.01	53	3
KANLQIDQINTDLNLER	+2	999.5437	1997.0729	1997.0541	0.02	120	4
QLEEAEEEAQRANASR	+3	610.9622	1829.8648	1829.8503	0.01	46	6
IAQLEEQLDNETK	+2	765.8928	1529.7711	1529.7573	0.01	75	6
VVQEQGTHPK	+2	560.8441	1119.6736	1121.5829	-1.9	62	16
YKASIAALEAK	+2	582.8396	1163.6646	1163.6550	0.01	45	4
KFDQLLAEEK	+2	610.8358	1219.6570	1219.6448	0.01	47	1
QTLENERGELANEVK	+2	865.4470	1728.8794	1728.8642	0.02	56	2
KVEAQLQELQVK	+2	706.9152	1411.8158	1411.8034	0.01	86	9
NKHEAMITDLEER	+3	529.2632	1584.7679	1584.7566	0.01	74	5
IAQLEEQLDNETKER	+2	908.4672	1814.9199	1814.9010	0.02	90	14
LKDVLLQVEDERR	+3	538.3088	1611.9045	1611.8944	0.01	49	2
LQKDLEGLSQRLEEK	+2	893.4967	1784.9789	1784.9632	0.02	66	2
KQELEEICHDLEAR	+2	856.9293	1711.8441	1711.8199	0.02	107	3
HSQAVEELAEQLEQTK	+2	920.4673	1838.9200	1838.9010	0.02	113	3
HSQAVEELAEQLEQTKR	+3	666.0126	1995.0159	1995.0021	0.01	71	3
IMGIPEDEQMGLLR	+2	801.4113	1600.8081	1600.7952	0.01	60	6
EKHLAAENR	+2	534.2875	1066.5605	1066.5519	0.01	52	3
QSVSNLEKK	+2	516.7911	1031.5676	1031.5611	0.01	41	2
VKVNKDDIQK	+2	593.8477	1185.6809	1185.6717	0.01	69	8
TELADKVSK	+2	495.7803	989.5461	989.5393	0.01	53	8
YAEERDRAEAEAR	+2	783.3743	1564.7341	1564.7229	0.01	44	3
RQLEEAEEEAQR	+2	744.3644	1486.7143	1486.7011	0.01	67	3
NAEQFKDQADKASTR	+2	854.9249	1707.8353	1707.8176	0.02	76	6
THEAQIQEMR	+2	622.3306	1242.6466	1241.5822	1.06	50	4

ASREEILAQAKENEK	+2	858.4590	1714.9035	1714.8849	0.02	77	3
LQKDLEGLSQR	+2	643.8605	1285.7064	1285.6990	0.01	49	4
AKQTLENERGELANEVK	+2	965.0170	1928.0195	1927.9962	0.02	103	5
LKNKHEAMITDLEER	+2	913.9836	1825.9527	1825.9356	0.02	92	10
KFDQLLAEEKTISAK	+2	860.9836	1719.9526	1719.9406	0.01	84	3
LDPHLVLDQLR	+2	659.8826	1317.7507	1317.7405	0.01	52	17
KLQAQMK	+2	423.7498	845.4850	845.4793	0.01	55	105
ALLQGKGDSEHK	+2	641.8460	1281.6775	1281.6677	0.01	50	20
RQQQLTAMK	+2	552.3073	1102.6000	1102.5917	0.01	43	7
VRTELADKVSK	+2	623.3666	1244.7187	1244.7088	0.01	55	5
TVGQLYKEQLAK	+2	689.3959	1376.7773	1376.7663	0.01	71	9
QIATLHAQVTDMK	+2	728.3907	1454.7669	1454.7551	0.01	96	5
HEMPPHIYAITDTAYR	+3	638.9833	1913.9280	1913.9094	0.02	43	1
QLLQANPILEAFGNAK	+2	863.9836	1725.9526	1725.9413	0.01	96	101
SFVEKVVQEQGTHPK	+3	571.6407	1711.9002	1711.8893	0.01	46	2
KKVEAQLQELQVK	+2	770.9622	1539.9099	1539.8984	0.01	97	16
LRLEVNLQAMK	+2	657.8853	1313.7560	1313.7489	0.01	53	6
VSHLLGINVTDFTR	+2	786.4365	1570.8584	1570.8467	0.01	90	34
VISGVLQLGNIVFK	+2	743.9583	1485.9020	1485.8918	0.01	101	34
VIQYLAHVASSHK	+2	726.9067	1451.7989	1451.7885	0.01	79	52
QRYEILTPNSIPK	+2	779.9386	1557.8626	1557.8515	0.01	55	8
ALLQGKGDSEHKR	+2	719.8974	1437.7802	1437.7688	0.01	83	29
QIATLHAQVTDMKK	+2	792.4373	1582.8601	1582.8501	0.01	77	9
KVIQYLAHVASSHK	+2	790.9553	1579.8961	1579.8834	0.01	95	25
VISGVLQLGNIVFKK	+2	808.0068	1613.9991	1613.9868	0.01	78	18
AGKLDPHLVLDQLR	+2	787.9604	1573.9063	1573.8940	0.01	77	30

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
673.	IPI00199655	N	Y	0.22	1	0	2	0	5

*Des: 25 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 11.84%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EALENANTNTEVLK	+2	773.8572	1545.6998	1544.7682	0.93	59	4
KIEQELTAAKK	+3	420.2541	1257.7406	1257.7292	0.01	43	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
674.	IPI00209115	Y	Y	0.32	1	3	2	7	8

*Des: Slc25a3 protein

SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 11.01%

Seq	Charge	Xcor	Delta	Probility	PepHits
GIFNGFSITLK	+2	2.814	0.410	0.9991	2
IQTQPGYANTLR	+2	3.413	0.480	0.9999	3
LPRPPPPEMPESLK	+3	3.925	0.397	0.9999	2

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 6.88%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
IQTQPGYANTLR	+2	681.37	1360.72	1360.71	0.01	75	6

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                        GIFNGFSITLK             +2          598.84      1195.68     1195.66     0.02        45          3

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
675.        IPI00208241             Y           N           0.13        1           3           0           5           0
*Des:       Splice Isoform Stat5A1 of Signal transducer and activator of transcription 5A
            SEQUEST:(PepMatched Observed.Hits Coverage)                 3           1           4.95%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LGHYATQLQNTYDR          +2          4.353       0.612       1.0000      3
                        LAEIIWQNR               +2          3.618       0.165       0.9928      4
                        FSDSEIGGITIAWK          +2          3.006       0.396       0.9981      1
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
676.        IPI00199657             Y           Y           1.69        1           2           2           3           4
*Des:       21 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)                 2           2           12.62%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        KSNQQAVSPK              +2          2.961       0.269       0.9899      2
                        SGNSGNQRPSYQK           +2          3.748       0.389       0.9994      3
            MASCOT:(PepMatched Observed.Hits Coverage)                  2           2           12.62%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        KSNQQAVSPK              +2          543.8026    1085.5907   1085.5829   0.01        57          2
                        SGNSGNQRPSYQK           +2          711.8446    1421.6747   1421.6647   0.01        61          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
677.        IPI00551558             Y           Y           0.06        1           2           2           3           6
*Des:       Type II keratin Kb2
            SEQUEST:(PepMatched Observed.Hits Coverage)                 2           1           4.01%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        GFSSGSAVVSGGSR                      +2          3.833       0.435       1.0000      3
                        LLRDYQELMNVK            +3          3.098       0.268       0.9979      2
            MASCOT:(PepMatched Observed.Hits Coverage)                  2           1           4.01%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        GFSSGSAVVSGGSR                      +2          627.8087    1253.6029   1253.5999   0           83          6
                        LLRDYQELMNVK            +2          761.4108    1520.8070   1520.8020   0.01        42          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
678.        IPI00364715             Y           Y           0.63        1           3           3           8           3
*Des:       PREDICTED: similar to Auh protein
            SEQUEST:(PepMatched Observed.Hits Coverage)                 3           1           13.7%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        MHSSEVGPFVSK            +2          3.157       0.475       0.9998      6
                        GIVVLGINR               +2          3.399       0.354       0.9995      1
                        AVGLISHVLEQNQEGDAAYR                +2          5.030       0.383       0.9999      4
            MASCOT:(PepMatched Observed.Hits Coverage)                  3           1           13.7%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        MHSSEVGPFVSK            +2          652.82      1303.63     1303.62     0.01        56          6
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		GIVVLGINR		+2	470.80	939.59	939.59	0	58	1		
		AVGLISHVLEQNQEGDAAYR			+3	724.04	2169.10	2169.08	0.02	43	3	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
679.	IPI00208315		N	Y	0.04	4	0	10	0	539		
*Des:	PREDICTED: similar to myosin-VIIb											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					10	17	4.27%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GYSFTTTAER		+2	566.77	1131.52	1131.52	0	59	4		
		VAPEEHPVLLTEAPLNPK			+2	977.54	1953.06	1953.06	0	65	4	
		KDLYANTVLSGGTTMYPGIADR				+3	781.73	2342.16	2342.16	0	74	2
		AGFAGDDAPR		+2	488.73	975.44	975.44	0	53	5		
		AVFPSIVGRPR		+2	599.86	1197.70	1197.70	0	49	5		
		DSYVGDEAQSKR		+2	677.82	1353.62	1353.62	0	47	5		
		HQGVMVGMGQKDSYVGDEAQSK				+3	784.36	2350.07	2350.07	0	56	10
		HQGVMVGMGQKDSYVGDEAQSKR				+3	836.40	2506.17	2506.17	0	70	15
		HQGVMVGMGQK		+2	586.29	1170.56	1170.56	0	52	30		
		SYELPDGQVITIGNER			+2	895.95	1789.88	1789.88	0	90	6	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
680.	IPI00231643		Y	N	0.5	1	2	0	2	0		
*Des:	Superoxide dismutase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	25.64%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		GDGPVQGVIHFEQK		+2	2.728	0.500	0.9826	1				
		DGVANVSIEDRVISLSGEHSIIGR				+3	6.881	0.791	1.0000	1		
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
681.	IPI00366247		Y	Y	0.7	1	3	3	5	5		
*Des:	PREDICTED: similar to RIKEN cDNA 4921531G14											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	15.23%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		YAGWAANQINR		+2	3.183	0.501	0.9996	2				
		YTQGGLENLELSR		+2	3.445	0.429	0.9990	2				
		NSEQIMEVGEELINDYASK			+3	5.070	0.610	1.0000	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	15.23%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YAGWAANQINR		+2	632.32	1262.62	1262.62	0	49	2		
		YTQGGLENLELSR		+2	740.38	1478.75	1478.74	0.01	65	2		
		NSEQIMEVGEELINDYASK			+3	723.68	2168.00	2167.99	0.01	50	1	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
682.	IPI00206712		Y	Y	0.33	1	3	3	6	8		
*Des:	Inositol monophosphatase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	13.82%				

Seq	Charge	Xcor	Delta	Probility	PepHits
SSPADLVTVTDQK	+2	3.112	0.386	0.9989	2
IIAASNIALAER	+2	3.049	0.488	0.9998	5
SLLVTELGSSR	+2	3.134	0.392	0.9994	1

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 13.82%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
SSPADLVTVTDQK	+2	680.85	1359.69	1359.69	0	51	2
IIAASNIALAER	+2	622.34	1242.67	1240.71	1.96	54	6
SLLVTELGSSR	+2	581.33	1160.65	1160.64	0.01	61	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
683.	IPI00188225	Y	N	1.68	1	3	0	3	0

*Des: C-reactive protein precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 14.95%

Seq	Charge	Xcor	Delta	Probility	PepHits
TSFNEILLFWTR	+2	2.727	0.348	0.9955	1
VFSPNVLNWR	+2	2.731	0.382	0.9985	4
SFSIFSYATK	+2	2.803	0.457	0.9997	13

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
684.	IPI00195372	Y	Y	0.3	2	5	3	7	24

*Des: Elongation factor 1-alpha 1

SEQUEST:(PepMatched Observed.Hits Coverage) 5 2 16.8%

Seq	Charge	Xcor	Delta	Probility	PepHits
IGGIGTVPVGR	+2	3.415	0.392	0.9928	4
THINIVVIGHVDSGK	+3	3.378	0.477	0.9998	1
YYVTIIDAPGHR	+3	2.654	0.467	0.9996	2
EHALLAYTLGVK	+3	3.856	0.473	0.9999	2
VETGVLKPGMVVTFAPVNVTTEVK	+3	3.503	0.393	0.9989	1

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 8.93%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
YYVTIIDAPGHR	+3	468.9119	1403.7139	1403.7197	0	42	7
THINIVVIGHVDSGK	+3	530.2991	1587.8754	1587.8732	0	52	15
EHALLAYTLGVK	+2	657.8748	1313.7350	1313.7343	0	52	28

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
685.	IPI00208249	Y	Y	0.53	3	4	5	15	17

*Des: Chloride intracellular channel protein 4

SEQUEST:(PepMatched Observed.Hits Coverage) 4 5 21.31%

Seq	Charge	Xcor	Delta	Probility	PepHits
EEDKEPLIELFVK	+2	3.591	0.371	0.9810	5
HPESNTAGMDIFAK	+2	3.621	0.465	0.9999	4
NSRPEANEALER	+2	2.927	0.288	0.9889	2
GVVFSVTTVDLK	+2	4.086	0.532	1.0000	14

MASCOT:(PepMatched Observed.Hits Coverage) 5 2 24.8%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits

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                    YLTNAYSR            +2        494.25    986.49    986.48    0.01      47        3
                    NSRPEANEALER        +2        693.34    1384.67   1384.67   0         48        2
                    HPESNTAGMDIFAK      +2        759.36    1516.71   1516.70   0.01      69        4
                    GVVFSVTTVDLK        +2        632.87    1263.72   1263.71   0.01      91        12
                    EEDKEPLIELFVK       +2        794.93    1587.84   1587.84   0         51        5

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
686.      IPI00230775         N         Y         0.56      3         0         4         0         33
*Des:     Splice Isoform 1 of Tropomyosin beta chain
          SEQUEST:(PepMatched Observed.Hits Coverage)
          MASCOT:(PepMatched Observed.Hits Coverage)        4         3         14.87%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    ATDAEADVASLNR       +2        666.8300  1331.6455 1331.6317 0.01      76        7
                    MELQEMQLK           +2        575.2916  1148.5687 1148.5569 0.01      45        3
                    RIQLVEEELDR         +2        700.3923  1398.7700 1398.7466 0.02      51        13
                    AMKDEEKMELQEMQLK              +2        990.9909  1979.9673 1979.9366 0.03      121       12

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
687.      IPI00363847         Y         Y         0.8       2         6         3         14        21
*Des:     PREDICTED: similar to ARP2/3 complex 16 kDa subunit (p16-ARC) (Actin-related protein 2/3 complex subunit 5)
          SEQUEST:(PepMatched Observed.Hits Coverage)       6         2         25.52%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    ALAAGGVGSIVR        +2        3.729     0.458     0.9933    3
                    AVQSLDKNGVDLLMK               +3        3.332     0.671     0.9997    2
                    QGNMTAALQAALKNPPINTK          +2        3.799     0.555     0.9894    3
                    YIYKGFESPSDNSSAMLLQWHEK                 +3        5.938     0.724     1.0000    2
                    GFESPSDNSSAMLLQWHEKALAAGGVGSIVR                   +3        5.525     0.741     1.0000    3
                    AVQSLDKNGVDLLMKYIYK           +3        4.617     0.617     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)        3         1         13.15%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    ALAAGGVGSIVR        +2        535.8227  1069.6308 1069.6243 0.01      73        15
                    AVQSLDKNGVDLLMK               +2        815.9519  1629.8893 1629.8759 0.01      66        4
                    QGNMTAALQAALKNPPINTK          +2        1041.0742 2080.1339 2080.1098 0.02      67        5

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
688.      IPI00568946         Y         N         0.56      1         2         0         2         0
*Des:     22 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)       2         1         9.42%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    IAYQRNDDDEEEAAR               +3        4.613     0.429     1.0000    1
                    IAYQRNDDDEEEAARER             +3        3.791     0.271     0.9976    1
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
689.      IPI00360362         Y         Y         0.81      4         23        16        105       150
*Des:     PREDICTED: similar to CDNA sequence BC032204
          SEQUEST:(PepMatched Observed.Hits Coverage)       23        25        45.05%
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Seq	Charge	Xcor	Delta	Probility	PepHits
LTQLYEQAR	+2	3.573	0.428	0.9998	9
VFVGEEDPEAQSVTLR	+2	5.263	0.400	1.0000	5
SQDEAPGDPIQQLNLK	+2	4.880	0.471	1.0000	6
ILEAHQNVAQLSLTEAQLR	+2	6.397	0.589	1.0000	10
TASGDYIDSSWELR	+2	4.988	0.532	1.0000	4
AGDVLWLR	+2	3.072	0.280	0.9946	6
QWNVNWDIR	+2	2.739	0.172	0.9555	3
DEILGIANNR	+2	2.792	0.281	0.9892	1
IDLAVGDVVK	+2	3.173	0.423	0.9993	5
VTLSGDVGELASGDPGLDDLDAALNNLEVK	+3	6.136	0.583	1.0000	2
GEELDEDLFLQLTGGHEAF	+2	5.271	0.631	1.0000	2
LLVPSPEGMSEIYLR	+3	5.250	0.532	1.0000	8
GEELDEDLFLQLTGGHEA	+2	5.233	0.683	1.0000	1
EKEPEEEVHDLTR	+3	3.355	0.347	0.9996	6
KQDWSDHAIWWEQK	+3	3.516	0.319	0.9997	1
KDEILGIANNR	+3	3.249	0.323	0.9996	11
VTGESHIGGVLLK	+2	4.027	0.440	0.9997	6
KQDWSDHAIWWEQKK	+3	4.567	0.379	1.0000	3
VVLAGGVAPTLFR	+2	4.514	0.560	1.0000	42
LKGSAPSDMLDSLTTIPELKDHLR	+3	5.517	0.520	1.0000	24
LIRIDLAVGDVVK	+2	2.941	0.502	0.9973	5
ASFSKPLFQTVAAICR	+2	4.875	0.600	1.0000	22
PSSLLDKTQLHSR	+3	3.779	0.470	0.9999	7

MASCOT:(PepMatched Observed.Hits Coverage) 16 27 41.06%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LTQLYEQAR	+2	561.30	1120.59	1120.59	0	59	6
KDEILGIANNR	+2	621.84	1241.68	1241.67	0.01	51	3
VTGESHIGGVLLK	+2	655.38	1308.74	1308.74	0	46	6
SQDEAPGDPIQQLNLK	+2	876.94	1751.87	1751.87	0	89	5
VFVGEEDPEAQSVTLR	+2	888.44	1774.88	1774.87	0.01	102	12
AGDVLWLR	+2	465.74	929.47	928.51	0.96	56	6
TASGDYIDSSWELR	+2	800.37	1598.73	1598.72	0.01	83	2
KQWLLQTHWTLDK	+2	848.96	1695.92	1695.91	0.01	49	2
ILEAHQNVAQLSLTEAQLR	+3	712.06	2133.16	2133.15	0.01	57	4
AGGTNGGSGNKPQGLEASAEGLNPYGLVAPR	+3	980.82	2939.44	2938.45	0.99	44	2
YYSFFDLDPK	+2	647.80	1293.59	1293.59	0	55	2
VVLAGGVAPTLFR	+2	650.39	1298.77	1298.77	0	64	8
FIQAWQSLPDFGISYVIVR	+3	747.07	2238.18	2238.18	0	43	1
TMADSSYASEVQAILAFLSLQR	+3	801.07	2400.20	2400.20	0	62	3
GSAPSDMLDSLTTIPELK	+2	937.97	1873.93	1873.93	0	52	9
VTLSGDVGELASGDPGLDDLDAALNNLEVK	+3	999.84	2996.49	2996.48	0.01	77	4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
690. IPI00210381 Y Y 0.17 2 2 4 6 10
*Des: Ras-related protein Rab-11B
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 12.61%

		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AQIWDTAGQER		+2	3.736	0.564	1.0000	6				
		DHADSNIVIMLVGNK		+2	5.051	0.528	1.0000	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					4	2	19.81%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AITSAYYR		+2	472.7452	943.4759	943.4763	0	43	8		
		VVLIGDSGVGK		+2	522.3075	1042.6004	1042.6022	0	34	4		
		STIGVEFATR		+2	540.7875	1079.5604	1079.5611	0	36	4		
		AQIWDTAGQER		+2	637.8096	1273.6046	1273.6051	0	40	2		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
691.	IPI00328073		Y	Y	0.37	5	21	25	36	46		
*Des:	Splice Isoform PDE5A2 of cGMP-specific 3',5'-cyclic phosphodiesterase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					21	9	35.41%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		EEVVGVAQAINK		+2	4.171	0.405	0.9998	5				
		FNAEVDQITGYK		+2	3.977	0.503	0.9999	2				
		KELNMEPADLMNR		+2	3.636	0.404	0.9995	2				
		INYMYAQYVK		+2	3.115	0.357	0.9987	1				
		NTMEPLNIPDVTK		+2	3.684	0.445	0.9998	2				
		KNEFSFEDPLQK		+2	2.887	0.331	0.9951	3				
		ELQALAAAVVPSAQTLK			+2	4.253	0.566	1.0000	2			
		VFQMEWEEVGK		+2	3.321	0.534	0.9999	1				
		QMVTLEVLSYHASAAEEETR			+2	5.209	0.573	1.0000	3			
		RGEFFELIR		+2	2.730	0.208	0.9744	2				
		IAELVAAEFFDQGDRER			+2	3.756	0.446	0.9923	2			
		IAATIISFMQVQK		+3	4.645	0.408	1.0000	3				
		IAELVAAEFFDQGDR			+2	5.058	0.480	1.0000	2			
		MFTDLNLVQNFQMK			+2	4.674	0.507	1.0000	2			
		QAILATDLALYIK		+2	3.327	0.464	0.9997	1				
		NHREEVVGVAQAINK			+3	4.265	0.404	0.9987	1			
		LTDLETLALLIAALSHDLDHR			+4	5.107	0.538	1.0000	11			
		NQVLLDLASLIFEEQQSLEVILKK				+3	4.925	0.486	1.0000	4		
		RNQVLLDLASLIFEEQQSLEVILK				+3	3.282	0.417	0.9996	1		
		EEVVGVAQAINKK		+2	3.440	0.386	0.9991	2				
		WQALADQQEK		+2	2.830	0.226	0.9806	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					25	12	37.42%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GVNNSYIQR		+2	525.77	1049.53	1049.53	0	43	1		
		EEVVGVAQAINK		+2	628.85	1255.68	1255.68	0	86	4		
		EEVVGVAQAINKK		+2	692.90	1383.78	1383.77	0.01	59	1		
		NHREEVVGVAQAINK			+3	555.30	1662.88	1662.88	0	53	1	
		FNAEVDQITGYK		+2	692.84	1383.67	1383.67	0	72	2		
		KELNMEPADLMNR		+2	780.88	1559.75	1559.74	0.01	59	1		
		DSEGTVSFLSDSGK		+2	714.83	1427.65	1427.64	0.01	86	4		
		DSEGTVSFLSDSGKK			+2	778.88	1555.75	1555.74	0.01	58	4	
		INYMYAQYVK		+2	646.82	1291.63	1291.63	0	46	1		

NTMEPLNIPDVTK	+2	736.38	1470.75	1470.74	0.01	59	2
KNEFSFEDPLQK	+2	741.87	1481.73	1480.72	1.01	52	2
GEFFELIR	+2	505.77	1009.52	1009.52	0	44	1
VFQMEWEEVGK	+2	691.33	1380.65	1380.64	0.01	55	1
IAATIISFMQVQK	+3	483.94	1448.81	1448.81	0	60	2
IAELVAAEFFDQGDR	+2	840.92	1679.82	1679.82	0	106	4
ELQALAAAVVPSAQTLK	+2	855.50	1708.98	1708.97	0.01	67	2
MFTDLNLVQNFQMK	+2	864.93	1727.84	1727.84	0	83	2
IAELVAAEFFDQGDRER	+2	983.49	1964.96	1964.96	0	56	3
QMVTLEVLSYHASAAEEETR	+3	755.37	2263.09	2263.08	0.01	41	1
DMVNAWFSER	+2	627.79	1253.56	1253.55	0.01	60	2
GIVGHVAAFGEPLNIK	+2	811.46	1620.91	1620.90	0.01	56	4
QAILATDLALYIK	+2	716.93	1431.84	1431.83	0.01	46	1
LTDLETLALLIAALSHDLDHR	+3	777.43	2329.28	2329.26	0.02	55	2
NQVLLDLASLIFEEQQSLEVILK	+3	881.50	2641.48	2641.46	0.02	81	3
NQVLLDLASLIFEEQQSLEVILKK	+3	924.20	2769.58	2769.55	0.03	64	3

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
692.	IPI00554034	Y	Y	1.31	3	2	4	6	31

*Des: 24 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 13.2%

Seq	Charge	Xcor	Delta	Probility	PepHits
VAAALPGMESTQDR	+2	3.034	0.429	0.9964	4
ELNVMFIETSAK	+2	3.557	0.510	0.9997	2

MASCOT:(PepMatched Observed.Hits Coverage) 4 3 24.52%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LVFLGEQSVGK	+2	588.8753	1175.7360	1175.6550	0.08	39	1
LQLWDTAGQER	+2	658.8825	1315.7504	1315.6520	0.1	62	2
ELNVMFIETSAK	+2	691.4074	1380.8002	1380.6958	0.1	60	1
VAAALPGMESTQDR	+2	723.4117	1444.8088	1444.6980	0.11	73	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
693.	IPI00551702	Y	Y	0.51	1	2	4	5	5

*Des: Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex, mitochondrial precursor

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.57%

Seq	Charge	Xcor	Delta	Probility	PepHits
NVETMNYADIER	+2	4.123	0.551	1.0000	2
ASAFALQEQPVVNAVIDDATK	+2	6.116	0.583	1.0000	3

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 12.33%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
NVETMNYADIER	+2	727.83	1453.65	1453.65	0	64	2
LGFMSAFVK	+2	500.27	998.53	998.53	0	61	1
VEGGTPLFTLR	+2	595.34	1188.66	1188.65	0.01	44	1
ASAFALQEQPVVNAVIDDATK	+3	729.72	2186.13	2186.12	0.01	42	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
694.	IPI00388249	Y	Y	0.44	4	6	7	9	12

***Des:** Calpain-2 catalytic subunit

SEQUEST:(PepMatched Observed.Hits Coverage) 6 6 12.23%

Seq	Charge	Xcor	Delta	Probility	PepHits			
EAAEGLGSHER		+2	3.488	0.289	0.9993	2		
DREAAEGLGSHER		+2	3.955	0.502	1.0000	6		
MGEDMHTIGFGIYEVPEELTGQTNIHLSK				+3	3.898	0.471	1.0000	3
RPTEICADPQFIIGGATR			+2	3.757	0.555	1.0000	2	
LAKDREAAEGLGSHER			+3	4.412	0.508	1.0000	8	
GHAYSVTGAEEVESSGSLQK			+3	3.854	0.420	1.0000	3	

MASCOT:(PepMatched Observed.Hits Coverage) 7 6 16.17%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
SGTMNSYEMR		+2	588.24	1174.47	1174.47	0	47	3		
IMVDMLDEDGSGK		+2	705.32	1408.62	1408.62	0	73	2		
NPWGQVEWTGK		+2	650.38	1298.74	1300.62	-1.87	53	3		
FADDELIIDFDNFVR		+3	610.29	1827.86	1827.87	0	64	4		
QEDGEFWMSFSDFLR			+2	947.41	1892.81	1892.80	0.01	54	1	
LFAQLAGEDAEISAFELQTILR			+3	812.44	2434.29	2434.27	0.02	41	2	
DGELLFVHSAEGSEFWSALLEK				+3	822.07	2463.20	2463.20	0	54	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
695.	IPI00551632	N	Y	0.3	1	0	7	0	24

***Des:** Alpha-ETF

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 7 1 42.18%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
GTSFEAAAASGGSASSEK			+2	807.87	1613.73	1613.72	0.01	112	2	
APSSSSAGISEWLDQK			+2	831.90	1661.80	1661.79	0.01	84	2	
AAVDAGFVPNDMQVGQTGK			+2	952.97	1903.92	1903.91	0.01	76	4	
LLYDLADQLHAAVGASR			+2	906.99	1811.96	1811.95	0.01	106	2	
GLLPEELTPLILETQK			+2	897.52	1793.02	1793.02	0	55	4	
IVAPELYIAVGISGAIQHLAGMK			+3	784.12	2349.33	2350.31	-0.97	55	10	
TIVAINKDPEAPIFQVADYGIVADLFK				+3	983.21	2946.59	2946.57	0.02	86	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
696.	IPI00554039	N	Y	0.47	1	0	6	0	293

***Des:** PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 6 1 26.54%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
GAAQNIIPASTGAAK		+2	685.38	1368.74	1368.74	0	101	238		
VGVNGFGR		+2	403.22	804.43	804.42	0.01	58	141		
LVNNGKPITIFQER		+2	814.98	1627.94	1627.90	0.04	72	2		
LISWYDNEYGYSNR		+2	890.40	1778.79	1778.79	0	80	97		
RVIISAPSADAPMFVMGVNHEK			+3	790.41	2368.21	2368.20	0.01	57	8	
VVDLMAYMASK		+2	614.31	1226.61	1226.60	0.01	87	90		

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)

697.	IPI00372810	Y	Y	0.07	1	2	2	4	3

*Des: PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 1.62%

Seq	Charge	Xcor	Delta	Probility	PepHits
LLDMDGIIVEK	+2	3.638	0.482	0.9999	3
DLYNWLEVEFNPLK	+2	4.069	0.437	0.9997	1

MASCOT:(PepMatched Observed.Hits Coverage) 2 1 1.62%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LLDMDGIIVEK	+2	623.35	1244.68	1244.67	0.01	57	3
DLYNWLEVEFNPLK	+2	890.46	1778.90	1778.89	0.01	54	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
698.	IPI00454532	N	Y	0.27	1	0	4	0	10

*Des: Similar to enthoprotin; epsin 4; clathrin interacting protein localized in the trans-Golgi region

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 4 2 11.04%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
IGSTIDDTISK	+2	575.30	1148.59	1148.59	0	43	3
TIDLGAAAHYTGDK	+2	716.86	1431.70	1431.70	0	42	3
ATNVVMNYSEIESK	+2	792.88	1583.75	1583.75	0	50	1
SLLLLAYLIR	+2	587.88	1173.75	1173.75	0	75	3

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
699.	IPI00471519	Y	Y	2.6	4	18	16	75	260

*Des: Bridging integrator 2

SEQUEST:(PepMatched Observed.Hits Coverage) 18 14 43.99%

Seq	Charge	Xcor	Delta	Probility	PepHits
ASGGGLSSPPGSAEASK	+2	4.180	0.519	1.0000	10
SATQVVSNDENTEL	+2	2.999	0.212	0.9642	1
TMENYVSQFSEVKER	+2	4.697	0.544	1.0000	5
VSETLQEIYNSDWDGHEDLK	+2	4.957	0.526	1.0000	9
AIVGNNDLLWEDYEEK	+2	5.708	0.567	1.0000	2
AIVGNNDLLWEDYEEKLADQALR	+3	4.886	0.654	1.0000	8
MAKAEEDFSK	+2	2.815	0.386	0.9896	2
SQEEAAPCSPTSSLGR	+2	3.731	0.516	1.0000	2
SATQVVSNDENTE	+2	3.462	0.383	0.9826	3
TMENYVSQFSEVK	+2	3.448	0.524	1.0000	1
FEQSASNFYQQQAEGHR	+2	4.830	0.540	1.0000	3
AGGAAGLFAK	+2	3.561	0.430	0.9997	8
RVSETLQEIYNSDWDGHEDLK	+3	6.161	0.484	1.0000	2
EGTGSSGPKEPHASSTK	+2	3.337	0.544	0.9990	3
EMSKLNHSLYEVMSK	+2	3.906	0.442	0.9982	1
HHLEAVQNAK	+2	3.049	0.313	0.9960	68
TSAPPSRPPPPK	+3	2.542	0.534	1.0000	157
GQTGKEHSPPGEVVLR	+2	4.834	0.478	1.0000	21

MASCOT:(PepMatched Observed.Hits Coverage) 16 15 36.24%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits

MAKAEEDFSK	+2	578.2744	1154.5343	1154.5277	0.01	46	10
LVDYDSAR	+2	469.7354	937.4562	937.4505	0.01	41	34
SQEEAAPCSPTSSLGR	+2	810.3764	1618.7383	1618.7257	0.01	59	4
ASGGGLSSPPGSAEASK	+2	730.3602	1458.7058	1458.6950	0.01	77	14
TMENYVSQFSEVK	+2	781.3688	1560.7231	1560.7130	0.01	59	12
AIVGNNDLLWEDYEEK	+2	954.4615	1906.9085	1906.8948	0.01	123	6
TMENYVSQFSEVKER	+2	923.9434	1845.8722	1845.8566	0.02	103	10
AGGAAGLFAK	+2	431.7452	861.4758	861.4708	0	94	12
KLVDYDSAR	+2	533.7838	1065.5531	1065.5454	0.01	61	13
EMSKLNHSLYEVMSK	+2	898.4476	1794.8806	1794.8644	0.02	59	2
DLKNFLSAVK	+2	567.8340	1133.6535	1133.6444	0.01	42	4
EGTGSSGPKEPHASSTK	+2	828.9039	1655.7933	1655.7750	0.02	50	8
TSAPPSRPPPPK	+2	616.3484	1230.6823	1230.6721	0.01	79	274
HHLEAVQNAK	+2	573.8085	1145.6024	1145.5941	0.01	61	106
GQTGKEHSPPGEVVLR	+2	845.9539	1689.8933	1689.8798	0.01	92	34
HHLEAVQNAKK	+2	637.8570	1273.6994	1273.6891	0.01	48	6

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
700.	IPI00199663	N	Y	0.1	1	0	3	0	6

*Des: Glycerol-3-phosphate dehydrogenase, mitochondrial precursor

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 6.08%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
MNLAIALTAAR	+2	572.83	1143.64	1143.64	0	45	2
LAFLNVQAAEEALPK	+2	807.45	1612.89	1612.88	0.01	44	2
YGAATANYMEVVSLLK	+2	864.96	1727.90	1728.88	-0.97	47	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
701.	IPI00231721	Y	Y	0.71	1	2	4	2	11

*Des: Protein-L-isoaspartate (D-aspartate) O-methyltransferase 1

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 22.07%

Seq	Charge	Xcor	Delta	Probility	PepHits
MGFAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR	+3	5.902	0.638	1.0000	5
SGGASHSELIHNLRK	+3	2.828	0.313	0.9983	3

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 33.76%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LILPVGPAGGNQMLEQYDKLQDGSVK	+3	924.1584	2769.4535	2769.4370	0.02	41	2
MGFAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR	+3	1163.6112	3487.8118	3487.7921	0.02	93	8
SGGASHSELIHNLR	+3	493.2581	1476.7524	1476.7433	0.01	55	2
SGGASHSELIHNLRK	+2	803.4318	1604.8490	1604.8382	0.01	57	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
702.	IPI00370130	Y	N	0.16	1	2	0	3	0

*Des: PREDICTED: similar to serine/threonine protein kinase MST4a

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 5.96%

Seq	Charge	Xcor	Delta	Probility	PepHits
AANVLLSEQGDVK	+2	2.991	0.334	0.9591	1

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                        LWIIMEYLGGGSALDLLR     +3          5.907       0.553       1.0000      2
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
703.        IPI00231726             Y           Y           0.28        2           3           2           5           2
*Des:       Guanine nucleotide-binding protein G(k), alpha subunit
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           1           13.64%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        ISQTNYIPTQQDVLR +2      3.837       0.383       0.9992      1
                        NVQFVFDAVTDVIIK +2      5.362       0.425       1.0000      3
                        VVVYSNTIQSIIAIIR +2     3.987       0.422       0.9996      2
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           4.73%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        LLLLGAGESGK             +2          529.3199    1056.6252   1056.6178   0.01        60          1
                        LLLLGAGESGKSTIVK                    +3          529.3199    1584.9378   1584.9450   0           43          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
704.        IPI00382295             N           Y           0.14        2           0           5           0           23
*Des:       Ac2-125
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      5           2           5.48%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        EVLEYNTVGGK             +2          604.82      1207.62     1207.61     0.01        66          12
                        VLTEDELGHPEK            +2          683.85      1365.69     1365.68     0.01        51          12
                        VLTEDELGHPEKGDAITR                  +3          660.68      1979.00     1979.00     0           44          12
                        IKEVLEYNTVGGK           +3          483.94      1448.80     1448.79     0.01        44          4
                        GLTVVQTFQELVEPR                     +2          858.48      1714.94     1714.93     0.01        76          4

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
705.        IPI00230925             Y           Y           16.42       2           5           2           20          26
*Des:       Thymosin beta-4
            SEQUEST:(PepMatched Observed.Hits Coverage)     5           3           120.45%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        ETIEQEKQAGE             +2          3.993       0.365       0.9694      3
                        TETQEKNPLPSK            +2          3.875       0.237       0.9801      4
                        TETQEKNPLPSKETIEQEK                 +3          4.709       0.483       1.0000      2
                        NPLPSKETIEQEKQAGES                  +2          3.869       0.527       1.0000      1
                        KTETQEKNPLPSK           +2          4.266       0.486       1.0000      22
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           31.81%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        TETQEKNPLPSK            +2          686.3647    1370.7149   1370.7041   0.01        65          6
                        KTETQEKNPLPSK           +2          750.4125    1498.8105   1498.7991   0.01        86          34

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
706.        IPI00569825             N           Y           0.22        1           0           2           0           3
*Des:       35 kDa protein
            SEQUEST:(PepMatched Observed.Hits Coverage)
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Identified Human Platelet Proteins

	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	4.06%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GAWSNVLR		+2	451.7454	901.4763	901.4770	0	46	1		
		AFCKGAWSNVLR		+3	451.7454	1352.2144	1350.6866	1.53	41	2		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
707.	IPI00208256		Y	Y	0.51	3	14	10	26	30		
*Des:	Heat shock protein 86											
	SEQUEST:(PepMatched Observed.Hits Coverage)					14	5	26.8%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		EGLELPEDEEEKKK	+2		3.384	0.367	0.9626	1				
		EGLELPEDEEEKK	+2		3.057	0.366	0.9976	1				
		YYTSASGDEMVSLK	+2		3.911	0.575	1.0000	2				
		HIYFITGETK	+2		3.090	0.428	0.9995	4				
		VILHLKEDQTEYLEER			+3	4.437	0.565	1.0000	4			
		ELHINLIPNKQDR	+2		3.406	0.461	0.9922	3				
		NPDDITNEEYGEFYK			+2	5.117	0.519	1.0000	2			
		HFSVEGQLEFR	+3		3.560	0.430	0.9999	4				
		HNDDEQYAWESSAGGSFTVR		+2		6.744	0.718	1.0000	3			
		HLEINPDHSIIETLR	+3		3.668	0.479	1.0000	3				
		ADLINNLGTIAK	+2		3.589	0.475	0.9998	3				
		APFDLFENR	+2		2.968	0.511	0.9999	2				
		DLVILLYETALLSSGFSLEDPQTHANR				+3	6.074	0.646	1.0000	4		
		DQVANSAFVER	+2		2.801	0.368	0.9972	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					10	4	18.49%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DNSTMGYMAAK		+2	594.76	1187.50	1187.50	0	54	2		
		DQVANSAFVER		+2	618.31	1234.60	1234.59	0.01	54	2		
		ELISNSSDALDK		+2	646.33	1290.64	1290.63	0.01	63	4		
		YYTSASGDEMVSLK		+2	775.86	1549.71	1549.70	0.01	77	2		
		ELHINLIPNKQDR		+2	795.44	1588.87	1588.87	0	44	4		
		TLTIVDTGIGMTK		+2	675.37	1348.73	1348.73	0	81	3		
		NPDDITNEEYGEFYK			+2	917.40	1832.78	1832.77	0.01	78	2	
		HLEINPDHSIIETLR		+3	596.32	1785.94	1785.94	0	43	4		
		APFDLFENR		+2	554.77	1107.53	1107.53	0	50	4		
		HSQFIGYPITLFVEK		+2	889.98	1777.95	1777.94	0.01	74	24		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
708.	IPI00372748		Y	Y	0.51	1	4	2	4	3		
*Des:	PREDICTED: similar to adenylosuccinate synthetase, non muscle											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	1	14.65%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VTVVLGAQWGDEGK			+2	3.090	0.282	0.9899	2			
		VGIGAFPTEQDNEIGELLQTR			+3	3.822	0.314	0.9975	1			
		SIYPTLEIDIEGELQQLK			+2	5.005	0.456	1.0000	2			
		LDILDMFTEIK	+2		4.156	0.412	0.9999	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	5.17%				

Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ELPVNAQNYVR +2 651.85 1301.68 1301.67 0.01 47 2
LDILDMFTEIK +2 669.60 1337.19 1336.69 0.5 69 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
709. IPI00230857 Y Y 0.55 2 4 4 19 11
*Des: Adenylate kinase isoenzyme 2, mitochondrial
SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 21.81%
Seq Charge Xcor Delta Probility PepHits
SYHEEFNPPK +3 3.084 0.295 0.9973 5
LEAYHTQTTPLVEYYR +2 4.966 0.521 1.0000 5
NGFLLDGFPR +2 3.379 0.496 1.0000 17
LVSDEMVVELIEK +2 4.434 0.468 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 4 3 23.86%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
APNALAPEPEHPK +2 685.86 1369.71 1369.70 0.01 53 2
AVLLGPPGAGK +2 490.30 978.59 978.59 0 43 7
LEAYHTQTTPLVEYYR +2 992.50 1982.99 1982.97 0.02 76 5
EAMKDDITGEPLIR +2 794.42 1586.82 1586.80 0.02 51 4

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
710. IPI00364585 Y Y 0.25 1 2 2 2 2
*Des: Serine/threonine kinase receptor associated protein
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 8.93%
Seq Charge Xcor Delta Probility PepHits
YDYNSGEELESYK +2 3.494 0.522 0.9998 1
SFEAPATINSASLHPEK +2 3.631 0.527 0.9998 1
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 8.93%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
YDYNSGEELESYK +2 798.84 1595.67 1595.66 0.01 57 1
SFEAPATINSASLHPEK +2 899.96 1797.90 1797.89 0.01 74 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
711. IPI00194728 Y Y 0.79 4 8 8 24 23
*Des: Integrin-linked kinase ILK
SEQUEST:(PepMatched Observed.Hits Coverage) 8 10 23.91%
Seq Charge Xcor Delta Probility PepHits
YGEMPVDKAK +2 2.451 0.380 0.9743 3
MYAPAWVAPEALQK +2 4.040 0.593 1.0000 4
SAVVEMLIMR +2 3.454 0.385 0.9993 3
EVPFADLSNMEIGMK +2 4.897 0.537 1.0000 5
SVMIDEDMTAR +2 3.343 0.481 0.9997 4
LNENHSGELWK +2 3.256 0.366 0.9984 1
GDDTPLHLAASHGHR +3 4.508 0.514 1.0000 13
MGQNLNRIPYKDTFWK +2 2.927 0.344 0.9684 1
MASCOT:(PepMatched Observed.Hits Coverage) 8 9 24.56%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

		GDDTPLHLAASHGHR			+2	792.39	1582.77	1582.76	0.01	79	2	
		WQGNDIVVK		+2	529.79	1057.56	1057.56	0	45	2		
		SVMIDEDMTAR		+2	634.29	1266.56	1266.56	0	60	4		
		SAVVEMLIMR		+2	574.81	1147.61	1147.61	0	62	2		
		MYAPAWVAPEALQK			+2	787.91	1573.80	1573.80	0	59	2	
		EVPFADLSNMEIGMK			+2	840.91	1679.80	1679.79	0.01	64	1	
		GMAFLHTLEPLIPR		+3	532.30	1593.87	1593.87	0	44	2		
		SADMWSFAVLLWELVTR			+3	675.35	2023.03	2023.02	0.01	48	2	
No.	Protein	Matched (SEQUEST		MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST		MASCOT)	SpectraMatched(SEQUEST		MASCOT)
712.	IPI00365388		Y	N	0.16	1	2	0	2	0		
*Des:	PREDICTED: similar to tumor protein D53											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	2.97%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		THETLSHAGQK		+2	2.678	0.491	0.9991	6				
		KTHETLSHAGQK		+2	3.145	0.499	0.9996	1				
	MASCOT:(PepMatched Observed.Hits Coverage)											
No.	Protein	Matched (SEQUEST		MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST		MASCOT)	SpectraMatched(SEQUEST		MASCOT)
713.	IPI00194583		N	Y	2.16	1	0	3	0	8		
*Des:	PREDICTED: similar to Apolipoprotein C2											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	22.22%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AAAGELYQK		+2	475.7531	949.4917	949.4868	0	63	7		
		TYLTSVDEK		+2	528.2704	1054.5263	1054.5182	0.01	43	4		
		TYLTSVDEKLR		+2	662.8635	1323.7125	1323.7034	0.01	43	1		
No.	Protein	Matched (SEQUEST		MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST		MASCOT)	SpectraMatched(SEQUEST		MASCOT)
714.	IPI00230859		Y	Y	1.11	2	6	6	14	16		
*Des:	Alcohol dehydrogenase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	2	25.45%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ALEALVAK		+2	2.576	0.288	0.9920	7				
		YALSVGYR		+2	2.831	0.404	0.9992	4				
		ALGLSNFSSR		+2	3.164	0.333	0.9981	3				
		GLEVTAYSPLGSSDR			+2	4.365	0.534	1.0000	2			
		HPDEPVLLEEPVVLALAEK			+3	5.591	0.525	1.0000	6			
		ILQNIQVFDFTFSPEEMK			+3	3.669	0.373	0.9994	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					6	2	23.03%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ALEALVAK		+2	407.76	813.50	813.50	0	51	9		
		SPAQILLR		+2	449.28	896.55	896.54	0.01	48	5		
		ALGLSNFSSR		+2	526.28	1050.55	1050.55	0	57	3		
		GLEVTAYSPLGSSDR			+2	776.40	1550.78	1550.76	0.02	73	2	
		MPLIGLGTWK		+2	558.32	1114.63	1114.62	0.01	44	22		
		HPDEPVLLEEPVVLALAEK			+3	700.06	2097.15	2097.14	0.01	89	3	

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No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
715.	IPI00208188	Y	Y	0.2	2	4	4	10	9

*Des: Syntaxin binding protein 2

SEQUEST:(PepMatched Observed.Hits Coverage) 4 3 12.41%

Seq	Charge	Xcor	Delta	Probility	PepHits
MSDILAEGITIVEDINK	+3	4.298	0.322	0.9999	1
SVQALIADFQGTPTFTYK	+2	3.071	0.506	0.9994	1
KGPEDTAQLAHAVLAK	+3	5.402	0.567	1.0000	7
ATEGKWEVLIGSSHILTPTR	+3	4.915	0.530	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage) 4 2 10.92%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
MSDILAEGITIVEDINK	+3	620.9976	1859.9708	1859.9550	0.02	48	2
LTTDKANIK	+2	502.2964	1002.5783	1002.5709	0.01	47	1
KGPEDTAQLAHAVLAK	+2	824.9622	1647.9098	1647.8944	0.02	63	7
ATEGKWEVLIGSSHILTPTR	+3	732.4061	2194.1964	2194.1746	0.02	44	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
716.	IPI00358099	Y	N	0.34	1	2	0	22	0

*Des: PREDICTED: similar to actin alpha 1 skeletal muscle protein

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 8.13%

Seq	Charge	Xcor	Delta	Probility	PepHits
MGQKDSYVGDEAQSKR	+3	5.685	0.499	1.0000	20
MGQKDSYVGDEAQSK	+3	3.757	0.509	1.0000	6

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
717.	IPI00204046	Y	N	0.06	3	8	0	33	0

*Des: Myosin heavy chain, nonmuscle type B

SEQUEST:(PepMatched Observed.Hits Coverage) 8 9 3.18%

Seq	Charge	Xcor	Delta	Probility	PepHits
FDQLLAEEK	+2	2.735	0.328	0.9950	2
ADEWLMK	+2	3.099	0.250	0.9965	3
VDYKADEWLMK	+3	3.269	0.285	0.9983	6
AGVLAHLEEER	+2	3.595	0.478	1.0000	3
LDPHLVLDQLR	+3	2.761	0.379	0.9998	8
VIQYLAHVASSHK	+2	4.515	0.587	1.0000	22
KVIQYLAHVASSHK	+2	4.599	0.520	1.0000	12
AGKLDPHLVLDQLR	+2	4.228	0.517	1.0000	9

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
718.	IPI00201713	Y	Y	0.15	1	3	4	4	14

*Des: Splice Isoform B of Adapter-related protein complex 1 beta 1 subunit

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 7.41%

Seq	Charge	Xcor	Delta	Probility	PepHits
LASQANIAQVLAELK	+2	3.677	0.534	0.9999	2

LGAPVSSGLSDLFDLTSGVGTLSGSYVAPK +3 2.939 0.413 0.9992 2
NNIDVFYFSTLYPLHVLFVEDGK +3 3.847 0.504 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 4 1 8.76%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LTNGIWVLAELR +2 692.37 1382.72 1383.79 -1.06 44 2
NNIDVFYFSTLYPLHVLFVEDGK +3 910.80 2729.38 2729.37 0.01 51 2
LGAPVSSGLSDLFDLTSGVGTLSGSYVAPK +3 965.84 2894.50 2894.49 0.01 44 4
LASQANIAQVLAELK +3 523.64 1567.90 1567.89 0.01 61 8

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
719. IPI00211336 N Y 2.76 1 0 4 0 12
*Des: PREDICTED: similar to SH3 domain binding glutamic acid-rich protein-like 3
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 4 2 46.31%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VYSTSVTGSR +2 528.7722 1055.5299 1055.5247 0.01 68 4
IQYQLVDISQDNALRDEMR +3 769.7202 2306.1388 2306.1324 0.01 45 1
RIQYQLVDISQDNALRDEMR +3 821.7519 2462.2338 2462.2336 0 41 1
EIKSQQSEVTR +2 652.8442 1303.6739 1303.6732 0 49 8

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
720. IPI00200773 Y N 0.07 3 5 0 29 0
*Des: Skeletal muscle-specific alpha-actinin 3
SEQUEST:(PepMatched Observed.Hits Coverage) 5 7 7.65%
Seq Charge Xcor Delta Probility PepHits
FAIQDISVEETSAK +2 4.215 0.537 1.0000 3
AGTQIENIEEDFR +2 3.210 0.442 0.9994 1
HEAFESDLAAHQDR +3 3.849 0.388 0.9998 1
LMLLLEVISGER +2 3.877 0.374 0.9996 6
MTLGMIWTIILR +2 4.935 0.521 1.0000 8
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
721. IPI00200847 Y Y 0.17 2 5 6 7 11
*Des: T-complex protein 1, alpha subunit
SEQUEST:(PepMatched Observed.Hits Coverage) 5 2 13.07%
Seq Charge Xcor Delta Probility PepHits
ICDDELILIK +2 2.908 0.342 0.9965 1
MLVDDIGDVTITNDGATILK +2 5.452 0.568 1.0000 2
FATEAAITILR +2 3.030 0.420 0.9989 1
SQNVMAAASIANIVK +2 3.967 0.324 0.9981 1
AFHNEAQVNPERK +3 3.972 0.371 1.0000 5
MASCOT:(PepMatched Observed.Hits Coverage) 6 3 14.48%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ICDDELILIK +2 587.8248 1173.6350 1173.6315 0 53 3
EQLAIAEFAR +2 574.3136 1146.6126 1146.6033 0.01 44 1
FATEAAITILR +2 603.3526 1204.6906 1204.6815 0.01 42 1

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                      LGVQVVITDPEKLDQIR          +3         641.7086   1922.1040  1922.0836  0.02       52         1
                      SQNVMAAASIANIVK+2          758.9182   1515.8219  1515.8078  0.01       68         1
                      AFHNEAQVNPERK  +2          770.3968   1538.7790  1538.7589  0.02       54         4

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
722.       IPI00365600           Y          Y          0.62       2          8          9          20         26
*Des:      cAMP-dependent protein kinase type II-beta regulatory subunit
           SEQUEST:(PepMatched Observed.Hits Coverage)      8          4          31.04%
                      Seq        Charge     Xcor       Delta      Probility  PepHits
                      SDIEENGAVEIAR         +2         4.235      0.449      0.9999     4
                      GVNFAEEPMR            +2         3.002      0.249      0.9869     3
                      EGEHVIDQGDDGDNFYVIDR             +3         4.773      0.571      1.0000     1
                      AATITATSPGALWGLDR                +2         4.462      0.598      1.0000     1
                      KMYESFIESLPFLK  +2               4.000      0.430      0.9998     2
                      HQPADLLEFALQHFTR                 +3         5.275      0.517      1.0000     4
                      NLDPEQMSQVLDAMFEK                +2         5.478      0.616      1.0000     2
                      TWGDAGAAAGGGTPSK                 +2         3.700      0.367      0.9990     1
           MASCOT:(PepMatched Observed.Hits Coverage)       9          4          34.83%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore   PepHits
                      SDIEENGAVEIAR         +2         701.85     1401.68    1401.67    0.01       70         4
                      TWGDAGAAAGGGTPSK                 +2         702.34     1402.66    1402.65    0.01       61         1
                      GVNFAEEPMR            +2         575.27     1148.53    1148.53    0          50         3
                      EGEHVIDQGDDGDNFYVIDR             +3         765.01     2292.00    2291.99    0.01       48         1
                      GQYFGELALVTNKPR                  +2         846.86     1691.70    1691.90    -0.19      87         4
                      AATITATSPGALWGLDR                +2         850.96     1699.90    1699.89    0.01       73         1
                      KMYESFIESLPFLK  +2               866.46     1730.91    1730.90    0.01       74         1
                      HQPADLLEFALQHFTR                 +3         641.67     1921.98    1921.98    0          66         4
                      NLDPEQMSQVLDAMFEK                +2         997.97     1993.92    1993.91    0.01       91         2

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
723.       IPI00561192           N          Y          0.79       1          0          8          0          93
*Des:      57 kDa protein
           SEQUEST:(PepMatched Observed.Hits Coverage)
           MASCOT:(PepMatched Observed.Hits Coverage)       8          1          23.61%
                      Seq        Charge     ObservedMS            ExpectedMS            CalculatedMS                     Pepscore   PepHits
                      QSVAVNESCGK           +2         561.2704   1120.5263  1120.5182  0.01       67         18
                      VNPFRPGDSESPVAAGAQR              +2         977.9990   1953.9834  1953.9656  0.02       94         38
                      QHPLPPPAQNQNQVR                  +3         575.3083   1722.9030  1722.8914  0.01       75         31
                      VVALDKNFHMK           +2         651.3597   1300.7049  1300.6961  0.01       72         23
                      FSPGAPSGPGPQPSQK                 +2         769.8878   1537.7610  1537.7525  0.01       49         8
                      GPLSQAPTPAPK          +2         582.3276   1162.6407  1162.6346  0.01       60         6
                      FAPVVAPKPK            +2         526.4513   1050.8880  1052.6382  -1.74      53         14
                      SVPLEAPSSVGTGSPQPPSFTYAQQK                  +3         887.4490   2659.3251  2659.3129  0.01       42         1

No.        Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
724.       IPI00471525           N          Y          0.23       2          0          8          0          47
*Des:      Eukaryotic translation elongation factor 1 delta
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	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					8	3	18.12%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		QENGASVILR		+2	544.30	1086.58	1085.58	1	60	8		
		FYEQMNGPVTAGSR			+2	778.87	1555.72	1555.71	0.01	82	9	
		SLAGSSGPGASSGPGGDHSDLIVR				+3	727.69	2180.06	2180.05	0.01	58	8
		IASLEVENQNLR		+2	693.38	1384.74	1384.73	0.01	85	6		
		FEEHVQSVDIAAFNK			+2	867.44	1732.86	1732.84	0.02	80	6	
		GVVQDLQQAISK		+2	643.36	1284.71	1284.70	0.01	71	30		
		VGTDLLEEEITK		+2	673.86	1345.71	1345.70	0.01	64	6		
		SIQLDGLVWGASK		+2	687.38	1372.75	1372.74	0.01	89	9		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
725.	IPI00324019		Y	Y	0.5	1	4	4	7	10		
*Des:	Alpha-1-antiproteinase precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	2	17.94%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VFNNDADLSGITEDAPLK			+2	5.437	0.626	1.0000	1			
		ISSNLADFAFSLYR		+2	4.129	0.485	0.9999	2				
		FDHPFIFMIVESETQSPLFVGK			+3	4.303	0.496	0.9999	2			
		QLDEDTVFALVNYIFFK			+2	5.138	0.600	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					4	2	14.59%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VFNNDADLSGITEDAPLK			+2	959.98	1917.94	1917.93	0.01	102	2	
		SAILYFPK		+2	469.77	937.53	937.53	0	54	2		
		ISSNLADFAFSLYR		+2	802.41	1602.82	1602.80	0.02	68	4		
		QLDEDTVFALVNYIFFK			+3	688.02	2061.05	2061.05	0	76	2	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
726.	IPI00365531		Y	Y	0.77	1	7	6	10	9		
*Des:	PREDICTED: similar to DNA segment, Chr 12, ERATO Doi 553, expressed											
	SEQUEST:(PepMatched Observed.Hits Coverage)					7	1	37.99%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DAIQNPNDIQLQEK		+2	3.691	0.376	0.9983	1				
		TLSNATMHFVSENK		+2	3.314	0.343	0.9953	1				
		NPAIQNDFSYYR		+2	3.519	0.414	0.9991	1				
		INNMHLDIENEVNNEMANR			+3	3.929	0.440	0.9997	2			
		MSLFYAEATPMLK		+2	3.062	0.383	0.9964	2				
		EIENYPHFFLDFENAQPTEGER			+3	3.883	0.423	0.9995	2			
		EIWNQISAVLQDSESILSDLQAYK				+2	5.691	0.644	1.0000	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					6	1	30.39%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DAIQNPNDIQLQEK		+2	813.41	1624.81	1624.81	0	65	1		
		TLSNATMHFVSENK		+2	789.88	1577.75	1577.75	0	43	2		
		NPAIQNDFSYYR		+2	744.35	1486.69	1486.68	0.01	68	2		
		INNMHLDIENEVNNEMANR			+3	757.35	2269.02	2269.02	0	41	4	
		EFAEILHFTLR		+2	688.38	1374.74	1374.73	0.01	51	1		

EIWNQISAVLQDSESILSDLQAYK +3 917.47 2749.39 2749.38 0.01 69 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
727. IPI00365460 N Y 0.52 1 0 2 0 2
*Des: PREDICTED: similar to ubiquitin-conjugating enzyme E2M
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 11.22%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LFEQNVQR +2 518.2332 1034.4519 1032.5352 1.92 51 1
VGQGYPHDPPK +2 597.8059 1193.5973 1193.5829 0.01 46 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
728. IPI00358316 N Y 0.12 1 0 2 0 2
*Des: PREDICTED: similar to Myotubularin-related protein 7
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 3.27%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ADYLNPLFR +2 554.79 1107.56 1107.57 0 43 1
AIMDAGIFIAK +2 575.32 1148.63 1148.63 0 46 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
729. IPI00363930 Y Y 0.29 3 4 5 7 9
*Des: PREDICTED: similar to SEPT11 protein
SEQUEST:(PepMatched Observed.Hits Coverage) 4 4 9.04%
Seq Charge Xcor Delta Probility PepHits
SYELQESNVR +2 3.010 0.445 0.9993 3
AAAQLLQSQAQQSGAQQTK +2 6.020 0.607 1.0000 2
KAAAQLLQSQAQQSGAQQTK +3 5.937 0.357 1.0000 2
AAAQLLQSQAQQSGAQQTKK +3 3.279 0.392 0.9999 2
MASCOT:(PepMatched Observed.Hits Coverage) 5 5 10.4%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VNMEDLR +2 438.7179 875.4213 875.4171 0 50 3
SYELQESNVR +2 612.8006 1223.5866 1223.5782 0.01 44 2
AAAQLLQSQAQQSGAQQTK +2 979.0156 1956.0167 1956.0024 0.01 104 2
AAAQLLQSQAQQSGAQQTKK +3 695.7108 2084.1104 2084.0974 0.01 57 2
KAAAQLLQSQAQQSGAQQTK +3 695.7135 2084.1187 2084.0974 0.02 70 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
730. IPI00359982 Y Y 0.07 1 3 3 3 3
*Des: PREDICTED: similar to Early endosome antigen 1
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 2.73%
Seq Charge Xcor Delta Probility PepHits
LQQQAAQAAQELAVEK +2 5.656 0.636 1.0000 1
LALAQEDLISNR +2 2.808 0.297 0.9783 1
AAQLATEIADIK +2 2.861 0.303 0.9889 1
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 2.6%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

		LQQQAAQAAQELAVEK			+2	863.47	1724.92	1724.91	0.01	116	1	
		AAQLATEIADIK		+2	622.35	1242.68	1242.68	0	59	1		
		IQNLEALLQK		+2	585.35	1168.68	1168.68	0	47	1		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
731.	IPI00231734		Y	Y	0.87	4	7	11	26	73		
*Des:	Fructose-bisphosphate aldolase A											
	SEQUEST:(PepMatched Observed.Hits Coverage)					7	3	26.48%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VDKGVVPLAGTNGETTTQGLDGLSER				+3	4.172	0.465	1.0000	2		
		GGVVGIKVDKGVVPLAGTNGETTTQGLDGLSER					+3	6.674	0.576	1.0000	2	
		YTPSGQSGAAASESLFISNHAY			+2	5.548	0.665	1.0000	8			
		KELADIAHR		+2	2.797	0.350	0.9993	6				
		FSNEEIAMATVTALRR			+2	2.959	0.243	0.9914	11			
		YTPSGQSGAAASESLFISNHA			+2	5.589	0.637	1.0000	5			
		ENLKAAQEEYIKR		+3	3.492	0.398	1.0000	14				
	MASCOT:(PepMatched Observed.Hits Coverage)					11	8	33.24%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GILAADESTGSIAK		+2	666.8596	1331.7046	1331.6932	0.01	83	8		
		ELADIAHR		+2	462.7511	923.4877	923.4825	0.01	48	3		
		GILAADESTGSIAKR		+2	744.9116	1487.8087	1487.7943	0.01	107	13		
		FSNEEIAMATVTALR		+2	826.9241	1651.8336	1651.8239	0.01	83	1		
		AAQEEYIKR		+2	554.2971	1106.5796	1106.5720	0.01	69	4		
		ALQASALK		+2	402.2093	802.4040	800.4756	1.93	43	4		
		ALANSLACQGK		+2	538.2852	1074.5559	1074.5491	0.01	74	4		
		RLQSIGTENTEENRR			+2	901.9678	1801.9210	1801.9030	0.02	46	5	
		KELADIAHR		+2	526.7999	1051.5852	1051.5774	0.01	68	3		
		IGEHTPSSLAIMENANVLAR			+2	1062.0568	2122.0990	2122.0840	0.02	88	3	
		SKGGVVGIKVDK		+2	593.3029	1184.5912	1185.7080	-1.11	53	3		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
732.	IPI00189981		Y	Y	0.29	1	2	4	3	5		
*Des:	Prothrombin precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	3.66%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		QTVTSLLQAGYK		+2	3.459	0.506	0.9999	2				
		YGFYTHVFR		+2	2.982	0.469	0.9997	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	7.48%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		YQNFDPEVK		+2	570.27	1138.53	1138.53	0	45	2		
		YGFYTHVFR		+2	595.30	1188.58	1188.57	0.01	59	2		
		QTVTSLLQAGYK		+2	654.87	1307.72	1307.71	0.01	69	2		
		TTDAEFHTFFDER		+2	808.36	1614.70	1614.70	0	51	2		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
733.	IPI00231662		Y	Y	2.17	1	7	6	14	11		
*Des:	NADH-cytochrome b5 reductase											

SEQUEST:(PepMatched Observed.Hits Coverage) 7 1 40.32%
Seq Charge Xcor Delta Probility PepHits
GPNGLLVYQGK +2 3.416 0.472 0.9996 3
SSPAITLENPDIK +2 3.514 0.407 0.9988 1
APDAWDYSQGFVNEEMIR +2 5.412 0.611 1.0000 2
MSQYLENMNIGDTIEFR +2 5.473 0.626 1.0000 2
SVGMIAGGTGITPMLQVIR +2 4.646 0.526 1.0000 4
FALPSPQHILGLPIGQHIYLSTR +3 5.043 0.505 0.9999 1
VVLSPVWFVYSLFMK +3 4.702 0.540 1.0000 2
MASCOT:(PepMatched Observed.Hits Coverage) 6 1 32.45%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LIDKEIISHDTR +2 720.40 1438.78 1438.78 0 56 1
GPNGLLVYQGK +2 573.32 1144.63 1144.62 0.01 68 7
SSPAITLENPDIK +2 692.87 1383.73 1383.72 0.01 69 1
SVGMIAGGTGITPMLQVIR +2 951.02 1900.03 1900.03 0 84 4
FALPSPQHILGLPIGQHIYLSTR +3 853.48 2557.43 2557.42 0.01 60 1
VVLSPVWFVYSLFMK +2 908.01 1814.00 1813.98 0.02 95 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
734. IPI00231736 Y Y 0.19 1 2 2 3 7
*Des: Fructose-bisphosphate aldolase C
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 8.1%
Seq Charge Xcor Delta Probility PepHits
DNAGAATEEFIK +2 3.169 0.400 0.9989 2
TPSALAILENANVLAR +2 4.271 0.450 0.9998 1
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 9.18%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
DNAGAATEEFIK +2 633.31 1264.60 1264.59 0.01 53 6
ISDRTPSALAILENANVLAR +3 708.37 2122.10 2123.17 -1.06 47 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
735. IPI00358175 Y N 0.02 1 3 0 29 0
*Des: PREDICTED: similar to gamma-filamin
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 1.11%
Seq Charge Xcor Delta Probility PepHits
LIALLEVLSQK +2 3.517 0.423 0.9995 78
KIQQNTFTR +2 2.752 0.254 0.9862 5
LLGWIQNK +2 3.020 0.166 0.9800 4
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
736. IPI00372829 Y Y 0.2 2 3 3 4 3
*Des: PREDICTED: similar to Dendritic cell protein GA17
SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 7.91%
Seq Charge Xcor Delta Probility PepHits
VMVELLGSYTEDNASQAR +2 4.489 0.573 1.0000 1
LLTFMGMAVENK +2 3.248 0.491 0.9997 1

		LQLLSNLFHGMDK		+2	2.819	0.267	0.9826	3				
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	7.91%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VMVELLGSYTEDNASQAR			+2	991.99	1981.96	1981.94	0.02	82	1	
		LLTFMGMAVENK		+2	677.35	1352.69	1352.68	0.01	68	1		
		LQLLSNLFHGMDK		+2	758.91	1515.80	1514.79	1.01	46	4		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
737.	IPI00208265		Y	Y	0.42	3	2	6	3	23		
*Des:	Serine/threonine protein phosphatase PP1-alpha catalytic subunit											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	2	7.14%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		NVQLTENEIR		+2	2.826	0.267	0.9876	4				
		YGQFSGLNPGGR		+2	2.952	0.481	0.9980	6				
	MASCOT:(PepMatched Observed.Hits Coverage)					6	3	25.89%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NVQLTENEIR		+2	608.32	1214.63	1214.63	0	46	2		
		AHQVVEDGYEFFAK		+3	547.26	1638.77	1638.77	0	52	8		
		LNLDSIIGR		+2	501.74	1001.46	999.57	1.89	56	2		
		YPENFFLLR		+2	599.82	1197.62	1197.62	0	45	8		
		EIFLSQPILLELEAPLK			+2	977.07	1952.13	1952.12	0.01	79	9	
		LFEYGGFPPESNYLFLGDYVDR				+3	866.75	2597.23	2597.21	0.02	57	6

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
738.	IPI00213015		Y	Y	0.43	2	3	3	3	4		
*Des:	Dynactin 2											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	2	12.71%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LLHEVQELTTEVEK		+2	4.624	0.412	0.9999	2				
		ENLATVEGNFASIDAR			+2	4.537	0.461	0.9993	2			
		LLGPDAAINLADPDGALAK			+2	4.970	0.523	1.0000	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	2	12.71%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LLHEVQELTTEVEK		+2	834.45	1666.89	1666.88	0.01	57	1		
		ENLATVEGNFASIDAR			+2	854.43	1706.85	1705.83	1.02	83	2	
		LLGPDAAINLADPDGALAK			+2	918.00	1833.99	1833.98	0.01	85	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
739.	IPI00566421		N	Y	0.32	1	0	2	0	8		
*Des:	75 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	5.24%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LMSLDSGLLANLGALTELR			+2	994.0620	1986.1095	1986.0819	0.03	117	9	
		TLPGDVFAALPQLTR			+2	799.9623	1597.9101	1597.8828	0.03	41	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		

740.	IPI00371957		Y	Y	0.62	1	3	2	5	4		
*Des:	PREDICTED: similar to pyrophosphatase											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	18.7%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VIAINVDDPDAANYHDISDVER			+3	3.591	0.404	0.9994	1			
		LKPGYLEATVDWFR		+3	3.312	0.433	0.9997	3				
		VLGILAMIDEGETDWK			+2	5.155	0.623	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	13.6%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VIAINVDDPDAANYHDISDVER			+3	814.39	2440.16	2440.15	0.01	42	1	
		VLGILAMIDEGETDWK			+2	895.46	1788.90	1788.90	0	92	3	

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
741.	IPI00370073		N	Y	0.02	1	0	2	0	2		
*Des:	Type I keratin KA17											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	4.98%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LASYLDKVR		+2	532.8090	1063.6035	1063.6026	0	40	4		
		TRLEQEIATYR		+2	690.3661	1378.7177	1378.7204	0	48	1		

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
742.	IPI00212070		Y	N	1.03	1	4	0	13	0		
*Des:	16 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	3	40.97%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TNLLQVCER		+2	3.171	0.356	0.9987	3				
		TNISDEESEQATEMLVHNAQNLMQSVK				+3	4.966	0.551	1.0000	7		
		IRTNLLQVCER		+2	2.832	0.471	0.9963	1				
		TNLLQVCERIPTISTQLK			+2	5.299	0.552	1.0000	7			
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
743.	IPI00230868		Y	Y	0.37	1	3	4	4	7		
*Des:	Guanine nucleotide bindinG protein, alpha q polypeptide											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	13.69%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VADPSYLPTQQDVLR			+2	3.953	0.395	0.9994	2			
		VSAFENPYVDAIK		+2	2.767	0.547	0.9996	2				
		VPTTGIIEYPFDLQSVIFR			+3	4.072	0.429	0.9999	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	16.43%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VADPSYLPTQQDVLR			+2	851.45	1700.89	1700.87	0.02	47	2	
		DTILQLNLK		+2	529.32	1056.63	1056.62	0.01	51	3		
		VSAFENPYVDAIK		+2	726.88	1451.74	1451.73	0.01	62	2		
		VPTTGIIEYPFDLQSVIFR			+3	732.40	2194.19	2194.17	0.02	45	1	

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
744. IPI00208197 Y N 0.26 1 2 0 3 0
*Des: [Protein ADP-ribosylarginine] hydrolase
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 8.67%
Seq Charge Xcor Delta Probility PepHits
AYVTQSGYFVK +2 3.126 0.443 0.9995 3
FPHPSQLDTLIQVSIESGR +3 3.394 0.429 0.9997 1
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
745. IPI00476545 N Y 0.12 1 0 3 0 10
*Des: Ac1262
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 3.39%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
SFSIFSYATK +2 575.80 1149.58 1149.57 0.01 59 15
VFSPNVLNWR +2 616.34 1230.66 1230.65 0.01 46 4
TSFNEILLFWTR +2 763.91 1525.81 1525.79 0.02 44 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
746. IPI00326561 Y Y 0.37 1 2 3 3 4
*Des: Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 9.3%
Seq Charge Xcor Delta Probility PepHits
MMADEALDSGLVSR +2 4.263 0.537 1.0000 2
EVDVGLAADVGTLQR +2 4.746 0.494 0.9999 1
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 16.21%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
MMADEALDSGLVSR +2 747.85 1493.69 1493.69 0 117 2
EVDVGLAADVGTLQR +2 771.91 1541.80 1541.80 0 75 1
VFPDKDVMLNAAFALAADISSK+3 775.07 2322.20 2322.19 0.01 41 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
747. IPI00327509 Y Y 2.16 1 3 3 3 4
*Des: Glia maturation factor gamma
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 28.96%
Seq Charge Xcor Delta Probility PepHits
NRLVQIAELTK +2 2.554 0.534 0.9650 3
QMVVLEDEFQNVSPEELKLELPER +3 4.722 0.653 1.0000 1
NRLVQIAELTKVFEIR +3 3.465 0.635 0.9995 1
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 33.1%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ETNNAAIIMK +2 552.79 1103.57 1103.56 0.01 42 1
NRLVQIAELTK +2 642.89 1283.76 1283.76 0 42 3
QMVVLEDEFQNVSPEELKLELPER +3 957.83 2870.45 2870.44 0.01 94 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

748.	IPI00202384		Y	Y	0.15	2	3	2	5	3		
*Des:	PREDICTED: similar to chromosome 10 open reading frame 45											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	2	4.52%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		RTGQEVAQAQE		+2	2.892	0.388	0.9687	1				
		KSDLEIELLKR		+3	3.491	0.317	0.9998	1				
		GLAPQNKPELQK		+2	3.128	0.318	0.9952	4				
	MASCOT:(PepMatched Observed.Hits Coverage)					2	2	3.05%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		KSDLEIELLKR		+3	448.6030	1342.7871	1342.7820	0.01	41	1		
		GLAPQNKPELQK		+2	661.8792	1321.7439	1321.7354	0.01	48	4		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
749.	IPI00392216		N	Y	0.11	1	0	4	0	25		
*Des:	Liver regeneration protein lrryan											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					4	2	8.36%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VFSQQADLSR		+2	575.8004	1149.5863	1149.5778	0.01	49	16		
		AVLDVAETGTEAAAATGVK			+2	888.4487	1774.8828	1772.9155	1.97	83	6	
		IAELFSDLEER		+2	661.3403	1320.6660	1320.6561	0.01	78	6		
		WKDSLIPR		+2	507.7935	1013.5725	1013.5658	0.01	44	2		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
750.	IPI00476478		N	Y	0.5	1	0	2	0	16		
*Des:	31 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	8.86%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		IGVTVLSR		+2	422.77	843.52	843.52	0	55	8		
		SETITEEELVGLMNK		+2	846.93	1691.84	1691.83	0.01	73	12		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
751.	IPI00367214		N	Y	0.51	1	0	2	0	6		
*Des:	Hypothetical LOC313163											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	12.27%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NLQYYDISAK		+2	607.8523	1213.6900	1213.5979	0.09	43	3		
		GPIKFNVWDTAGQEK			+3	563.9938	1688.9596	1688.8522	0.11	40	3	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
752.	IPI00471608		Y	Y	0.32	4	10	7	14	21		
*Des:	Staphylococcal nuclease domain containing protein 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					10	8	20.43%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ETDGSETPEPFAAEAK			+2	4.011	0.541	0.9999	1			

		VITEYLNAQESAK		+2	4.034	0.607	1.0000	3				
		VMQVLNADAIVVK		+2	3.261	0.269	0.9927	1				
		DTNGENIAESLVAEGLASR			+2	4.259	0.480	0.9999	2			
		NLPGLVQEGEPFSEEATLFTK			+2	5.811	0.583	1.0000	1			
		LRPLYDIPYMFEAR		+2	3.112	0.252	0.9853	1				
		VLPAQATEYAFAFIQVPQDEDAR				+3	5.543	0.559	1.0000	2		
		ALLLPDHYLVTVMLSGIK			+2	2.727	0.424	0.9975	1			
		AGNFIGWLHMDGANLSVLLVEHALSK				+3	3.687	0.419	0.9997	2		
		SDISSHPPVEGAYAPR			+3	4.458	0.517	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					7	8	12.54%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ETDGSETPEPFAAEAK			+2	839.88	1677.74	1677.74	0	67	2	
		SDISSHPPVEGAYAPR			+2	841.91	1681.81	1681.81	0	50	4	
		GDVGLGLVK		+2	429.74	857.48	856.50	0.98	42	3		
		VITEYLNAQESAK		+2	733.38	1464.75	1464.75	0	76	9		
		VMQVLNADAIVVK		+2	700.41	1398.80	1398.79	0.01	52	1		
		DTNGENIAESLVAEGLASR			+2	973.49	1944.96	1944.94	0.02	52	2	
		VLPAQATEYAFAFIQVPQDEDAR				+3	860.43	2578.28	2578.27	0.01	56	6
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
753.	IPI00421995		Y	Y	0.63	3	4	5	25	25		
*Des:	Chloride intracellular channel 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	5	28.04%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		NSNPALNDNLEK		+2	3.927	0.401	0.9999	5				
		LFMVLWLK		+2	2.860	0.199	0.9847	4				
		VLDNYLTSPLPEEVDETSAEDEGISQR				+3	5.805	0.591	1.0000	1		
		LAALNPESNTSGLDIFAK			+2	5.698	0.618	1.0000	21			
	MASCOT:(PepMatched Observed.Hits Coverage)					5	5	26.42%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		NSNPALNDNLEK		+2	664.8304	1327.6463	1327.6368	0.01	82	4		
		GVTFNVTTVDTK		+2	641.3607	1280.7068	1280.6612	0.05	51	2		
		LAALNPESNTSGLDIFAK			+2	930.9965	1859.9785	1859.9628	0.02	95	4	
		LFMVLWLK		+2	525.8184	1049.6223	1048.6143	1.01	45	4		
		LHIVQVVCKK		+2	583.8607	1165.7068	1165.7005	0.01	41	1		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
754.	IPI00231810		N	Y	0.13	1	0	3	0	10		
*Des:	Splice Isoform 2 of Alpha adducin											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	7.16%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VNLQGDIVDR		+2	564.8091	1127.6036	1127.5934	0.01	44	6		
		TSTSAVPNLFVPLNTNPK			+2	950.5234	1899.0323	1899.0101	0.02	43	3	
		AAVVTSPPPTTAPHK			+2	737.4166	1472.8186	1472.7987	0.02	43	1	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		

755.	IPI00324893	Y	Y	2.73	5	13	13	191	344

*Des: 14-3-3 protein zeta/delta

SEQUEST:(PepMatched Observed.Hits Coverage) 13 10 60.4%

Seq	Charge	Xcor	Delta	Probility	PepHits			
DICNDVLSLLEK		+2	4.720	0.492	1.0000	21		
YLAEVAAGDDKK		+3	3.075	0.354	0.9998	9		
SVTEQGAELSNEER		+2	5.297	0.533	1.0000	6		
FLIPNASQPESK		+2	3.295	0.444	0.9994	10		
LAEQAERYDDMAACMK			+2	4.240	0.546	1.0000	9	
GIVDQSQQAYQEAFEISK			+2	6.053	0.590	1.0000	3	
TAFDEAIAELDTLSEESYK			+2	5.362	0.670	1.0000	6	
IETELRDICNDVLSLLEK			+2	3.692	0.318	0.9865	2	
TAFDEAIAELDTLSEESYKDSTLIMQLLR				+3	7.696	0.709	1.0000	5
VVSSIEQKTEGAEKK			+2	4.048	0.370	0.9960	2	
VVSSIEQKTEGAEK		+2	4.039	0.346	0.9951	1		
GIVDQSQQAYQEAFEISKK			+2	4.881	0.579	1.0000	4	
SVTEQGAELSNEERNLLSVAYK				+2	3.652	0.539	1.0000	3

MASCOT:(PepMatched Observed.Hits Coverage) 13 11 51.2%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
DICNDVLSLLEK		+2	681.3577	1360.7009	1360.6908	0.01	93	48		
VVSSIEQK		+2	445.2557	888.4969	888.4916	0.01	66	4		
YLAEVAAGDDKK		+2	640.3353	1278.6560	1278.6455	0.01	73	28		
SVTEQGAELSNEER		+2	774.8674	1547.7202	1547.7063	0.01	96	20		
YDDMAACMK		+2	524.2044	1046.3943	1046.3871	0.01	48	12		
LAEQAERYDDMAACMK			+2	922.9102	1843.8059	1843.7902	0.02	75	24	
FLIPNASQPESK		+2	665.8585	1329.7024	1329.6928	0.01	72	20		
VVSSIEQKTEGAEK		+2	752.9042	1503.7939	1503.7780	0.02	70	2		
VVSSIEQKTEGAEKK			+2	816.9540	1631.8935	1631.8729	0.02	75	6	
DSTLIMQLLR		+2	595.3376	1188.6606	1188.6536	0.01	75	14		
LGLALNFSVFYYEILNSPEK			+2	1159.1243	2316.2340	2316.2041	0.03	130	3	
EMQPTHPIR		+2	554.7859	1107.5572	1107.5495	0.01	54	11		
EMQPTHPIRLGLALNFSVFYYEILNSPEK				+3	1136.2618	3405.7637	3405.7430	0.02	89	6

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

756.	IPI00366416	Y	Y	0.56	1	2	3	4	6

*Des: PREDICTED: similar to cytochrome c-1

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 9.03%

Seq	Charge	Xcor	Delta	Probility	PepHits		
LSDYFPKPYPNPEAAR			+2	3.471	0.475	0.9999	4
GLLSSLDHTSIR		+2	2.728	0.367	0.9968	2	

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 14.15%

Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
LSDYFPKPYPNPEAAR			+2	932.97	1863.93	1863.92	0.01	62	4	
GLLSSLDHTSIR		+2	649.86	1297.71	1297.70	0.01	57	2		
AANNGALPPDLSYIVR			+2	835.95	1669.89	1669.88	0.01	49	4	

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

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757.     IPI00551729      N     Y     0.27    1     0     2     0     12
*Des:    50 kDa protein
         SEQUEST:(PepMatched Observed.Hits Coverage)
         MASCOT:(PepMatched Observed.Hits Coverage)   2     1     5.31%
               Seq        Charge     ObservedMS    ExpectedMS    CalculatedMS          Pepscore PepHits
               IGGIGTVPVGR    +2     514.24    1026.47   1024.60   1.87    65    8
               EHALLAYTLGVK   +2     657.88    1313.74   1313.73   0.01    50    7

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
758.     IPI00209216      Y     Y     0.34    1     6     5     7     12
*Des:    Splice Isoform 2 of Gamma adducin
         SEQUEST:(PepMatched Observed.Hits Coverage)  6     1     16.59%
               Seq        Charge     Xcor      Delta     Probility  PepHits
               TAGPQSQLLAGIVVDKPPSTMR          +3        3.880     0.525    1.0000   1
               LTTSTTIENIEITIK    +2   3.743   0.447     0.9997    1
               VNIIGEVVDQGSTNLK       +2       4.608     0.621     1.0000   2
               VGEIEFEGLMR    +2     3.319     0.484     0.9973    1
               FEDDDQGPPAPPNPFSHLMEGELEEYTK +3     4.685     0.546    1.0000   1
               AFTHGVAMTGGGGVNMGSHQK           +3        3.599     0.404    0.9997   2
         MASCOT:(PepMatched Observed.Hits Coverage)   5     1     12.55%
               Seq        Charge     ObservedMS    ExpectedMS    CalculatedMS          Pepscore PepHits
               AFTHGVAMTGGGGVNMGSHQK           +3        681.99    2042.94  2042.94  0    47    4
               VGEIEFEGLMR    +2     640.86    1279.70   1278.63   1.07    47    2
               LTTSTTIENIEITIK    +2   838.97  1675.93   1675.92   0.01    50    2
               VNIIGEVVDQGSTNLK       +2       843.46    1684.91   1684.90  0.01   97    4
               TAGPQSQLLAGIVVDKPPSTMR          +3        756.08    2265.23  2265.22  0.01   50    2

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
759.     IPI00230941      Y     Y     0.16    2     2     3     3     3
*Des:    Vimentin
         SEQUEST:(PepMatched Observed.Hits Coverage)  2     2     5.49%
               Seq        Charge     Xcor      Delta     Probility  PepHits
               FADLSEAANR     +2     2.715     0.338     0.9956    5
               KVESLQEEIAFLKK +3     3.197     0.176     0.9638    1
         MASCOT:(PepMatched Observed.Hits Coverage)   3     1     7.82%
               Seq        Charge     ObservedMS    ExpectedMS    CalculatedMS          Pepscore PepHits
               ILLAELEQLKGQGK +2     771.3616  1540.7086 1538.9031 1.81    50    2
               KVESLQEEIAFLKK +3     554.6533  1660.9379 1660.9399 0       43    2
               FLEQQNKILLAELEQLKGQGK +3  809.7935  2426.3585 2426.3532 0.01  53    2

No.      Protein  Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
760.     IPI00362201      Y     N     0.28    1     2     0     3     0
*Des:    PREDICTED: similar to IAP-associated factor VIAF1
         SEQUEST:(PepMatched Observed.Hits Coverage)  2     1     10.24%
               Seq        Charge     Xcor      Delta     Probility  PepHits
               FGEVLEISGK     +2     2.905     0.340     0.9948    2
               AGEGLWVVLHLYK  +3     3.852     0.512     0.9999    1
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MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
761.	IPI00214905	Y	Y	11.41	5	13	22	70	282

*Des: Tropomyosin alpha 4 chain

SEQUEST:(PepMatched Observed.Hits Coverage) 13 10 48.41%

Seq	Charge	Xcor	Delta	Probility	PepHits
IQALQQQADDAEDR	+2	5.151	0.502	1.0000	5
KIQALQQQADDAEDRAQGLQR	+2	5.143	0.506	1.0000	10
SSDLEEELKNVTNNLK	+2	5.083	0.470	1.0000	19
EENVGLHQTLDQTLNELNCI	+2	5.219	0.604	1.0000	2
EKAEGDAAALNR	+2	3.912	0.481	1.0000	10
TIDDLEEKLAQAK	+2	3.625	0.293	0.9843	2
EENVGLHQTLDQTLNELNC	+2	5.250	0.491	1.0000	2
LAQAKEENVGLHQTLDQTLNELNCI	+2	4.234	0.607	1.0000	3
LAQAKEENVGLHQTLDQTLNELNC	+3	3.990	0.471	0.9997	3
REKAEGDAAALNR	+2	5.305	0.409	1.0000	5
KIQALQQQADDAEDR	+2	5.051	0.531	1.0000	3
KLVILEGELERAEER	+2	3.585	0.453	0.9976	4
LLSDKLKEAETR	+2	3.819	0.402	0.9978	8

MASCOT:(PepMatched Observed.Hits Coverage) 22 13 73.01%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
EKAEGDAAALNR	+2	622.8203	1243.6260	1243.6156	0.01	87	10
IQALQQQADDAEDR	+2	800.8884	1599.7623	1599.7489	0.01	111	9
MEIQEMQLK	+2	575.2896	1148.5647	1148.5569	0.01	49	2
IQLVEEELDR	+2	622.3340	1242.6534	1242.6455	0.01	82	29
TIDDLEEKLAQAK	+2	737.3972	1472.7799	1472.7722	0.01	70	2
SSDLEEELKNVTNNLK	+2	916.9730	1831.9314	1831.9163	0.02	97	26
LVILEGELER	+2	585.8451	1169.6756	1169.6655	0.01	59	17
LEEAEKAADESER	+2	738.8504	1475.6863	1475.6739	0.01	70	91
IQLVEEELDRAQER	+2	864.4552	1726.8958	1726.8849	0.01	64	143
AMKDEEKMEIQEMQLK	+2	990.9833	1979.9520	1979.9366	0.02	101	13
LATALQKLEEAEK	+2	722.4111	1442.8077	1442.7980	0.01	88	69
RIQLVEEELDRAQER	+2	942.5091	1883.0036	1882.9860	0.02	53	114
KLVILEGELER	+3	433.5968	1297.7685	1297.7605	0.01	59	5
LVILEGELERAEER	+2	828.4581	1654.9017	1654.8889	0.01	59	5
KLVILEGELERAEER	+2	892.5059	1782.9972	1782.9839	0.01	41	4
REKAEGDAAALNR	+2	700.8725	1399.7304	1399.7167	0.01	89	6
AEGDAAALNRR	+2	572.3012	1142.5879	1142.5792	0.01	43	1
EKAEGDAAALNRR	+2	700.8723	1399.7301	1399.7167	0.01	67	6
KIQALQQQADDAEDR	+2	864.9382	1727.8619	1727.8438	0.02	116	3
LEEAEKAADESERGMK	+2	896.9334	1791.8521	1791.8308	0.02	54	10
HIAEEADRKYEEVAR	+2	908.4594	1814.9042	1814.8911	0.01	66	56
LLSDKLKEAETR	+2	701.9042	1401.7938	1401.7827	0.01	72	5

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
762.	IPI00199688	Y	Y	0.54	1	3	7	5	39

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*Des:       Mitogen-activated protein kinase 1
            SEQUEST:(PepMatched Observed.Hits Coverage)  3           1           12.36%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        APEIMLNSK               +2          2.857       0.517       0.9998      5
                        VADPDHDHTGFLTEYVATR     +3          4.509       0.577       1.0000      1
                        FRHENIIGINDIIR          +3          4.046       0.421       0.9988      2
            MASCOT:(PepMatched Observed.Hits Coverage)   7           1           20.87%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        APEIMLNSK               +2          501.77      1001.53     1001.52     0.01        51          12
                        GQVFDVGPR               +2          487.76      973.50      973.50      0           48          21
                        ELIFEETAR               +2          554.29      1106.57     1106.56     0.01        55          9
                        VADPDHDHTGFLTEYVATR     +3          715.34      2143.01     2143.00     0.01        54          3
                        FDMELDDLPK              +2          611.79      1221.57     1221.56     0.01        41          6
                        HENIIGINDIIR            +2          703.90      1405.78     1405.77     0.01        46          6
                        FRHENIIGINDIIR          +3          570.65      1708.94     1708.94     0           63          6

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
763.        IPI00198887             Y           Y           0.36        1           9           9           13          10
*Des:       Protein disulfide-isomerase precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)  9           2           30.88%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        LGETYKDHENIVIAK +3      3.758       0.440       0.9971      3
                        NFEEVAFDEKK             +2          3.074       0.312       0.9963      1
                        VDATEESDLAQQYGVR        +2          5.065       0.593       1.0000      2
                        EADDIVNWLK              +2          2.792       0.370       0.9978      2
                        HNQLPLVIEFTEQTAPK       +2          4.136       0.555       1.0000      2
                        ILFIFIDSDHTDNQR +2      4.257       0.508       0.9999      2
                        QFLLAAEAVDDIPFGITSNSDVFSK           +3          5.725       0.559       1.0000      1
                        TGPAATTLSDTAAAESLVDSSEVTVIGFFK                  +3          4.854       0.648       1.0000      1
                        MDSTANEVEAVK            +2          3.427       0.485       0.9999      1
            MASCOT:(PepMatched Observed.Hits Coverage)   9           2           30.69%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        MDSTANEVEAVK            +2          647.31      1292.60     1292.59     0.01        58          1
                        LGETYKDHENIVIAK +2      865.46      1728.91     1728.90     0.01        71          2
                        NFEEVAFDEKK             +2          678.33      1354.65     1354.64     0.01        43          1
                        VDATEESDLAQQYGVR        +2          890.92      1779.83     1779.83     0           84          2
                        THILLFLPK               +2          541.34      1080.67     1080.67     0           46          2
                        ILFIFIDSDHTDNQR +2      917.46      1832.91     1832.91     0           64          2
                        HNQLPLVIEFTEQTAPK       +2          983.03      1964.05     1964.04     0.01        62          2
                        QFLLAAEAVDDIPFGITSNSDVFSK           +3          895.46      2683.35     2683.34     0.01        61          1
                        TGPAATTLSDTAAAESLVDSSEVTVIGFFK                  +3          995.84      2984.50     2984.49     0.01        77          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
764.        IPI00212220             Y           Y           0.29        2           2           7           2           12
*Des:       Protein disulfide-isomerase A4 precursor
            SEQUEST:(PepMatched Observed.Hits Coverage)  2           1           3.36%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
```

VDATEQTDLAK +2 3.111 0.378 0.9982 2
FIDEHATKR +2 2.801 0.298 0.9934 3
MASCOT:(PepMatched Observed.Hits Coverage) 7 2 14.98%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
IDATSASMLASK +2 597.81 1193.60 1193.60 0 92 5
MDATANDITNDR +2 668.79 1335.57 1335.57 0 81 2
MHVMDVQGSTEASAIK +2 852.41 1702.80 1702.80 0 98 2
FDVSGYPTIK +2 563.52 1125.02 1125.57 -0.54 60 5
RFDVSGYPTLK +3 428.23 1281.67 1281.67 0 43 3
FAMEPEEFDSDALR +2 828.86 1655.71 1655.71 0 54 2
YGIVDYMVEQSGPPSK +2 885.43 1768.84 1768.83 0.01 77 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
765. IPI00206743 N Y 0.3 1 0 2 0 2
*Des: 30 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 11.65%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
AGPELLLDSNIR +2 649.36 1296.71 1296.70 0.01 52 1
SIYSLILGQDNAADQSR +2 925.98 1849.94 1849.92 0.02 79 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
766. IPI00215564 Y Y 1.03 2 2 4 3 6
*Des: Ras-related protein Rab-7
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 15.16%
Seq Charge Xcor Delta Probility PepHits
EAINVEQAFQTIAR +2 3.273 0.428 0.9977 2
TLDSWRDEFLIQASPR +3 3.165 0.247 0.9569 1
MASCOT:(PepMatched Observed.Hits Coverage) 4 1 24.64%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ATIGADFLTK +2 518.8194 1035.6242 1035.5600 0.06 56 3
VIILGDSGVGK +2 529.3469 1056.6792 1056.6178 0.06 72 3
DPENFPFVVLGNK +2 738.4340 1474.8534 1474.7456 0.11 50 1
EAINVEQAFQTIAR +2 795.4725 1588.9304 1588.8209 0.11 81 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
767. IPI00230874 Y Y 1.05 1 5 5 6 6
*Des: Biliverdin reductase A precursor
SEQUEST:(PepMatched Observed.Hits Coverage) 5 1 30.66%
Seq Charge Xcor Delta Probility PepHits
MTVQLETQNK +2 2.731 0.360 0.9943 1
YVNFQFTSGSLEEVPSVGVNK +3 3.498 0.288 0.9906 1
VLHEEHVELLMEEFEFLR +3 3.246 0.352 0.9968 2
SAAFLNLIGFVSR +2 3.809 0.455 0.9996 2
HVLVEYPMTLSFAAAQELWELAAQK +3 4.412 0.449 0.9997 2
MASCOT:(PepMatched Observed.Hits Coverage) 5 1 27.33%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits

```
                        FGVVVVGVGR              +2          494.80      987.59      987.59      0           53          1
                        FGFPAFSGISR             +2          593.31      1184.60     1184.60     0           44          2
                        SAAFLNLIGFVSR           +2          697.89      1393.77     1393.77     0           51          1
                        VLHEEHVELLMEEFEFLR                  +3          767.06      2298.15     2298.14     0.01        43          1
                        HVLVEYPMTLSFAAAQELWELAAQK           +3          949.17      2844.48     2844.45     0.03        48          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
768.        IPI00231749             Y           Y           0.85        1           6           3           8           4
*Des:       Phosphatidylinositol transfer protein alpha isoform
            SEQUEST:(PepMatched Observed.Hits Coverage)                 6           2           36.36%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        MLAPEGALNIHEK           +2          3.381       0.451       0.9995      2
                        NETGGGEGVEVLVNEPYEK                 +2          5.247       0.592       1.0000      1
                        HVEAIYIDIADR            +2          3.300       0.650       1.0000      2
                        WVDLTMDDIR              +2          2.942       0.359       0.9977      2
                        VILPVSVDEYQVGQLYSVAEASK                         +2          5.333       0.628       1.0000      2
                        IETWHKPDLGTQENVHK                   +3          3.263       0.260       0.9923      2
            MASCOT:(PepMatched Observed.Hits Coverage)                  3           2           18.54%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        MLAPEGALNIHEK           +2          711.88      1421.74     1421.73     0.01        44          1
                        HVEAIYIDIADR            +2          707.87      1413.72     1413.73     0           54          2
                        VILPVSVDEYQVGQLYSVAEASK                         +3          832.11      2493.30     2493.30     0           45          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
769.        IPI00231677             Y           Y           1.55        5           10          8           74          137
*Des:       14-3-3 protein eta
            SEQUEST:(PepMatched Observed.Hits Coverage)                 10          7           55.6%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        YLAEVASGEKK             +2          3.109       0.375       0.9982      3
                        NCNDFQYESK              +2          3.610       0.508       1.0000      4
                        NSVVEASEAAYK            +2          4.402       0.572       1.0000      4
                        AVTELNEPLSNEDR          +2          4.856       0.470       1.0000      2
                        LAEQAERYDDMASAMK                    +3          3.080       0.453       0.9999      3
                        QAFDDAIAELDTLNEDSYK                 +2          4.987       0.642       1.0000      3
                        QAFDDAIAELDTLNEDSYKDSTLIMQLLR       +3          5.879       0.607       1.0000      2
                        ELETVCNDVLALLDKFLIK                 +2          4.347       0.454       1.0000      2
                        IEKELETVCNDVLALLDKFLIK              +3          5.829       0.361       1.0000      7
                        EAFEISKEHMQPTHPIR                   +3          3.963       0.410       1.0000      2
            MASCOT:(PepMatched Observed.Hits Coverage)                  8           8           43.6%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore    PepHits
                        YLAEVASGEK              +2          533.7823    1065.5501   1065.5342   0.02        43          5
                        NCNDFQYESK              +2          624.2593    1246.5040   1246.4924   0.01        55          6
                        NSVVEASEAAYK            +2          634.3166    1266.6187   1266.6091   0.01        95          6
                        AVTELNEPLSNEDR          +2          793.8927    1585.7708   1585.7583   0.01        78          4
                        LAEQAERYDDMASAMK                    +2          914.9235    1827.8325   1827.8131   0.02        64          5
                        YLAEVASGEKK             +2          597.8267    1193.6389   1193.6291   0.01        47          3
                        IEKELETVCNDVLALLDKFLIK              +3          849.4840    2545.4302   2545.4076   0.02        69          2
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		EAFEISKEHMQPTHPIR			+2	1025.5305	2049.0465	2049.0101	0.04	43	1	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
770.	IPI00207475		Y	Y	0.37	1	3	2	4	2		
*Des:	Endothelial cell adhesion molecule											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	13.71%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LDALQEGDSGTYR		+2	3.778	0.515	0.9999	1				
		LAPSSQVFFGPALDTVR			+2	4.712	0.593	1.0000	2			
		EESSSHPWEAPFLIWFLEQEGK				+3	3.225	0.312	0.9947	1		
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	7.98%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LDALQEGDSGTYR		+2	712.84	1423.66	1423.66	0	61	1		
		LAPSSQVFFGPALDTVR			+2	902.98	1803.95	1803.95	0	58	2	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
771.	IPI00204206		Y	Y	0.59	2	5	4	5	44		
*Des:	Tropomyosin alpha isoform											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	2	21.1%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AEADVASLNR		+2	2.842	0.387	0.9979	2				
		EENLSMHQMLDQTLLELNN			+2	4.605	0.472	1.0000	1			
		AELSEGQVR		+2	2.824	0.209	0.9779	1				
		VAHAKEENLSMHQMLDQTLLELNNM				+3	4.419	0.443	1.0000	1		
		SKQLEEDISAKEK		+3	3.593	0.168	0.9740	1				
	MASCOT:(PepMatched Observed.Hits Coverage)					4	3	17.3%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AELSEGQVR		+2	494.7593	987.5041	987.4985	0.01	61	5		
		QLEEDISAKEK		+2	645.3393	1288.6640	1288.6510	0.01	42	2		
		AEADVASLNR		+2	523.2709	1044.5272	1044.5199	0.01	41	3		
		AQKDEEKMEIQEIQLK			+2	980.5159	1959.0173	1958.9982	0.02	110	36	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
772.	IPI00190530		Y	Y	0.97	1	7	7	14	24		
*Des:	41 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					7	1	31.42%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TLFPGTDHIDQLK		+2	3.407	0.269	0.9945	3				
		NYIQSLAQMPK		+2	3.591	0.407	0.9996	3				
		YIHSADIIHR		+3	3.339	0.392	0.9998	4				
		HENVIGLLDVFTPAR		+2	5.647	0.579	1.0000	4				
		LTDDHVQFLIYQILR		+3	3.396	0.413	0.9997	1				
		SLEEFNDVYLVTHLMGADLNNIVK				+3	5.632	0.524	1.0000	1		
		MNFANVFIGANPLAVDLLEK			+3	4.769	0.441	0.9999	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					7	1	29.78%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MLVLDSDKR		+2	538.79	1075.57	1075.57	0	46	4		

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                    YIHSADIIHR         +3        408.89    1223.65   1223.64   0.01      52        8
                    TLFPGTDHIDQLK      +2        742.90    1483.78   1483.77   0.01      56        4
                    NYIQSLAQMPK        +2        646.84    1291.67   1291.66   0.01      59        3
                    HENVIGLLDVFTPAR+2            840.98    1679.94   1679.90   0.04      119       10
                    MNFANVFIGANPLAVDLLEK +3                726.06    2175.15   2175.14   0.01      54        2
                    SLEEFNDVYLVTHLMGADLNNIVK               +3        912.14    2733.40   2733.37   0.03      59        2

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
773.      IPI00370158         Y         N         0.61      1         2         0         2         0
*Des:     RAS-related C3 botulinum substrate 2
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         6.12%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    TVFDEAIR            +2        2.732     0.149     0.9521    1
                    GLKTVFDEAIR         +3        3.602     0.208     0.9938    1
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
774.      IPI00203406         Y         N         0.08      1         2         0         2         0
*Des:     Oxysterol-binding protein
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         2.89%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    NDFSIWSILR          +2        3.045     0.429     0.9995    1
                    ITMPVIFNEPLSFLQR              +2        4.580     0.597     1.0000    1
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
775.      IPI00190462         Y         Y         0.24      1         2         2         3         8
*Des:     Serine/threonine protein phosphatase 2A, catalytic subunit, beta isoform
          SEQUEST:(PepMatched Observed.Hits Coverage)   2         1         13.33%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    SPDTNYLFMGDYVDR               +2        5.138     0.635     1.0000    1
                    GAGYTFGQDISETFNHANGLTLVSR     +3        4.956     0.587     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    2         1         13.33%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    SPDTNYLFMGDYVDR               +2        896.90    1791.78   1791.78   0         84        4
                    GAGYTFGQDISETFNHANGLTLVSR     +3        885.77    2654.28   2654.27   0.01      61        8

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
776.      IPI00190392         Y         N         0.26      1         4         0         6         0
*Des:     51 kDa protein
          SEQUEST:(PepMatched Observed.Hits Coverage)   4         1         13.47%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    MNVSPDVNYEELAR+2              3.588     0.402     0.9994    1
                    VDILDPALLR          +2        2.721     0.360     0.9969    2
                    TMLELLNQLDGFQPNTQVK +3        3.500     0.251     0.9907    1
                    QTYFLPVIGLVDAEK+2             2.959     0.432     0.9987    2
          MASCOT:(PepMatched Observed.Hits Coverage)
```

Identified Human Platelet Proteins

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
777.	IPI00324102	Y	Y	0.37	4	4	5	15	25

*Des: Prothrombinase FGL2

SEQUEST:(PepMatched Observed.Hits Coverage) 4 8 16.8%

Seq	Charge	Xcor	Delta	Probility	PepHits
NAKEEIQGLQGR	+3	3.696	0.268	0.9986	5
TLQEAVDSLKK	+2	2.913	0.411	0.9984	4
EFWLGNDKIHLLTK	+2	4.412	0.487	1.0000	9
NGIFWGTWPGVSQAHPGGYK	+2	4.496	0.515	1.0000	10

MASCOT:(PepMatched Observed.Hits Coverage) 5 7 19.28%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
AGFGNLER	+2	432.2249	862.4353	862.4297	0.01	59	8
NAKEEIQGLQGR	+2	671.8618	1341.7091	1341.7000	0.01	71	5
TLQEAVDSLKK	+2	616.3517	1230.6889	1230.6819	0.01	46	2
EFWLGNDKIHLLTK	+2	857.4759	1712.9372	1712.9249	0.01	74	6
NGIFWGTWPGVSQAHPGGYK	+2	1080.0363	2158.0580	2158.0384	0.02	74	11

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
778.	IPI00392151	N	Y	0.23	1	0	3	0	5

*Des: 59 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 8.48%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
HKSETDTSLIR	+2	643.8428	1285.6710	1285.6626	0.01	43	1
DGNVLLHEMQIQHPTASLIAK	+3	772.4177	2314.2312	2314.2103	0.02	56	3
GPNKHTLTQIK	+2	618.8608	1235.7070	1235.6986	0.01	44	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
779.	IPI00565497	N	Y	0.88	1	0	4	0	15

*Des: 46 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 13.52%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
GYDVIAQAQSGTGK	+2	697.8556	1393.6966	1393.6837	0.01	71	6
MFVLDEADEMLSR	+2	778.3652	1554.7159	1554.7058	0.01	100	5
ATQALVLAPTR	+2	570.8439	1139.6732	1139.6662	0.01	43	3
KGVAINMVTEEDKR	+3	530.6196	1588.8369	1588.8242	0.01	45	1

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
780.	IPI00200794	Y	Y	0.38	1	2	3	5	7

*Des: L-xylulose reductase

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 14.45%

Seq	Charge	Xcor	Delta	Probility	PepHits
GVPGAIVNVSSQASQR	+2	5.037	0.545	1.0000	2
FAEVENVVDTILFLLSNR	+2	4.851	0.533	1.0000	3

MASCOT:(PepMatched Observed.Hits Coverage) 3 1 19.27%

```
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                            Pepscore    PepHits
                        GVPGAIVNVSSQASQR                    +2          785.42      1568.83     1568.83     0           87          2
                        AVVQVSQIVAR             +2          585.32      1168.62     1168.69     -0.06       42          5
                        FAEVENVVDTILFLLSNR                  +3          693.71      2078.12     2078.10     0.02        46          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
781.        IPI00325847             Y           N           0.15        1           3           0           4           0
*Des:       GPI-anchored ceruloplasmin
            SEQUEST:(PepMatched Observed.Hits Coverage)     3           1           4.44%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        ALYSEYTDGTFTK           +2          3.031       0.426       0.9986      1
                        AGLQAFFQVR              +2          2.859       0.407       0.9985      2
                        GPDEEHLGILGPVIWAEVGDIIR+3           4.883       0.449       1.0000      1
            MASCOT:(PepMatched Observed.Hits Coverage)

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
782.        IPI00358331             Y           Y           0.14        1           2           2           2           3
*Des:       PREDICTED: similar to dead end protein
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           3.37%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        ASAEQIEEEVTK            +2          3.669       0.380       0.9995      1
                        DQGGELLSLR              +2          3.054       0.160       0.9637      1
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           3.37%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                            Pepscore    PepHits
                        ASAEQIEEEVTK            +2          667.33      1332.65     1332.64     0.01        64          2
                        DQGGELLSLR              +2          544.29      1086.57     1086.57     0           59          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
783.        IPI00358404             Y           Y           0.23        1           2           2           3           3
*Des:       Eukaryotic translation termination factor 1
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           5.84%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        FGATLEIVTDK             +2          2.810       0.438       0.9991      2
                        LSVLGAITSVQQR           +2          3.103       0.396       0.9818      1
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           5.84%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                            Pepscore    PepHits
                        FGATLEIVTDK             +2          597.33      1192.64     1192.63     0.01        58          2
                        LSVLGAITSVQQR           +2          687.36      1372.71     1370.79     1.92        46          1

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
784.        IPI00551592             Y           Y           0.47        2           2           2           17          26
*Des:       Myosin regulatory light chain 2-A, smooth muscle isoform
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           28.73%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        DGFIDKEDLHDMLASMGK                  +2          5.640       0.641       1.0000      3
                        NPTDEYLDAMMNEAPGPINFTMFLTMFGEK                  +3          6.548       0.443       1.0000      14
            MASCOT:(PepMatched Observed.Hits Coverage)      2           1           13.21%
```

		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits	
		GNFNYIEFTR		+2	630.8568	1259.6990	1259.5934	0.11	52	15			
		LNGTDPEDVIR		+2	614.8630	1227.7114	1227.6095	0.1	85	29			
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)											
785.	IPI00207550		N	Y	2.17	4	0	25	0	4153			
*Des:	PREDICTED: similar to Actin, cytoplasmic 2 (Gamma-actin)												
	SEQUEST:(PepMatched Observed.Hits Coverage)												
	MASCOT:(PepMatched Observed.Hits Coverage)					25	9	46.45%					
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits	
		AGFAGDDAPR		+2	488.7993	975.5841	975.4410	0.14	91	567			
		CDVDIRK	+2	424.7206	847.4267	847.4222	0	44	6				
		DSYVGDEAQSK		+2	599.7686	1197.5227	1197.5149	0.01	78	28			
		SYELPDGQVITIGNER			+2	895.9565	1789.8984	1789.8846	0.01	115	1554		
		GYSFTTTAEREIVR		+2	815.4221	1628.8296	1628.8158	0.01	53	28			
		VAPEEHPVLLTEAPLNPK			+2	977.5460	1953.0775	1953.0571	0.02	96	72		
		DLTDYLMK		+2	499.7492	997.4839	997.4790	0	62	181			
		DSYVGDEAQSKR		+2	677.8203	1353.6261	1353.6160	0.01	91	280			
		EITALAPSTMK		+2	581.5111	1161.0077	1160.6111	0.4	84	849			
		GYSFTTTAER		+2	565.7974	1129.5802	1131.5196	-1.93	75	183			
		LDLAGRDLTDYLMK		+2	812.4302	1622.8458	1622.8338	0.01	49	308			
		QEYDESGPSIVHR		+3	506.2422	1515.7047	1515.6953	0.01	58	89			
		QEYDESGPSIVHRK		+2	822.9086	1643.8027	1643.7903	0.01	60	19			
		KDLYANTVLSGGTTMYPGIADR				+2	1172.0969	2342.1793	2342.1576	0.02	121	10	
		HQGVMVGMGQK		+2	585.5645	1169.1145	1170.5637	-1.44	83	763			
		HQGVMVGMGQKDSYVGDEAQSKR				+2	1254.1031	2506.1917	2506.1692	0.02	110	476	
		MQKEITALAPSTMK		+2	774.9154	1547.8163	1547.8051	0.01	86	141			
		IWHHTFYNELR		+2	758.3823	1514.7500	1514.7419	0.01	41	12			
		AVFPSIVGRPR		+2	599.9666	1197.9186	1197.6982	0.22	86	894			
		YSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHR					+3	1367.3589	4099.0548	4099.0148	0.04	141	25
		MTQIMFETFNTPAMYVAIQAVLSLYASGR					+3	1085.2173	3252.6300	3252.6021	0.03	93	36
		IIAPPERK	+2	461.8878	921.7611	922.5600	-0.79	52	497				
		MQKEITALAPSTMKIK			+2	895.5047	1788.9948	1788.9841	0.01	74	25		
		VAPEEHPVLLTEAPLNPKANREK				+3	851.4714	2551.3925	2551.3757	0.02	41	3	
		VAPEEHPVLLTEAPLNPKANR			+3	765.7600	2294.2582	2294.2382	0.02	63	7		
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)											
786.	IPI00209082		Y	Y	0.46	5	31	16	62	158			
*Des:	Alpha-actinin 1												
	SEQUEST:(PepMatched Observed.Hits Coverage)					31	13	49.94%					
		Seq	Charge	Xcor	Delta	Probility	PepHits						
		DHSGTLGPEEFK		+2	2.857	0.368	0.9970	1					
		LSNRPAFMPSEGR		+2	3.188	0.486	0.9997	4					
		GISQEQMNEFR		+2	3.411	0.483	0.9998	3					
		NYITGDELR		+2	2.744	0.268	0.9825	3					
		QKDYETATLSEIK		+2	3.119	0.416	0.9751	3					
		ASFNHFDRDHSGTLGPEEFK			+3	4.222	0.327	0.9908	1				

IMSIVDPNR	+2	2.891	0.234	0.9885	2
ILAGDKNYITGDELR	+2	4.582	0.446	0.9973	3
LAILGIHNEVSK	+2	3.639	0.436	0.9997	6
MLDAEDIVGTARPDEK	+2	3.699	0.414	0.9995	4
TINEVENQILTR	+2	3.282	0.349	0.9983	2
VLAVNQENEQLMEDYEK	+2	5.652	0.536	1.0000	3
IVQTYHVNMAGTNPYTTITPQEINGK	+3	4.045	0.468	0.9999	2
LVSIGAEEIVDGNVK	+2	4.748	0.534	1.0000	2
RDQALTEEHSR	+3	3.503	0.279	0.9986	1
ETADTDTADQVMASFK	+2	5.266	0.646	1.0000	4
ISIEMHGTLEDQLSHLR	+2	4.940	0.603	1.0000	5
NVNIQNFHISWK	+2	4.012	0.456	0.9999	2
KDDPLTNLNTAFDVAER	+2	4.689	0.567	1.0000	4
QFGAQANVIGPWIQTK	+2	3.606	0.315	0.9973	1
AGTQIENIEEDFRDGLK	+2	4.332	0.440	0.9961	2
IDQLEGDHQLIQEALIFDNK	+2	5.638	0.589	1.0000	3
KHEAFESDLAAHQDR	+3	3.791	0.501	1.0000	2
VEQIAAIAQELNELDYYDSPSVNAR	+3	6.111	0.579	1.0000	3
LLETIDQLYLEYAK	+2	5.231	0.549	1.0000	3
AIMTYVSSFYHAFSGAQK	+2	5.322	0.584	1.0000	1
LASDLLEWIR	+2	3.304	0.308	0.9981	2
VGWEQLLTTIAR	+2	3.904	0.454	0.9999	3
VPENTMQAMQQK	+2	3.567	0.380	0.9994	1
LGVVTFQAFIDFMSR	+2	5.284	0.586	1.0000	6
IMSIVDPNRLGVVTFQAFIDFMSR	+3	4.533	0.570	1.0000	4

MASCOT:(PepMatched Observed.Hits Coverage) 16 9 26.13%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
TINEVENQILTR	+2	716.3560	1430.6974	1428.7572	1.94	77	8
LVSIGAEEIVDGNVK	+2	771.9271	1541.8396	1541.8300	0.01	63	4
MLDAEDIVGTARPDEK	+2	880.4343	1758.8540	1758.8458	0.01	77	20
ALDFIASK	+2	432.7474	863.4803	863.4752	0.01	56	11
FAIQDISVEETSAK	+2	769.3969	1536.7792	1536.7671	0.01	81	18
KDDPLTNLNTAFDVAER	+2	959.9879	1917.9612	1917.9432	0.02	127	4
AGTQIENIEEDFRDGLK	+2	967.9816	1933.9486	1933.9381	0.01	71	2
VGWEQLLTTIAR	+2	693.8954	1385.7763	1385.7667	0.01	80	12
LMLLLEVISGER	+2	686.9023	1371.7901	1371.7795	0.01	87	91
RDQALTEEHSR	+3	447.8917	1340.6533	1340.6433	0.01	60	4
ILAGDKNYITGDELRR	+2	917.5018	1832.9890	1832.9744	0.01	47	28
LAILGIHNEVSK	+2	648.3389	1294.6632	1292.7452	1.92	66	24
TIPWLENRVPENTMQAMQQK	+3	805.4089	2413.2050	2413.1882	0.02	44	6
HRPELIDYGK	+3	409.8900	1226.6482	1226.6407	0.01	45	26
QFGAQANVIGPWIQTK	+2	879.4825	1756.9504	1756.9260	0.02	70	6
LSNRPAFMPSEGR	+2	731.3718	1460.7291	1460.7194	0.01	47	4

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
787.	IPI00371972	Y	Y	0.22	1	3	4	6	7

*Des: PREDICTED: similar to chromosome 10 open reading frame 42

	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	7.22%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DLLSHENAETLNDVK			+2	4.464	0.503	0.9999	3			
		DAIAQAEMDLK		+2	2.982	0.354	0.9955	2				
		VAASTGIDLLLLDDFK			+2	5.009	0.564	1.0000	2			
	MASCOT:(PepMatched Observed.Hits Coverage)					4	1	9.3%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DLLSHENAETLNDVK			+2	849.43	1696.84	1696.83	0.01	86	3	
		DAIAQAEMDLK		+2	602.80	1203.58	1203.58	0	68	2		
		LRDPLQVHLPLR		+3	486.30	1455.86	1455.87	0	53	2		
		VAASTGIDLLLLDDFK			+2	845.97	1689.93	1689.92	0.01	80	2	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
788.	IPI00188338		Y	Y	0.29	3	3	8	3	39		
*Des:	PREDICTED: similar to inter-alpha trypsin inhibitor, heavy chain 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	2	5.23%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		KAAISGENAGLVR		+2	3.020	0.407	0.9981	3				
		GSLVPASHANLQAAQDFVR			+2	4.911	0.553	1.0000	1			
		FSLAGATNLNGGLLR			+2	2.779	0.334	0.9891	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					8	3	11.62%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		AAISGENAGLVR		+2	579.32	1156.63	1156.62	0.01	77	6		
		LWAYLTIQELLAK		+2	781.46	1560.90	1560.89	0.01	75	4		
		QAVDTTVNGVSIR		+2	680.37	1358.72	1358.72	0	73	1		
		QYYDGSEIVVAGR		+2	728.86	1455.71	1455.70	0.01	66	10		
		FAHYVITSQVVNSANK			+2	889.47	1776.93	1776.92	0.01	96	18	
		VNCKVTSRFAHYVITSQVVNSANK				+3	889.47	2665.39	2664.38	1.01	43	2
		LDAQASFLSK		+2	540.29	1078.57	1078.57	0	61	18		
		GSLVPASHANLQAAQDFVR			+2	991.02	1980.03	1980.02	0.01	90	4	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
789.	IPI00213033		Y	N	0.92	2	3	0	4	0		
*Des:	15 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	2	30.76%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		VIKDFMIQGGDFTR		+2	4.274	0.627	0.9961	2				
		TVDNFVALATGEK		+2	2.862	0.381	0.9563	1				
		VYFDFQIGDEPVGR		+2	3.084	0.487	0.9875	1				
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
790.	IPI00215574		Y	Y	0.79	1	5	3	10	8		
*Des:	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	1	28.23%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ALQLGTLFPPAEALK			+2	4.628	0.378	0.9999	1			

GVILTSERPGIFSAGLDLMEMYGR +3 3.893 0.465 0.9999 1
NPAHYAEYWK +2 2.863 0.374 0.9983 3
VGLVDEVVPEDQVHSK +2 4.700 0.420 0.9999 4
EADIQNFTSFISR +2 3.894 0.424 0.9999 5
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 15.98%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VGLVDEVVPEDQVHSK +2 875.46 1748.91 1748.89 0.02 86 4
EADIQNFTSFISR +2 764.38 1526.75 1526.74 0.01 95 5
ALQLGTLFPPAEALK +2 784.96 1567.91 1567.90 0.01 69 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
791. IPI00362070 Y Y 0.14 1 2 2 2 2
*Des: PREDICTED: similar to uridindiphosphoglucosepyrophosphorylase 2
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 4.86%
Seq Charge Xcor Delta Probility PepHits
TLDGGLNVIQLETAVGAAIK +2 3.412 0.331 0.9738 1
IFNTNNLWISLAAVK +2 4.933 0.435 0.9999 1
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 4.86%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
IFNTNNLWISLAAVK +2 852.49 1702.96 1702.94 0.02 99 1
TLDGGLNVIQLETAVGAAIK +2 992.51 1983.01 1982.10 0.91 52 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
792. IPI00370090 Y Y 0.02 1 2 4 3 32
*Des: Type I keratin KA15
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 7.91%
Seq Charge Xcor Delta Probility PepHits
VTMQNLNDRLASYLDKVR +3 4.191 0.502 1.0000 2
TLQGLEIELQSQLSMK +2 3.140 0.227 0.9876 1
MASCOT:(PepMatched Observed.Hits Coverage) 4 4 5.93%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VTMQNLNDRLASYLDKVR +3 712.7253 2135.1542 2135.1157 0.04 48 2
LASYLDKVR +2 532.8175 1063.6205 1063.6026 0.02 61 3
VTMQNLNDR +2 545.7769 1089.5393 1089.5237 0.02 51 10
LAADDFR +2 404.2094 806.4042 806.3922 0.01 43 17

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
793. IPI00195629 Y N 0.35 1 3 0 13 0
*Des: 25 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 16.89%
Seq Charge Xcor Delta Probility PepHits
IEDGNNFGVAVQEK +2 4.644 0.438 1.0000 8
TENLLGSYFPK +2 3.510 0.371 0.9996 6
ISELDAFLK +2 2.749 0.458 0.9977 3
MASCOT:(PepMatched Observed.Hits Coverage)

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)

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794.    IPI00208286    Y    Y    1.09    1    4    3    7    18
*Des:   Ubiqutin carboxyl-terminal hydrolase l3
        SEQUEST:(PepMatched Observed.Hits Coverage)    4    1    28.63%
                Seq    Charge    Xcor    Delta    Probility    PepHits
                FLEESVAMSPEER    +2    3.690    0.303    0.9986    2
                VTHETSAHEGQTEAPSIDEK    +3    5.717    0.557    1.0000    1
                SQGQDVTSSVYFMK    +2    3.848    0.535    1.0000    2
                WLPLEANPEVTNQFLK    +2    4.292    0.503    1.0000    3
        MASCOT:(PepMatched Observed.Hits Coverage)    3    1    22.64%
                Seq    Charge    ObservedMS    ExpectedMS    CalculatedMS    Pepscore    PepHits
                VTHETSAHEGQTEAPSIDEK    +3    722.68    2165.01    2164.99    0.02    67    2
                SQGQDVTSSVYFMK    +2    788.87    1575.73    1575.72    0.01    73    8
                WLPLEANPEVTNQFLK    +2    950.01    1898.01    1897.99    0.02    61    12

No.     Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
795.    IPI00360541    Y    Y    0.24    1    4    4    5    5
*Des:   PREDICTED: similar to CD18 antigen preprotein
        SEQUEST:(PepMatched Observed.Hits Coverage)    4    1    8.45%
                Seq    Charge    Xcor    Delta    Probility    PepHits
                SFADLHPQYQVQR    +2    3.525    0.432    0.9996    2
                SAVGELSDDSSNVVQLIK    +2    3.699    0.431    0.9996    1
                LGGDLLQALNEITESGR    +2    4.538    0.584    1.0000    1
                LTDNSNQFQTEVGK    +2    3.719    0.531    0.9999    1
        MASCOT:(PepMatched Observed.Hits Coverage)    4    1    8.45%
                Seq    Charge    ObservedMS    ExpectedMS    CalculatedMS    Pepscore    PepHits
                LTDNSNQFQTEVGK    +2    790.88    1579.75    1579.75    0    65    1
                SFADLHPQYQVQR    +2    794.90    1587.79    1587.78    0.01    53    2
                SAVGELSDDSSNVVQLIK    +2    930.99    1859.96    1859.95    0.01    63    1
                LGGDLLQALNEITESGR    +2    893.47    1784.93    1784.93    0    69    1

No.     Protein    Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
796.    IPI00362072    Y    Y    2.2    4    7    7    24    35
*Des:   Actin-like protein 2
        SEQUEST:(PepMatched Observed.Hits Coverage)    7    4    25.68%
                Seq    Charge    Xcor    Delta    Probility    PepHits
                SMLEVNYPMENGIVR    +2    4.832    0.463    1.0000    3
                GYAFNHSADFETVR    +2    3.773    0.549    1.0000    3
                RLDIAGR    +2    3.122    0.187    0.9918    7
                KVVVCDNGTGFVK    +2    3.117    0.444    0.9990    1
                ILLTEPPMNPTK    +2    2.991    0.530    0.9997    5
                HMVFLGGAVLADIMK    +2    5.066    0.607    1.0000    10
                HIVLSGGSTMYPGLPSRLER    +3    3.516    0.572    1.0000    2
        MASCOT:(PepMatched Observed.Hits Coverage)    7    4    27.43%
                Seq    Charge    ObservedMS    ExpectedMS    CalculatedMS    Pepscore    PepHits
                DLMVGDEASELR    +2    667.82    1333.63    1333.62    0.01    47    1
                ILLTEPPMNPTK    +2    677.38    1352.75    1352.74    0.01    45    1
                GYAFNHSADFETVR    +2    807.38    1612.74    1612.73    0.01    70    3
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		HIVLSGGSTMYPGLPSR			+2	886.47	1770.92	1770.91	0.01	83	3	
		SMLEVNYPMENGIVR			+2	876.43	1750.85	1750.84	0.01	65	6	
		LALETTVLVESYTLPDGR			+2	989.04	1976.06	1976.05	0.01	60	3	
		HMVFLGGAVLADIMK			+2	801.44	1600.86	1600.85	0.01	106	3	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
797.	IPI00213036		Y	N	0.04	1	2	0	2	0		
*Des:	Complement C4 precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	2	2.49%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		ILSLAQEQIGDSPEK		+2	5.073	0.604	1.0000	1				
		NPSEPVPQAPALWIETTAYGLLHLLLR				+3	4.369	0.588	1.0000	2		
	MASCOT:(PepMatched Observed.Hits Coverage)											
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
798.	IPI00559080		Y	Y	0.13	1	2	2	5	6		
*Des:	PREDICTED: similar to Nicotinamide nucleotide adenylyltransferase 3											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	11.2%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DSHIQEIVEK		+2	2.746	0.305	0.9965	2				
		VDPWESEQAQWMETVK			+2	5.194	0.526	1.0000	4			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	11.2%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DSHIQEIVEK		+2	599.3203	1196.6261	1196.6037	0.02	41	2		
		VDPWESEQAQWMETVK			+2	981.9713	1961.9280	1961.8829	0.05	84	4	
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
799.	IPI00476630		N	Y	0.22	1	0	2	0	5		
*Des:	31 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	10.56%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		SEFIGLQLLDILTR		+2	809.4698	1616.9250	1616.9137	0.01	84	5		
		QLSQALDTSNVMVK		+2	768.3745	1534.7343	1532.7868	1.95	54	1		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)		SpectraMatched(SEQUEST MASCOT)			
800.	IPI00476704		N	Y	0.23	1	0	5	0	20		
*Des:	111 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					5	1	8.38%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		MLDYEMLQR		+2	599.7880	1197.5614	1197.5522	0.01	42	4		
		ATLNSGPGAQQK		+2	586.3111	1170.6076	1170.5993	0.01	48	12		
		ALVEGIKMEHQLELGNLQAK			+3	741.0787	2220.2144	2220.1935	0.02	43	1	
		KISGTTALQEALKEK			+3	539.6492	1615.9259	1615.9144	0.01	51	8	
		HSSPVGRPSIGSASSSVVASASGSK				+3	767.0664	2298.1774	2298.1563	0.02	50	2

Identified Human Platelet Proteins

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
801. IPI00205957 N Y 0.3 1 0 2 0 6
*Des: 30 kDa protein
SEQUEST:(PepMatched Observed.Hits Coverage)
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 13.18%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VLALIQAWADAFR +2 737.4160 1472.8175 1472.8139 0 74 3
KGIEFPMADLDALSPIHTPQR +3 779.9518 2336.8337 2335.1994 1.63 60 3

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
802. IPI00370169 Y Y 0.14 1 2 2 2 2
*Des: PREDICTED: similar to adaptor protein Gads
SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 4.35%
Seq Charge Xcor Delta Probility PepHits
ASQSSPGDFSISVR +2 3.489 0.550 0.9999 1
ALYDFEALEEDELGLR +2 4.593 0.552 1.0000 1
MASCOT:(PepMatched Observed.Hits Coverage) 2 1 4.35%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
ASQSSPGDFSISVR +2 719.36 1436.70 1436.69 0.01 59 1
ALYDFEALEEDELGLR +2 941.96 1881.91 1881.90 0.01 71 1

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
803. IPI00202616 Y Y 0.71 1 4 3 8 7
*Des: PREDICTED: similar to NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (Complex I-30KD) (CI-30KD)
SEQUEST:(PepMatched Observed.Hits Coverage) 4 1 19.7%
Seq Charge Xcor Delta Probility PepHits
LSAFGEYVAEILPK +2 4.266 0.439 0.9999 2
FEIVYNLLSLR +2 3.200 0.393 0.9995 3
VVAEPVELAQEFR +2 3.294 0.556 1.0000 2
DFPLTGYVELR +2 3.113 0.470 0.9998 6
MASCOT:(PepMatched Observed.Hits Coverage) 3 1 15.24%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
VVAEPVELAQEFR +2 743.91 1485.80 1485.78 0.02 60 3
DFPLTGYVELR +2 655.35 1308.68 1308.67 0.01 60 5
LSAFGEYVAEILPK +2 768.93 1535.84 1535.82 0.02 95 2

No. Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
804. IPI00202543 Y Y 0.08 2 3 3 10 9
*Des: Hexokinase, type I
SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 3.96%
Seq Charge Xcor Delta Probility PepHits
ASGVEGADVVK +2 3.154 0.402 0.9975 4
HIDLVEGDEGR +2 4.032 0.596 1.0000 5
LSDEILIDILTR +2 3.118 0.402 0.9966 3
MASCOT:(PepMatched Observed.Hits Coverage) 3 2 4.38%
Seq Charge ObservedMS ExpectedMS CalculatedMS Pepscore PepHits
LSDEILIDILTR +2 700.9086 1399.8027 1399.7922 0.01 81 7

HIDLVEGDEGR	+2	620.3051	1238.5956	1238.5891	0.01	42	2
SANLVAATLGAILNR	+3	495.2935	1482.8585	1482.8518	0.01	66	3

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
805.	IPI00210635	N	Y	0.13	1	0	4	0	6

*Des: N-ethylmaleimide sensitive factor

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 4 1 7.39%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
GHQLLSADVDIK	+2	648.35	1294.68	1294.69	0	53	2
VLDDGELLVQQTK	+2	729.40	1456.78	1456.78	0	57	2
NFSGAELEGLVR	+2	646.34	1290.66	1290.66	0	58	1
MGIGGLDKEFSDIFR	+3	562.28	1683.83	1683.83	0	64	2

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
806.	IPI00192076	Y	N	0.09	2	3	0	5	0

*Des: 100 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 3 2 4.66%

Seq	Charge	Xcor	Delta	Probility	PepHits
TDPAALTDDEINR	+2	3.394	0.509	0.9999	2
AYTEEDLDLVEK	+2	2.975	0.347	0.9981	1
EIGLLTEEVELYGETK	+2	4.436	0.572	1.0000	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
807.	IPI00567177	N	Y	2.75	3	0	11	0	482

*Des: PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase

SEQUEST:(PepMatched Observed.Hits Coverage)

MASCOT:(PepMatched Observed.Hits Coverage) 11 5 41.59%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LISWYDNEYGYSNR	+2	890.4091	1778.8036	1778.7900	0.01	82	35
VGVNGFGR	+2	403.2222	804.4298	804.4242	0.01	60	17
GAAQNIIPASTGAAK	+2	685.3809	1368.7472	1368.7361	0.01	99	96
DGRGAAQNIIPASTGAAK	+2	849.4615	1696.9085	1696.8856	0.02	48	4
VIISAPSADAPMFVMGVNHEK	+2	1107.0680	2212.1214	2212.1020	0.02	106	5
LEKPAKYDDIKK	+2	724.4164	1446.8182	1446.8082	0.01	64	29
VIISAPSADAPMFVMGVNHEKYDNSLK	+3	978.4977	2932.4712	2932.4462	0.03	78	81
VKVGVNGFGR	+2	515.8327	1029.6509	1031.5875	-1.93	55	39
VPTPNVSVVDLTCR	+2	750.4030	1498.7914	1498.7813	0.01	113	49
VIHDNFGIVEGLMTTVHAITATQK	+2	1298.1926	2594.3707	2594.3526	0.02	111	362
LVINGKPITIFQER	+2	814.4849	1626.9552	1626.9457	0.01	58	9

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
808.	IPI00554213	Y	Y	0.35	2	2	3	4	5

*Des: PREDICTED: similar to methylenetetrahydrofolate dehydrogenase (NAD) (EC 1.5.1.15) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) precursor - mouse

SEQUEST:(PepMatched Observed.Hits Coverage) 2 2 10.7%

Identified Human Platelet Proteins

		Seq	Charge	Xcor	Delta	Probility	PepHits					
		QEVEEWVASGNK		+2	3.687	0.448	0.9999	2				
		TLNDDENVDGLLVQLPLPEHIDER				+3	6.120	0.537	1.0000	2		
	MASCOT:(PepMatched Observed.Hits Coverage)					3	2	14.36%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		EGATVIDVGINR		+2	622.34	1242.66	1242.66	0	64	2		
		QEVEEWVASGNK		+2	688.33	1374.65	1374.64	0.01	64	1		
		TLNDDENVDGLLVQLPLPEHIDER				+3	915.47	2743.38	2743.37	0.01	70	3
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
809.	IPI00211299		N	Y	1.49	1	0	2	0	2		
*Des:	Neuropeptide Y precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	23%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		SSPETLISDLLMR		+2	730.4301	1458.8456	1460.7545	-1.9	51	5		
		HYINLITR	+2	515.2983	1028.5821	1028.5767	0.01	43	1			
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
810.	IPI00551812		Y	Y	1.42	5	22	19	63	48		
*Des:	ATP synthase beta chain, mitochondrial precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					22	9	63.94%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		IMDPNIVGSEHYDVAR			+2	4.767	0.632	1.0000	5			
		VALVYGQMNEPPGAR			+2	4.931	0.501	1.0000	7			
		AHGGYSVFAGVGER			+2	3.938	0.541	1.0000	4			
		IMNVIGEPIDER		+2	3.939	0.476	0.9999	3				
		LVLEVAQHLGESTVR			+2	4.315	0.592	1.0000	4			
		IGLFGGAGVGK		+2	3.236	0.463	0.9998	6				
		IPSAVGYQPTLATDMGTMQER			+2	5.297	0.658	1.0000	2			
		VLDSGAPIKIPVGPETLGR			+2	4.468	0.530	1.0000	2			
		FTQAGSEVSALLGR		+2	3.913	0.459	0.9999	3				
		VVDLLAPYAK		+2	2.765	0.357	0.9971	2				
		TREGNDLYHEMIESGVINLK			+2	5.736	0.401	0.9993	3			
		AIAELGIYPAVDPLDSTSR			+2	4.755	0.592	1.0000	5			
		VALTGLTVAEYFR		+2	3.902	0.603	1.0000	1				
		FLSQPFQVAEVFTGHMGK			+2	4.544	0.608	1.0000	5			
		QFAPIHAEAPEFIEMSVEQEILVTGIK				+3	4.402	0.416	0.9997	3		
		GFQQILAGDYDHLPEQAFYMVGPIEEAVAK					+3	4.736	0.543	1.0000	3	
		TVLIMELINNVAK		+2	4.801	0.455	1.0000	7				
		SLQDIIAILGMDELSEEDKLTVSR				+3	5.878	0.646	1.0000	6		
		SLQDIIAILGMDELSEEDK			+2	4.647	0.454	0.9999	2			
		IGLFGGAGVGKTVLIMELINNVAK				+3	3.949	0.411	0.9934	2		
		DQEGQDVLLFIDNIFR			+2	6.025	0.590	1.0000	7			
		VALTGLTVAEYFRDQEGQDVLLFIDNIFR				+3	5.606	0.553	1.0000	3		
	MASCOT:(PepMatched Observed.Hits Coverage)					19	9	52.04%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits

		IPVGPETLGR		+2	519.80	1037.59	1037.59	0	63	6		
		IMDPNIVGSEHYDVAR			+2	908.44	1814.87	1814.86	0.01	88	4	
		IGLFGGAGVGK		+2	489.27	976.53	974.55	1.98	50	6		
		TIAMDGTEGLVR		+2	631.83	1261.64	1261.63	0.01	65	2		
		IMNVIGEPIDER		+2	693.37	1384.72	1384.70	0.02	52	1		
		AHGGYSVFAGVGER			+2	703.85	1405.68	1405.67	0.01	87	4	
		VALVYGQMNEPPGAR			+2	801.41	1600.81	1600.80	0.01	93	5	
		LVLEVAQHLGESTVR			+2	825.97	1649.92	1649.91	0.01	86	5	
		IPSAVGYQPTLATDMGTMQER			+3	756.04	2265.09	2265.08	0.01	62	1	
		VVDLLAPYAK		+2	544.82	1087.63	1087.63	0	45	2		
		FTQAGSEVSALLGR		+2	718.38	1434.75	1434.75	0	92	3		
		VALTGLTVAEYFR		+2	720.40	1438.79	1438.78	0.01	78	2		
		VLDSGAPIKIPVGPETLGR			+2	960.06	1918.10	1918.09	0.01	80	2	
		AIAELGIYPAVDPLDSTSR			+2	994.52	1987.03	1987.03	0	72	5	
		TREGNDLYHEMIESGVINLK			+3	773.39	2317.14	2317.14	0	58	1	
		TVLIMELINNVAK		+2	729.43	1456.84	1456.83	0.01	86	6		
		DQEGQDVLLFIDNIFR			+2	961.49	1920.97	1920.96	0.01	101	7	
		IGLFGGAGVGKTVLIMELINNVAK				+3	805.47	2413.39	2413.38	0.01	53	2
		SLQDIIAILGMDELSEEDKLTVSR				+3	892.47	2674.39	2674.37	0.02	89	4

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
811.	IPI00209300		Y	Y	0.09	3	2	4	4	17		
*Des:	Density-enhanced phosphatase-1 precursor											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	2	1.85%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		NTEVGNEVPGQK		+2	3.365	0.446	0.9989	2				
		YAAEIAENR		+2	3.604	0.460	0.9997	2				
	MASCOT:(PepMatched Observed.Hits Coverage)					4	3	4.44%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VTIYSQAADGTEGQPGNK			+2	918.45	1834.88	1834.87	0.01	102	2	
		FSGFEASHGPIK		+2	638.82	1275.63	1275.62	0.01	49	6		
		NNEVSFSQIKPK		+2	695.87	1389.73	1389.73	0	52	5		
		TGTFIAIDR		+2	497.28	992.54	992.53	0.01	63	18		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
812.	IPI00373722		Y	Y	0.09	1	2	2	2	2		
*Des:	PREDICTED: similar to RAN binding protein 5											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	3.39%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LVLEQVVTSIASVADTAEEK			+3	4.168	0.566	1.0000	2			
		QLALEVIVTLSETAAAMLR			+3	3.814	0.532	1.0000	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	3.39%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LVLEQVVTSIASVADTAEEK			+3	701.39	2101.14	2101.12	0.02	47	2	
		QLALEVIVTLSETAAAMLR			+3	677.05	2028.14	2028.13	0.01	58	1	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		

813.	IPI00367234		Y	Y	0.05	1	2	2	2	2		
*Des:	PREDICTED: similar to Expressed sequence AI314180											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	1.6%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TEALSVIELLLK		+2	3.777	0.224	0.9932	1				
		ELQLESLLGAFESLGK			+2	4.313	0.600	1.0000	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	1.6%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TEALSVIELLLK		+2	664.91	1327.80	1327.80	0	67	1		
		ELQLESLLGAFESLGK			+2	867.48	1732.95	1732.92	0.03	71	1	
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
814.	IPI00189212		Y	Y	0.32	2	4	4	5	5		
*Des:	PREDICTED: similar to hypothetical protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					4	2	12.92%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DIYDQGGEQAIK		+2	3.381	0.419	0.9996	1				
		LISQAYEVLSDPK		+2	3.314	0.423	0.9994	2				
		ILFHGEGDQEPELEPGDVIIVLDQK				+3	3.715	0.410	0.9993	1		
		NVVHQLSVTLEDLYNGITK			+3	3.611	0.342	0.9983	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					4	2	12.92%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		DIYDQGGEQAIK		+2	668.83	1335.64	1335.63	0.01	46	1		
		LISQAYEVLSDPK		+2	731.90	1461.78	1461.77	0.01	59	2		
		ILFHGEGDQEPELEPGDVIIVLDQK				+3	930.82	2789.43	2789.41	0.02	41	1
		NVVHQLSVTLEDLYNGITK			+3	715.05	2142.14	2142.13	0.01	47	2	
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
815.	IPI00209232		Y	Y	0.61	3	6	5	9	9		
*Des:	GMP reductase 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					6	4	27.06%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		STCTYVGAAK		+2	3.043	0.535	1.0000	3				
		MSLILEAVPQVK		+2	3.967	0.489	1.0000	3				
		TVEVPYKGDVENTILDILGGLR			+3	4.542	0.432	1.0000	4			
		HAGGVAEYR		+2	2.333	0.485	0.9985	5				
		VGVGPGSVCTTR		+2	3.315	0.481	0.9996	8				
		TKTGVGYPQLSAVIECADSAHGLK				+3	5.622	0.531	1.0000	1		
	MASCOT:(PepMatched Observed.Hits Coverage)					5	4	20.51%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		STCTYVGAAK		+2	501.7241	1001.4337	999.4695	1.96	43	6		
		HAGGVAEYR		+2	480.2398	958.4651	958.4620	0	47	5		
		MSLILEAVPQVK		+2	664.3912	1326.7678	1326.7581	0.01	72	2		
		VGVGPGSVCTTR		+2	566.7957	1131.5769	1131.5706	0.01	84	5		
		TKTGVGYPQLSAVIECADSAHGLK				+3	815.7589	2444.2547	2444.2369	0.02	83	1
No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										

816.	IPI00324986		Y	Y	0.2	1	3	3	11	20		
*Des:	Rab GDP dissociation inhibitor alpha											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	10.54%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		TFEGVDPQTTSMR		+2	3.100	0.213	0.9741	1				
		FQLLEGPPESMGR		+2	2.865	0.332	0.9926	1				
		SPYLYPLYGLGELPQGFAR			+2	6.059	0.666	1.0000	9			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	10.54%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		TFEGVDPQTTSMR		+2	734.8456	1467.6767	1467.6664	0.01	52	2		
		FQLLEGPPESMGR		+2	730.8682	1459.7218	1459.7129	0.01	46	1		
		SPYLYPLYGLGELPQGFAR			+2	1071.0686	2140.1227	2140.0992	0.02	106	23	

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
817.	IPI00364904		Y	Y	0.06	2	2	2	2	13		
*Des:	PREDICTED: kinesin family member 5B											
	SEQUEST:(PepMatched Observed.Hits Coverage)					2	1	3.16%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		DQDNMQAELNR		+2	3.344	0.318	0.9993	1				
		QLDDKDEEINQQSQLVEK			+3	3.980	0.272	0.9988	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	3.46%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		KSAEVDSDDTGGSAAQKQK			+3	641.3102	1920.9089	1920.9024	0.01	81	2	
		HVAVTNMNEHSSR		+2	741.3511	1480.6876	1480.6841	0	69	14		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
818.	IPI00372924		N	Y	0.1	1	0	2	0	5		
*Des:	Cytokeratin 19											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	5.6%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		ALEQANGELEVK		+2	651.3420	1300.6695	1299.6670	1	34	2		
		LASYLDKVR		+2	532.8174	1063.6203	1063.6026	0.02	59	4		

No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
819.	IPI00231690		Y	Y	0.82	3	3	3	6	3		
*Des:	Cysteine and glycine-rich protein 1											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	4	17.34%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		NLDSTTVAVHGEEIYCK			+2	4.998	0.619	1.0000	2			
		GFGFGQGAGALVHS			+2	2.951	0.456	0.9945	3			
		GFGFGQGAGALVHSE			+2	3.966	0.477	1.0000	6			
	MASCOT:(PepMatched Observed.Hits Coverage)					3	1	28.06%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		GYGYGQGAGTLSMDK			+2	752.84	1503.67	1503.67	0	68	1	
		GLESTTLADKDGEIYCKGCYAK				+3	788.70	2363.08	2364.10	-1.01	43	1
		GFGFGQGAGALVHSE			+2	717.35	1432.68	1432.67	0.01	71	1	

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No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
820.        IPI00198978             Y           Y           0.26        1           2           3           3           4
*Des:       Proteasome 26S non-ATPase subunit 12
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           8.4%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        EWDLLNENIMLLSK +2       3.239       0.355       0.9977      1
                        MAQLLDLSVDESEAFLSNLVVNK             +3          5.888       0.442       0.9999      2
            MASCOT:(PepMatched Observed.Hits Coverage)      3           1           10.77%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        LNSLMSLVNK  +2          559.82      1117.62     1117.62     0           54          1
                        EWDLLNENIMLLSK +2       859.45      1716.88     1716.88     0           43          1
                        MAQLLDLSVDESEAFLSNLVVNK             +3          845.77      2534.30     2534.29     0.01        80          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
821.        IPI00231765             N           Y           0.13        1           0           3           0           8
*Des:       Splice Isoform 1 of Reticulon 4
            SEQUEST:(PepMatched Observed.Hits Coverage)
            MASCOT:(PepMatched Observed.Hits Coverage)      3           1           4.14%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        GPLPAAPPAAPER +2        622.35      1242.68     1242.67     0.01        47          4
                        YSNSALGHVNSTIK +2       745.89      1489.77     1489.75     0.02        58          1
                        SPAAPAPSLPPAAAVLPSK     +2          871.50      1740.99     1740.98     0.01        73          6

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
822.        IPI00189148             Y           Y           0.61        4           6           4           27          15
*Des:       Serine (Or cysteine) proteinase inhibitor, clade B (Ovalbumin), member 6
            SEQUEST:(PepMatched Observed.Hits Coverage)     6           9           26.68%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
                        KFYEAEMEELDFKGDTEQSR    +3          5.405       0.515       1.0000      2
                        TEEKPVQMMFMK +2         3.280       0.244       0.9924      2
                        MTYIGEIFTK  +2          2.940       0.380       0.9989      1
                        LDMLDEEEVEVFLPR         +2          2.951       0.256       0.9798      2
                        FLADHPFLFFIQHVK +3      3.946       0.319       0.9997      4
                        ILLLPYAGNELNMIIMLPDEHIELK           +3          4.368       0.467       1.0000      4
            MASCOT:(PepMatched Observed.Hits Coverage)      4           7           14.24%
                        Seq         Charge      ObservedMS              ExpectedMS              CalculatedMS                        Pepscore PepHits
                        LGMTDAFMEGR +2          614.28      1226.55     1226.54     0.01        65          2
                        GMTASQMVQTLSLDK         +2          805.41      1608.80     1608.79     0.01        78          1
                        MTYIGEIFTK  +2          601.81      1201.61     1201.61     0           49          5
                        FLADHPFLFFIQHVK +3      620.34      1858.01     1857.99     0.02        48          2

No.         Protein     Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
823.        IPI00205023             Y           N           0.07        1           2           0           2           0
*Des:       cGMP-inhibited 3',5'-cyclic phosphodiesterase B
            SEQUEST:(PepMatched Observed.Hits Coverage)     2           1           1.33%
                        Seq         Charge      Xcor        Delta       Probility   PepHits
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                    FLVIEAILATDLKK  +2        3.816     0.382     0.9992    2
                    FLVIEAILATDLK   +2        3.961     0.503     0.9999    1
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
824.      IPI00231694         Y         N         0.11      1         2         0         2         0
*Des:     Xanthine dehydrogenase/oxidase
          SEQUEST:(PepMatched Observed.Hits Coverage) 2         1         2.36%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    IPAFGSIPIEFR    +2        3.545     0.475     0.9998    1
                    TLLRPEEILLSIEIPYSK        +3        3.485     0.383     0.9997    2
          MASCOT:(PepMatched Observed.Hits Coverage)

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
825.      IPI00231767         Y         Y         0.65      2         4         4         13        34
*Des:     Triosephosphate isomerase
          SEQUEST:(PepMatched Observed.Hits Coverage) 4         3         24.9%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    RHIFGESDELIGQK  +3        4.390     0.368     0.9999    3
                    VTNGAFTGEISPGMIK          +2        4.516     0.500     1.0000    5
                    DLGATWVVLGHSER            +2        4.350     0.596     1.0000    4
                    VVLAYEPVWAIGTGK           +2        4.428     0.551     1.0000    5
          MASCOT:(PepMatched Observed.Hits Coverage)    4         2         24.9%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    RHIFGESDELIGQK  +3        543.62    1627.84   1627.83   0.01      57        6
                    DLGATWVVLGHSER            +2        770.40    1538.79   1538.78   0.01      86        4
                    VTNGAFTGEISPGMIK          +2        811.91    1621.81   1620.82   0.99      82        5
                    VVLAYEPVWAIGTGK           +2        801.95    1601.89   1601.88   0.01      85        28

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
826.      IPI00373587         Y         Y         1.57      1         5         4         20        16
*Des:     PREDICTED: similar to Protein phosphatase 2A, regulatory subunit B (PR 53)
          SEQUEST:(PepMatched Observed.Hits Coverage) 5         1         22.44%
                    Seq       Charge    Xcor      Delta     Probility PepHits
                    WIDETPPVDQPSR   +2        4.011     0.536     1.0000    5
                    VDDQVAIVFK      +2        2.974     0.215     0.9842    5
                    LVALLDTLDR      +2        3.607     0.465     0.9998    20
                    TGPFAEHSNQLWNISAVPSWSK              +3        4.242     0.414     0.9998    3
                    SQAYADYIGFILTLNEGVK       +2        6.032     0.525     1.0000    2
          MASCOT:(PepMatched Observed.Hits Coverage)    4         1         19.31%
                    Seq       Charge    ObservedMS          ExpectedMS          CalculatedMS                  Pepscore  PepHits
                    WIDETPPVDQPSR   +2        770.38    1538.75   1538.74   0.01      71        5
                    LVALLDTLDR      +2        564.84    1127.66   1127.65   0.01      70        22
                    TGPFAEHSNQLWNISAVPSWSK              +3        819.41    2455.22   2455.19   0.03      59        3
                    SQAYADYIGFILTLNEGVK       +3        701.37    2101.09   2101.07   0.02      48        1

No.       Protein   Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
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827.    IPI00211512     N       Y       0.32    2       0       6       0       26
*Des:   Actin-related protein 2/3 complex subunit 1B
        SEQUEST:(PepMatched Observed.Hits Coverage)
        MASCOT:(PepMatched Observed.Hits Coverage)      6       3       22.19%
                Seq     Charge  ObservedMS      ExpectedMS      CalculatedMS            Pepscore PepHits
                EVEERPAPTPWGSK+2        791.90  1581.79 1581.78 0.01    57      3
                ASSEGGAATGAGLDSLHK      +2      814.90  1627.79 1627.78 0.01    72      5
                NSVSQISVLSGGK   +2      638.35  1274.69 1274.68 0.01    88      10
                IFSAYIK +2      420.72  839.42  840.47  -1.04   53      1
                EHNGQVTGIDWAPESNR       +2      955.45  1908.89 1908.87 0.02    95      10
                TWKPTLVILR      +3      409.93  1226.76 1225.75 1.01    62      14

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
828.    IPI00212314     Y       N       0.42    3       9       0       16      0
*Des:   Moesin
        SEQUEST:(PepMatched Observed.Hits Coverage)     9       5       16.89%
                Seq     Charge  Xcor    Delta   Probility       PepHits
                FYPEDVSEELIQDITQR       +3      4.442   0.483   1.0000  3
                AKFYPEDVSEELIQDITQR     +3      3.712   0.368   0.9997  1
                ERQEAEEAKEALLQASR       +3      3.552   0.363   0.9997  1
                IGFPWSEIR       +2      3.023   0.322   0.9971  4
                KTTNDMIHAENMR   +2      4.643   0.623   1.0000  3
                KPDTIEVQQMK     +2      3.367   0.362   0.9986  1
                SGYLAGDKLLPQR   +2      3.358   0.462   0.9977  6
                RKPDTIEVQQMK    +3      3.295   0.362   0.9999  5
                VLEQHKLNK       +2      2.842   0.301   0.9743  2
        MASCOT:(PepMatched Observed.Hits Coverage)

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
829.    IPI00362229     Y       N       0.19    1       2       0       3       0
*Des:   42 kDa protein
        SEQUEST:(PepMatched Observed.Hits Coverage)     2       1       9.39%
                Seq     Charge  Xcor    Delta   Probility       PepHits
                TLFSNIVLSGGSTLFK        +2      5.104   0.605   1.0000  2
                LYSTWIGGSILASLDTFK      +2      3.230   0.247   0.9842  1
        MASCOT:(PepMatched Observed.Hits Coverage)

No.     Protein Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)
830.    IPI00230897     Y       Y       1       5       4       7       13      28
*Des:   Hemoglobin beta chain, major-form
        SEQUEST:(PepMatched Observed.Hits Coverage)     4       7       50.33%
                Seq     Charge  Xcor    Delta   Probility       PepHits
                VNPDDVGGEALGR   +2      4.499   0.505   1.0000  3
                YFDSFGDLSSASAIMGNPK     +2      6.193   0.575   1.0000  4
                GTFAHLSELHCDKLHVDPENFR          +3      4.757   0.573   1.0000  2
                VHLTDAEKAAVNGLWGK       +3      3.249   0.477   1.0000  2
        MASCOT:(PepMatched Observed.Hits Coverage)      7       7       53.69%
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Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
LHVDPENFR	+2	563.8232	1125.6318	1125.5567	0.08	51	1
KVINAFNDGLK	+2	609.8846	1217.7546	1217.6768	0.08	41	1
VNPDDVGGEALGR	+2	649.8675	1297.7204	1297.6262	0.09	48	4
YFDSFGDLSSASAIMGNPK	+2	1004.0267	2006.0388	2005.9091	0.13	90	1
VINAFNDGLK	+2	545.8290	1089.6434	1089.5818	0.06	44	5
LLVVYPWTQR	+2	637.8884	1273.7622	1273.7183	0.04	47	31
VVAGVASALAHK	+2	561.8705	1121.7264	1121.6556	0.07	60	10

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
831.	IPI00191354	Y	N	0.45	3	6	0	15	0

*Des: 33 kDa protein

SEQUEST:(PepMatched Observed.Hits Coverage) 6 6 22.83%

Seq	Charge	Xcor	Delta	Probility	PepHits
MLDQTLLDLNE	+2	4.021	0.517	1.0000	5
TIDDLEDKLK	+2	3.255	0.308	0.9870	7
MLDQTLLDLNEM	+2	3.442	0.366	0.9986	4
KLVIIEGDLER	+3	2.829	0.343	0.9996	3
ALKDEEKMELQEIQLK	+2	5.286	0.499	1.0000	4
ILTDKLKEAETR	+2	3.740	0.446	0.9987	3

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
832.	IPI00212249	Y	N	0.09	1	2	0	4	0

*Des: PREDICTED: similar to pyruvate kinase 3

SEQUEST:(PepMatched Observed.Hits Coverage) 2 1 3.57%

Seq	Charge	Xcor	Delta	Probility	PepHits
ITLPVDFVTADKFDENAK	+2	4.886	0.540	1.0000	4
AGGFLMKK	+2	2.767	0.260	0.9878	2

MASCOT:(PepMatched Observed.Hits Coverage)

No.	Protein	Matched (SEQUEST	MASCOT)	emPAI	Strategy.Hits	PepMatched(SEQUEST	MASCOT)	SpectraMatched(SEQUEST	MASCOT)
833.	IPI00200013	Y	Y	0.99	2	3	7	6	24

*Des: PREDICTED: cAMP-dependent protein kinase catalytic subunit alpha

SEQUEST:(PepMatched Observed.Hits Coverage) 3 1 15.68%

Seq	Charge	Xcor	Delta	Probility	PepHits
KWETPSQNTAQLDHFDR	+3	4.812	0.446	1.0000	2
DLKPENLLIDQQGYIQVTDFGFAK	+3	7.422	0.648	1.0000	3
ILQAVNFPFLVK	+2	4.182	0.302	0.9991	2

MASCOT:(PepMatched Observed.Hits Coverage) 7 2 31.65%

Seq	Charge	ObservedMS	ExpectedMS	CalculatedMS		Pepscore	PepHits
TLGTGSFGR	+2	448.24	894.46	894.46	0	45	12
KWETPSQNTAQLDHFDR	+3	691.67	2071.99	2071.97	0.02	55	2
NLLQVDLTK	+2	522.31	1042.61	1042.60	0.01	48	1
ILQAVNFPFLVK	+2	694.92	1387.83	1387.82	0.01	71	4
DLKPENLLIDQQGYIQVTDFGFAK	+3	918.15	2751.43	2751.41	0.02	58	6
WFATTDWIAIYQR	+2	835.93	1669.84	1669.83	0.01	84	4

		DNSNLYMVMEYVPGGEMFSHLR				+3	863.73	2588.17	2588.15	0.02	44	8

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
834.	IPI00476644		N	Y	0.77	1	0	5	0	9		
*Des:	50 kDa protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)											
	MASCOT:(PepMatched Observed.Hits Coverage)					5	1	20.72%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		VVQQSVLEVDER		+2	700.87	1399.73	1399.73	0	73	1		
		IFSTSADLSELSAVAR			+2	833.94	1665.86	1665.86	0	74	2	
		LILVDYILFK		+2	618.88	1235.75	1235.75	0	59	4		
		HDGNVIFSPFGLSVAMVNLMLGAK				+3	839.77	2516.30	2516.29	0.01	51	2
		VQVENGLNLQALSQAGPLILPALFK				+3	878.51	2632.50	2632.50	0	56	2

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
835.	IPI00203358		Y	N	0.26	2	5	0	11	0		
*Des:	Splice Isoform Gamma-1 of Serine/threonine protein phosphatase PP1-gamma catalytic subunit											
	SEQUEST:(PepMatched Observed.Hits Coverage)					5	2	23.1%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		AHQVVEDGYEFFAK		+3	3.998	0.560	1.0000	2				
		LNIDSIIQR		+2	2.743	0.177	0.9531	2				
		YPENFFLLR		+2	2.702	0.399	0.9983	2				
		LFEYGGFPPESNYLFLGDYVDR				+3	5.890	0.513	1.0000	4		
		EIFLSQPILLELEAPLK			+2	4.949	0.520	1.0000	3			
	MASCOT:(PepMatched Observed.Hits Coverage)											

No.	Protein	Matched (SEQUEST MASCOT) emPAI Strategy.Hits PepMatched(SEQUEST MASCOT) SpectraMatched(SEQUEST MASCOT)										
836.	IPI00190557		Y	Y	0.59	4	10	8	21	16		
*Des:	B-cell receptor-associated protein 37											
	SEQUEST:(PepMatched Observed.Hits Coverage)					10	4	48.02%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LGLDYEER		+2	2.780	0.497	0.9995	3				
		VLSRPNAQELPSMYQR			+2	4.281	0.415	0.9995	2			
		FNASQLITQR		+2	3.550	0.359	0.9988	2				
		LLLGAGAVAYGVR		+2	4.513	0.486	0.9999	1				
		DLQMVNISLR		+2	2.853	0.246	0.9773	2				
		IGGVQQDTILAEGLHFR			+3	5.074	0.532	1.0000	3			
		IVQAEGEAEAAK		+2	3.815	0.507	0.9998	1				
		IYLTADNLVLNLQDESFTR			+2	5.646	0.595	1.0000	3			
		IPWFQYPIIYDIR		+2	4.146	0.496	0.9998	4				
		DFSLILDDVAITELSFSR			+2	3.612	0.512	0.9997	1			
	MASCOT:(PepMatched Observed.Hits Coverage)					8	4	34.53%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		LGLDYEER		+2	497.75	993.48	993.48	0	54	4		
		IVQAEGEAEAAK		+2	608.32	1214.62	1214.61	0.01	72	1		
		VLSRPNAQELPSMYQR			+2	944.99	1887.97	1887.96	0.01	42	2	
		AQVSLLIR		+2	451.27	900.53	898.56	1.97	42	3		

		FNASQLITQR		+2	589.32	1176.63	1176.63	0	55	3		
		LLLGAGAVAYGVR		+2	630.38	1258.74	1258.74	0	76	1		
		IGGVQQDTILAEGLHFR			+2	927.50	1852.99	1852.98	0.01	87	3	
		IPWFQYPIIYDIR		+2	862.46	1722.91	1722.91	0	49	4		
No.	Protein	Matched (SEQUEST MASCOT)			emPAI	Strategy.Hits	PepMatched(SEQUEST MASCOT)			SpectraMatched(SEQUEST MASCOT)		
837.	IPI00190559		Y	Y	0.62	2	3	2	3	5		
*Des:	Bendless protein											
	SEQUEST:(PepMatched Observed.Hits Coverage)					3	1	39.35%				
		Seq	Charge	Xcor	Delta	Probility	PepHits					
		LLAEPVPGIKAEPDESNAR			+2	4.020	0.671	1.0000	1			
		SNEAQAIETAR		+2	3.471	0.549	0.9966	1				
		TVLLSIQALLSAPNPDDPLANDVAEQWK				+3	4.556	0.628	0.9998	1		
	MASCOT:(PepMatched Observed.Hits Coverage)					2	1	15.48%				
		Seq	Charge	ObservedMS		ExpectedMS		CalculatedMS			Pepscore	PepHits
		SNEAQAIETAR		+2	595.2975	1188.5804	1188.5734	0.01	54	4		
		IYHPNVDKLGR		+2	656.3666	1310.7186	1310.7095	0.01	41	2		