Mascot Search Results

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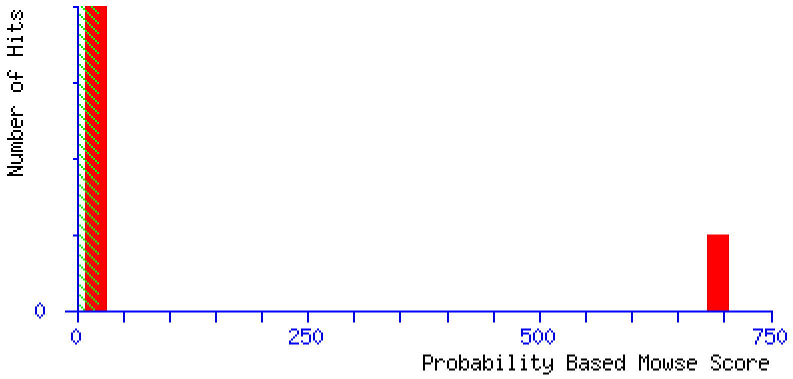
User           :  Julie Kadrmas; gel band: #38
Email          : 110223FT_JulieKadrmas_38
Search title   : NCBI Drosophila DB trypsin specific search: Oxidation (MHW)
MS data file   : C:\Documents and Settings\cnelson\Desktop\Merge Files_2011\February_2011\merge_110223FT_JulieKad
Database       : NCBInr  (5335292 sequences; 1845185051 residues)
Taxonomy       : Drosophila (fruit flies) (50248 sequences)
Timestamp      : 24 Feb 2011 at 19:10:11 GMT
Protein hits   : gi|18860063 Rpt3 CG16916-PA [Drosophila melanogaster]
                 gi|3426089  polyprotein [Drosophila melanogaster]
                 gi|11323019 pol [Drosophila melanogaster]
```

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 23 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

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Significance threshold p< 0.05 Max. number of hits AUTO

Standard scoring ● MudPIT scoring ○ Ions score or expect cut-off 20 Show sub-sets 0

Show pop-ups ○ Suppress pop-ups ● Sort unassigned Decreasing Score Require bold red ☑

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. gi|18860063 **Mass:** 46969 **Score:** 693 **Queries matched:** 24 **emPAI:** 3.77

Rpt3 CG16916-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1366	706.4517	705.4444	705.4425	2.68	0	21	0.03	1	R.YIVLAK.D
☑	1471	396.2069	790.3993	790.3973	2.47	0	21	0.18	1	K.YLGEGPR.M
☑	1600	469.7492	937.4838	937.4804	3.62	1	26	0.028	1	R.MVRDVFR.L + Oxidation (M)
☑	1621	496.7754	991.5362	991.5339	2.35	0	59	1.1e-005	1	R.VVGSEFVQK.Y
☑	1624	995.5785	994.5712	994.5699	1.29	0	(30)	0.0089	1	R.LVFSTITSK.M
☑	1625	498.2930	994.5714	994.5699	1.52	0	45	0.00025	1	R.LVFSTITSK.M
☑	1663	576.3441	1150.6737	1150.6710	2.38	1	36	0.0012	1	K.RLVFSTITSK.M
☑	1672	613.3465	1224.6785	1224.6754	2.53	1	49	9.8e-005	1	R.YIVLAKDFEK.G
☑	1673	409.2339	1224.6798	1224.6754	3.62	1	(23)	0.028	1	R.YIVLAKDFEK.G
☑	1681	424.2481	1269.7223	1269.7193	2.36	2	31	0.0056	1	R.KIEFPLPDRR.Q
☑	1686	437.5707	1309.6902	1309.6891	0.83	0	(37)	0.0028	1	K.AVAHHTTASFIR.V
☑	1687	655.8548	1309.6951	1309.6891	4.57	0	49	0.00016	1	K.AVAHHTTASFIR.V
☑	1694	701.3615	1400.7084	1400.7048	2.59	1	(35)	0.004	1	K.EYLHAQEEVKR.I
☑	1695	467.9104	1400.7095	1400.7048	3.37	1	44	0.00059	1	K.EYLHAQEEVKR.I
☑	1698	498.2438	1491.7097	1491.7066	2.05	1	36	0.0029	1	R.FDAQTGADREVQR.I
☑	1699	746.8630	1491.7114	1491.7066	3.21	1	(26)	0.03	1	R.FDAQTGADREVQR.I
☑	1705	824.9144	1647.8142	1647.8077	3.96	2	31	0.016	1	K.RFDAQTGADREVQR.I
☑	1711	844.9510	1687.8874	1687.8821	3.12	0	46	0.00042	1	R.EAVELPLTHFELYK.Q
☑	1739	675.3043	2022.8910	2022.8840	3.46	0	22	0.032	1	K.DAHSSLDELDMEDLYVR.Y + Oxidation (M
☑	1743	708.3394	2121.9963	2121.9888	3.54	0	29	0.016	1	K.MNLSEDVDLEEFVARPDK.I + Oxidation (
☑	1748	1085.0417	2168.0688	2168.0637	2.34	1	76	3.7e-007	1	K.TLEFIEVQEEYIKDEQR.N
☑	1749	723.6969	2168.0690	2168.0637	2.43	1	(47)	0.00034	1	K.TLEFIEVQEEYIKDEQR.N
	1752	1104.5680	2207.1214	2207.1144	3.17	0	71	1.5e-006	1	R.ILLELLNQMDGFDQTTNVK.V + Oxidation

☑

☑	1753	736.7148	2207.1225	2207.1144	3.69	0	(61)	1.5e-005	1	R.ILLELLNQMDGFDQTTNVK.V + Oxidation

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2. gi|3426089 **Mass:** 177601 **Score:** 31 **Queries matched:** 5 **emPAI:** 0.02
polyprotein [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1295	672.4048	671.3975	671.3966	1.27	0	(27)	0.028	1	K.TVSLPR.L
☑	1296	672.4049	671.3976	671.3966	1.42	0	31	0.01	1	K.TVSLPR.L
☑	1297	672.4050	671.3977	671.3966	1.60	0	(21)	0.12	1	K.TVSLPR.L
☑	1298	672.4052	671.3979	671.3966	1.95	0	(23)	0.077	1	K.TVSLPR.L
☑	1299	672.4055	671.3982	671.3966	2.37	0	(27)	0.027	1	K.TVSLPR.L

Proteins matching the same set of peptides:

gi|21214752 **Mass:** 206214 **Score:** 31 **Queries matched:** 5
gag-pol polyprotein precursor; hypothetical protein [Drosophila melanogaster]
gi|25009978 **Mass:** 83774 **Score:** 31 **Queries matched:** 5
GH06606p [Drosophila melanogaster]

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3. gi|11323019 **Mass:** 139125 **Score:** 23 **Queries matched:** 1
pol [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1520	423.2277	844.4409	844.4443	-4.06	0	23	0.082	1	K.SPALWGSK.Q

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1473	791.4439	790.4366	790.4371	-0.65	1	19	0.33	1	QMLKQK + Oxidation (M)
☑	1525	423.7204	845.4263	845.4243	2.42	0	19	0.22	1	ALAEAESR
☑	1594	466.7462	931.4778	931.4770	0.82	2	19	0.16	1	ACSPRRSR

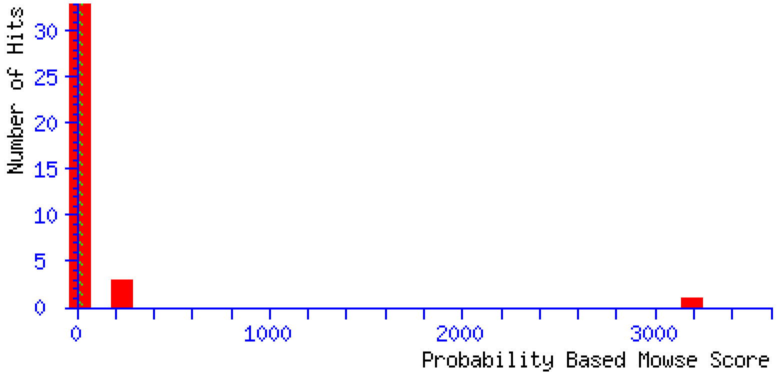
Mascot Search Results

User : **Julie Kadrmas; gel band: #40**
Email : **110223FT_JulieKadrmas_40**
Search title : **NCBI Drosophila DB trypsin specific search: Oxidation (MHW)**
MS data file : **C:\Documents and Settings\cnelson\Desktop\Merge Files_2011\February_2011\merge_110223FT_JulieKad**
Database : **NCBInr (5335292 sequences; 1845185051 residues)**
Taxonomy : **Drosophila (fruit flies) (50248 sequences)**
Timestamp : **24 Feb 2011 at 19:12:43 GMT**
Protein hits :

gi|45551086	ERp60 CG8983-PA, isoform A [Drosophila melanogaster]
gi|157570	gamma-tubulin
gi|158739	beta-1 tubulin
gi|20129399	Aldehyde dehydrogenase CG3752-PA [Drosophila melanogaster]
gi|6942155	putative cytoplasmic aminopeptidase [Drosophila melanogaster]
gi|1923274	Tpr homolog [Drosophila melanogaster]
gi|17944482	RH04336p [Drosophila melanogaster]
gi|17945899	RE40293p [Drosophila melanogaster]
gi|3426089	polyprotein [Drosophila melanogaster]
gi|304728	transcription factor
gi|19920576	CG3557-PA [Drosophila melanogaster]
gi|21429138	RE42508p [Drosophila melanogaster]
gi|9799628	Nut2 [Drosophila melanogaster]
gi|45550970	CG5792-PB, isoform B [Drosophila melanogaster]
gi|24644950	CG2767-PA [Drosophila melanogaster]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 24 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary ▾ | Help

Significance threshold p< 0.05 | Max. number of hits AUTO

Standard scoring ● MudPIT scoring ○ | Ions score or expect cut-off 20 | Show sub-sets 0

Show pop-ups ○ Suppress pop-ups ● | Sort unassigned Decreasing Score ▾ | Require bold red ☑

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. gi|45551086 **Mass:** 55336 **Score:** 3195 **Queries matched:** 146 **emPAI:** 159.92
ERp60 CG8983-PA, isoform A [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	636	487.3243	486.3170	486.3166	0.88	0	29	0.062	1	K.VAVAK.N
☑	637	487.3243	486.3170	486.3166	0.88	0	(24)	0.21	1	K.VAVAK.N
☑	638	487.3243	486.3171	486.3166	1.01	0	(29)	0.063	1	K.VAVAK.N
☑	1105	603.3359	602.3286	602.3275	1.78	0	30	0.03	1	K.EVLDK.Q
☑	1106	603.3367	602.3295	602.3275	3.19	0	(23)	0.17	1	K.EVLDK.Q
☑	1146	613.4402	612.4330	612.4323	1.16	0	27	0.022	1	K.IVLIR.A
	1147	613.4403	612.4331	612.4323	1.30	0	(23)	0.049	1	K.IVLIR.A

☑										
☑	1148	613.4406	612.4333	612.4323	1.65	0	(26)	0.03	1	K.IVLIR.A
☑	1187	623.3413	622.3340	622.3326	2.28	0	28	0.026	1	K.FLDTK.D
	1291	660.3943	659.3870	659.3854	2.53	0	(31)	0.013	4	R.TVAELK.K
	1292	660.3946	659.3874	659.3854	3.03	0	32	0.011	4	R.TVAELK.K
☑	1338	675.3682	674.3610	674.3599	1.59	0	(28)	0.039	1	R.EASGIAK.Y
☑	1339	675.3683	674.3610	674.3599	1.68	0	(26)	0.061	1	R.EASGIAK.Y
☑	1340	675.3689	674.3617	674.3599	2.63	0	(25)	0.1	1	R.EASGIAK.Y
☑	1341	675.3690	674.3617	674.3599	2.72	0	29	0.035	1	R.EASGIAK.Y
☑	1482	746.4059	745.3987	745.3970	2.25	1	29	0.03	1	R.DEKNLK.Y
☑	1503	379.2143	756.4140	756.4130	1.37	0	(36)	0.0025	1	R.AQVGPASK.T
☑	1504	379.2143	756.4141	756.4130	1.45	0	51	9.6e-005	1	R.AQVGPASK.T
☑	1505	757.4215	756.4142	756.4130	1.56	0	(21)	0.08	1	R.AQVGPASK.T
☑	1506	757.4215	756.4142	756.4130	1.64	0	(34)	0.0042	1	R.AQVGPASK.T
☑	1507	379.2145	756.4145	756.4130	2.02	0	(48)	0.00018	1	R.AQVGPASK.T
☑	1508	757.4221	756.4148	756.4130	2.37	0	(23)	0.05	1	R.AQVGPASK.T
☑	1524	383.7147	765.4149	765.4133	2.10	0	(26)	0.019	1	R.APHLSNK.F
☑	1525	383.7148	765.4150	765.4133	2.14	0	34	0.0031	1	R.APHLSNK.F
☑	1526	766.4226	765.4153	765.4133	2.64	0	(24)	0.03	1	R.APHLSNK.F
☑	1555	394.7482	787.4818	787.4803	1.85	1	29	0.014	1	R.TVAELKK.F
	1556	394.7483	787.4820	787.4803	2.09	1	(20)	0.12	2	R.TVAELKK.F
☑	1558	394.7484	787.4823	787.4803	2.54	1	(28)	0.019	1	R.TVAELKK.F
☑	1559	394.7485	787.4825	787.4803	2.70	1	(28)	0.017	1	R.TVAELKK.F
☑	1560	788.4915	787.4842	787.4803	4.89	1	(21)	0.085	1	R.TVAELKK.F
☑	1579	791.4162	790.4089	790.4072	2.12	0	(29)	0.02	1	K.EATTELK.G
☑	1580	791.4162	790.4090	790.4072	2.18	0	(21)	0.15	1	K.EATTELK.G
☑	1581	396.2118	790.4091	790.4072	2.36	0	31	0.013	1	K.EATTELK.G
☑	1586	398.6911	795.3676	795.3664	1.57	0	25	0.021	1	K.GTNYWR.N
☑	1589	399.2061	796.3976	796.3967	1.23	0	25	0.02	1	K.FESSSIK.F
☑	1593	799.3848	798.3775	798.3759	1.94	0	31	0.0036	1	K.DDDPPIK.L
☑	1674	424.7482	847.4818	847.4803	1.80	0	28	0.015	1	R.LKPEYAK.A
☑	1725	433.2195	864.4244	864.4229	1.69	0	36	0.0035	1	R.EVDDFLK.Y
☑	1871	502.7991	1003.5837	1003.5814	2.25	1	(27)	0.017	1	K.RLKPEYAK.A
	1872	502.7998	1003.5851	1003.5814	3.68	1	33	0.0046	1	K.RLKPEYAK.A

☑										
☑	1968	557.7924	1113.5702	1113.5706	-0.41	0	(29)	0.016	1	K.YSVSGYPTLK.I
☑	1969	1114.5789	1113.5716	1113.5706	0.87	0	(32)	0.0082	1	K.YSVSGYPTLK.I
☑	1970	557.7931	1113.5717	1113.5706	0.97	0	50	0.00014	1	K.YSVSGYPTLK.I
☑	1971	557.7944	1113.5743	1113.5706	3.27	0	(39)	0.0016	1	K.YSVSGYPTLK.I
☑	1972	557.7946	1113.5747	1113.5706	3.65	0	(28)	0.02	1	K.YSVSGYPTLK.I
☑	1982	565.3100	1128.6054	1128.6026	2.48	0	55	4.9e-005	1	K.LQDEDVAIVK.M
☑	1988	571.2880	1140.5615	1140.5597	1.57	1	32	0.0074	1	R.EASGIAKYMR.A + Oxidation (M)
☑	2007	389.2011	1164.5813	1164.5788	2.13	0	(21)	0.1	1	K.ENFHGLVGHR.T
☑	2008	583.2981	1164.5816	1164.5788	2.35	0	49	0.00019	1	K.ENFHGLVGHR.T
☑	2032	603.3402	1204.6658	1204.6645	1.10	0	(35)	0.0045	1	R.GFPTLFWLPK.D
☑	2034	603.3405	1204.6665	1204.6645	1.66	0	36	0.0029	1	R.GFPTLFWLPK.D
☑	2044	611.3376	1220.6607	1220.6594	1.08	0	(27)	0.034	1	R.GFPTLFWLPK.D + Oxidation (HW)
☑	2045	611.3381	1220.6617	1220.6594	1.90	0	(26)	0.034	1	R.GFPTLFWLPK.D + Oxidation (HW)
☑	2046	611.3383	1220.6620	1220.6594	2.11	0	(26)	0.034	1	R.GFPTLFWLPK.D + Oxidation (HW)
☑	2080	422.8834	1265.6283	1265.6252	2.48	1	(31)	0.019	1	K.EATTELKGFDR.S
☑	2081	633.8216	1265.6287	1265.6252	2.79	1	47	0.00044	1	K.EATTELKGFDR.S
☑	2087	424.5831	1270.7273	1270.7245	2.24	1	(37)	0.0019	1	K.QGETDKIVLIR.A
☑	2088	636.3712	1270.7279	1270.7245	2.72	1	51	7.8e-005	1	K.QGETDKIVLIR.A
☑	2093	646.3444	1290.6742	1290.6707	2.70	0	53	8.9e-005	1	K.LSPIYEELAEK.L
☑	2099	651.8699	1301.7253	1301.7231	1.69	0	59	2e-005	1	K.LLANELEPYIK.S
☑	2100	651.8703	1301.7260	1301.7231	2.25	0	(47)	0.00025	1	K.LLANELEPYIK.S
☑	2101	1302.7347	1301.7275	1301.7231	3.39	0	(30)	0.0082	1	K.LLANELEPYIK.S
☑	2127	670.8601	1339.7057	1339.7023	2.52	1	51	0.00012	1	R.EVDDFLKYIAK.E
☑	2131	459.2345	1374.6818	1374.6779	2.78	1	(37)	0.0029	1	R.FGHSSEKEVLDK.Q
☑	2132	688.3488	1374.6831	1374.6779	3.75	1	56	4.6e-005	1	R.FGHSSEKEVLDK.Q
☑	2159	704.3120	1406.6095	1406.6062	2.35	0	(75)	1.5e-007	1	R.QDEVSQDYNGPR.E
☑	2160	704.3121	1406.6097	1406.6062	2.43	0	(77)	8.6e-008	1	R.QDEVSQDYNGPR.E
☑	2161	704.3125	1406.6105	1406.6062	3.04	0	81	3.7e-008	1	R.QDEVSQDYNGPR.E
☑	2168	470.9217	1409.7434	1409.7402	2.27	1	(34)	0.0047	1	K.AAEIVKDDDPPIK.L
☑	2169	470.9218	1409.7434	1409.7402	2.30	1	(33)	0.0053	1	K.AAEIVKDDDPPIK.L
☑	2170	705.8790	1409.7434	1409.7402	2.31	1	(35)	0.0034	1	K.AAEIVKDDDPPIK.L
☑	2171	705.8794	1409.7443	1409.7402	2.91	1	62	6.9e-006	1	K.AAEIVKDDDPPIK.L

☑	2175	710.3921	1418.7696	1418.7656	2.77	1	64	4.9e-006	1	K.KLSPIYEELAEK.L
☑	2178	712.3850	1422.7554	1422.7507	3.30	0	(85)	3.3e-008	1	K.EFVGQINFAIASK.D
☑	2179	712.3852	1422.7559	1422.7507	3.65	0	90	1.2e-008	1	K.EFVGQINFAIASK.D
☑	2230	760.4210	1518.8274	1518.8235	2.55	1	45	0.00039	1	R.GFPTLFWLPKDAK.N
☑	2235	766.8612	1531.7078	1531.7042	2.34	0	94	3.4e-009	1	K.FEGSSESDLSTFVK.E
☑	2236	766.8620	1531.7095	1531.7042	3.45	0	(72)	4.9e-007	1	K.FEGSSESDLSTFVK.E
☑	2237	766.8624	1531.7102	1531.7042	3.93	0	(50)	8.3e-005	1	K.FEGSSESDLSTFVK.E
☑	2243	515.6085	1543.8036	1543.7994	2.67	1	(21)	0.11	1	R.APHLSNKFESSSIK.F
☑	2244	772.9107	1543.8069	1543.7994	4.82	1	49	0.00022	1	R.APHLSNKFESSSIK.F
☑	2263	791.8500	1581.6854	1581.6835	1.20	0	(38)	0.00053	1	K.DTTLFGYFSDSDSK.L
☑	2264	791.8512	1581.6878	1581.6835	2.75	0	55	2.2e-005	1	K.DTTLFGYFSDSDSK.L
☑	2265	791.8518	1581.6890	1581.6835	3.48	0	(29)	0.01	1	K.DTTLFGYFSDSDSK.L
☑	2266	791.8523	1581.6901	1581.6835	4.17	0	(42)	0.00051	1	K.DTTLFGYFSDSDSK.L
☑	2298	559.2640	1674.7701	1674.7672	1.75	0	(39)	0.0013	1	K.MDATANDVPPEFNVR.G
☑	2299	838.3934	1674.7723	1674.7672	3.04	0	(40)	0.0011	1	K.MDATANDVPPEFNVR.G
☑	2300	838.3936	1674.7726	1674.7672	3.25	0	(57)	1.9e-005	1	K.MDATANDVPPEFNVR.G
☑	2301	838.3936	1674.7727	1674.7672	3.29	0	(82)	5.9e-008	1	K.MDATANDVPPEFNVR.G
☑	2309	846.3901	1690.7656	1690.7621	2.08	0	102	5.6e-010	1	K.MDATANDVPPEFNVR.G + Oxidation (M)
☑	2310	846.3905	1690.7665	1690.7621	2.58	0	(60)	8.1e-006	1	K.MDATANDVPPEFNVR.G + Oxidation (M)
☑	2311	846.3907	1690.7668	1690.7621	2.80	0	(59)	1e-005	1	K.MDATANDVPPEFNVR.G + Oxidation (M)
☑	2312	564.5964	1690.7673	1690.7621	3.08	0	(36)	0.0021	1	K.MDATANDVPPEFNVR.G + Oxidation (M)
☑	2313	846.3911	1690.7677	1690.7621	3.31	0	(81)	7.2e-008	1	K.MDATANDVPPEFNVR.G + Oxidation (M)
☑	2319	565.6227	1693.8464	1693.8424	2.38	2	35	0.0045	1	K.YRFGHSSEKEVLDK.Q
☑	2326	849.8990	1697.7834	1697.7784	2.90	0	61	9.7e-006	1	K.DEFSVENLQDFVEK.L
☑	2342	861.4851	1720.9557	1720.9512	2.64	1	45	0.00028	1	K.VAKEFVGQINFAIASK.D
☑	2343	574.6594	1720.9564	1720.9512	3.00	1	(40)	0.00071	1	K.VAKEFVGQINFAIASK.D
☑	2344	861.9870	1721.9595	1721.9563	1.85	2	(36)	0.0015	1	K.AAEIVKDDDPPIKLAK.V
☑	2345	574.9941	1721.9603	1721.9563	2.33	2	(47)	0.00013	1	K.AAEIVKDDDPPIKLAK.V
☑	2346	574.9941	1721.9605	1721.9563	2.43	2	(45)	0.00023	1	K.AAEIVKDDDPPIKLAK.V
☑	2347	861.9884	1721.9622	1721.9563	3.41	2	55	2.1e-005	1	K.AAEIVKDDDPPIKLAK.V
☑	2348	581.3102	1740.9087	1740.9046	2.35	2	(46)	0.00038	1	K.YIAKEATTELKGFDR.S
☑	2349	581.3104	1740.9094	1740.9046	2.77	2	54	5e-005	1	K.YIAKEATTELKGFDR.S
☑	2367	608.6283	1822.8631	1822.8598	1.78	1	(38)	0.0021	1	K.IFRQDEVSQDYNGPR.E

☑	2368	608.6288	1822.8647	1822.8598	2.68	1	(41)	0.0011	1	K.IFRQDEVSQDYNGPR.E
☑	2369	912.4398	1822.8651	1822.8598	2.92	1	(61)	1.1e-005	1	K.IFRQDEVSQDYNGPR.E
☑	2370	912.4403	1822.8660	1822.8598	3.39	1	63	6.5e-006	1	K.IFRQDEVSQDYNGPR.E
☑	2386	617.6690	1849.9851	1849.9785	3.56	1	(33)	0.0076	1	K.SEPIPESNDAPVKVAVAK.N
☑	2387	925.9999	1849.9853	1849.9785	3.65	1	88	2.6e-008	1	K.SEPIPESNDAPVKVAVAK.N
☑	2392	619.3565	1855.0477	1855.0415	3.36	2	50	5.7e-005	1	K.EVLDKQGETDKIVLIR.A
☑	2398	947.9589	1893.9032	1893.8996	1.87	1	64	8.1e-006	1	K.DTTLFGYFSDSDSKLAK.I
☑	2399	632.3086	1893.9040	1893.8996	2.28	1	(28)	0.032	1	K.DTTLFGYFSDSDSKLAK.I
☑	2440	678.6660	2032.9760	2032.9702	2.89	2	39	0.002	1	R.FGHSSEKEVLDKQGETDK.I
☑	2444	688.6591	2062.9554	2062.9556	-0.06	1	33	0.0071	1	R.QDEVSQDYNGPREASGIAK.Y
☑	2445	1033.0011	2063.9877	2063.9840	1.79	0	(89)	2e-008	1	K.DFQNPLITAYYSVDYQK.N
☑	2446	1033.0017	2063.9889	2063.9840	2.38	0	95	4.7e-009	1	K.DFQNPLITAYYSVDYQK.N
☑	2447	689.0041	2063.9905	2063.9840	3.16	0	(64)	5.8e-006	1	K.DFQNPLITAYYSVDYQK.N
☑	2457	725.3622	2173.0647	2173.0579	3.14	1	(50)	0.00019	1	K.YALKDEFSVENLQDFVEK.L
☑	2458	1087.5414	2173.0682	2173.0579	4.72	1	85	5.8e-008	1	K.YALKDEFSVENLQDFVEK.L
☑	2459	729.6779	2186.0119	2186.0056	2.91	1	(46)	0.00038	1	K.FLDTKDTTLFGYFSDSDSK.L
☑	2460	1094.0135	2186.0125	2186.0056	3.16	1	106	3.4e-010	1	K.FLDTKDTTLFGYFSDSDSK.L
☑	2461	729.6788	2186.0145	2186.0056	4.08	1	(21)	0.12	1	K.FLDTKDTTLFGYFSDSDSK.L
☑	2496	771.0404	2310.0994	2310.0903	3.92	1	47	0.00033	1	K.FESSSIKFEGSSESDLSTFVK.E
☑	2497	771.0408	2310.1007	2310.0903	4.48	1	(41)	0.00094	1	K.FESSSIKFEGSSESDLSTFVK.E
☑	2499	772.3745	2314.1015	2314.1005	0.43	2	34	0.0073	1	K.KFLDTKDTTLFGYFSDSDSK.L
☑	2504	801.4305	2401.2696	2401.2628	2.85	1	(50)	8.8e-005	1	K.LSPIYEELAEKLQDEDVAIVK.M
☑	2505	1201.6422	2401.2699	2401.2628	2.98	1	65	2.7e-006	1	K.LSPIYEELAEKLQDEDVAIVK.M
☑	2506	1202.5951	2403.1757	2403.1747	0.43	1	47	0.00039	1	K.DFQNPLITAYYSVDYQKNPK.G
☑	2507	1202.5988	2403.1830	2403.1747	3.48	1	(35)	0.0058	1	K.DFQNPLITAYYSVDYQKNPK.G
☑	2508	802.0683	2403.1831	2403.1747	3.50	1	(37)	0.0041	1	K.DFQNPLITAYYSVDYQKNPK.G
☑	2509	802.0685	2403.1836	2403.1747	3.73	1	(28)	0.029	1	K.DFQNPLITAYYSVDYQKNPK.G
☑	2513	827.4123	2479.2151	2479.2091	2.42	2	34	0.0079	1	K.IFRQDEVSQDYNGPREASGIAK.Y
☑	2516	1250.1217	2498.2289	2498.2217	2.89	2	(50)	0.00017	1	K.FLDTKDTTLFGYFSDSDSKLAK.I
☑	2517	833.7509	2498.2307	2498.2217	3.62	2	56	5.2e-005	1	K.FLDTKDTTLFGYFSDSDSKLAK.I
☑	2518	844.1299	2529.3680	2529.3577	4.06	2	55	3.1e-005	1	K.KLSPIYEELAEKLQDEDVAIVK.M
☑	2524	889.4711	2665.3916	2665.3850	2.46	1	(36)	0.0038	1	K.LLANELEPYIKSEPIPESNDAPVK.V
☑	2525	889.4717	2665.3933	2665.3850	3.12	1	39	0.0016	1	K.LLANELEPYIKSEPIPESNDAPVK.V

☑ 2534	908.4475	2722.3207	2722.3126	2.97	1	(42)	0.0011	1	R.TQDSVKDFQNPLITAYYSVDYQK.N
☑ 2535	1362.1676	2722.3207	2722.3126	2.97	1	50	0.00018	1	R.TQDSVKDFQNPLITAYYSVDYQK.N
☑ 2536	908.4482	2722.3226	2722.3126	3.67	1	(48)	0.00025	1	R.TQDSVKDFQNPLITAYYSVDYQK.N
☑ 2540	934.7944	2801.3613	2801.3542	2.54	1	(41)	0.0014	1	K.LQDEDVAIVKMDATANDVPPEFNVR.G + Oxid
☑ 2541	934.7952	2801.3637	2801.3542	3.39	1	44	0.00068	1	K.LQDEDVAIVKMDATANDVPPEFNVR.G + Oxid
☑ 2542	934.7963	2801.3672	2801.3542	4.63	1	(25)	0.059	1	K.LQDEDVAIVKMDATANDVPPEFNVR.G + Oxid
☑ 2545	1021.5118	3061.5135	3061.5033	3.35	2	83	1.1e-007	1	R.TQDSVKDFQNPLITAYYSVDYQKNPK.G
☑ 2546	1045.5743	3133.7010	3133.6910	3.19	2	59	5.3e-006	1	K.LLANELEPYIKSEPIPESNDAPVKVAVAK.N

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2. gi|157570 **Mass:** 53278 **Score:** 244 **Queries matched:** 5 **emPAI:** 0.27

gamma-tubulin

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1894	513.3047	1024.5949	1024.5917	3.13	0	37	0.00093	1	R.AVLLDLEPR.V
☑ 1895	513.3051	1024.5956	1024.5917	3.84	0	(32)	0.0034	1	R.AVLLDLEPR.V
☑ 2118	664.3521	1326.6896	1326.6853	3.23	0	71	7.5e-007	1	R.VINTIMGSVYSK.L + Oxidation (M)
☑ 2122	670.3494	1338.6842	1338.6819	1.68	0	45	0.00067	1	K.LYNPENVYLSK.H
☑ 2395	937.0079	1872.0013	1871.9953	3.20	0	90	1.3e-008	1	R.LTTAADSVVVLDNTALNR.I

Proteins matching the same set of peptides:

gi|3342456 **Mass:** 37046 **Score:** 244 **Queries matched:** 5

gamma-tubulin [Drosophila melanogaster]

gi|17136618 **Mass:** 53306 **Score:** 244 **Queries matched:** 5

gamma-Tubulin at 23C CG3157-PA [Drosophila melanogaster]

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3. gi|158739 **Mass:** 50119 **Score:** 222 **Queries matched:** 5 **emPAI:** 0.29

beta-1 tubulin

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1923	527.3098	1052.6051	1052.6019	3.06	0	42	0.00051	1	R.YLTVAAIFR.G
☑ 2062	623.3017	1244.5889	1244.5860	2.37	0	51	7.5e-005	1	R.ISEQFTAMFR.R + Oxidation (M)

☑	2275	809.4142	1616.8138	1616.8080	3.61	0	64	6.8e-006	1	R.AVLVDLEPGTMDSVR.S + Oxidation (M)
☑	2329	854.4365	1706.8584	1706.8549	2.06	0	24	0.069	1	R.ALTVPELTQQMFDAK.N + Oxidation (M)
☑	2425	662.6392	1984.8957	1984.8904	2.66	1	41	0.00078	1	R.MSMKEVDEQMLNIQNK.N + 3 Oxidation (M

Proteins matching the same set of peptides:

gi|24655737 **Mass:** 50115 **Score:** 222 **Queries matched:** 5
beta-Tubulin at 56D CG9277-PB, isoform B [Drosophila melanogaster]

gi|24655741 **Mass:** 51264 **Score:** 222 **Queries matched:** 5
beta-Tubulin at 56D CG9277-PA, isoform A [Drosophila melanogaster]

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4. gi|20129399 **Mass:** 56983 **Score:** 126 **Queries matched:** 2 **emPAI:** 0.12
Aldehyde dehydrogenase CG3752-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2250	778.3931	1554.7717	1554.7678	2.52	0	93	1e-008	1	R.ANNSEYGLAAAVFTK.D
☑	2357	597.2946	1788.8619	1788.8570	2.74	1	33	0.0064	1	R.TFVEDKIYDEFVER.S

Proteins matching the same set of peptides:

gi|68051705 **Mass:** 61886 **Score:** 126 **Queries matched:** 2
GH22814p [Drosophila melanogaster]

gi|125986975 **Mass:** 56964 **Score:** 126 **Queries matched:** 2
GA17661-PA [Drosophila pseudoobscura]

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5. gi|6942155 **Mass:** 60188 **Score:** 42 **Queries matched:** 1 **emPAI:** 0.05
putative cytoplasmic aminopeptidase [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1942	543.8117	1085.6089	1085.6081	0.79	0	42	0.00074	1	K.GAQETIALVGK.G

Proteins matching the same set of peptides:

gi|21357381 **Mass:** 60132 **Score:** 42 **Queries matched:** 1

granny smith CG7340-PB, isoform B [Drosophila melanogaster]
gi|24646410 **Mass:** 71134 **Score:** 42 **Queries matched:** 1
granny smith CG7340-PA, isoform A [Drosophila melanogaster]
gi|24646412 **Mass:** 62705 **Score:** 42 **Queries matched:** 1
granny smith CG7340-PC, isoform C [Drosophila melanogaster]
gi|25009916 **Mass:** 71132 **Score:** 42 **Queries matched:** 1
AT31511p [Drosophila melanogaster]
gi|125774513 **Mass:** 56357 **Score:** 42 **Queries matched:** 1
GA20276-PA [Drosophila pseudoobscura]

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6. gi|1923274 **Mass:** 262206 **Score:** 32 **Queries matched:** 1 **emPAI:** 0.01
Tpr homolog [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1422	**718.3640**	**717.3567**	**717.3544**	**3.19**	**0**	**32**	**0.012**	**1**	**R.EELAEK.V**

Proteins matching the same set of peptides:
gi|24652825 **Mass:** 262194 **Score:** 32 **Queries matched:** 1
Megator CG8274-PA [Drosophila melanogaster]

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7. gi|17944482 **Mass:** 56834 **Score:** 31 **Queries matched:** 2 **emPAI:** 0.06
RH04336p [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1996	**574.3413**	**1146.6680**	**1146.6648**	**2.76**	**0**	**(26)**	**0.0095**	**1**	**R.SFAQVEILLK.H**
☑	1997	**574.3420**	**1146.6695**	**1146.6648**	**4.04**	**0**	**31**	**0.0026**	**1**	**R.SFAQVEILLK.H**

Proteins matching the same set of peptides:
gi|24659664 **Mass:** 56825 **Score:** 31 **Queries matched:** 2
CG9953-PA [Drosophila melanogaster]

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8. gi|17945899 **Score:** 31 **Queries matched:** 1

RE40293p [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**ppm**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
☑	1214	637.3203	636.3131	636.3119	1.85	0	31	0.0065	1	K.DDFIK.T

Proteins matching the same set of peptides:

gi|24650758 **Score:** 31 **Queries matched:** 1
gi|24650760 **Score:** 31 **Queries matched:** 1
gi|24667151 **Score:** 31 **Queries matched:** 1
gi|24667155 **Score:** 31 **Queries matched:** 1
gi|125980730 **Score:** 31 **Queries matched:** 1

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9. gi|3426089 **Mass:** 177601 **Score:** 29 **Queries matched:** 5 **emPAI:** 0.02

polyprotein [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**ppm**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
☑	1327	672.4047	671.3974	671.3966	1.13	0	(25)	0.049	1	K.TVSLPR.L
☑	1328	672.4049	671.3976	671.3966	1.42	0	29	0.019	1	K.TVSLPR.L
☑	1329	672.4049	671.3976	671.3966	1.51	0	(29)	0.019	1	K.TVSLPR.L
☑	1331	672.4051	671.3978	671.3966	1.78	0	(22)	0.09	1	K.TVSLPR.L
☑	1333	672.4058	671.3985	671.3966	2.77	0	(24)	0.056	1	K.TVSLPR.L

Proteins matching the same set of peptides:

gi|21214752 **Mass:** 206214 **Score:** 29 **Queries matched:** 5
gag-pol polyprotein precursor; hypothetical protein [Drosophila melanogaster]
gi|25009978 **Mass:** 83774 **Score:** 29 **Queries matched:** 5
GH06606p [Drosophila melanogaster]

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10. gi|304728 **Score:** 28 **Queries matched:** 2

transcription factor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	569	475.2880	474.2807	474.2802	1.12	0	(25)	0.33	1	K.SGIAK.Q
☑	570	475.2881	474.2808	474.2802	1.27	0	28	0.15	1	K.SGIAK.Q

Proteins matching the same set of peptides:

gi|17737765 **Score:** 28 **Queries matched:** 2
gi|28572995 **Score:** 28 **Queries matched:** 2
gi|41616160 **Score:** 28 **Queries matched:** 2
gi|62472391 **Score:** 28 **Queries matched:** 2
gi|92109928 **Score:** 28 **Queries matched:** 2

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11. gi|19920576 **Mass:** 29241 **Score:** 26 **Queries matched:** 2 **emPAI:** 0.11
CG3557-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1991	572.3413	1142.6680	1142.6713	-2.85	1	(21)	0.094	1	K.WLWTRLIR.G
☑	1992	572.3413	1142.6681	1142.6713	-2.75	1	26	0.033	1	K.WLWTRLIR.G

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12. gi|21429138 **Mass:** 24766 **Score:** 26 **Queries matched:** 1 **emPAI:** 0.14
RE42508p [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1945	1091.5658	1090.5585	1090.5553	2.96	2	26	0.036	1	R.KMSLEDGRR.A

Proteins matching the same set of peptides:

gi|116007254 **Mass:** 21260 **Score:** 26 **Queries matched:** 1
Rab21 CG17515-PA, isoform A [Drosophila melanogaster]

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13. gi|9799628 **Score:** 25 **Queries matched:** 2
Nut2 [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1363	687.4418	686.4345	686.4326	2.69	1	(25)	0.072	1	K.IEGLKK.F
☑	1364	687.4433	686.4360	686.4326	4.95	1	25	0.064	1	K.IEGLKK.F

Proteins matching the same set of peptides:
gi|24665095 **Score:** 25 **Queries matched:** 2

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14. gi|45550970 **Mass:** 154737 **Score:** 25 **Queries matched:** 2 **emPAI:** 0.02
CG5792-PB, isoform B [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1717	432.7330	863.4514	863.4501	1.49	1	(24)	0.062	1	K.LEKFGDR.N
☑	1718	432.7330	863.4515	863.4501	1.56	1	25	0.049	1	K.LEKFGDR.N

Proteins matching the same set of peptides:
gi|90855623 **Mass:** 130026 **Score:** 25 **Queries matched:** 2
IP16022p [Drosophila melanogaster]

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15. gi|24644950 **Mass:** 36839 **Score:** 25 **Queries matched:** 1
CG2767-PA [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1914	523.2861	1044.5576	1044.5564	1.19	0	25	0.062	1	K.LSSLDQNIR.I

Peptide matches not assigned to protein hits: (no details means no match)

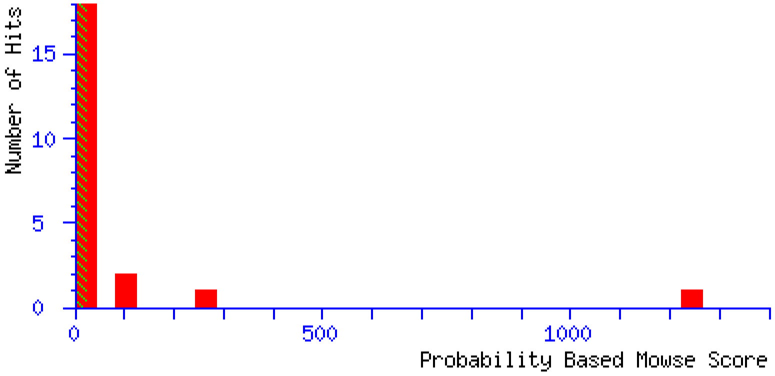
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1292	660.3946	659.3874	659.3854	3.05	0	43	0.00085	1	AEISLK
☑	1291	660.3943	659.3870	659.3854	2.55	0	38	0.0028	1	AEISLK
☑	1556	394.7483	787.4820	787.4803	2.11	1	28	0.017	1	LSALEKK
	1669	424.2139	846.4133	846.4157	-2.79	0	24	0.023	1	DPDLMLK + Oxidation (M)

Mascot Search Results

```
User            :  Julie Kadrmas; gel band: #63
Email           : 110223FT_JulieKadrmas_63
Search title    : NCBI Drosophila DB trypsin specific search: Oxidation (MHW)
MS data file    : C:\Documents and Settings\cnelson\Desktop\Merge Files_2011\February_2011\merge_110223FT_JulieKad
Database        : NCBInr  (5335292 sequences; 1845185051 residues)
Taxonomy        : Drosophila (fruit flies) (50248 sequences)
Timestamp       : 24 Feb 2011 at 19:14:32 GMT
Protein hits    : gi|17137738 Rpt1 CG1341-PA [Drosophila melanogaster]
                  gi|20129399 Aldehyde dehydrogenase CG3752-PA [Drosophila melanogaster]
                  gi|24643390 CG32528-PA [Drosophila melanogaster]
                  gi|386043   tubulin alpha-2 chain {internal fragment} [Drosophila melanogaster, CME W2 wing imag
                  gi|1699220  D-ERp60=protein disulphide isomerase isoform/multifunctional endoplasmic reticulum l
                  gi|7946     unnamed protein product [Drosophila melanogaster]
                  gi|45552677 CG33456-PA [Drosophila melanogaster]
                  gi|3426089  polyprotein [Drosophila melanogaster]
                  gi|17946230 RE57556p [Drosophila melanogaster]
                  gi|24644950 CG2767-PA [Drosophila melanogaster]
                  gi|24648138 CG11779-PA, isoform A [Drosophila melanogaster]
```

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 23 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary ▾ | Help

Significance threshold p< 0.05 | Max. number of hits AUTO

Standard scoring ● MudPIT scoring ○ | Ions score or expect cut-off 20 | Show sub-sets 0

Show pop-ups ○ Suppress pop-ups ● | Sort unassigned Decreasing Score ▾ | Require bold red ☑

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. gi|17137738 **Mass:** 48511 **Score:** 1244 **Queries matched:** 34 **emPAI:** 6.68

Rpt1 CG1341-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1621	646.3420	645.3347	645.3333	2.13	0	22	0.13	1	K.EQIEK.L
☑	2122	456.2190	910.4235	910.4218	1.83	0	30	0.0052	1	R.ELFEMAR.S + Oxidation (M)
☑	2123	456.2192	910.4238	910.4218	2.17	0	(20)	0.053	1	R.ELFEMAR.S + Oxidation (M)
☑	2124	456.2193	910.4241	910.4218	2.50	0	(23)	0.026	1	R.ELFEMAR.S + Oxidation (M)
☑	2158	481.2464	960.4783	960.4764	1.99	0	51	0.00017	1	K.SIEEDIQK.A
☑	2181	486.7908	971.5670	971.5651	1.91	0	52	0.00016	1	R.VIGSELVQK.Y
	2209	501.2860	1000.5575	1000.5553	2.23	0	40	0.0017	1	K.QVNELTGIK.E

☑										
☑	2255	539.7449	1077.4753	1077.4727	2.37	0	51	3e-005	1	M.PDYLGDDQR.K
☑	2260	544.2685	1086.5225	1086.5193	2.94	0	48	7.5e-005	1	K.IINADSDDPK.Y
☑	2277	557.3190	1112.6234	1112.6230	0.41	0	33	0.0044	1	K.FVNLGIEPPK.G
☑	2280	373.5493	1117.6260	1117.6244	1.48	1	(27)	0.018	1	R.DIRFDLLAR.L
☑	2281	559.8207	1117.6269	1117.6244	2.23	1	40	0.00097	1	R.DIRFDLLAR.L
☑	2291	571.8329	1141.6512	1141.6496	1.39	0	36	0.0055	1	K.GVLLFGPPGTGK.T
☑	2327	402.8639	1205.5698	1205.5677	1.81	1	(49)	0.00013	1	M.PDYLGDDQRK.V
☑	2328	603.7931	1205.5717	1205.5677	3.37	1	65	2.9e-006	1	M.PDYLGDDQRK.V
☑	2343	616.3266	1230.6387	1230.6343	3.56	0	55	4.1e-005	1	K.SLDEGDIELLK.T
☑	2344	616.7998	1231.5850	1231.5833	1.35	0	35	0.0038	1	K.VEFGLPDQDGR.S
☑	2352	630.3472	1258.6798	1258.6768	2.38	1	52	9.2e-005	1	K.SIEEDIQKAVK.Q
☑	2353	420.5673	1258.6800	1258.6768	2.54	1	(28)	0.026	1	K.SIEEDIQKAVK.Q
☑	2382	454.2341	1359.6806	1359.6783	1.68	1	(37)	0.0032	1	R.KVEFGLPDQDGR.S
☑	2383	680.8485	1359.6824	1359.6783	3.03	1	48	0.0002	1	R.KVEFGLPDQDGR.S
☑	2389	690.2971	1378.5797	1378.5750	3.43	0	81	4e-008	1	R.FDDGAGGDNEVQR.T
☑	2407	493.2814	1476.8224	1476.8188	2.47	2	51	4.4e-005	1	K.VATEKDFLEAVKK.V
☑	2412	768.9312	1535.8478	1535.8420	3.77	0	61	6.7e-006	1	K.QILQNEQPLQVAR.C
☑	2424	553.9866	1658.9381	1658.9355	1.53	1	29	0.0058	1	K.LREVVETPLLHPEK.F
☑	2432	852.9684	1703.9222	1703.9206	0.90	1	26	0.03	1	R.VIGSELVQKYVGEGAR.M
☑	2437	881.4490	1760.8834	1760.8767	3.80	0	(47)	0.00032	1	R.TMLELINQLDGFDPR.G
☑	2442	889.4456	1776.8766	1776.8716	2.81	0	80	1.7e-007	1	R.TMLELINQLDGFDPR.G + Oxidation (M)
☑	2451	606.6608	1816.9607	1816.9570	1.98	1	(35)	0.0039	1	K.IINADSDDPKYIINVK.Q
☑	2452	909.4882	1816.9618	1816.9570	2.60	1	84	5.1e-008	1	K.IINADSDDPKYIINVK.Q
☑	2481	1040.5005	2078.9865	2078.9830	1.65	0	(80)	1.8e-007	1	K.FVVDLADSVAPTDIEEGMR.V + Oxidation
☑	2482	694.0036	2078.9891	2078.9830	2.89	0	96	4.3e-009	1	K.FVVDLADSVAPTDIEEGMR.V + Oxidation
☑	2496	746.4299	2236.2680	2236.2620	2.67	1	44	0.00014	1	K.FVNLGIEPPKGVLLFGPPGTGK.T
☑	2529	869.4323	2605.2750	2605.2694	2.15	1	36	0.005	1	K.FVVDLADSVAPTDIEEGMRVGVDR.N + Oxida

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2. gi\|20129399 **Mass:** 56983 **Score:** 251 **Queries matched:** 5 **emPAI:** 0.32
Aldehyde dehydrogenase CG3752-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2258	541.2808	1080.5470	1080.5452	1.73	0	52	0.0001	1	K.VAFTGSTDVGK.L
☑	2402	717.3935	1432.7724	1432.7674	3.46	1	50	0.00017	1	K.DLDKANYIVGGLR.A
☑	2415	778.3935	1554.7725	1554.7678	3.02	0	86	4.5e-008	1	R.ANNSEYGLAAAVFTK.D
☑	2446	597.2944	1788.8613	1788.8570	2.38	1	(29)	0.017	1	R.TFVEDKIYDEFVER.S
☑	2447	895.4390	1788.8634	1788.8570	3.58	1	63	6.2e-006	1	R.TFVEDKIYDEFVER.S

Proteins matching the same set of peptides:

gi|68051705 **Mass:** 61886 **Score:** 251 **Queries matched:** 5
GH22814p [Drosophila melanogaster]
gi|125986975 **Mass:** 56964 **Score:** 251 **Queries matched:** 5
GA17661-PA [Drosophila pseudoobscura]

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3. gi|24643390 **Mass:** 41837 **Score:** 65 **Queries matched:** 1 **emPAI:** 0.08
CG32528-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2422	805.4469	1608.8793	1608.8723	4.36	0	65	2.6e-006	1	R.AVIDPQSISDPQVIK.L

---

4. gi|386043 **Mass:** 1687 **Score:** 63 **Queries matched:** 1 **emPAI:** 2.57
tubulin alpha-2 chain {internal fragment} [Drosophila melanogaster, CME W2 wing imaginal disc cell line, Pep

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2429	844.4505	1686.8864	1686.8829	2.08	0	63	9e-006	1	-.AVFVDLEPTVVDEVR.-

Proteins matching the same set of peptides:

gi|17136564 **Mass:** 49876 **Score:** 63 **Queries matched:** 1
alpha-Tubulin at 84B CG1913-PA [Drosophila melanogaster]
gi|17737821 **Mass:** 49859 **Score:** 63 **Queries matched:** 1
alpha-Tubulin at 84D CG2512-PA, isoform A [Drosophila melanogaster]

gi|17865841 **Mass:** 49935 **Score:** 63 **Queries matched:** 1
alpha-Tubulin at 85E CG9476-PA [Drosophila melanogaster]
gi|21064813 **Mass:** 50034 **Score:** 63 **Queries matched:** 1
RH71862p [Drosophila melanogaster]
gi|38047815 **Mass:** 28524 **Score:** 63 **Queries matched:** 1
similar to Drosophila melanogaster alphaTub84B [Drosophila yakuba]

---

5. gi|1699220 **Mass:** 55338 **Score:** 36 **Queries matched:** 1 **emPAI:** 0.06
D-ERp60=protein disulphide isomerase isoform/multifunctional endoplasmic reticulum luminal polypeptide [Dros

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2279	**557.7929**	**1113.5713**	**1113.5706**	**0.63**	**0**	**36**	**0.0035**	**1**	**K.YSVSGYPTLK.I**

Proteins matching the same set of peptides:
gi|45551086 **Mass:** 55336 **Score:** 36 **Queries matched:** 1
ERp60 CG8983-PA, isoform A [Drosophila melanogaster]
gi|66804043 **Mass:** 55334 **Score:** 36 **Queries matched:** 1
Erp60 [Drosophila simulans]

---

6. gi|7946 **Mass:** 46534 **Score:** 32 **Queries matched:** 1 **emPAI:** 0.07
unnamed protein product [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2233	**522.7832**	**1043.5518**	**1043.5499**	**1.85**	**0**	**32**	**0.0086**	**1**	**R.IEEEIGAGVK.F**

Proteins matching the same set of peptides:
gi|17137654 **Mass:** 46633 **Score:** 32 **Queries matched:** 1
Enolase CG17654-PA, isoform A [Drosophila melanogaster]
gi|21392248 **Mass:** 54304 **Score:** 32 **Queries matched:** 1
SD23356p [Drosophila melanogaster]
gi|24580914 **Mass:** 54276 **Score:** 32 **Queries matched:** 1
Enolase CG17654-PB, isoform B [Drosophila melanogaster]

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7. gi|45552677 **Mass:** 74415 **Score:** 32 **Queries matched:** 1 **emPAI:** 0.04
CG33456-PA [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2244	530.7865	1059.5585	1059.5560	2.33	0	32	0.013	1	R.TLIDQESVR.D

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8. gi|3426089 **Mass:** 177601 **Score:** 32 **Queries matched:** 3 **emPAI:** 0.02
polyprotein [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1715	672.4047	671.3974	671.3966	1.13	0	(31)	0.01	1	K.TVSLPR.L
☑	1716	672.4049	671.3976	671.3966	1.42	0	(27)	0.028	1	K.TVSLPR.L
☑	1718	672.4054	671.3981	671.3966	2.24	0	32	0.01	1	K.TVSLPR.L

Proteins matching the same set of peptides:
gi|21214752 **Mass:** 206214 **Score:** 32 **Queries matched:** 3
gag-pol polyprotein precursor; hypothetical protein [Drosophila melanogaster]
gi|25009978 **Mass:** 83774 **Score:** 32 **Queries matched:** 3
GH06606p [Drosophila melanogaster]

---

9. gi|17946230 **Mass:** 43594 **Score:** 25 **Queries matched:** 1 **emPAI:** 0.08
RE57556p [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2076	866.4293	865.4220	865.4181	4.50	0	25	0.033	1	K.EYADLQK.R

Proteins matching the same set of peptides:
gi|24584126 **Mass:** 43654 **Score:** 25 **Queries matched:** 1
CG9267-PA [Drosophila melanogaster]

---

10. gi|24644950 **Mass:** 36839 **Score:** 25 **Queries matched:** 2
CG2767-PA [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2235	523.2860	1044.5575	1044.5564	1.08	0	25	0.064	1	K.LSSLDQNIR.I
☑	2236	523.2864	1044.5583	1044.5564	1.83	0	(25)	0.065	1	K.LSSLDQNIR.I

---

11. gi|24648138 **Mass:** 52842 **Score:** 25 **Queries matched:** 1 **emPAI:** 0.06
CG11779-PA, isoform A [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1961	787.4594	786.4522	786.4487	4.40	0	25	0.045	1	R.GDLEILK.D

Proteins matching the same set of peptides:
gi|24648140 **Mass:** 48895 **Score:** 25 **Queries matched:** 1
CG11779-PB, isoform B [Drosophila melanogaster]
gi|25009742 **Mass:** 52856 **Score:** 25 **Queries matched:** 1
AT09326p [Drosophila melanogaster]
gi|63093891 **Mass:** 52816 **Score:** 25 **Queries matched:** 1
hypothetical protein [Drosophila parabipectinata]
gi|63093892 **Mass:** 48814 **Score:** 25 **Queries matched:** 1
hypothetical protein [Drosophila parabipectinata]
gi|78706782 **Mass:** 49345 **Score:** 25 **Queries matched:** 1
CG11779-PC, isoform C [Drosophila melanogaster]
gi|125773847 **Mass:** 51199 **Score:** 25 **Queries matched:** 1
GA11194-PA [Drosophila pseudoobscura]

Peptide matches not assigned to protein hits: (no details means no match)

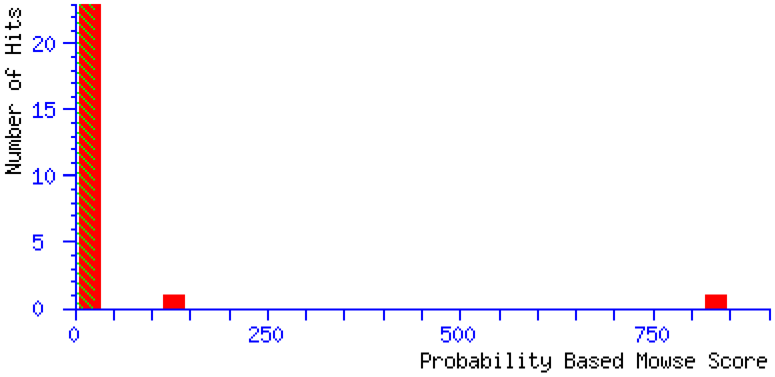
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2351	630.3420	1258.6695	1258.6710	-1.22	0	22	0.1	1	SLPFSPSHFLK
	2042	423.7203	845.4261	845.4243	2.14	0	21	0.13	1	ALAEAESR

Mascot Search Results

User : Julie Kadrmas; gel band: #64
Email : 110224FT_JulieKadrmas_64
Search title : NCBI Drosophila DB trypsin specific search: Oxidation (MHW)
MS data file : C:\Documents and Settings\cnelson\Desktop\Merge Files_2011\February_2011\merge_110224FT_JulieKad
Database : NCBInr (5335292 sequences; 1845185051 residues)
Taxonomy : Drosophila (fruit flies) (50248 sequences)
Timestamp : 24 Feb 2011 at 19:39:26 GMT
Protein hits : gi|24643390 CG32528-PA [Drosophila melanogaster]
gi|62862344 CG10837-PB.3 [Drosophila melanogaster]
gi|3426089 polyprotein [Drosophila melanogaster]
gi|66771585 IP12293p [Drosophila melanogaster]
gi|63146399 rhino [Drosophila simulans]
gi|125811483 GA21181-PA [Drosophila pseudoobscura]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 24 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary ▾ | Help

Significance threshold p< 0.05 | Max. number of hits AUTO

Standard scoring ● MudPIT scoring ○ | Ions score or expect cut-off 20 | Show sub-sets 0

Show pop-ups ○ Suppress pop-ups ● | Sort unassigned Decreasing Score ▾ | Require bold red ☑

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. gi|24643390 **Mass:** 41837 **Score:** 832 **Queries matched:** 21 **emPAI:** 3.57
CG32528-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1589	350.2425	698.4704	698.4690	2.00	0	40	0.00037	1	K.LNIVLK.A
☑	1590	699.4780	698.4708	698.4690	2.45	0	(28)	0.0063	1	K.LNIVLK.A
☑	1842	457.7573	913.5000	913.4981	2.06	0	33	0.0064	1	K.NAGVLNAQK.F
☑	1848	461.2746	920.5346	920.5331	1.66	0	47	0.00019	1	K.SLITFVNK.H
☑	1887	500.7650	999.5155	999.5138	1.76	0	49	9.5e-005	1	K.WSVASVHSK.N
☑	1919	525.3225	1048.6305	1048.6281	2.29	1	56	1.2e-005	1	K.KSLITFVNK.H
☑	1980	417.8921	1250.6545	1250.6520	2.02	0	36	0.0036	1	K.AVNHTLGFHQK.I
☑	1981	626.3352	1250.6558	1250.6520	3.03	0	(36)	0.0045	1	K.AVNHTLGFHQK.I
☑	1985	646.8401	1291.6657	1291.6635	1.70	0	80	1.5e-007	1	R.VLYSLFTMFR.D + Oxidation (M)
☑	1996	456.8869	1367.6390	1367.6357	2.37	2	27	0.022	1	K.KGEKEDSFWDK.F
☑	1999	472.9110	1415.7111	1415.7078	2.28	0	(42)	0.00083	1	K.ARPEDIVNMDLK.S + Oxidation (M)
☑	2000	708.8635	1415.7124	1415.7078	3.20	0	48	0.00024	1	K.ARPEDIVNMDLK.S + Oxidation (M)
☑	2012	779.4503	1556.8861	1556.8814	3.01	0	69	9e-007	1	R.LPENVFVTVVIAEK.N
☑	2018	537.2992	1608.8757	1608.8723	2.10	0	(57)	2.5e-005	1	R.AVIDPQSISDPQVIK.L
☑	2019	805.4462	1608.8778	1608.8723	3.42	0	67	2e-006	1	R.AVIDPQSISDPQVIK.L
☑	2020	805.4467	1608.8789	1608.8723	4.14	0	(64)	3.5e-006	1	R.AVIDPQSISDPQVIK.L
☑	2030	857.4455	1712.8765	1712.8733	1.83	0	82	9.7e-008	1	R.ILVDWINDELAEQR.I
☑	2038	924.4119	1846.8092	1846.8043	2.62	0	98	7.6e-010	1	K.FQEQITSEYDDLGMR.C + Oxidation (M)
☑	2039	616.6106	1846.8099	1846.8043	2.99	0	(65)	1.9e-006	1	K.FQEQITSEYDDLGMR.C + Oxidation (M)
	2051	651.3306	1950.9699	1950.9647	2.68	1	66	4.1e-006	1	K.KLDVPEVTQSEQGQHEK.L

☑

☑	2064	728.3658	2182.0755	2182.0728	1.23	0	34	0.0072	1	R.IIVQHLEEDMYDGQVLHK.L + Oxidation (M

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2. gi|62862344 **Mass:** 52171 **Score:** 131 **Queries matched:** 3 **emPAI:** 0.20
CG10837-PB.3 [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1845	458.7419	915.4692	915.4661	3.37	0	23	0.055	1	R.ELEIEQR.L
☑	2002	716.8398	1431.6650	1431.6590	4.22	0	83	6.2e-008	1	R.IELSNENDQQSR.Q
☑	2015	528.2625	1581.7657	1581.7634	1.44	2	25	0.047	1	R.TNQDYKESDKINK.C

Proteins matching the same set of peptides:
gi|62862346 **Mass:** 44097 **Score:** 131 **Queries matched:** 3
CG10837-PE.3 [Drosophila melanogaster]
gi|62862348 **Mass:** 44197 **Score:** 131 **Queries matched:** 3
CG10837-PA.3 [Drosophila melanogaster]

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3. gi|3426089 **Mass:** 177601 **Score:** 31 **Queries matched:** 3 **emPAI:** 0.02
polyprotein [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1530	672.4047	671.3974	671.3966	1.13	0	(27)	0.029	1	K.TVSLPR.L
☑	1531	672.4047	671.3974	671.3966	1.18	0	31	0.01	1	K.TVSLPR.L
☑	1532	672.4049	671.3977	671.3966	1.55	0	(31)	0.01	1	K.TVSLPR.L

Proteins matching the same set of peptides:
gi|21214752 **Mass:** 206214 **Score:** 31 **Queries matched:** 3
gag-pol polyprotein precursor; hypothetical protein [Drosophila melanogaster]
gi|25009978 **Mass:** 83774 **Score:** 31 **Queries matched:** 3
GH06606p [Drosophila melanogaster]

---

4. gi|66771585 **Mass:** 7369 **Score:** 31 **Queries matched:** 1 **emPAI:** 0.48

IP12293p [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1732	401.7252	801.4359	801.4345	1.85	1	31	0.026	1	K.DLGRTLAG.-

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5. gi|63146399 **Mass:** 55283 **Score:** 25 **Queries matched:** 1

rhino [Drosophila simulans]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1773	845.4495	844.4422	844.4403	2.35	1	25	0.053	1	K.SSSPPKSR.G

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6. gi|125811483 **Mass:** 144257 **Score:** 25 **Queries matched:** 1 **emPAI:** 0.02

GA21181-PA [Drosophila pseudoobscura]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1400	628.3429	627.3356	627.3340	2.56	0	25	0.051	1	R.AHGISK.Q + Oxidation (HW)

Peptide matches not assigned to protein hits: (no details means no match)

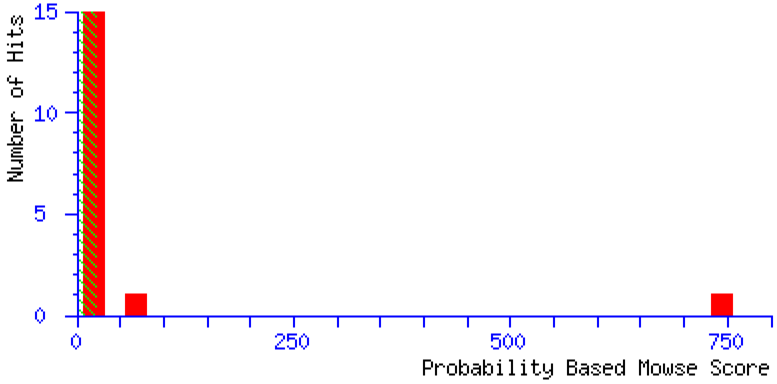
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1852	466.7444	931.4742	931.4770	-3.04	2	24	0.072	1	ACSPRRSR
☑	1856	466.7448	931.4751	931.4770	-2.02	2	23	0.098	1	ACSPRRSR
☑	1921	530.7869	1059.5592	1059.5560	3.03	0	23	0.1	1	TLIDQESVR
☑	1763	416.7486	831.4826	831.4814	1.42	0	21	0.096	1	SLSLSLGR
☑	1778	846.4351	845.4278	845.4243	4.14	0	21	0.15	1	NNLDSVGK
☑	1772	423.2281	844.4417	844.4443	-3.09	0	20	0.16	1	SPALWGSK
☑	1290	586.3934	585.3861	585.3850	1.93	0	20	0.11	1	GIGVIK
☑	1240	573.3362	572.3289	572.3282	1.25	0	20	0.34	1	INAQK
☑	1898	510.7725	1019.5305	1019.5321	-1.64	0	20	0.16	1	AIMVGTVGEK + Oxidation (M)

Mascot Search Results

```
User            : Julie Kadrmas; gel band: #66
Email           : 110224FT_JulieKadrmas_66
Search title    : NCBI Drosophila DB trypsin specific search: Oxidation (MHW)
MS data file    : C:\Documents and Settings\cnelson\Desktop\Merge Files_2011\February_2011\merge_110224FT_JulieKad
Database        : NCBInr  (5335292 sequences; 1845185051 residues)
Taxonomy        : Drosophila (fruit flies) (50248 sequences)
Timestamp       : 25 Feb 2011 at 18:43:33 GMT
Protein hits    : gi|21357547  CG8863-PA, isoform A [Drosophila melanogaster]
                  gi|158767    ubiquitin
                  gi|157891    myosin heavy chain
                  gi|3426089   polyprotein [Drosophila melanogaster]
                  gi|3915856   40S ribosomal protein S3a (C3 protein)
                  gi|1150726   transcription factor
                  gi|41619832  TPA: TPA_inf: HDC15749 [Drosophila melanogaster]
                  gi|45552677  CG33456-PA [Drosophila melanogaster]
                  gi|125982242 GA22115-PA [Drosophila pseudoobscura]
                  gi|19922798  CG3085-PA [Drosophila melanogaster]
                  gi|24668309  CG11248-PA, isoform A [Drosophila melanogaster]
```

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 23 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary ▾ | Help

Significance threshold p< 0.05 | Max. number of hits AUTO

Standard scoring ● MudPIT scoring ○ | Ions score or expect cut-off 20 | Show sub-sets 0

Show pop-ups ○ Suppress pop-ups ● | Sort unassigned Decreasing Score ▾ | Require bold red ☑

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. gi|21357547 **Mass:** 45202 **Score:** 743 **Queries matched:** 24 **emPAI:** 2.82
CG8863-PA, isoform A [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2430	379.2510	756.4875	756.4857	2.27	1	30	0.022	1	R.KLQLQK.N
☑	2785	483.7856	965.5567	965.5546	2.22	0	45	0.00019	1	K.VLEVHIEK.G
☑	2878	365.5578	1093.6516	1093.6495	1.88	1	(31)	0.003	1	R.KVLEVHIEK.G
☑	2879	547.8334	1093.6523	1093.6495	2.50	1	39	0.00056	1	R.KVLEVHIEK.G
☑	2928	587.2765	1172.5384	1172.5363	1.77	0	57	1.2e-005	1	K.FFGAGFGGSGGGR.R
☑	2994	640.3137	1278.6129	1278.6092	2.91	0	62	6.3e-006	1	R.QVYDEGGEAAIK.K
	3034	469.9095	1406.7067	1406.7041	1.83	1	(55)	4.6e-005	1	R.QVYDEGGEAAIKK.G

☑										
☑	3035	704.3610	1406.7074	1406.7041	2.30	1	63	7.9e-006	1	R.QVYDEGGEAAIKK.G
☑	3041	714.3345	1426.6545	1426.6477	4.75	1	23	0.044	1	K.YHPDKNPNEGEK.F
☑	3092	555.9539	1664.8397	1664.8369	1.69	1	(30)	0.023	1	K.AISQAYEVLSDADKR.Q
☑	3093	833.4276	1664.8406	1664.8369	2.21	1	(74)	9.5e-007	1	K.AISQAYEVLSDADKR.Q
☑	3094	833.4284	1664.8422	1664.8369	3.16	1	87	5e-008	1	K.AISQAYEVLSDADKR.Q
☑	3105	851.9160	1701.8174	1701.8111	3.74	2	21	0.12	1	K.YHPDKNPNEGEKFK.A
☑	3106	852.8282	1703.6419	1703.6369	2.93	0	82	6.8e-009	1	R.MAYDEDDGGYQDGPR.V + Oxidation (M)
☑	3138	618.3261	1851.9565	1851.9479	4.67	2	31	0.013	1	K.LALKYHPDKNPNEGEK.F
☑	3140	635.9423	1904.8050	1904.7999	2.63	1	34	0.00083	1	K.GGADSGDFRNPMDFFEK.F + Oxidation (M)
☑	3141	635.9429	1904.8070	1904.7999	3.69	1	(27)	0.0059	1	K.GGADSGDFRNPMDFFEK.F + Oxidation (M)
☑	3167	676.3653	2026.0742	2026.0695	2.30	1	33	0.0047	1	K.TLDDRDLIVSTQPGEVIR.H
☑	3168	678.6398	2032.8977	2032.8949	1.36	2	(20)	0.066	1	K.KGGADSGDFRNPMDFFEK.F + Oxidation (M
☑	3169	678.6418	2032.9037	2032.8949	4.34	2	32	0.0051	1	K.KGGADSGDFRNPMDFFEK.F + Oxidation (M
☑	3226	797.3996	2389.1770	2389.1696	3.08	1	49	0.00026	1	R.GKDVVHQMSVQLEELYNGATR.K + Oxidation
☑	3234	885.1814	2652.5224	2652.5142	3.06	0	28	0.0028	1	K.GTLIIQFEVIFPEVINPSVVPTLK.Q
☑	3235	890.4575	2668.3505	2668.3490	0.57	2	(24)	0.077	1	K.TLDDRDLIVSTQPGEVIRHEMTK.C + Oxidati
☑	3236	890.4596	2668.3569	2668.3490	2.93	2	32	0.01	1	K.TLDDRDLIVSTQPGEVIRHEMTK.C + Oxidati

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2. gi|158767 **Mass:** 8540 **Score:** 45 **Queries matched:** 1 **emPAI:** 0.41
ubiquitin
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	3126	894.4700	1786.9255	1786.9200	3.04	0	45	0.00089	1	K.TITLEVEPSDTIENVK.A

Proteins matching the same set of peptides:

gi|158769 **Mass:** 8428 **Score:** 45 **Queries matched:** 1
ubiquitin
gi|158771 **Mass:** 8543 **Score:** 45 **Queries matched:** 1
ubiquitin
gi|17136570 **Mass:** 14720 **Score:** 45 **Queries matched:** 1
Ribosomal protein L40 CG2960-PA [Drosophila melanogaster]

gi|17136574 **Mass:** 17929 **Score:** 45 **Queries matched:** 1
Ribosomal protein S27A CG5271-PA [Drosophila melanogaster]
gi|51701919 **Mass:** 8560 **Score:** 45 **Queries matched:** 1
Ubiquitin
gi|158763 **Score:** 43 **Queries matched:** 1
gi|158765 **Score:** 43 **Queries matched:** 1
gi|225319 **Score:** 43 **Queries matched:** 1
gi|225320 **Score:** 43 **Queries matched:** 1
gi|24640094 **Mass:** 34314 **Score:** 43 **Queries matched:** 1
CG11700-PA [Drosophila melanogaster]
gi|158753 **Mass:** 25955 **Score:** 42 **Queries matched:** 1
ubiquitin
gi|21428336 **Mass:** 34369 **Score:** 42 **Queries matched:** 1
GH17513p [Drosophila melanogaster]
gi|24640086 **Mass:** 59993 **Score:** 40 **Queries matched:** 1
CG32744-PA [Drosophila melanogaster]
gi|24657014 **Mass:** 85746 **Score:** 39 **Queries matched:** 1
Ubiquitin-63E CG11624-PA, isoform A [Drosophila melanogaster]
gi|21429768 **Mass:** 119913 **Score:** 39 **Queries matched:** 1
AT20865p [Drosophila melanogaster]

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3. gi|157891 **Mass:** 224288 **Score:** 31 **Queries matched:** 1 **emPAI:** 0.01
myosin heavy chain
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2530	819.3864	818.3791	818.3770	2.59	0	31	0.0089	1	R.LADEESR.E

Proteins matching the same set of peptides:
gi|157892 **Mass:** 224488 **Score:** 31 **Queries matched:** 1
myosin heavy chain
gi|2546936 **Mass:** 135522 **Score:** 31 **Queries matched:** 1
muscle myosin heavy chain [Drosophila melanogaster]
gi|2546937 **Mass:** 135517 **Score:** 31 **Queries matched:** 1
muscle myosin heavy chain [Drosophila melanogaster]

gi|2546938 **Mass:** 138464 **Score:** 31 **Queries matched:** 1
muscle myosin heavy chain [Drosophila melanogaster]
gi|2546939 **Mass:** 138459 **Score:** 31 **Queries matched:** 1
muscle myosin heavy chain [Drosophila melanogaster]
gi|7579901 **Mass:** 44936 **Score:** 31 **Queries matched:** 1
myosin heavy chain; MHC [Drosophila melanogaster]
gi|24584692 **Mass:** 224278 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PC, isoform C [Drosophila melanogaster]
gi|24584694 **Mass:** 224395 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PG, isoform G [Drosophila melanogaster]
gi|24584696 **Mass:** 224496 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PE, isoform E [Drosophila melanogaster]
gi|24584698 **Mass:** 224269 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PJ, isoform J [Drosophila melanogaster]
gi|24584700 **Mass:** 224391 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PF, isoform F [Drosophila melanogaster]
gi|24584702 **Mass:** 224355 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PD, isoform D [Drosophila melanogaster]
gi|24584704 **Mass:** 224472 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PA, isoform A [Drosophila melanogaster]
gi|24584706 **Mass:** 224456 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PI, isoform I [Drosophila melanogaster]
gi|24584710 **Mass:** 224272 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PB, isoform B [Drosophila melanogaster]
gi|24584712 **Mass:** 221271 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PK, isoform K [Drosophila melanogaster]
gi|24584714 **Mass:** 221339 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PL, isoform L [Drosophila melanogaster]
gi|24584716 **Mass:** 221330 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PM, isoform M [Drosophila melanogaster]
gi|28574239 **Mass:** 224573 **Score:** 31 **Queries matched:** 1
Myosin heavy chain CG17927-PH, isoform H [Drosophila melanogaster]

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4. gi|3426089 **Mass:** 177601 **Score:** 29 **Queries matched:** 4 **emPAI:** 0.02
polyprotein [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2177	672.4046	671.3974	671.3966	1.09	0	(27)	0.028	1	K.TVSLPR.L
☑	2178	672.4051	671.3978	671.3966	1.82	0	29	0.02	1	K.TVSLPR.L
☑	2180	672.4052	671.3980	671.3966	2.00	0	(23)	0.079	1	K.TVSLPR.L
☑	2181	672.4055	671.3982	671.3966	2.37	0	(28)	0.022	1	K.TVSLPR.L

Proteins matching the same set of peptides:

gi|21214752 **Mass:** 206214 **Score:** 29 **Queries matched:** 4
gag-pol polyprotein precursor; hypothetical protein [Drosophila melanogaster]
gi|25009978 **Mass:** 83774 **Score:** 29 **Queries matched:** 4
GH06606p [Drosophila melanogaster]

5\. gi|3915856 **Mass:** 30337 **Score:** 28 **Queries matched:** 1 **emPAI:** 0.11
40S ribosomal protein S3a (C3 protein)

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2510	405.2244	808.4342	808.4330	1.48	0	28	0.014	1	R.IASDYLK.G

Proteins matching the same set of peptides:

gi|17864162 **Mass:** 30321 **Score:** 28 **Queries matched:** 1
Ribosomal protein S3A CG2168-PA, isoform A [Drosophila melanogaster]
gi|17945018 **Mass:** 25085 **Score:** 28 **Queries matched:** 1
RE04220p [Drosophila melanogaster]
gi|38047857 **Mass:** 30307 **Score:** 28 **Queries matched:** 1
similar to Drosophila melanogaster RpS3A [Drosophila yakuba]
gi|38048393 **Mass:** 25024 **Score:** 28 **Queries matched:** 1
similar to Drosophila melanogaster RpS3A [Drosophila yakuba]
gi|126002490 **Mass:** 30307 **Score:** 28 **Queries matched:** 1
GA15280-PA [Drosophila pseudoobscura]

6\. gi|1150726 **Mass:** 112844 **Score:** 26 **Queries matched:** 1
transcription factor

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2556	416.2510	830.4874	830.4862	1.55	0	26	0.067	1	R.SLVVANTK.T

Proteins matching the same set of peptides:

gi\|24664166 **Mass:** 112804 **Score:** 26 **Queries matched:** 1
stonewall CG3836-PA [Drosophila melanogaster]
gi\|125979313 **Mass:** 107544 **Score:** 26 **Queries matched:** 1
GA17720-PA [Drosophila pseudoobscura]

---

7. gi\|41619832 **Mass:** 27811 **Score:** 24 **Queries matched:** 1 **emPAI:** 0.12
TPA: TPA_inf: HDC15749 [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2870	541.7511	1081.4877	1081.4896	-1.75	1	24	0.034	1	K.MEMEKVQR.V + 2 Oxidation (M)

---

8. gi\|45552677 **Mass:** 74415 **Score:** 24 **Queries matched:** 1 **emPAI:** 0.04
CG33456-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2858	530.7866	1059.5587	1059.5560	2.51	0	24	0.084	1	R.TLIDQESVR.D

---

9. gi\|125982242 **Mass:** 50218 **Score:** 24 **Queries matched:** 1
GA22115-PA [Drosophila pseudoobscura]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2501	401.7252	801.4359	801.4344	1.77	1	24	0.16	1	R.EREQIK.R

---

10. gi|19922798 **Mass:** 50665 **Score:** 23 **Queries matched:** 1
CG3085-PA [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2380	731.4070	730.3998	730.3973	3.34	0	23	0.22	1	R.ISELNR.W

Proteins matching the same set of peptides:
gi|27374258 **Mass:** 50627 **Score:** 23 **Queries matched:** 1
CG3085-PA [Drosophila erecta]
gi|125807457 **Mass:** 50658 **Score:** 23 **Queries matched:** 1
GA15915-PA [Drosophila pseudoobscura]

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11. gi|24668309 **Mass:** 96012 **Score:** 23 **Queries matched:** 1 **emPAI:** 0.03
CG11248-PA, isoform A [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2584	846.4335	845.4262	845.4243	2.29	0	23	0.089	1	K.ALAEAESR.I

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1656	559.3458	558.3385	558.3377	1.42	0	22	0.17	1	IAEVK
☑	2741	466.7448	931.4751	931.4770	-1.99	2	21	0.15	1	ACSPRRSR
☑	2738	466.7435	931.4724	931.4770	-4.94	2	21	0.14	1	ACSPRRSR
☑	1990	625.3202	624.3130	624.3119	1.76	0	21	0.099	1	SYLDK
☑	2490	794.3867	793.3794	793.3817	-2.88	1	20	0.092	1	SSSEKEK
☑	2511	405.2246	808.4346	808.4330	1.93	0	20	0.068	1	IASDYLK
☑	2509	807.4024	806.3951	806.3956	-0.63	0	20	0.15	1	MSSPTLR + Oxidation (M)
☑	2557	831.4952	830.4879	830.4862	2.10	0	20	0.25	1	SLVVANTK
☑	1657	559.3466	558.3393	558.3377	2.96	0	20	0.3	1	IAEVK
☑	2789	487.2707	972.5268	972.5240	2.86	0	20	0.17	1	LLTDELNR
☑	2011	628.3781	627.3708	627.3704	0.68	0	19	0.15	1	GSVLPR

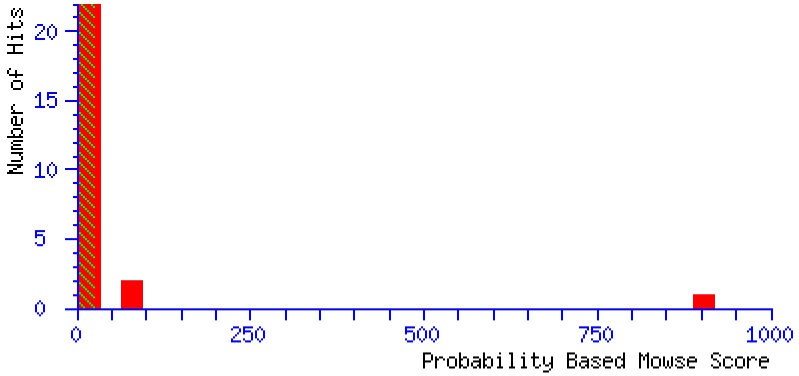
Mascot Search Results

User : **Julie Kadrmas; gel band: #92**
Email : **110224FT_JulieKadrmas_92**
Search title : **NCBI Drosophila DB trypsin specific search: Oxidation (MHW)**
MS data file : **C:\Documents and Settings\cnelson\Desktop\Merge Files_2011\February_2011\merge_110224FT_JulieKad**
Database : **NCBInr (5335292 sequences; 1845185051 residues)**
Taxonomy : **Drosophila (fruit flies) (50248 sequences)**
Timestamp : **25 Feb 2011 at 18:51:51 GMT**
Protein hits :

gi|17737405	Proteasome 35kD subunit CG4904-PA [Drosophila melanogaster]
gi|62862344	CG10837-PB.3 [Drosophila melanogaster]
gi|17136226	Ecdysone-inducible gene L3 CG10160-PA [Drosophila melanogaster]
gi|82466274	kl-2 protein [Drosophila bipectinata]
gi|3426089	polyprotein [Drosophila melanogaster]
gi|24653473	CG30484-PA [Drosophila melanogaster]
gi|8630	unnamed protein product [Drosophila melanogaster]
gi|125985389	GA19998-PA [Drosophila pseudoobscura]
gi|21358649	CG3508-PA, isoform A [Drosophila melanogaster]
gi|16768410	GM04011p [Drosophila melanogaster]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 24 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary ▾ | Help

Significance threshold p< 0.05 | Max. number of hits AUTO

Standard scoring ● MudPIT scoring ○ | Ions score or expect cut-off 20 | Show sub-sets 0

Show pop-ups ○ Suppress pop-ups ● | Sort unassigned Decreasing Score ▾ | Require bold red ☑

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. gi|17737405 **Mass:** 31040 **Score:** 905 **Queries matched:** 33 **emPAI:** 10.46

Proteasome 35kD subunit CG4904-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1356	638.4000	637.3927	637.3911	2.44	0	29	0.0077	1	K.HVAIAK.E
☑	1376	645.3580	644.3507	644.3493	2.13	0	24	0.14	1	K.DEIIR.H
☑	1407	653.3519	652.3447	652.3432	2.29	0	24	0.019	1	R.TYLEK.N
☑	1762	436.7645	871.5145	871.5127	2.04	0	41	0.0015	1	R.LITNLGNK.M
☑	1763	872.5224	871.5151	871.5127	2.79	0	(37)	0.004	1	R.LITNLGNK.M
☑	1764	872.5232	871.5160	871.5127	3.76	0	(33)	0.0096	1	R.LITNLGNK.M
	1967	561.8131	1121.6116	1121.6080	3.18	1	30	0.0066	1	R.TYLEKNLNK.F

☑										
☑	1980	581.8100	1161.6054	1161.6030	2.12	0	39	0.002	1	K.DQPFTILSNK.D
☑	2041	441.5707	1321.6903	1321.6878	1.89	1	(47)	0.00032	1	K.FLDSSKDEIIR.H
☑	2042	661.8534	1321.6923	1321.6878	3.43	1	66	2.8e-006	1	K.FLDSSKDEIIR.H
☑	2043	663.3113	1324.6080	1324.6048	2.43	0	56	2.5e-005	1	K.HSYDTTYPVSR.L
☑	2048	671.8659	1341.7172	1341.7140	2.39	0	53	7.4e-005	1	R.AILGTLPTDEQGK.D
☑	2052	677.3563	1352.6981	1352.6936	3.33	0	84	5.7e-008	1	R.DPEVLVATEQRP.-
☑	2065	478.5754	1432.7043	1432.7020	1.59	0	(29)	0.019	1	R.LHQVEYAMEAVK.L + Oxidation (M)
☑	2066	478.5758	1432.7057	1432.7020	2.55	0	(45)	0.0004	1	R.LHQVEYAMEAVK.L + Oxidation (M)
☑	2067	717.3605	1432.7064	1432.7020	3.05	0	45	0.00051	1	R.LHQVEYAMEAVK.L + Oxidation (M)
☑	2096	782.4060	1562.7974	1562.7940	2.16	1	(23)	0.073	1	K.DQPFTILSNKDSAK.H
☑	2097	521.9399	1562.7979	1562.7940	2.48	1	35	0.0055	1	K.DQPFTILSNKDSAK.H
☑	2117	578.9785	1733.9136	1733.9094	2.43	1	(48)	0.00031	1	R.LITNLGNKMQTTTQR.Y + Oxidation (M)
☑	2118	867.9645	1733.9145	1733.9094	2.92	1	72	1.3e-006	1	R.LITNLGNKMQTTTQR.Y + Oxidation (M)
☑	2119	867.9646	1733.9146	1733.9094	2.98	1	(51)	0.00017	1	R.LITNLGNKMQTTTQR.Y + Oxidation (M)
☑	2122	876.4050	1750.7954	1750.7911	2.45	0	(61)	9.2e-006	1	R.NQYDSDVTVWSPQGR.L
☑	2123	584.6061	1750.7966	1750.7911	3.14	0	(40)	0.001	1	R.NQYDSDVTVWSPQGR.L
☑	2124	876.4057	1750.7968	1750.7911	3.25	0	67	1.9e-006	1	R.NQYDSDVTVWSPQGR.L
☑	2133	884.4024	1766.7903	1766.7860	2.44	0	(47)	0.00015	1	R.NQYDSDVTVWSPQGR.L + Oxidation (HW)
☑	2134	884.4025	1766.7905	1766.7860	2.54	0	(64)	2.9e-006	1	R.NQYDSDVTVWSPQGR.L + Oxidation (HW)
☑	2143	597.9941	1790.9606	1790.9526	4.45	2	48	0.00027	1	K.NLNKFLDSSKDEIIR.H
☑	2167	687.7181	2060.1324	2060.1266	2.82	0	(31)	0.0063	1	K.IIPIDDHLGISIAGLTADAR.V
☑	2168	1031.0739	2060.1332	2060.1266	3.22	0	96	2.1e-009	1	K.IIPIDDHLGISIAGLTADAR.V
☑	2169	687.7188	2060.1344	2060.1266	3.80	0	(32)	0.0046	1	K.IIPIDDHLGISIAGLTADAR.V
☑	2170	1031.0756	2060.1366	2060.1266	4.88	0	(77)	1.5e-007	1	K.IIPIDDHLGISIAGLTADAR.V
☑	2176	700.3624	2098.0655	2098.0596	2.80	1	29	0.022	1	R.YDRRPYGVGLLVAGYDER.G
☑	2183	730.4163	2188.2270	2188.2215	2.47	1	69	5.6e-007	1	R.KIIPIDDHLGISIAGLTADAR.V

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2. gi|62862344 **Mass:** 52171 **Score:** 62 **Queries matched:** 2 **emPAI:** 0.13
CG10837-PB.3 [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

☑	1830	458.7409	915.4672	915.4661	1.17	0	26	0.033	1	R.ELEIEQR.L
☑	2111	851.4325	1700.8505	1700.8441	3.75	1	36	0.0046	1	R.IRIELSNENDQQSR.Q

Proteins matching the same set of peptides:

gi|62862346 **Mass:** 44097 **Score:** 62 **Queries matched:** 2
CG10837-PE.3 [Drosophila melanogaster]
gi|62862348 **Mass:** 44197 **Score:** 62 **Queries matched:** 2
CG10837-PA.3 [Drosophila melanogaster]

3. gi|17136226 **Mass:** 35515 **Score:** 53 **Queries matched:** 1 **emPAI:** 0.09
Ecdysone-inducible gene L3 CG10160-PA [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	2091	763.9261	1525.8376	1525.8352	1.62	0	53	5.8e-005	1	K.QILTPTEVEQLQK.S

Proteins matching the same set of peptides:

gi|78214230 **Mass:** 35524 **Score:** 53 **Queries matched:** 1
RE54418p [Drosophila melanogaster]

4. gi|82466274 **Mass:** 19078 **Score:** 35 **Queries matched:** 1 **emPAI:** 0.18
kl-2 protein [Drosophila bipectinata]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1907	515.3014	1028.5882	1028.5866	1.54	0	35	0.0047	1	K.DELVLTIAR.N

Proteins matching the same set of peptides:

gi|82466286 **Mass:** 19064 **Score:** 35 **Queries matched:** 1
kl-2 protein [Drosophila pseudoananassae nigrens]

5. gi|3426089 **Mass:** 177601 **Score:** 31 **Queries matched:** 3 **emPAI:** 0.02
polyprotein [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1453	672.4046	671.3974	671.3966	1.09	0	31	0.01	1	K.TVSLPR.L
☑	1456	672.4051	671.3978	671.3966	1.78	0	(29)	0.019	1	K.TVSLPR.L
☑	1457	672.4051	671.3978	671.3966	1.82	0	(31)	0.011	1	K.TVSLPR.L

Proteins matching the same set of peptides:

gi|21214752 **Mass:** 206214 **Score:** 31 **Queries matched:** 3
gag-pol polyprotein precursor; hypothetical protein [Drosophila melanogaster]
gi|25009978 **Mass:** 83774 **Score:** 31 **Queries matched:** 3
GH06606p [Drosophila melanogaster]

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6. gi|24653473 **Mass:** 101560 **Score:** 30 **Queries matched:** 1 **emPAI:** 0.03
CG30484-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1812	453.7388	905.4631	905.4640	-1.06	1	30	0.019	1	K.MLEGKANK.I + Oxidation (M)

---

7. gi|8630 **Mass:** 42958 **Score:** 27 **Queries matched:** 1 **emPAI:** 0.08
unnamed protein product [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1522	697.3347	696.3274	696.3265	1.41	0	27	0.016	1	-.MAANYK.S

Proteins matching the same set of peptides:

gi|17136490 **Mass:** 42928 **Score:** 27 **Queries matched:** 1
snail CG3956-PA [Drosophila melanogaster]
gi|125984502 **Mass:** 44640 **Score:** 27 **Queries matched:** 1
GA17803-PA [Drosophila pseudoobscura]

---

8. gi|125985389 **Mass:** 238718 **Score:** 26 **Queries matched:** 1 **emPAI:** 0.01
GA19998-PA [Drosophila pseudoobscura]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1895	501.7645	1001.5144	1001.5141	0.24	1	28	0.046	1	K.AEEEQRLK.A

---

9. gi|21358649 **Mass:** 38035 **Score:** 25 **Queries matched:** 2 **emPAI:** 0.09
CG3508-PA, isoform A [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1446	664.3349	663.3276	663.3261	2.24	0	25	0.046	1	-.MAEAVK.N + Oxidation (M)
☑	1447	664.3359	663.3286	663.3261	3.71	0	(21)	0.11	1	-.MAEAVK.N + Oxidation (M)

Proteins matching the same set of peptides:
gi|24646884 **Mass:** 39187 **Score:** 25 **Queries matched:** 2
CG3508-PB, isoform B [Drosophila melanogaster]
gi|25012395 **Mass:** 39158 **Score:** 25 **Queries matched:** 2
RE11603p [Drosophila melanogaster]
gi|125774419 **Mass:** 34857 **Score:** 25 **Queries matched:** 2
GA17490-PA [Drosophila pseudoobscura]

---

10. gi|16768410 **Score:** 24 **Queries matched:** 1
GM04011p [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1031	545.3055	544.2982	544.2969	2.41	0	24	0.28	1	R.NLGNK.F

Proteins matching the same set of peptides:
gi|24582135 **Score:** 24 **Queries matched:** 1
gi|45580808 **Score:** 24 **Queries matched:** 1

Peptide matches not assigned to protein hits: (no details means no match)

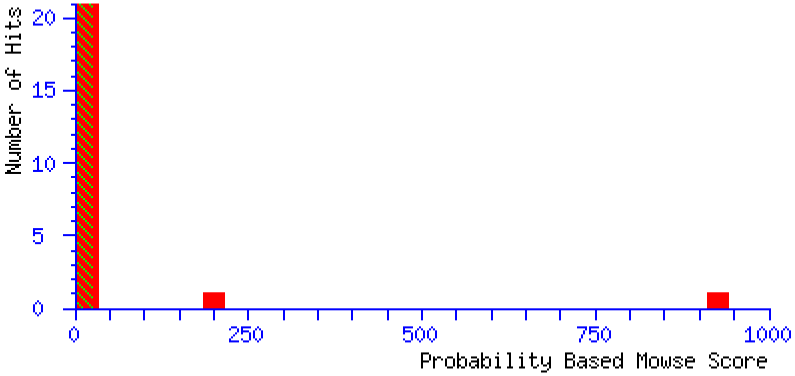
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1987	588.3181	1174.6216	1174.6167	4.22	2	24	0.06	1	RASSQSQQKR
☑	1836	466.7445	931.4745	931.4770	-2.65	2	23	0.076	1	ACSPRRSR
☑	1386	646.3533	645.3460	645.3446	2.25	0	23	0.17	1	NTLNGK
☑	1767	437.7542	873.4939	873.4920	2.26	1	22	0.11	1	DGKINLSK
☑	1919	523.2869	1044.5592	1044.5564	2.72	0	22	0.12	1	LSSLDQNIR
☑	1859	947.5165	946.5093	946.5056	3.82	2	22	0.09	1	SSRAQSRR
☑	1766	874.4898	873.4826	873.4807	2.10	0	21	0.12	1	SLVEAEVK
☑	1846	468.2707	934.5268	934.5236	3.47	1	21	0.11	1	AAYDKVLR
☑	1724	423.2281	844.4417	844.4443	-3.09	0	20	0.15	1	SPALWGSK
☑	1725	423.2283	844.4420	844.4443	-2.72	0	20	0.16	1	SPALWGSK
☑	1860	474.2621	946.5097	946.5058	4.06	0	20	0.14	1	TWIMIQR
☑	888	515.3307	514.3234	514.3227	1.40	0	20	0.49	1	LGAVR
☑	1525	699.4147	698.4075	698.4075	-0.09	0	19	0.19	1	QVSLPR
☑	1755	432.7511	863.4877	863.4899	-2.49	1	19	0.16	1	SMLTKIR + Oxidation (M)
☑	1778	439.7332	877.4519	877.4480	4.46	0	19	0.19	1	LMQWLR + Oxidation (HW); Oxidation (M
☑	1408	653.3521	652.3448	652.3432	2.50	0	19	0.059	1	TYLEK
☑	1715	421.2614	840.5083	840.5069	1.71	0	18	0.072	1	IGGPGSLIK
☑	1671	791.4434	790.4361	790.4371	-1.19	1	18	0.47	1	QMLKQK + Oxidation (M)
☑	1698	827.3995	826.3923	826.3895	3.39	0	18	0.16	1	MEAAYVK + Oxidation (M)
☑	1026	543.3514	542.3442	542.3428	2.54	0	18	0.11	1	SPLVK
☑	1918	523.2862	1044.5579	1044.5564	1.48	0	18	0.32	1	LSSLDQNIR
☑	886	515.3307	514.3234	514.3227	1.34	0	18	0.81	1	LGAVR
☑	889	515.3308	514.3235	514.3227	1.52	0	17	0.83	1	LGAVR
☑	891	515.3309	514.3236	514.3227	1.73	0	17	0.83	1	LGAVR
☑	887	515.3307	514.3234	514.3227	1.40	0	17	0.83	1	LGAVR
☑	1455	672.4049	671.3976	671.3966	1.51	0	17	0.26	1	TVSLPR
☑	890	515.3308	514.3235	514.3227	1.56	0	17	0.84	1	LGAVR
☑	1729	423.7202	845.4259	845.4243	1.99	0	17	0.36	1	ALAEAESR
☑	1428	663.3853	662.3780	662.3752	4.35	0	17	0.42	1	GQAFLK
☑	1427	663.3851	662.3778	662.3752	3.99	0	17	0.44	1	GQAFLK

MATRIX SCIENCE Mascot Search Results

User : **Julie Kadrmas; gel band: #111**
Email : **110224FT_JulieKadrmas_111**
Search title : **NCBI Drosophila DB trypsin specific search: Oxidation (MHW)**
MS data file : **C:\Documents and Settings\cnelson\Desktop\Merge Files_2011\February_2011\merge_110224FT_JulieKad**
Database : **NCBInr (5335292 sequences; 1845185051 residues)**
Taxonomy : **Drosophila (fruit flies) (50248 sequences)**
Timestamp : **25 Feb 2011 at 18:54:28 GMT**
Protein hits : **gi|21428580** LD43891p [Drosophila melanogaster]
gi|24644197 CG11999-PA [Drosophila melanogaster]
gi|2582508 20S proteasome alpha7 subunit [Drosophila melanogaster]
gi|24584030 CG16972-PA [Drosophila melanogaster]
gi|3426089 polyprotein [Drosophila melanogaster]
gi|17862878 SD01389p [Drosophila melanogaster]
gi|8380 unnamed protein product [Drosophila melanogaster]
gi|24644950 CG2767-PA [Drosophila melanogaster]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 24 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary ▾ | Help

Significance threshold p< 0.05 | Max. number of hits AUTO

Standard scoring ● MudPIT scoring ○ | Ions score or expect cut-off 20 | Show sub-sets 0

Show pop-ups ○ Suppress pop-ups ● | Sort unassigned Decreasing Score ▾ | Require bold red ☑

Select All | Select None | Search Selected | ☐ **Error tolerant** | Archive Report

1. gi|21428580 **Mass:** 30698 **Score:** 925 **Queries matched:** 34 **emPAI:** 12.03
LD43891p [Drosophila melanogaster]
☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1534	673.3901	672.3828	672.3806	3.23	0	25	0.056	1	K.EVGQLK.N
☑	1604	702.3796	701.3724	701.3708	2.25	0	(24)	0.1	1	K.VLDEAR.E
☑	1606	702.3803	701.3730	701.3708	3.12	0	32	0.015	1	K.VLDEAR.E
☑	1733	787.4331	786.4258	786.4236	2.88	0	26	0.04	1	R.EVGDLVR.L
☑	1763	406.7358	811.4570	811.4552	2.24	0	33	0.0046	1	R.LTLSHNK.I
☑	1794	415.7409	829.4673	829.4657	1.87	1	(37)	0.0044	1	K.KVLDEAR.E
☑	1795	415.7412	829.4679	829.4657	2.64	1	42	0.0013	1	K.KVLDEAR.E
☑	1886	463.7932	925.5719	925.5709	1.08	0	46	0.00013	1	K.NLQILGLR.D
☑	1887	463.7938	925.5731	925.5709	2.40	0	(36)	0.0011	1	K.NLQILGLR.D
☑	1888	464.7831	927.5516	927.5501	1.56	0	(39)	0.0015	1	R.ILNVSINR.L
☑	1889	464.7831	927.5516	927.5501	1.59	0	(59)	1.6e-005	1	R.ILNVSINR.L
☑	1891	464.7832	927.5519	927.5501	1.88	0	60	1.4e-005	1	R.ILNVSINR.L
☑	1892	464.7837	927.5529	927.5501	2.97	0	(59)	1.5e-005	1	R.ILNVSINR.L
☑	1944	497.2732	992.5319	992.5291	2.83	1	47	0.00029	1	R.SGPPPPKADK.S
☑	1952	512.2713	1022.5281	1022.5257	2.35	0	27	0.04	1	R.ELHIQNNR.L
☑	1969	542.7868	1083.5591	1083.5560	2.86	0	63	4.8e-006	1	R.DNDLLELPR.E
☑	1993	599.3775	1196.7405	1196.7353	4.30	1	49	4.9e-005	1	K.LRILNVSINR.L
☑	2009	431.5785	1291.7137	1291.7109	2.21	1	37	0.002	1	R.LRELHIQNNR.L

☑ 2010	646.8644	1291.7142	1291.7109	2.58	1	(33)	0.0045	1	R.LRELHIQNNR.L
☑ 2014	650.8500	1299.6855	1299.6823	2.51	1	39	0.0022	1	K.TETYKIIYNR.H
☑ 2022	461.2256	1380.6548	1380.6521	1.98	0	(33)	0.0047	1	R.ETHNPELDLADK.G
☑ 2023	691.3359	1380.6573	1380.6521	3.74	0	69	1e-006	1	R.ETHNPELDLADK.G
☑ 2037	545.6759	1634.0059	1633.9991	4.14	1	47	2.2e-005	1	R.ILNVSINRLINLPR.G
☑ 2038	829.4126	1656.8107	1656.8035	4.32	0	63	7.4e-006	1	R.ALYLGDNDFEYIPK.E
☑ 2060	618.3314	1851.9723	1851.9690	1.79	1	36	0.0036	1	R.DNDLLELPREVGDLVR.L
☑ 2061	946.0439	1890.0733	1890.0826	-4.92	0	(38)	0.00053	1	R.LQVLPPEIAQLDLLSNK.S
☑ 2062	631.0356	1890.0850	1890.0826	1.29	0	(53)	1.8e-005	1	R.LQVLPPEIAQLDLLSNK.S
☑ 2063	946.0505	1890.0865	1890.0826	2.05	0	54	1.5e-005	1	R.LQVLPPEIAQLDLLSNK.S
☑ 2064	946.0511	1890.0876	1890.0826	2.64	0	(47)	6.5e-005	1	R.LQVLPPEIAQLDLLSNK.S
☑ 2072	996.5666	1991.1186	1991.1163	1.12	1	49	7.8e-005	1	K.NLQILGLRDNDLLELPR.E
☑ 2073	664.7149	1991.1228	1991.1163	3.24	1	(41)	0.00035	1	K.NLQILGLRDNDLLELPR.E
☑ 2080	689.0135	2064.0186	2064.0123	3.05	1	34	0.0078	1	K.VLDEARETHNPELDLADK.G
☑ 2083	1064.5235	2127.0325	2127.0306	0.88	0	(45)	0.00047	1	K.GLSSFEELPGLFNMSNITR.L + Oxidation
☑ 2084	710.0181	2127.0326	2127.0306	0.90	0	49	0.00022	1	K.GLSSFEELPGLFNMSNITR.L + Oxidation

Proteins matching the same set of peptides:

gi|45550188 **Mass:** 31830 **Score:** 925 **Queries matched:** 34
Ras suppressor-1 CG9031-PA [Drosophila melanogaster]

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2. gi|24644197 **Mass:** 23619 **Score:** 188 **Queries matched:** 4 **emPAI:** 0.70
CG11999-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑ 1975	549.7837	1097.5529	1097.5505	2.15	0	45	0.00034	1	K.LLNSDYAFR.L
☑ 2017	681.3785	1360.7424	1360.7391	2.44	0	57	2.5e-005	1	R.WTTAEGLFIVPK.E
☑ 2020	688.2942	1374.5738	1374.5688	3.63	0	27	0.0047	1	K.SSTHDEYAHSEL.-
☑ 2049	580.2861	1737.8364	1737.8291	4.22	1	61	1.3e-005	1	R.LRHIDTGMYLGMSGR.S + 2 Oxidation (M)

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3. gi|2582508 **Mass:** 27444 **Score:** 43 **Queries matched:** 1 **emPAI:** 0.12
20S proteasome alpha7 subunit [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1966	535.7814	1069.5482	1069.5444	3.54	0	43	0.00056	1	R.VFQIDYASK.V

Proteins matching the same set of peptides:

gi|24652204 **Mass:** 27658 **Score:** 43 **Queries matched:** 1
Proteasome alpha7 subunit CG1519-PA, isoform A [Drosophila melanogaster]
gi|28573936 **Mass:** 25656 **Score:** 43 **Queries matched:** 1
Proteasome alpha7 subunit CG1519-PB, isoform B [Drosophila melanogaster]
gi|125811303 **Mass:** 53546 **Score:** 43 **Queries matched:** 1
GA13558-PA [Drosophila pseudoobscura]

4. gi|24584030 **Score:** 38 **Queries matched:** 1
CG16972-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1138	558.3253	557.3180	557.3173	1.35	0	38	0.0025	1	K.KPADK.S

5. gi|3426089 **Mass:** 177601 **Score:** 29 **Queries matched:** 5 **emPAI:** 0.02
polyprotein [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1527	672.4048	671.3975	671.3966	1.27	0	29	0.019	1	K.TVSLPR.L
☑	1528	672.4049	671.3976	671.3966	1.46	0	(24)	0.051	1	K.TVSLPR.L
☑	1529	672.4054	671.3981	671.3966	2.24	0	(29)	0.019	1	K.TVSLPR.L
☑	1530	672.4055	671.3982	671.3966	2.37	0	(28)	0.023	1	K.TVSLPR.L
☑	1532	672.4060	671.3988	671.3966	3.19	0	(28)	0.021	1	K.TVSLPR.L

Proteins matching the same set of peptides:

gi|21214752 **Mass:** 206214 **Score:** 29 **Queries matched:** 5

gag-pol polyprotein precursor; hypothetical protein [Drosophila melanogaster]
gi|25009978 **Mass:** 83774 **Score:** 29 **Queries matched:** 5
GH06606p [Drosophila melanogaster]

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6. gi|17862878 **Mass:** 232888 **Score:** 28 **Queries matched:** 1 **emPAI:** 0.01
SD01389p [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1537	674.3734	673.3662	673.3646	2.26	0	28	0.027	1	K.IDLADK.E

Proteins matching the same set of peptides:
gi|19527661 **Mass:** 141204 **Score:** 28 **Queries matched:** 1
SD03956p [Drosophila melanogaster]
gi|24650843 **Mass:** 232920 **Score:** 28 **Queries matched:** 1
CG10011-PA [Drosophila melanogaster]
gi|125773229 **Mass:** 229479 **Score:** 28 **Queries matched:** 1
GA10007-PA [Drosophila pseudoobscura]

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7. gi|8380 **Mass:** 29436 **Score:** 25 **Queries matched:** 1 **emPAI:** 0.11
unnamed protein product [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1967	536.8000	1071.5855	1071.5812	4.03	0	25	0.031	1	K.LLDSAIPSEK.I

Proteins matching the same set of peptides:
gi|17136420 **Mass:** 29393 **Score:** 25 **Queries matched:** 1
Proteasome 29kD subunit CG9327-PA [Drosophila melanogaster]
gi|125811518 **Mass:** 29205 **Score:** 25 **Queries matched:** 1
GA21704-PA [Drosophila pseudoobscura]

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8. gi|24644950 **Mass:** 36839 **Score:** 25 **Queries matched:** 2
CG2767-PA [Drosophila melanogaster]

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	1957	523.2861	1044.5577	1044.5564	1.30	0	25	0.063	1	K.LSSLDQNIR.I
☑	1959	523.2873	1044.5601	1044.5564	3.58	0	(22)	0.14	1	K.LSSLDQNIR.I

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
☑	781	499.2993	498.2920	498.2914	1.20	0	23	0.12	1	GGIPR
☑	782	499.2996	498.2923	498.2914	1.72	0	23	0.13	1	GGIPR
☑	1300	603.3106	602.3034	602.3024	1.65	0	22	0.22	1	DLEAR
☑	1330	612.3845	611.3772	611.3755	2.80	0	21	0.1	1	LNIPR
☑	1170	571.3574	570.3501	570.3489	2.11	0	21	0.05	1	VSIPR
☑	1881	920.4873	919.4800	919.4763	4.05	1	21	0.18	1	EKYPVER
☑	1302	603.3113	602.3040	602.3024	2.77	0	21	0.32	1	DLEAR
☑	1809	423.2281	844.4416	844.4443	-3.19	0	20	0.16	1	SPALWGSK
☑	1304	603.3116	602.3043	602.3024	3.16	0	20	0.37	1	DLEAR
☑	1650	725.4692	724.4620	724.4595	3.35	0	20	0.06	1	LINLPR
☑	1732	394.2197	786.4249	786.4236	1.66	0	19	0.19	1	EVGDLVR
☑	1895	466.7426	931.4706	931.4723	-1.80	0	19	0.16	1	INDSLQSR
☑	2110	771.4011	2311.1815	2311.1736	3.44	1	19	0.23	1	ALYLGDNDFEYIPKEVGQLK
☑	1382	628.3793	627.3721	627.3704	2.63	0	19	0.16	1	GSVLPR
☑	1605	702.3798	701.3725	701.3708	2.50	0	19	0.3	1	VLDEAR
☑	1890	928.5590	927.5518	927.5501	1.76	0	19	0.17	1	ILNVSINR
☑	1303	603.3114	602.3041	602.3024	2.92	0	19	0.49	1	DLEAR
☑	1168	571.3568	570.3495	570.3489	0.99	0	19	0.087	1	VSIPR
☑	1489	658.3905	657.3832	657.3810	3.46	0	18	0.44	1	EAAIVR
☑	1535	673.3908	672.3835	672.3806	4.32	0	18	0.27	1	EVGQLK
☑	1566	681.3808	680.3735	680.3718	2.54	0	18	0.062	1	HLQAGR
☑	1989	587.8335	1173.6525	1173.6506	1.62	0	18	0.18	1	YVLPLGTQQR
☑	922	515.3309	514.3237	514.3227	1.81	0	17	0.83	1	LGAVR
☑	920	515.3309	514.3236	514.3227	1.69	0	17	0.84	1	LGAVR