Mascot Search Results

User : PRL_NUCLEI
Email :
Search title : Submitted from linz a flav 2Da by Mascot Daemon on D55NS391
MS data file : C:\Xcalibur\sequest\Linz\v2009121702.mgf
Database : Aspergillus flavus-AY371490_parasiticus (14799 sequences; 6103753 residues)
Timestamp : 18 Dec 2009 at 14:30:48 GMT
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 2 Da (# ^{13}C = 1)
Fragment Mass Tolerance: ± 0.6 Da
Max Missed Cleavages : 2
Instrument type : ESI-TRAP
Number of queries : 16412
Protein hits :

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gi|220697217|gb|EED53558.1|	NADPH cytochrome P450 reductase (CprA), putative [Aspergillus flav
gi|220691248|gb|EED47596.1|	cell division control protein Cdc48 [Aspergillus flavus NRRL3357]
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gi|220699027|gb|EED55366.1|	polyubiquitin UbiD/Ubi4, putative [Aspergillus flavus NRRL3357]
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gi|220699259|gb|EED55598.1|	ubiquitin UbiA, putative [Aspergillus flavus NRRL3357]
gi|220694536|gb|EED50880.1|	V-type ATPase, B subunit, putative [Aspergillus flavus NRRL3357]
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gi|220697382|gb|EED53723.1|	conserved hypothetical protein [Aspergillus flavus NRRL3357]
gi|220700631|gb|EED56969.1|	phospholipase PldA, putative [Aspergillus flavus NRRL3357]
gi|220694211|gb|EED50555.1|	conserved hypothetical protein [Aspergillus flavus NRRL3357]
gi|220697584|gb|EED53925.1|	methionine aminopeptidase, type II, putative [Aspergillus flavus N
gi|220698460|gb|EED54800.1|	ribosomal protein S15, putative [Aspergillus flavus NRRL3357]
gi|220701477|gb|EED57815.1|	Sec23/Sec24 family protein [Aspergillus flavus NRRL3357]
gi|220697844|gb|EED54184.1|	protein phosphatase 2A catalytic subunit Pph21, putative [Aspergil
gi|220700656|gb|EED56994.1|	metallopeptidase MepB [Aspergillus flavus NRRL3357]
gi|220691491|gb|EED47839.1|	arylsulfatase, putative [Aspergillus flavus NRRL3357]
gi|220700052|gb|EED56391.1|	carbon catabolite repression protein CreD, putative [Aspergillus f
gi|220698436|gb|EED54776.1|	glycolipid transfer protein HET-C2, putative [Aspergillus flavus N
gi|220691415|gb|EED47763.1|	actin interacting protein 2 [Aspergillus flavus NRRL3357]
gi|220694306|gb|EED50650.1|	orotate phosphoribosyltransferase [Aspergillus flavus NRRL3357]
gi|46370483|gb|AAS90018.1|	OmtA [Aspergillus flavus]
gi|220693839|gb|EED50184.1|	conserved hypothetical protein [Aspergillus flavus NRRL3357]
gi|220696817|gb|EED53158.1|	phosphoserine aminotransferase [Aspergillus flavus NRRL3357]
gi|220699236|gb|EED55575.1|	transmembrane protein 14, putative [Aspergillus flavus NRRL3357]
gi|1762235|gb|AAC23536.1|	polyketide synthase PKSL2 [Aspergillus parasiticus]
gi|220688427|gb|EED44780.1|	polyketide synthase, putative [Aspergillus flavus NRRL3357]
gi|220699699|gb|EED56038.1|	phosphatidylinositol transporter, putative [Aspergillus flavus NRR
gi|220696458|gb|EED52800.1|	aspartate transaminase, putative [Aspergillus flavus NRRL3357]
gi|220692426|gb|EED48773.1|	oligosaccharyl transferase subunit (alpha), putative [Aspergillus
gi|220694178|gb|EED50522.1|	Arp2/3 complex subunit (Arp3), putative [Aspergillus flavus NRRL33
gi|220700573|gb|EED56911.1|	structure-specific recognition protein, putative [Aspergillus flav
gi|220691595|gb|EED47943.1|	exonuclease Kem1, putative [Aspergillus flavus NRRL3357]

gi|220690781|gb|EED47130.1|	tubulin beta subunit [Aspergillus flavus NRRL3357]
gi|220694223|gb|EED50567.1|	KH domain RNA-binding protein [Aspergillus flavus NRRL3357]
gi|220698074|gb|EED54414.1|	NADH-ubiquinone oxidoreductase 12 kda subunit, putative [Aspergill

	Aspergillus	Decoy	False discovery rate
Peptide matches above identity threshold	2604	22	0.84 %
Peptide matches above homology or identity threshold	3345	97	2.90 %

Select Summary Report

Format As: Select Summary (protein hits) Help

Significance threshold p< 0.05 Max. number of hits AUTO

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

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

1. gi|220689386|gb|EED45737.1| **Mass:** 55369 **Score:** 4307 **Queries matched:** 231 **emPAI:** 16.94
ATP synthase F1, beta subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4	609.3310	608.3237	608.2806	0.0431	0	17	2.5	1	K.FEGEK.L
763	488.5926	975.1707	974.5549	0.6158	0	44	0.0071	1	K.IGLFGGAGVGK.T 758 759 761 765 767
887	500.8601	999.7057	999.5600	0.1457	1	45	0.0055	1	K.LLAELENKA.- 882 884 885
1221	537.6926	1073.3707	1071.6288	1.7419	1	33	0.084	1	K.LVDLKDTIR.S
1448	558.8551	1115.6957	1115.6339	0.0618	0	52	0.0011	1	K.VVDLLAPYAR.G 1447 1449 1451 1463 1464
1727	583.7901	1165.5657	1165.5801	-0.0144	0	75	4.9e-06	1	R.VQQMLQEYK.S 1732
2322	632.6851	1263.3557	1262.7347	0.6210	0	29	0.21	1	K.VHQVIGAVVDVK.F 2314 2315 2317 2320 2323 2328 2330 2
2475	640.1306	1278.2467	1277.6285	0.6182	0	(62)	0.00011	1	R.TIAMEGTEGLTR.G 2474 2476 2492
2625	648.6861	1295.3577	1293.6235	1.7343	0	77	3.2e-06	1	R.TIAMEGTEGLTR.G 2598 2602 2607 2611 2612 2615 2618 2
2895	664.6266	1327.2387	1326.6779	0.5608	0	62	0.00011	1	R.ILNVTGDPVDER.G 2884 2894 2898 2924 2926
3381	688.3971	1374.7797	1374.6528	0.1269	0	62	0.00013	1	R.IVGQDHYDTATR.V 3378 3385 3397 3400
3879	718.6546	1435.2947	1434.7467	0.5480	0	81	1.3e-06	1	R.FTQAGSEVSALLGR.I 3877 3888 3889 3895 3898 3902 3905
3883	718.8501	1435.6857	1435.6844	0.0013	0	79	1.9e-06	1	K.AHGGYSVFTGVGER.T 3894 3899 3900 3907 3912 3918
4053	727.5011	1452.9877	1452.7977	0.1901	0	90	1.6e-07	1	R.VALTGLTIAEYFR.D 4060 4074
4472	752.4016	1502.7887	1501.8504	0.9383	0	87	3.4e-07	1	K.TVFIQELINNIAK.A 4454 4456 4458 4473 4474 4476 4480
5292	793.6841	1585.3537	1584.8082	0.5455	0	78	2.4e-06	1	K.VALVFGQMNEPPGAR.A 5307 5308 5312
5463	801.2826	1600.5507	1600.8032	-0.2524	0	(70)	1.5e-05	1	K.VALVFGQMNEPPGAR.A 5454 5470 5477 5478 5483 5490 549
5739	811.7191	1621.4237	1620.8835	0.5402	0	63	7.4e-05	1	R.DTGAPITIPVGPGTLGR.I 5729 5738
6698	847.0141	1692.0137	1690.9366	1.0771	0	58	0.00026	1	K.LVLEVSQHLGENVVR.T 6661 6673 6682 6685 6686 6687 669

6920	855.5741	1709.1337	1707.9156	1.2182	1	45	0.0045	1	R.ILNVTGDPVDERGPVK.A 6906 6918
7069	863.2091	1724.4037	1723.9104	0.4933	0	86	3.5e-07	1	K.LPAILNAIETENNGQK.L 7082 7085 7087 7088
7578	888.1171	1774.2197	1772.9196	1.3001	0	44	0.0057	1	R.GISELGIYPAVDPLDSK.S 7568 7570 7571 7575
8391	619.2879	1854.8417	1853.0047	1.8370	1	1	1.2e+02	9	K.VHQVIGAVVDVKFEGEK.L
9375	985.0011	1967.9877	1968.0357	-0.0480	0	99	1.7e-08	1	R.FLSQPFTVAQVFTGIEGK.L 9374 9383 9386 9389 9391 9392
9760	672.7395	2015.1967	2016.0528	-0.8560	1	14	5.1	1	R.GISELGIYPAVDPLDSKSR.M 9761
10106	684.0532	2049.1377	2047.1174	2.0203	1	0	1.3e+02	3	R.GAAARDTGAPITIPVGPGTLGR.I
10208	1031.2881	2060.5617	2060.0347	0.5270	0	(110)	1.4e-09	1	K.SLQDIIAILGMDELSEADK.L 10210 10213 10220 10232
10350	1039.9356	2077.8567	2076.0296	1.8271	0	111	9.7e-10	1	K.SLQDIIAILGMDELSEADK.L 10335 10342 10349
11399	1110.7321	2219.4497	2219.0715	0.3783	0	95	4e-08	1	R.IPSAVGYQPTLAVDMGGMQER.I 11400 11405
11498	1118.8276	2235.6407	2235.0664	0.5743	0	(46)	0.0029	1	R.IPSAVGYQPTLAVDMGGMQER.I 11499
11515	1119.5021	2236.9897	2235.0664	1.9233	0	(7)	25	2	R.IPSAVGYQPTLAVDMGGMQER.I 11514
11592	1126.9181	2251.8217	2251.0613	0.7604	0	(41)	0.0094	1	R.IPSAVGYQPTLAVDMGGMQER.I
12070	773.0085	2316.0037	2314.1804	1.8233	1	34	0.045	1	K.FEGEKLPAILNAIETENNGQK.L
13386	836.2849	2505.8327	2505.1329	0.6998	0	53	0.00058	1	R.EGNDLYHEMQETGVIQLEGESK.V 13397 13400 13402
13498	841.2899	2520.8477	2521.1278	-0.2801	0	(2)	71	9	R.EGNDLYHEMQETGVIQLEGESK.V
14303	1330.5031	2658.9917	2658.3786	0.6132	1	119	1.4e-10	1	K.SLQDIIAILGMDELSEADKLTVER.A 14302 14307 14314 1432
14349	1334.4561	2666.8977	2666.2534	0.6444	0	94	4.1e-08	1	K.AIINGEADDLPEAAFYMVGDLESAR.A 14357 14359 14362 143
14430	892.9522	2675.8347	2674.3735	1.4612	1	(55)	0.00038	1	K.SLQDIIAILGMDELSEADKLTVER.A 14410 14417 14426 1442
14478	1342.9146	2683.8147	2682.2483	1.5664	0	(53)	0.00052	1	K.AIINGEADDLPEAAFYMVGDLESAR.A 14476
15035	1415.0256	2828.0367	2827.4280	0.6088	0	73	5.2e-06	1	K.YAPIHAEAPEFVEQSTEGEILVTGIK.V 15036 15039 15040 15
15106	948.2915	2841.8527	2839.5080	2.3447	2	3	51	1	R.LASTEAGATGKVHQVIGAVVDVKFEGEK.L
15221	960.8539	2879.5397	2881.3803	-1.8406	1	2	68	1	K.AIINGEADDLPEAAFYMVGDLESARAK.G 15224
16210	1120.4445	3358.3117	3356.7292	1.5825	1	57	0.0002	1	R.VALTGLTIAEYFRDEEGQDVLLFIDNIFR.F

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2. gi|220700135|gb|EED56474.1| **Mass:** 47434 **Score:** 3041 **Queries matched:** 152 **emPAI:** 3.70

enolase/allergen Asp F 22 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
161	378.9596	755.9047	755.4653	0.4394	0	33	0.072	1	K.LNQILR.I 157 158 159 160 163
502	451.8541	901.6937	901.5055	0.1882	0	55	0.00066	1	K.ACNALLLK.V 500 501 503
590	922.9430	921.9357	921.4556	0.4801	0	21	1.2	1	R.QGAEVYQK.L
608	464.9511	927.8877	927.4702	0.4176	1	31	0.12	1	K.KYDLDFK.N
1191	535.2076	1068.4007	1067.6815	0.7193	1	11	11	5	R.LAKLNQILR.I
3215	681.1271	1360.2397	1359.6380	0.6017	0	(64)	6.6e-05	1	K.IAMDVASSEFYK.A 3214 3217 3219 3223 3227 3230 3234
3394	688.7436	1375.4727	1375.6329	-0.1602	0	64	6.4e-05	1	K.IAMDVASSEFYK.A 3392 3395 3401
4840	771.9471	1541.8797	1541.7766	0.1032	0	58	0.00022	1	K.WLTYEQLADLYK.T 4837 4838 4845 4867
4848	772.2606	1542.5067	1540.8249	1.6818	0	64	6e-05	1	K.GVPLYAHISDLAGTK.K 4834
5152	787.1736	1572.3327	1571.8519	0.4809	0	77	3.1e-06	1	K.VNQIGTLTESIQAAK.D 5148 5153 5154 5155 5170 5173 518
5621	806.8786	1611.7427	1610.9355	0.8072	0	95	4.6e-08	1	K.SNLGANAILGVSLAIAK.A 5598 5600 5601 5603 5605 5607 5
5849	544.4005	1630.1797	1629.7158	0.4639	1	31	0.11	1	K.YDLDFKNPDSDSSK.W

5907	818.7121	1635.4097	1635.7100	-0.3003	0	86	4.2e-07	1	K.DSYADNWGVMVSHR.S 5905 5917 5922 5934 5937
6121	826.6656	1651.3167	1648.7944	2.5224	0	23	0.76	1	R.IEEELGNNAIYAGEK.F
7292	874.0411	1746.0677	1744.8843	1.1834	0	108	2.3e-09	1	R.SGETEDVTIADIAVGLR.S 7264 7268 7274 7275 7279 7280 7
7376	879.8711	1757.7277	1757.8108	-0.0831	2	97	2.8e-08	1	K.KYDLDFKNPDSDSSK.W 7377 7381
8104	912.6196	1823.2247	1821.9221	1.3026	0	43	0.0065	1	R.GNPTVEVDVVTETGLHR.A 8090 8092 8095 8097 8098 8099
8214	613.2092	1836.6057	1836.0006	0.6051	2	11	12	2	K.THWGGKGVLKAVENVNK.T
8449	930.7696	1859.5247	1858.9286	0.5962	0	107	3e-09	1	R.AIVPSGASTGQHEAHELR.D 8432 8455 8458 8460
9563	996.7051	1991.3957	1990.0008	1.3950	0	91	1.1e-07	1	K.TSDFQIVGDDLTVTNPLR.I 9532 9534 9558 9567 9569 9573
10780	713.7889	2138.3447	2138.2059	0.1389	1	1	1.1e+02	7	K.SNLGANAILGVSLAIAKAGAAEK.G
12007	770.6239	2308.8497	2306.2284	2.6213	0	29	0.15	1	K.KPYVLPVPFQNVLNGGSHAGGR.L 11997 11999 12000 12001 1
12027	1156.3136	2310.6127	2310.1718	0.4409	0	66	3.1e-05	1	R.LAFQEFMIVPSAAPSFSEALR.Q 12022 12025 12028 12029 12
12149	1164.3561	2326.6977	2326.1667	0.5310	0	(66)	3.6e-05	1	R.LAFQEFMIVPSAAPSFSEALR.Q 12148 12150 12156 12157 12
12426	792.3479	2374.0217	2372.1172	1.9045	1	7	26	1	K.NPDSDSSKWLTYEQLADLYK.T
15197	1436.9706	2871.9267	2869.2799	2.6468	0	92	6.5e-08	1	K.YPIVSIEDPFAEDDWEAWSYFYK.T 15188 15189 15195
15210	959.1935	2874.5587	2872.4130	2.1457	2	5	35	2	K.NPDSDSSKWLTYEQLADLYKTLASK.Y

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3. gi|220699546|gb|EED55885.1| **Mass:** 63457 **Score:** 2763 **Queries matched:** 186 **emPAI:** 5.81

pyruvate decarboxylase PdcA, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
172	763.5390	762.5317	762.3483	0.1834	0	13	9.3	1	R.ECWIR.S
366	856.9270	855.9197	855.4086	0.5111	0	5	47	4	K.GAVDETHK.N
1923	603.6796	1205.3447	1203.6322	1.7125	0	(34)	0.064	1	K.SGLPTFVAPMGK.G 1925
2015	611.6426	1221.2707	1219.6271	1.6436	0	44	0.0069	1	K.SGLPTFVAPMGK.G 2007 2010 2019
2439	639.1111	1276.2077	1274.5489	1.6588	0	42	0.01	1	R.YSEYPDINMK.G 2429
2606	647.7731	1293.5317	1293.5626	-0.0309	0	67	3.3e-05	1	K.SDFNTTGFSYR.I 2600 2604 2608 2609 2615 2618 2634 26
3052	672.6726	1343.3307	1342.6769	0.6538	0	57	0.00032	1	R.VLDEVHEFVEK.S
3114	676.2246	1350.4347	1349.7343	0.7004	0	61	0.00012	1	R.KPIDVAEYLFR.R 3103 3116 3118 3119 3126 3127 3132
3158	678.2741	1354.5337	1353.7802	0.7535	0	66	3.7e-05	1	K.KPVILVDACAIR.H 3152 3153 3162
5119	785.6696	1569.3247	1567.7379	1.5868	0	68	2.7e-05	1	K.NYGGVYAGTGSNPGVR.E 5108 5117
5897	818.0826	1634.1507	1635.8369	-1.6862	1	1	1.2e+02	6	R.HRVLDEVHEFVEK.S 5895
6802	851.3951	1700.7757	1700.9196	-0.1439	0	116	3.4e-10	1	R.EQVESSDLILSIGAIK.S 6785 6786 6794 6798 6799 6803 6
6901	854.7931	1707.5717	1705.9073	1.6644	0	44	0.0057	1	R.SRPVYISLPTDMVTK.K 6893 6898
7062	862.7351	1723.4557	1721.9022	1.5535	0	(41)	0.01	1	R.SRPVYISLPTDMVTK.K 7041 7052 7056 7058
7437	882.6751	1763.3357	1762.8989	0.4368	0	2	90	4	R.LDTPLDLSLPPNDPEK.E
7440	882.7431	1763.4717	1762.9002	0.5715	0	81	1.1e-06	1	R.IGQLNTIDFHSTYVR.V 7439 7451 7452 7453 7456 7461 74
8477	622.3329	1863.9767	1860.9985	2.9782	1	4	50	4	K.EDYVVDVVLKYLHAAK.K
9602	998.4836	1994.9527	1993.9745	0.9782	0	30	0.14	1	K.DVVITETGTANFGIWDTR.F 9603
10008	1020.8191	2039.6237	2040.0680	-0.4443	0	89	1.8e-07	1	R.AVHGVPGDYNLVALDYLPK.C 10012 10014 10017 10027 100
10822	1072.9361	2143.8577	2143.0269	0.8308	0	53	0.00063	1	K.DGMLLHHTLGNGDFNVFTR.M 10824 10826 10852 10853
10955	721.4975	2161.4707	2159.0219	2.4489	0	(12)	7.1	1	K.DGMLLHHTLGNGDFNVFTR.M 10954

11175	1096.8091	2191.6037	2191.0943	0.5094	0	(64)	5.3e-05	1	R.MGNLNVGPVSPPSNLLPDNEK.A 11177 11208
11299	1104.8046	2207.5947	2207.0892	0.5055	0	67	2.7e-05	1	R.MGNLNVGPVSPPSNLLPDNEK.A 11298 11307
11612	752.2705	2253.7897	2251.1121	2.6776	1	52	0.00085	1	K.EKDVVITETGTANFGIWDTR.F 11588 11590 11594 11595 115
11771	1140.7841	2279.5537	2278.1416	1.4122	0	74	4.9e-06	1	R.NNLNPIIFVICNEGYTIER.Y 11757 11760 11762 11770 1177
12177	777.6382	2329.8927	2330.3157	-0.4230	2	4	54	5	K.YLHAAKKPVILVDACAIRHR.V
12773	1212.4586	2422.9027	2422.2434	0.6594	0	66	2.8e-05	1	K.ASTEQAITHAWLWPTVGQWLK.E 12760 12785 12786
14562	1351.5366	2701.0587	2700.3040	0.7548	0	52	0.00072	1	R.ELFANEEFASAPCLQLVELHMPR.D 14564 14566 14567 14573
14658	906.9689	2717.8847	2716.2989	1.5859	0	(38)	0.015	1	R.ELFANEEFASAPCLQLVELHMPR.D 14652 14660
15289	975.4579	2923.3517	2922.5114	0.8403	1	65	3.2e-05	1	R.LDTPLDLSLPPNDPEKEDYVVDVVLK.Y 15285 15286 15290 15
15375	1482.1936	2962.3727	2961.3994	0.9733	0	109	1.2e-09	1	R.MSADISCTLGCLNSTHEVATLIDNAIR.E 15373 15376 15378
15410	993.5282	2977.5627	2977.3943	0.1684	0	(47)	0.002	1	R.MSADISCTLGCLNSTHEVATLIDNAIR.E 15415 15416
15569	1018.2539	3051.7397	3049.5695	2.1702	0	67	2.2e-05	1	R.FPAGVTAISQVLWGSIGYSVGACQGAALAAK.E 15557 15561 155
15823	1055.4452	3163.3137	3162.5603	0.7534	0	46	0.0023	1	R.YIHGWEAVYNDIQPWDFLNIPVAFGAK.D 15826 15827 15828
15911	1071.5842	3211.7307	3212.7339	-1.0032	2	4	34	2	K.GVLQKIVQRMGNLNVGPVSPPSNLLPDNEK.A

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4. gi|220700832|gb|EED57170.1| **Mass:** 60129 **Score:** 2308 **Queries matched:** 173 **emPAI:** 2.40

mitochondrial F1 ATPase subunit alpha, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
101	359.0511	716.0877	715.4480	0.6398	0	36	0.053	1	R.LTELLK.Q 99
115	362.3291	722.6437	722.4439	0.1998	0	45	0.0047	1	K.APGILPR.R 112 114 116
190	777.3580	776.3507	776.3916	-0.0408	0	26	0.58	1	K.ETEASLK.E
256	815.3980	814.3907	814.4548	-0.0641	0	27	0.33	1	R.ELIIGDR.Q 257 258 259 261
270	818.4940	817.4867	817.4294	0.0574	1	10	23	5	K.EGETVKR.T
337	423.5326	845.0507	844.5018	0.5489	0	65	7.5e-05	1	R.STVAQLVK.T 334 335 336 339 340
385	431.1001	860.1857	859.4949	0.6908	0	(24)	0.92	1	R.QMSLLLR.R
436	438.9421	875.8697	875.4899	0.3799	0	31	0.16	2	R.QMSLLLR.R 437
537	456.1766	910.3387	909.5072	0.8315	0	37	0.028	1	K.LFLAQYR.E 532 534 536
816	986.5440	985.5367	985.5556	-0.0189	0	35	0.061	1	R.VLSVGDGIAR.V 814 821
895	501.6046	1001.1947	1000.6029	0.5918	1	9	23	5	K.RSTVAQLVK.T
1085	1048.5100	1047.5027	1047.5746	-0.0719	1	11	16	4	K.AMKQVAGSLK.L
1311	545.7766	1089.5387	1088.6012	0.9375	1	10	18	2	R.VGSAAQVKAMK.Q
1660	575.6406	1149.2667	1148.5318	0.7349	0	57	0.00036	1	K.CVDSMVPIGR.G 1661
1750	585.8456	1169.6767	1169.6404	0.0363	0	45	0.0055	1	R.SVNQPVQTGLK.C 1747 1748 1749 1754 1756
1881	1197.7070	1196.6997	1196.6401	0.0596	0	53	0.00078	1	R.VVDALGNPIDGK.G 1878 1882 1884 1887 1899
2055	615.2386	1228.4627	1228.6775	-0.2148	1	10	15	1	R.ELIIGDRQTGK.T 2058
2413	637.5896	1273.1647	1272.6714	0.4933	0	72	1.2e-05	1	R.HAVIIYDDLSK.Q 2408 2410 2412 2417 2420 2421 2422
2773	657.6781	1313.3417	1312.6849	0.6568	0	10	17	4	K.LYCIYVAVGQK.R
2793	658.8406	1315.6667	1315.6368	0.0299	0	84	6.3e-07	1	R.GVQEEAGLAETGR.V 2791 2792 2795 2797 2801 2805 2808
3273	683.2801	1364.5457	1363.6480	0.8977	2	6	42	6	K.RWNNTSDESKK.L
3334	1371.6890	1370.6817	1370.6677	0.0140	0	36	0.042	1	K.SNNPEIQEAIEK.E 3336

3714	708.7586	1415.5027	1415.7256	-0.2229	0	71	1.1e-05	1	K.ASPTEVSSILEQR.I 3717 3735 3739 3740
3867	478.5692	1432.6857	1429.7711	2.9146	1	8	26	5	K.TAVALDAMLNQKR.W
4926	517.4992	1549.4757	1547.8606	1.6151	1	4	61	7	K.QAVAYRQMSLLLR.R
4988	778.5981	1555.1817	1552.7310	2.4507	0	35	0.045	1	R.EAYPGDVFYLHSR.L 4982 4985 4991
5441	800.7646	1599.5147	1598.8457	0.6691	0	71	1.2e-05	1	K.ILQWESDFLAHLK.S 5428 5440 5447 5453 5455 5459 5462
6116	826.3686	1650.7227	1649.8988	0.8239	0	37	0.03	1	R.TGEIVDVPVGPELLGR.V 6103 6104 6117 6122 6129 6131 61
7242	871.4756	1740.9367	1739.8366	1.1001	0	79	2e-06	1	R.EVAAFAQFGSDLDAATK.Q 7179 7182 7188 7189 7193 7195 7
9915	678.6955	2033.0647	2032.0623	1.0025	2	4	57	4	K.RSTVAQLVKTLEENDAMK.Y 9913
10791	1071.2151	2140.4157	2138.9911	1.4246	0	(5)	45	2	K.GMCMNLEAGQVGVVLFGSDR.L 10789
10849	1073.8536	2145.6927	2144.0572	1.6355	0	107	2.7e-09	1	R.VHGMTNVQAEELVEFASGVK.G 10816 10820 10821 10828 108
10882	717.2365	2148.6877	2150.0855	-1.3978	1	4	48	1	R.TYAAEAKASPTEVSSILEQR.I
10924	719.5772	2155.7097	2154.9861	0.7237	0	(10)	13	3	K.GMCMNLEAGQVGVVLFGSDR.L 10919
10935	1079.4736	2156.9327	2154.9861	1.9467	0	19	1.4	2	K.GMCMNLEAGQVGVVLFGSDR.L
11050	1087.4826	2172.9507	2170.9810	1.9698	0	(7)	28	1	K.GMCMNLEAGQVGVVLFGSDR.L
12185	778.5979	2332.7717	2334.2120	-1.4403	2	14	4.9	1	R.EAYPGDVFYLHSRLLERAAK.M
12920	815.2602	2442.7587	2440.2679	2.4908	2	1	1e+02	4	R.RSVNQPVQTGLKCVDSMVPIGR.G
13315	833.0165	2496.0277	2495.2335	0.7942	1	3	61	1	K.GMCMNLEAGQVGVVLFGSDRLVK.E

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5. gi|220694557|gb|EED50901.1| **Mass:** 94681 **Score:** 1847 **Queries matched:** 122 **emPAI:** 1.77

translation elongation factor EF-2 subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
60	684.6450	683.6377	684.2901	-0.6524	0	4	48	6	R.FMDTR.A
737	485.5646	969.1147	968.5403	0.5744	0	60	0.00017	1	R.GGGQIIPTAR.R 732 734 735
782	978.8000	977.7927	977.4342	0.3585	0	9	22	1	K.FDDPEDLK.E
828	987.6260	986.6187	986.5396	0.0791	0	10	20	10	K.IIDAVTNNK.R 823 825
1018	518.3756	1034.7367	1034.5397	0.1971	0	36	0.047	1	K.ISDPVVSYR.E 1016 1017 1020
1034	520.1546	1038.2947	1036.7008	1.5939	0	22	1	1	R.IKPVLIINK.I 1028
1236	539.2191	1076.4237	1076.5866	-0.1629	0	46	0.0051	1	K.AVQYLNEIK.D 1237
1439	558.0276	1114.0407	1113.5124	0.5283	0	39	0.021	1	R.EGPVAEEPMR.A 1435
1545	566.0271	1130.0397	1129.5074	0.5324	0	(29)	0.26	1	R.EGPVAEEPMR.A
1841	1189.3780	1188.3707	1187.5782	0.7925	0	10	18	3	K.STDADGKPLER.A
2113	619.6521	1237.2897	1236.5928	0.6970	0	55	0.00054	1	R.LWGDNFFNPK.T 2111
2154	622.7826	1243.5507	1243.5292	0.0216	0	47	0.0031	1	K.EDLYQNFCR.I 2152
2204	625.3581	1248.7017	1248.6682	0.0335	1	4	65	10	K.IQRTVLMMGGK.T
2378	635.6601	1269.3057	1269.6928	-0.3871	1	14	5.7	3	R.SVEVKNAADLPK.L
2563	645.5886	1289.1627	1288.7503	0.4124	2	7	32	8	K.EDLFIKKIQR.T
2852	662.0566	1322.0987	1321.6514	0.4473	0	52	0.001	1	K.DLEEDHAGVPLK.I 2850 2855
3135	676.8951	1351.7757	1351.6521	0.1236	0	47	0.003	1	K.DSVVSGFQWATR.E
3421	690.1651	1378.3157	1377.6850	0.6307	0	21	1.3	2	K.EDPAPLMLYVSK.M
4098	730.3591	1458.7037	1455.7140	2.9897	1	1	1.1e+02	1	R.EGPVAEEPMRAVR.F

4567	759.2236	1516.4327	1514.7228	1.7099	0	56	0.00042	1	R.AFNQFCLDPIYK.I 4566
4711	765.7236	1529.4327	1528.8712	0.5615	1	2	1.1e+02	5	R.DQITTLVEKLEIK.L
5318	794.8286	1587.6427	1587.7457	-0.1029	1	50	0.0015	1	K.EVVPGYENYYDKL.- 5351 5356
5397	798.4086	1594.8027	1593.8304	0.9724	2	9	17	2	R.LWGDNFFNPKTKK.W 5404
5814	814.6956	1627.3767	1626.6984	0.6783	0	109	2e-09	1	R.LMADDYGWDVTDAR.K 5819
5996	822.6621	1643.3097	1642.6933	0.6164	0	(85)	5.2e-07	1	R.LMADDYGWDVTDAR.K 5972 5998
6890	569.8045	1706.3917	1704.8756	1.5161	1	22	0.84	1	K.AGSKEDPAPLMLYVSK.M
6917	855.4731	1708.9317	1707.8931	1.0387	0	48	0.0021	1	R.IIETVNVTIATYEDK.V 6914 6915 6919 6923 6924 6928 692
6958	857.1516	1712.2887	1713.9162	-1.6275	1	3	76	5	R.SGLQVRIQGPNYTPGK.K
7043	861.9651	1721.9157	1720.8705	1.0452	1	(4)	50	10	K.AGSKEDPAPLMLYVSK.M
7127	866.7591	1731.5037	1730.8563	0.6475	2	6	35	5	K.MVPTSDKGRFYAFGR.V 7121
7339	877.6446	1753.2747	1752.8948	0.3799	0	73	6.9e-06	1	K.GTVAFGSGLQGWAFTVR.Q 7334 7341 7348 7351
7661	891.5046	1780.9947	1778.9665	2.0282	2	0	1.2e+02	3	K.LTSEEKEYEGKLLLK.T 7654
7724	893.7286	1785.4427	1784.8734	0.5694	0	85	5e-07	1	K.AYLPVNESFGFTGDLR.A 7712 7713 7723 7725 7727 7730 77
8526	624.3235	1869.9487	1869.8316	0.1172	1	4	55	9	R.ARLMADDYGWDVTDAR.K 8523
10188	1030.3351	2058.6557	2058.0534	0.6023	0	76	3.6e-06	1	R.GHVYAEEQRPGTPIYTIK.A 10178 10185 10211
10336	1039.3371	2076.6597	2076.0528	0.6069	0	100	1.2e-08	1	K.IWTFGPDTTGANLLVDQTK.A 10343
10574	703.6252	2107.8537	2108.0282	-0.1745	2	1	1.1e+02	5	K.DCKAGSKEDPAPLMLYVSK.M
10705	710.3099	2127.9077	2126.9803	0.9274	2	2	88	3	K.TRARLMADDYGWDVTDAR.K
10753	1069.0151	2136.0157	2136.0483	-0.0325	1	0	1.2e+02	1	K.EDPAPLMLYVSKMVPTSDK.G
11286	1103.8516	2205.6887	2205.0874	0.6013	0	106	3.7e-09	1	R.LYVTAEPIEEECALAIEAGK.I 11288 11290 11291 11292 112
11287	1103.8716	2205.7287	2204.1478	1.5810	1	102	9e-09	1	R.KIWTFGPDTTGANLLVDQTK.A 11280 11283 11289
12104	774.4039	2320.1897	2318.2416	1.9481	2	4	46	1	M.VNFTIEEIRSLMDKPKNIR.N
12673	1206.4541	2410.8937	2410.2281	0.6656	1	97	2.4e-08	1	K.AVQYLNEIKDSVVSGFQWATR.E 12663 12674 12676 12678 12
12917	814.9439	2441.8097	2443.2264	-1.4167	2	0	1.1e+02	4	K.ISDPVVSYRESVSGKSSMTALSK.S
12963	817.7882	2450.3427	2449.2821	1.0606	2	1	95	5	-.MVNFTIEEIRSLMDKPKNIR.N
13433	1256.2961	2510.5777	2509.4124	1.1654	2	3	55	5	R.IKPVLIINKIDRSMMEQQLPK.E 13421 13426
13577	843.6995	2528.0767	2525.4073	2.6694	2	(2)	81	3	R.IKPVLIINKIDRSMMEQQLPK.E 13578
13854	1287.1696	2572.3247	2571.3255	0.9993	0	55	0.0004	1	K.TEAIDDVPCGNIVGLVGVDQFLLK.S 13847 13851
14251	885.6075	2653.8007	2652.3477	1.4530	0	76	3e-06	1	K.FLPAADAMLEMICIHLPSPVTAQK.Y 14244
14503	896.7875	2687.3407	2684.4511	2.8897	1	2	67	7	R.FNILDVTLHADAIHRGGGQIIPTAR.R
14911	927.9909	2780.9507	2780.4427	0.5080	1	18	1.9	1	R.KFLPAADAMLEMICIHLPSPVTAQK.Y
15743	1039.5429	3115.6067	3115.6021	0.0047	2	0	97	7	R.KFLPAADAMLEMICIHLPSPVTAQKYR.A

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6. gi|220698646|gb|EED54986.1| **Mass:** 69834 **Score:** 1546 **Queries matched:** 94 **emPAI:** 2.30

molecular chaperone Hsp70 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
741	485.6646	969.3147	968.4967	0.8180	0	48	0.0022	1	R.LVSDFFNK.E 740
1374	552.1451	1102.2757	1103.5869	-1.3112	2	4	80	3	R.LRTACERAK.R
1538	1130.4010	1129.3937	1129.6203	-0.2266	1	6	51	4	K.DLTTNARALR.R

1591	568.7021	1135.3897	1134.5768	0.8129	1	21	1.2	1	K.LTISDSDKEK.V
1887	599.6811	1197.3477	1196.6553	0.6924	0	42	0.011	1	K.FELTGIPPAPR.G 1880 1891 1893
1956	606.7396	1211.4647	1210.7034	0.7614	0	86	3.7e-07	1	K.DAGLIAGLNVLR.I 1945 1948 1952 1960
1982	608.7861	1215.5577	1214.7023	0.8554	0	36	0.041	1	K.GGKPIIQVEFK.G 1989
2166	623.7521	1245.4897	1243.6084	1.8813	0	35	0.059	1	K.NGLESYAYSLK.N
2168	624.0471	1246.0797	1245.6506	0.4291	0	42	0.011	1	R.LVNHFVNEFK.R 2185 2188 2197
2273	630.1846	1258.3547	1257.7153	0.6394	2	8	25	1	K.KDLTTNARALR.R 2278
3055	672.7771	1343.5397	1344.7725	-1.2328	2	0	1.6e+02	3	K.ITITNDKGRLSK.E
3175	679.1996	1356.3847	1355.6180	0.7667	0	61	0.00011	1	R.FEELCQDLFR.G 3174 3188 3194
3630	468.7292	1403.1657	1401.7517	1.4140	1	32	0.093	1	R.LVNHFVNEFKR.K 3633 3638
3870	478.6799	1433.0177	1432.6867	0.3310	1	8	24	9	K.EEIERMLADAEK.Y
3903	719.5571	1437.0997	1436.7300	0.3698	1	47	0.0032	1	R.LVSDFFNKEPNK.S 3911 3919 3924
3941	721.5541	1441.0937	1439.7733	1.3205	0	30	0.17	2	K.SSVHEIVLVGGSTR.I 3940
4206	737.1881	1472.3617	1470.6991	1.6626	0	81	1.2e-06	1	R.TTPSFVAFTDTER.L 4207
4471	752.3866	1502.7587	1502.6624	0.0963	0	48	0.0029	1	R.TADEVEEKPEELD.-
5274	792.6871	1583.3597	1582.7562	0.6035	1	52	0.00098	1	R.ARFEELCQDLFR.G 5259 5295
5397	798.4086	1594.8027	1594.7913	0.0115	0	76	3.7e-06	1	K.QFTPEEVSSMVLTK.M 5404 5423
5630	807.1846	1612.3547	1610.7862	1.5685	0	(18)	2.2	1	K.QFTPEEVSSMVLTK.M
5810	814.5691	1627.1237	1627.7914	-0.6677	1	33	0.083	1	R.DDRIEIIANDQGNR.T 5836
5978	821.8231	1641.6317	1638.9417	2.6900	1	3	80	10	R.QATKDAGLIAGLNVLR.I
6229	830.7866	1659.5587	1658.8879	0.6708	0	89	2.1e-07	1	R.IINEPTAAAIAYGLDK.K 6247
6452	559.4279	1675.2617	1674.7234	0.5383	0	62	9.8e-05	1	K.ATAGDTHLGGEDFDNR.L 6451 6453 6463
6603	843.6996	1685.3847	1684.7991	0.5856	0	85	4.6e-07	1	K.NQVAMNPHNTVFDAK.R 6600 6601 6604
6818	851.7491	1701.4837	1700.7941	0.6897	0	(63)	7.7e-05	1	K.NQVAMNPHNTVFDAK.R 6839
7247	871.7286	1741.4427	1739.8399	1.6028	2	1	1.1e+02	1	K.EEIERMLADAEKYK.A
7741	894.6246	1787.2347	1786.9828	0.2519	1	104	5.7e-09	1	R.IINEPTAAAIAYGLDKK.A 7737 7749 7757
8788	633.6059	1897.7957	1897.9278	-0.1320	1	7	29	1	K.QFTPEEVSSMVLTKMR.E
9498	992.7851	1983.5557	1981.9932	1.5625	0	54	0.00059	1	M.APAVGIDLGTTYSCVGVFR.D 9481 9486 9487 9488 9490 949
9855	676.3869	2026.1387	2025.9313	0.2075	2	3	60	6	R.MLADAEKYKAEDEAEASR.I
11294	736.6852	2207.0337	2204.1325	2.9012	1	1	98	5	K.VTSKVDEIIGWLDSNQTATK.E
13513	1261.8241	2521.6337	2520.2343	1.3994	0	129	1.5e-11	1	K.SINPDEAVAYGAAVQAAILSGDSSSK.S 13508 13509 13514 13
15256	968.2662	2901.7767	2899.3988	2.3779	0	10	9.3	1	R.ETAEAYLGGTVNNAVITVPAYFNDSQR.Q
15519	1519.0341	3036.0537	3034.5108	1.5429	0	103	4.6e-09	1	K.ELEGVANPIISAAYGGAAGAAPGGAPGAAPGGSTR.T

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7. gi|220696438|gb|EED52780.1| **Mass:** 61176 **Score:** 1334 **Queries matched:** 58 **emPAI:** 2.34

glucose-6-phosphate isomerase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
83	702.3110	701.3037	700.3755	0.9282	0	10	24	2	K.TPEQVK.T
482	447.9891	893.9637	893.4243	0.5394	0	15	5.2	1	K.EFSEQVR.S
686	480.4156	958.8167	958.4719	0.3448	0	28	0.29	1	K.EANVEELR.D

1992	609.5841	1217.1537	1216.5473	0.6065	0	51	0.0013	1	K.GEHINFTEDR.A 1987
2460	639.4591	1276.9037	1276.6412	0.2626	0	52	0.0012	1	K.TEGAPDNLVPHK.T 2461 2467
3487	694.7091	1387.4037	1385.6187	1.7851	0	59	0.00023	1	K.NMFGFESWVGGR.Y 3477
3616	701.5911	1401.1677	1401.6136	-0.4459	0	(19)	2.1	2	K.NMFGFESWVGGR.Y
3755	711.5751	1421.1357	1420.6987	0.4371	0	89	2.1e-07	1	M.PAFSQATDLSAWK.E 3762
4504	754.2666	1506.5187	1505.8341	0.6846	0	64	6.7e-05	1	K.NFLTEETLSLLVK.L 4493 4496 4503 4506 4508 4511 4515
4772	768.8941	1535.7737	1534.7879	0.9859	0	69	1.8e-05	1	K.DSNPETTLFLIASK.T 4769 4779
4895	773.8121	1545.6097	1544.7835	0.8263	0	55	0.00048	1	K.HFVALSTNEAEVTK.F 4880 4887
5006	779.6391	1557.2637	1556.7318	0.5319	0	71	1.2e-05	1	K.TFTTAETTTNANSAK.K
5291	793.6671	1585.3197	1584.7818	0.5380	0	96	3.9e-08	1	K.SVVEDVNSVLEHMK.E 5290 5294 5300
5651	808.2831	1614.5517	1613.7573	0.7944	0	96	4e-08	1	K.NTVDNSDILFDFSK.N 5664
6061	824.3266	1646.6387	1645.9151	0.7236	0	51	0.0012	1	K.TFLGNRPTTSILAQK.I 6049 6057
6963	857.6981	1713.3817	1711.8239	1.5578	0	27	0.27	1	R.FPAYLQQLSMESNGK.A 6965
7962	905.7866	1809.5587	1808.9164	0.6423	0	115	4.9e-10	1	R.MLASNFLAQSEALMVGK.T 7958 7963 7965 7989
8125	609.5842	1825.7307	1824.8101	0.9206	1	25	0.48	1	R.DAMFKGEHINFTEDR.A
8140	914.2486	1826.4827	1824.9114	1.5714	0	(62)	7.9e-05	1	R.MLASNFLAQSEALMVGK.T
8254	921.9626	1841.9107	1840.9063	1.0044	0	(16)	4	2	R.MLASNFLAQSEALMVGK.T
8475	622.2932	1863.8577	1863.9843	-0.1266	0	14	5.2	1	K.LHFVSNIDGTHIAEALK.D
10588	1056.3176	2110.6207	2111.0357	-0.4150	0	68	2.3e-05	1	K.LIPSDFIMAAESHNPVEGGK.H 10598 10603 10608
11655	754.5402	2260.5987	2262.1249	-1.5262	1	3	67	10	K.HQRMLASNFLAQSEALMVGK.T
13787	853.9669	2558.8787	2558.2612	0.6175	0	31	0.11	1	K.IQQELETSGAGAGHDASTSGLLAAFK.Q
14502	896.7679	2687.2817	2686.3562	0.9255	1	78	1.8e-06	1	K.KIQQELETSGAGAGHDASTSGLLAAFK.Q
15720	1034.8882	3101.6427	3102.5563	-0.9136	0	52	0.00058	1	K.YTTGPILFGEPATNAQHSFFQLLHQGTK.L 15722 15728

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8. gi|220692818|gb|EED49164.1| **Mass:** 27024 **Score:** 1226 **Queries matched:** 49 **emPAI:** 5.46

14-3-3 family protein ArtA, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
214	789.4630	788.4557	788.4279	0.0278	0	7	44	6	K.IESELAK.I
523	454.5191	907.0237	906.5174	0.5063	0	8	25	6	R.NLLSVAYK.N
575	917.6150	916.6077	916.5229	0.0848	0	44	0.0087	1	R.IVTSIEQK.E 576
1299	544.8626	1087.7107	1087.5873	0.1234	0	64	7e-05	1	K.GNESQVTLIK.E 1298 1301 1302
1348	549.2626	1096.5107	1094.5244	1.9864	0	38	0.026	1	K.GAADASLEAYK.A
1372	551.9041	1101.7937	1101.5455	0.2483	0	50	0.002	1	M.GHEDAVYLAK.L 1371 1373
1677	577.7566	1153.4987	1153.5768	-0.0780	0	38	0.025	1	R.YLAEFAIGDR.R
1850	595.6851	1189.3557	1188.6536	0.7021	0	56	0.00042	1	K.DSTLIMQLLR.D 1844 1851
2229	627.2591	1252.5037	1252.6411	-0.1374	0	86	3.6e-07	1	K.HLIPSAQSGESK.V 2230
2512	642.7016	1283.3887	1284.7163	-1.3276	2	11	13	1	K.NVIGARRASWR.I 2503 2521
2947	667.1666	1332.3187	1331.6643	0.6545	0	66	4.2e-05	1	K.ICDDILEVLDK.H 2948 2967 2968
3516	696.1961	1390.3777	1389.7351	0.6426	1	57	0.00035	1	R.IVTSIEQKEESK.G
4572	759.2771	1516.5397	1515.7780	0.7617	0	100	1.5e-08	1	K.VVASADVELTVEER.N 4557 4561 4563 4569 4570 4574 4575

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       7785   597.9672  1790.8797  1789.9323   0.9475  0    72  8.3e-06    1   K.AATEVAQTDLAPTHPIR.L 7765 7786 7788 7789
      10723  1066.2416  2130.4687  2129.0052   1.4636  0    84  5.3e-07    1   K.LAFDDAIAELDTLSEESYK.D 10724 10732 10736
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9.    gi|220699320|gb|EED55659.1|     Mass: 38287    Score: 1185   Queries matched: 89    emPAI: 3.09
      alcohol dehydrogenase, zinc-containing, putative [Aspergillus flavus NRRL3357]
      Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
        162   757.6070   756.5997   756.4858   0.1140  1    12       11    9   K.VKGIVNK.V
        227   793.4020   792.3947   792.3766   0.0181  0    14        7    2   K.GFEVGER.V 226
        798   982.6490   981.6417   981.5859   0.0558  0    44   0.0059    1   R.VVVAAPEGLK.M 797 800 804
       1096   525.5421  1049.0697  1048.4825   0.5872  0    39    0.021    1   R.QDPSAQFEK.L 1093
       1210   536.5266  1071.0387  1070.6084   0.4303  1    24     0.69    1   K.LRDNDVLVK.V 1209
       1228   538.0931  1074.1717  1073.6233   0.5484  0    21      1.4    1   K.HAVVDVPLPK.L 1221
       2011   611.5391  1221.0637  1220.6401   0.4236  0    67  3.2e-05    1   K.ILEDSINYVR.R 2013 2014
       2569   645.8406  1289.6667  1289.6615   0.0052  1     9       21    1   R.QDPSAQFEKLK.K
       2583   646.5996  1291.1847  1290.6788   0.5059  1     4       69    7   -.MSLPQTMKALR.Y
       2641   649.7531  1297.4917  1295.6398   1.8520  0    59  0.00018    1   K.FPAAIDYLDSGK.V 2610 2613 2616 2617 2646
       3558   698.3736  1394.7327  1395.7146  -0.9819  0     7       29    2   K.LVVYGVYNNEAR.V
       3671   705.7686  1409.5227  1408.6834   0.8393  0    69  1.9e-05    1   K.SLEAGDEYVALSR.Q 3663 3678
       5582   805.7571  1609.4997  1608.6912   0.8085  0    88  2.3e-07    1   K.LEEWEQCLESMR.N 5576
       5797   813.7386  1625.4627  1624.6861   0.7766  0  (11)       13    2   K.LEEWEQCLESMR.N
       6817   851.7386  1701.4627  1699.8498   1.6129  1     2       83    6   R.QCGGCRVVVAAPEGLK.M
       8135   914.1691  1826.3237  1823.8942   2.4296  0    54  0.00054    1   K.ENPYGFDIVVEATGSVK.I 8106 8109 8115 8118 8121 8122 8
       8570   626.0502  1875.1287  1873.0462   2.0825  0    62  9.3e-05    1   K.FPLVPGHETVGVVAAVGPK.V 8544 8554 8556 8561 8562 856
       8986   639.8092  1916.4057  1917.9982  -1.5925  2     4       52    3   M.SLPQTMKALRYEQPEK.H
       9021   961.3581  1920.7017  1918.9564   1.7453  0    41    0.012    1   K.IFGDEITILGSFSETYK.F 9000 9005 9013 9019 9025
       9445   989.6771  1977.3397  1977.8019  -0.4622  0    75    4e-06    1   R.VVADNSELCGECFYCR.R 9465 9470
       9511   662.7922  1985.3547  1982.9230   2.4317  1    49   0.0016    1   K.VFKLEEWEQCLESMR.N 9505 9512
      10617   705.8285  2114.4637  2111.9881   2.4756  0    18      2.1    1   K.ACGVCGTDLHIHEGQFIAK.F
      11367   739.2635  2214.7687  2213.2606   1.5081  0   (3)       69    6   K.MGSSVLLFGAGPTGLILAQLLR.Q
      11465  1116.0396  2230.0647  2229.2555   0.8092  0    97  2.3e-08    1   K.MGSSVLLFGAGPTGLILAQLLR.Q 11458 11467 11472 11475
      11911  1149.4116  2296.8087  2296.1005   0.7082  0    84  4.8e-07    1   K.NLSDVDATLLEPASCAAHGLDK.I 11906 11910 11915 11926
      15811  1052.2529  3153.7367  3154.6186  -0.8819  2     2       62    6   K.KENPYGFDIVVEATGSVKILEDSINYVR.R
```

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10.   gi|220697529|gb|EED53870.1|     Mass: 87338    Score: 1172   Queries matched: 118   emPAI: 1.61
      cobalamin-independent methionine synthase MetH/D [Aspergillus flavus NRRL3357]
      Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
         47   676.4920   675.4847   675.3704   0.1143  0    16      6.4    1   K.SAFPVR.L 46
         59   684.5530   683.5457   683.3966   0.1491  0    18      1.9    1   R.EGLPLR.S 58
        176   767.5170   766.5097   766.4225   0.0872  0    30     0.12    1   K.YAVSISK.K 177
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232	800.4920	799.4847	799.4803	0.0044	0	38	0.029	1	K.VELAIQK.L	233 234
264	816.6540	815.6467	815.4137	0.2330	0	21	1.6	2	K.NLDAEVR.D	262
294	831.4050	830.3977	830.4385	-0.0408	0	31	0.19	1	K.EIEDVVK.I	296 299 304
671	958.3960	957.3887	957.5131	-0.1244	0	27	0.36	1	R.GQTVDPITK.I	674
751	487.1471	972.2797	969.5243	2.7554	0	23	0.94	1	K.AVTEGPAAVR.E	
948	1017.2320	1016.2247	1015.5298	0.6949	1	28	0.29	1	R.DDLLAEGKR.L	
1129	1056.5860	1055.5787	1055.6199	-0.0412	2	6	41	1	K.EIRIQRNK.F	
1189	534.8451	1067.6757	1067.5287	0.1470	0	32	0.086	1	K.DAFKPAYEK.L	1188
1309	545.6866	1089.3587	1088.5979	0.7609	0	74	7.8e-06	1	M.VQSSVLGFPR.M	1303 1305 1314 1321
1379	1104.6170	1103.6097	1102.5804	1.0293	0	12	12	4	K.AALTNMVNAAK.Y	
1411	555.2721	1108.5297	1108.5553	-0.0256	0	(78)	2.7e-06	1	K.VFIDEAYPR.H	1417
1531	1129.7040	1128.6967	1127.5288	1.1680	0	26	0.5	1	R.DWFSFAVEK.T	1523 1525
1608	570.3821	1138.7497	1138.6346	0.1151	0	25	0.47	1	K.VIQVDEPALR.E	1612 1616 1617 1628 1629
1902	601.1736	1200.3327	1199.6146	0.7181	1	64	6.9e-05	1	R.VPSEQEIKDR.V	
2000	610.1736	1218.3327	1217.6261	0.7067	0	(43)	0.0083	1	K.GMLTGPITCLR.W	1996
2082	617.9781	1233.9417	1233.6210	0.3208	0	51	0.0015	1	K.GMLTGPITCLR.W	2088 2093 2094
2274	630.2026	1258.3907	1257.5448	0.8459	0	64	7.9e-05	1	R.NDMVQYFGER.L	2272
2401	637.1831	1272.3517	1271.6609	0.6909	0	13	9.2	4	R.DEVIDLEAAGIK.V	2393
2418	637.7901	1273.5657	1273.5397	0.0260	0	(45)	0.0059	1	R.NDMVQYFGER.L	2414 2430 2433
3080	674.6756	1347.3367	1347.7286	-0.3918	1	10	15	2	K.FIEKEIEDVVK.I	
3762	712.2931	1422.5717	1420.7497	1.8220	1	2	86	9	M.VQSSVLGFPRMGK.L	
4005	724.7316	1447.4487	1446.7368	0.7119	0	72	9.6e-06	1	R.HIGPGVYDIHSPR.V	4001 4014 4016
4769	768.7591	1535.5037	1535.7952	-0.2915	1	3	70	4	-.MVQSSVLGFPRMGK.L	
5312	794.7321	1587.4497	1587.7814	-0.3317	0	4	63	6	K.DGQAAIDVPSLEMVK.W	
6197	829.3821	1656.7497	1655.9498	0.7999	0	79	1.8e-06	1	K.INDLLPVYVELLQK.L	6195 6196 6204 6206 6220
6752	566.5959	1696.7657	1695.9559	0.8098	0	59	0.00017	1	K.LAEQPKPVVQFLEAK.E	6751 6754 6756
6944	856.6786	1711.3427	1710.7824	0.5603	0	43	0.0069	1	K.YNLHPVDEYFAMGR.G	
7095	864.5356	1727.0567	1726.7773	0.2794	0	(42)	0.0083	1	K.YNLHPVDEYFAMGR.G	7108 7112 7113
8015	908.1986	1814.3827	1812.8900	1.4927	2	1	1.1e+02	1	K.VKERQAAVTEEMHNR.K	
8210	613.0085	1836.0037	1836.9702	-0.9665	2	4	51	1	-.MVQSSVLGFPRMGKLR.D	
8624	628.6912	1883.0517	1880.0731	2.9786	1	2	85	7	K.TAEVVVIAKAVTEGPAAVR.E	
8805	634.0499	1899.1277	1897.1288	1.9989	1	3	62	8	K.INDLLPVYVELLQKLK.E	
9850	676.3005	2025.8797	2023.9851	1.8946	0	33	0.061	1	K.IQEELDLDVFVHGEPER.N	9822 9824 9826 9844 9845 9851
10225	1031.9156	2061.8167	2061.1147	0.7021	0	84	5.7e-07	1	K.SINLPLFPTTTIGSFPQTK.E	10219 10231 10234 10241
10320	1037.8371	2073.6597	2072.0116	1.6481	0	9	18	1	R.LTGYVFTTHAWVQSYGSR.C	
10429	697.0252	2088.0537	2088.1579	-0.1042	0	2	93	6	R.VIVATSSSLLHVPHTLASEK.N	
11101	728.0915	2181.2527	2180.2933	0.9594	0	62	7.7e-05	1	K.EAGIVTRPVILGPVSFLTLAK.A	11097 11098 11099 11100
13094	1234.9541	2467.8937	2466.3161	1.5777	2	1	1e+02	1	K.YAVSISKKPMKGMLTGPITCLR.W	13080 13103
13608	844.6452	2530.9137	2530.1917	0.7220	0	46	0.0028	1	K.WFDSNYHYVKPTLQDNQTFK.L	13592
13626	845.7395	2534.1967	2535.3665	-1.1698	1	8	21	1	R.CVRPPIVVGDISRPAPMTVKESK.Y	13640 13650
13986	1303.3926	2604.7707	2604.3508	0.4200	0	82	7e-07	1	R.NPEQLDTVVGALGPNQVLSAGVVDGR.N	13994

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11. gi|220690467|gb|EED46816.1| **Mass:** 37432 **Score:** 1162 **Queries matched:** 109 **emPAI:** 4.94

alcohol dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
832	988.5260	987.5187	987.5237	-0.0050	0	48	0.0033	1	K.TQDLVADVK.A 831 839
903	502.0581	1002.1017	1001.5658	0.5359	0	50	0.0022	1	R.APVFNTVVR.M 904
941	1016.6730	1015.6657	1015.5186	0.1471	0	41	0.016	1	R.VVAIDGGEEK.Q 943
1336	548.4836	1094.9527	1093.5478	1.4050	0	35	0.052	1	K.IFELMEQGK.I 1327 1331
2264	629.7411	1257.4677	1258.6921	-1.2244	1	12	11	2	K.IAGRYVLEIPE.- 2266
3129	676.5956	1351.1767	1350.7078	0.4689	1	4	55	4	R.MINIKGSYVGNR.Q
3149	677.7656	1353.5167	1352.6361	0.8806	0	87	2.8e-07	1	R.QDGVEAVDFFAR.G 3150
3295	684.6351	1367.2557	1366.7027	0.5530	1	(4)	60	10	R.MINIKGSYVGNR.Q
3952	722.2236	1442.4327	1440.8453	1.5874	0	9	17	2	R.GTVVAIGLPAGAFLR.A 3947 3954
4443	751.3976	1500.7807	1499.7191	1.0616	0	60	0.00018	1	R.YSGVCHTDLHALK.G
4917	517.2625	1548.7657	1547.8242	0.9415	0	(28)	0.25	1	K.MPLVGGHEGAGVVVAR.G 4905
5068	782.8416	1563.6687	1563.8192	-0.1504	0	81	1.1e-06	1	K.MPLVGGHEGAGVVVAR.G 5071 5074 5084 5089 5093
5843	815.7421	1629.4697	1628.9501	0.5196	0	40	0.016	1	K.QIPVPKPGPDEILVK.V 5842 5848 5851
6038	823.6196	1645.2247	1643.6895	1.5353	0	51	0.0013	1	K.WLNGSCLACEFCK.Q 6024 6043
6789	851.0226	1700.0307	1699.8417	0.1890	0	120	1.3e-10	1	R.GDLVTEFEIGDHAGLK.W 6772 6776 6783 6785 6786 6790 67
7353	878.6471	1755.2797	1754.8886	0.3911	1	16	3.6	2	K.VRYSGVCHTDLHALK.G
9313	981.3106	1960.6067	1959.8706	0.7361	0	33	0.066	1	K.QAMCEQLGAEAYVDFTK.T 9322
9646	1001.2456	2000.4767	1999.0812	1.3955	0	71	1.2e-05	1	K.NVPLDAVAPVLCAGITVYK.G 9625 9641 9645 9647 9651 965
12997	819.7555	2456.2447	2454.3304	1.9143	2	1	1e+02	4	K.TAPLQDLPKIFELMEQGKIAGR.Y
13512	841.5515	2521.6327	2519.2552	2.3775	1	2	72	5	-.MSIPEMQWAQVAEQKGGPLIYK.Q 13527
14278	886.5579	2656.6517	2655.4344	1.2173	0	81	8.8e-07	1	K.ESGVRPGQTVAIVGAGGGLGSLALQYAK.A 14262 14268 14270
15396	991.6642	2971.9707	2973.3736	-1.4029	1	3	57	3	R.VVAIDGGEEKQAMCEQLGAEAYVDFTK.T
15505	1011.3115	3030.9127	3029.4077	1.5051	0	29	0.14	1	K.QADEPLCPNASLSGYTVDGTFQQYAIGK.A
15754	1040.9625	3119.8657	3119.6767	0.1890	0	72	5.7e-06	1	K.AATPEGLGAHAVILLAVAEKPFQQAAEYVR.S 15758 15759 1576

Proteins matching the same set of peptides:

gi|226693510|sp|P41747.2|ADH1_ASPFN **Mass:** 37432 **Score:** 1162 **Queries matched:** 109

RecName: Full=Alcohol dehydrogenase 1; AltName: Full=Alcohol dehydrogenase I

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12. gi|220693770|gb|EED50115.1| **Mass:** 44399 **Score:** 1075 **Queries matched:** 124 **emPAI:** 4.59

phosphoglycerate kinase PgkA, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
11	632.4010	631.3937	631.3541	0.0397	0	36	0.077	1	K.TIAEAK.T 12
31	656.3770	655.3697	655.4493	-0.0796	1	11	8.2	6	K.RVLIR.V
109	721.5540	720.5467	720.4170	0.1297	0	15	5.4	2	K.ASGFLVK.K 108
129	738.5340	737.5267	737.3959	0.1308	0	18	1.9	1	K.SVELYK.K 128

349	849.5340	848.5267	848.5120	0.0147	1	19	2.6	4	K.ASGFLVKK.E
395	432.7376	863.4607	864.4341	-0.9734	0	13	10	3	K.YAIENGAK.A
422	872.6150	871.6077	871.5015	0.1062	0	40	0.019	1	K.IVGDIVEK.A 420 421 423
491	899.3260	898.3187	898.4436	-0.1249	0	24	0.57	1	K.ELEYFAK.A 495 496
539	911.6280	910.6207	910.5851	0.0356	0	30	0.15	1	R.IVGALPTIK.Y 538 541 543 546
692	481.2821	960.5497	960.4764	0.0734	0	16	5	4	K.ETEEIVNK.A
823	494.2406	986.4667	986.5648	-0.0981	0	47	0.0036	1	K.LAITDVDLK.D 825 828 830
1279	543.3551	1084.6957	1084.6128	0.0829	0	39	0.02	1	K.VLPGVDALSSK.- 1277 1278 1286 1287 1293
1470	1120.6600	1119.6527	1119.4832	0.1695	0	56	0.00046	1	R.FHAEEEGSSK.D
1729	584.0551	1166.0957	1165.7070	0.3887	0	57	0.00028	1	K.IQLIDNLLPK.V 1728 1731 1743
2025	612.6761	1223.3377	1222.6016	0.7361	0	61	0.00013	1	K.SVIFAENCVGK.E 2028
2107	619.4396	1236.8647	1236.5986	0.2661	0	82	9.8e-07	1	K.IGNSLFDEAGSK.I 2115 2116 2127 2129
3223	681.3686	1360.7227	1359.7034	1.0193	1	0	1.5e+02	9	R.VDFNVPLDADKK.I
3298	684.7226	1367.4307	1367.6867	-0.2560	0	72	8.5e-06	1	R.AHSSMVGVDLPQK.A 3297
3404	689.3251	1376.6357	1376.7551	-0.1194	0	13	9.3	1	K.YSLKPVATELEK.L 3424
3468	693.6516	1385.2887	1383.6817	1.6071	0	(41)	0.014	1	R.AHSSMVGVDLPQK.A 3459 3465
4293	494.3592	1480.0557	1478.8028	1.2530	0	(23)	0.74	1	K.AVVLMSHLGRPDGK.A 4286 4290
4414	748.7571	1495.4997	1494.7977	0.7020	0	32	0.088	1	K.AVVLMSHLGRPDGK.A 4402
5415	799.2961	1596.5777	1594.9294	1.6483	1	56	0.00038	1	K.VSDKIQLIDNLLPK.V 5403 5405 5411
5615	806.7766	1611.5387	1611.8694	-0.3307	0	(13)	7.8	2	K.VNSLIITGAMAFTFK.K 5621 5635 5636
5832	815.2796	1628.5447	1627.8644	0.6804	0	17	2.9	1	K.VNSLIITGAMAFTFK.K 5833 5834 5837 5838
5932	546.6879	1637.0417	1636.9624	0.0793	1	1	1.1e+02	8	K.ITNNQRIVGALPTIK.Y
7351	878.4806	1754.9467	1753.9210	1.0257	0	9	18	2	K.LSHVSTGGGASLELLEGK.V
7478	884.3486	1766.6827	1765.0574	1.6254	2	8	24	3	K.KITNNQRIVGALPTIK.Y 7450 7485
7484	590.1412	1767.4017	1767.0043	0.3975	0	62	0.0001	1	K.ALESPQRPFLAILGGAK.V 7479 7486 7499 7508 7511
7768	895.7651	1789.5157	1786.9829	2.5328	1	20	1.4	1	K.NNVKIVLPVDYVTADK.F 7754
8710	630.4475	1888.3207	1890.0132	-1.6925	2	4	65	4	-.MSLSNKLAITDVDLKDK.R
9574	665.0545	1992.1417	1989.9908	2.1509	0	60	0.00013	1	K.GLTALGDVYINDAFGTAHR.A 9542 9544 9547 9550 9556 956
10429	697.0252	2088.0537	2086.0881	1.9656	1	1	1.1e+02	8	R.AHSSMVGVDLPQKASGFLVK.K
10641	1060.7316	2119.4487	2118.0858	1.3629	1	7	24	3	R.KGLTALGDVYINDAFGTAHR.A
10983	722.7375	2165.1907	2165.0674	0.1233	1	4	54	8	K.SVIFAENCVGKETEEIVNK.A
11559	1123.2361	2244.4577	2243.9893	0.4685	0	111	9.7e-10	1	K.TGYATDADGIPDGYMGLDVGEK.S 11564 11565
11670	1131.9906	2261.9667	2259.9842	1.9825	0	(0)	1.2e+02	2	K.TGYATDADGIPDGYMGLDVGEK.S
11955	768.3372	2301.9897	2300.1841	1.8056	0	71	1.1e-05	1	K.TILWNGPPGVFELEPFANATK.K 11944 11947 11948 11949 11
12563	798.6969	2393.0687	2390.2845	2.7842	2	3	64	5	K.NNVKIVLPVDYVTADKFAADAK.T
12921	815.2799	2442.8177	2440.3400	2.4778	2	4	50	3	K.VNSLIITGAMAFTFKKTLENVK.I
13234	829.2935	2484.8587	2483.3860	1.4728	2	2	86	4	K.ITNNQRIVGALPTIKYAIENGAK.A
13597	844.3822	2530.1247	2527.3493	2.7754	0	15	3.8	1	K.TLDAAVAAAQSGSIVIIGGGDTATVAAK.Y 13572 13579 13585
14293	886.8319	2657.4737	2655.4443	2.0294	1	1	78	10	K.KTLDAAVAAAQSGSIVIIGGGDTATVAAK.Y 14292

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13.   gi|220698278|gb|EED54618.1|      Mass: 34593    Score: 1032    Queries matched: 48    emPAI: 2.00
      60S ribosomal protein L5, putative [Aspergillus flavus NRRL3357]
     Query   Observed    Mr(expt)    Mr(calc)     Delta Miss Score   Expect Rank   Peptide
        34   660.3000    659.2927    658.3261    0.9666    0    10       24    6    -.MPFHK.Q
       695   481.4921    960.9697    960.5393    0.4305    0    52   0.0014    1    K.AFLDVGLAR.T 694
      2095   618.6266   1235.2387   1234.6346    0.6041    0    55  0.00057    1    K.VFASAYAHELK.R 2079 2096
      3519   696.3401   1390.6657   1390.7357   -0.0700    1    63  9.6e-05    1    K.VFASAYAHELKR.Y 3524 3528 3533
      4525   755.5681   1509.1217   1507.7379    1.3838    0    56  0.00039    1    K.GASDGGILVPHSENR.F 4517 4522 4524
      4657   762.6946   1523.3747   1522.6787    0.6960    2    12      9.6    1    R.EDPFKKDEDEGSK.K
      6515   841.2901   1680.5657   1679.8618    0.7040    0    83  6.6e-07    1    R.DIITQIVYSEISGDK.V 6511 6512 6514 6518 6523 6528 653
     11024   724.1829   2169.5267   2171.0793   -1.5526    1     8       19    1    R.VFAAMKGASDGGILVPHSENR.F
     12038  1156.8551   2311.6957   2309.2168    2.4789    0    81  9.2e-07    1    R.YGITNGLTNWAAAYATGLLLAR.R 12015 12016 12020 12025 1
     12222  1170.7121   2339.4097   2337.0648    2.3449    0   109  1.7e-09    1    K.YLENEVEAGDIEDLYTEAHK.A 12207 12208 12214 12217 122
     15123   950.8869   2849.6387   2848.2398    1.3989    1    23     0.59    2    R.NYIFGGHVAEYMEGLADDDEERYR.G 15126
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14.   gi|220696531|gb|EED52873.1|      Mass: 62404    Score: 1028    Queries matched: 82    emPAI: 1.94
      antigenic mitochondrial protein HSP60, putative [Aspergillus flavus NRRL3357]
     Query   Observed    Mr(expt)    Mr(calc)     Delta Miss Score   Expect Rank   Peptide
       138   745.5370    744.5297    744.4382    0.0916    0    21      1.7    1    K.EGVITVK.E
       322   843.5790    842.5717    842.5226    0.0492    0    21      1.3    2    K.LSGGVAVIK.V 323
       424   873.5660    872.5587    872.4967    0.0620    0    33      0.1    1    R.LLQDVASK.T 426
       478   894.5330    893.5257    893.4858    0.0399    0    14      6.6    1    R.AIFSETVK.N 479
       556   457.7271    913.4397    912.5393    0.9005    0    30     0.18    1    R.GQLQVAAVK.A 551 563
       679   479.9816    957.9487    957.5243    0.4244    0    68  3.3e-05    1    R.VVDALNATR.A 680
      1048   521.6276   1041.2407   1040.4848    0.7559    0    16      3.6    1    K.GEYVDMISK.G
      1682   578.3381   1154.6617   1154.7387   -0.0770    1     9       17    2    R.LAKLSGGVAVIK.V 1678 1684
      2578   646.3106   1290.6067   1288.6510    1.9557    0    10       17    6    K.EDTIILNGEGTK.D
      2697   652.7286   1303.4427   1302.6820    0.7608    0    43   0.0092    1    R.NVLIDTPYGSPK.I 2685 2698
      2808   659.5696   1317.1247   1316.5965    0.5282    0  (61)  0.00014    1    K.NVAAGCNPMDLR.R 2797
      2957   667.5881   1333.1617   1332.5914    0.5703    0    62  0.00012    1    K.NVAAGCNPMDLR.R 2961
      3221   454.5569   1360.6487   1358.6579    1.9909    1    10       15    5    K.LTEEHAKDFNR.G
      3529   696.7471   1391.4797   1391.6609   -0.1812    0    85  5.1e-07    1    R.GYTSPYFITDTK.S 3535
      4642   762.3081   1522.6017   1520.7028    1.8989    0   (1) 1.2e+02    8    K.TLEDELEVTEGMR.F
      4801   770.3821   1538.7497   1536.6977    2.0520    0    28     0.25    1    K.TLEDELEVTEGMR.F 4778
      4855   772.8056   1543.5967   1543.8861   -0.2894    0    49   0.0018    1    K.VEFEKPLILLSEK.K 4865 4872 4876
      5326   795.2541   1588.4937   1587.8369    0.6568    1    54  0.00064    1    K.AVQLQDKFENLGAR.L 5327 5357
      5414   799.2446   1596.4747   1594.8930    1.5817    0    86  3.8e-07    1    R.AAVEEGILPGGGTALLK.A 5424
      5624   806.9131   1611.8117   1611.8832   -0.0715    0     8       25    3    R.QIVENAGLEGSVIVGK.L 5607 5614 5619 5635
      6106   826.0336   1650.0527   1649.8546    0.1981    0    85  5.4e-07    1    K.LTPDMLGSTGSITITK.E
      6607   562.8589   1685.5547   1683.7661    1.7886    1     8       25    3    R.GVMADPTTSEYEKEK.L
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7097	864.7131	1727.4117	1726.9115	0.5003	1	4	51	3	R.GQLQVAAVKAPGFGDNR.K
7327	876.6786	1751.3427	1750.8156	0.5271	0	98	2e-08	1	K.TNELAGDGTTTATCLAR.A 7328
7660	594.6512	1780.9317	1778.9124	2.0193	1	4	60	7	K.GEYVDMISKGIVDPLK.V
8057	909.7626	1817.5107	1816.9319	0.5788	0	89	1.9e-07	1	R.GIQAAVEAAVDYLQQNK.R 8050 8054 8058 8062 8066
8789	633.6189	1897.8347	1897.0520	0.7827	0	61	0.0001	1	K.ISAVQDIIPALEASTTLR.R 8783 8798 8799 8808
8834	634.8565	1901.5477	1902.7192	-1.1714	0	(2)	85	8	K.APAAPGGMGGMGGMGGMGGGMF.- 8862
8859	635.4175	1903.2307	1902.7192	0.5116	0	(0)	1.3e+02	4	K.APAAPGGMGGMGGMGGMGGGMF.-
9007	640.6975	1919.0707	1918.7141	0.3566	0	5	48	4	K.APAAPGGMGGMGGMGGMGGGMF.-
9426	659.2422	1974.7047	1973.0330	1.6717	1	43	0.0062	1	R.GIQAAVEAAVDYLQQNKR.D 9429
9869	676.6652	2026.9737	2025.1470	1.8268	1	3	57	4	K.KISAVQDIIPALEASTTLR.R
13231	829.1845	2484.5317	2482.3180	2.2138	0	49	0.0017	1	K.AAANGLDNVKPANFDQQLGVSIIK.N 13207 13223 13228
14118	876.6785	2627.0137	2626.2908	0.7229	1	47	0.0025	1	K.TNELAGDGTTTATCLARAIFSETVK.N 14119
14289	886.7782	2657.3127	2655.3855	1.9273	0	23	0.51	1	R.TALVDASGVASLLGTTEVAIVDAPEEK.A 14275 14276 14279 1
16071	1097.4175	3289.2307	3290.7167	-1.4860	2	1	78	3	K.LEKLTPDMLGSTGSITITKEDTIILNGEGTK.D

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15. gi\|220694869\|gb\|EED51212.1\| **Mass:** 34829 **Score:** 982 **Queries matched:** 47 **emPAI:** 1.72

malate dehydrogenase, NAD-dependent [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
51	339.9126	677.8107	677.3748	0.4359	0	26	0.48	1	K.GIDFVK.N 50
132	742.5000	741.4927	741.4497	0.0430	0	11	12	3	K.INAGIVR.D
228	793.4880	792.4807	792.4381	0.0426	0	28	0.26	1	R.FAESVIK.A 229
240	804.4610	803.4537	803.4178	0.0360	0	16	6.1	2	K.AAGVFDPK.R
1967	607.2641	1212.5137	1210.6710	1.8427	1	4	67	9	K.GIDFVKNPPPK.L
2003	610.6796	1219.3447	1218.6972	0.6475	0	72	1.1e-05	1	R.LFGVTTLDVVR.A 2004 2016
2043	614.1861	1226.3577	1225.6554	0.7023	0	39	0.019	1	K.TTPAIQIPEEK.Y 2046 2055
2453	639.3316	1276.6487	1275.6459	1.0028	0	40	0.016	1	R.VQFGGDEVVQAK.D 2456
2868	663.5951	1325.1757	1322.6653	2.5105	1	8	26	6	R.KPGMTRDDLFK.I
3191	453.7812	1358.3217	1359.7510	-1.4293	1	3	82	10	R.DDLFKINAGIVR.D
3365	687.6706	1373.3267	1371.6307	1.6961	0	57	0.00032	1	R.AETFTQEFSGQK.D 3342 3364
3632	702.6186	1403.2227	1402.7303	0.4924	1	6	42	4	K.ASNVLEGVTEKEK.K 3629
6662	845.7396	1689.4647	1688.9937	0.4710	0	92	1e-07	1	K.QALTGANIVVIPAGIPR.K 6675 6693
7455	883.3336	1764.6527	1764.0509	0.6018	0	107	2.9e-09	1	K.AAVLGASGGIGQPLSLLLK.T 7469 7478
11803	1142.1166	2282.2187	2280.3093	1.9094	0	84	5.6e-07	1	K.AFVLVISNPVNSTVPIAAEVLK.A 11801
12850	1217.9406	2433.8667	2433.2904	0.5763	0	77	2.5e-06	1	K.DPSAVQIPVVGGHSGETIVPLFSK.T 12859 12865 12875
13240	1243.9421	2485.8697	2485.3105	0.5593	0	73	6.4e-06	1	K.GQTGIVEPTFVYLPGIPGGDEIVK.A 13239 13241 13251 1325
15117	950.1915	2847.5527	2847.3498	0.2030	1	1	75	5	R.VQFGGDEVVQAKDGAGSATLSMAYAGYR.F
15234	963.8635	2888.5687	2887.6066	0.9622	2	2	69	10	K.DDGLKQALTGANIVVIPAGIPRKPGMTR.D
16038	1095.8569	3284.5487	3281.6853	2.8634	0	85	2.8e-07	1	K.TCPLVEELALYDVVNTPGVAADLSHISSIAK.I 16027 16035 160

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16. gi|220699482|gb|EED55821.1| **Mass:** 39810 **Score:** 921 **Queries matched:** 77 **emPAI:** 1.82
fructose-bisphosphate aldolase, class II [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
29	651.5710	650.5637	650.3639	0.1998	0	24	0.61	1	R.DYILK.K
350	425.2716	848.5287	848.5120	0.0168	0	15	5.6	7	K.LHPELLK.K
526	454.6286	907.2427	906.5538	0.6889	2	12	12	4	R.DYILKKK.D
707	965.5100	964.5027	964.5229	-0.0202	0	36	0.043	1	K.EAISYGVVK.V 708
774	977.6210	976.6137	976.6069	0.0068	1	25	0.6	1	K.LHPELLKK.H 771 773 775 778
1815	592.5971	1183.1797	1184.7241	-1.5444	2	4	67	6	M.GVGVLEKLSRK.T
2449	1277.5660	1276.5587	1276.6299	-0.0712	0	34	0.069	1	K.VALEDFNTAGQL.- 2454 2470
6581	842.7691	1683.5237	1682.8515	0.6722	0	67	3.3e-05	1	K.LLPWLDGLLDEDER.Y 6558 6577 6579 6588 6609
6749	849.3046	1696.5947	1694.8417	1.7530	0	80	1.3e-06	1	K.DKPVFFVFHGGSGSSK.E 6732 6738 6741 6743 6746
7983	906.8221	1811.6297	1810.9465	0.6832	1	75	4.4e-06	1	K.KLLPWLDGLLDEDER.Y 7980 7984 7985 7996 7998
8301	924.5401	1847.0657	1845.8390	1.2268	0	14	5.1	1	K.VNVDTDMQFAYMSGIR.D 8291 8293 8295 8303 8311
8471	932.5561	1863.0977	1861.8339	1.2638	0	(0)	1.2e+02	1	K.VNVDTDMQFAYMSGIR.D
10097	1025.2926	2048.5707	2048.0513	0.5194	0	79	1.6e-06	1	R.SLAPAYGIPVVLHTDHCAK.K 10098 10114
10545	702.2469	2103.7187	2105.0099	-1.2912	1	3	72	4	K.KDYLMTAVGNPEGEDKPNK.K
10656	1061.8266	2121.6387	2121.0782	0.5605	1	21	0.96	1	K.LLPWLDGLLDEDERYFK.L
10938	720.1879	2157.5417	2155.0770	2.4647	0	4	54	5	K.GVSNDGQQASIAGGIAAAHYIR.S 10936
11509	1119.3656	2236.7167	2236.0947	0.6221	0	117	2.4e-10	1	R.DQNCPIVLQLSQGGAAYFAGK.G 11492 11494 11497 11500 11
11579	751.1779	2250.5117	2249.1732	1.3385	2	51	0.00096	1	K.KLLPWLDGLLDEDERYFK.L
16072	1097.4349	3289.2827	3286.6582	2.6245	0	33	0.045	1	R.LFEHAQQNNYAIPAVNVTSSSTVVASLEAAR.D 16046 16052 160

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17. gi|220700638|gb|EED56976.1| **Mass:** 44602 **Score:** 913 **Queries matched:** 61 **emPAI:** 1.92
malate dehydrogenase, NAD-dependent [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
51	339.9126	677.8107	677.3748	0.4359	0	26	0.48	1	K.GIDFVK.A 50
244	807.4900	806.4827	806.4208	0.0620	0	24	0.76	1	R.MAESLLK.A
349	849.5340	848.5267	848.4756	0.0511	0	30	0.19	1	R.FISQVQK.T 348 350
774	977.6210	976.6137	976.5342	0.0796	0	23	0.93	2	R.QSFNLLQK.R 771
902	502.0561	1002.0977	1001.5254	0.5723	1	25	0.57	1	K.TRDELVNR.I
1127	528.6741	1055.3337	1053.5091	1.8247	0	9	20	7	R.AFSASASQASK.V
1320	546.6386	1091.2627	1090.5659	0.6968	0	41	0.016	1	R.IQFGGDEVVK.A 1313 1319 1325
1432	557.5816	1113.1487	1112.5139	0.6349	0	64	6.5e-05	1	K.DQGVDFFASK.V 1425 1428
1593	379.5369	1135.5887	1132.6353	2.9535	1	8	24	6	R.QSFNLLQKR.A
1795	589.8866	1177.7587	1177.6343	0.1245	0	96	4.2e-08	1	R.VSELALYDIR.G 1805
2003	610.6796	1219.3447	1218.6972	0.6475	0	72	1.1e-05	1	R.LFGVTTLDVVR.A 2004 2016
2280	630.4476	1258.8807	1258.6955	0.1852	1	28	0.27	1	K.LLEACLGDLKK.N
2723	654.6866	1307.3587	1306.7609	0.5978	0	71	1.4e-05	1	K.GSEIVLIPAGVPR.K 2732 2733
3264	682.9016	1363.7887	1363.6732	0.1155	0	52	0.001	1	R.DDLFNTNASIVR.D 3273 3278

3364	687.6541	1373.2937	1374.7177	-1.4239	1	8	31	4	R.MAESLLKAAQGEK.G
3942	481.3919	1441.1537	1442.7881	-1.6344	2	19	1.9	2	K.NIQKGIDFVKANP.- 3950
4102	730.6596	1459.3047	1458.7718	0.5329	0	77	3.3e-06	1	K.ILPVGQVNAYEEK.L 4104 4123
4172	734.7001	1467.3857	1465.6653	1.7204	0	(4)	58	3	K.DGAGSATLSMAMAGAR.M
4310	742.1826	1482.3507	1481.6602	0.6905	0	70	1.6e-05	1	K.DGAGSATLSMAMAGAR.M 4312 4317 4320
4319	742.6751	1483.3357	1481.6602	1.6755	0	(6)	39	2	K.DGAGSATLSMAMAGAR.M
4938	776.1921	1550.3697	1549.8028	0.5669	0	64	5.3e-05	1	K.GVVEPTFVDSPLYK.D 4956
6753	566.6849	1697.0327	1696.7872	0.2455	1	12	8.7	1	K.AKDGAGSATLSMAMAGAR.M 6736 6763
7598	889.0126	1776.0107	1776.0873	-0.0766	0	117	3.2e-10	1	K.VAVLGAAGGIGQPLSLLLK.L 7610 7611 7614 7618 7631
8036	606.4182	1816.2327	1816.9319	-0.6992	1	11	12	3	R.DELVNRIQFGGDEVVK.A
12971	818.3479	2452.0217	2453.2076	-1.1859	2	6	33	1	K.AKDGAGSATLSMAMAGARMAESLLK.A
14864	924.7632	2771.2677	2769.3426	1.9252	2	0	1e+02	5	R.IQFGGDEVVKAKDGAGSATLSMAMAGAR.M
15037	943.7829	2828.3267	2827.3737	0.9531	0	18	1.9	1	R.GGPGVAADLSHINTNSTVSGYEATPSGLR.D 15046
15627	1534.1771	3066.3397	3065.6284	0.7113	0	70	1.1e-05	1	K.AAAEASPEANILVISNPVNSTVPIVSEVFK.S 15629
16270	1134.8129	3401.4167	3398.7318	2.6849	0	17	2	1	K.TDPSNEAVTVVGGHSGVTIVPLLSQSSHPSIEGK.T

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18. gi|220698199|gb|EED54539.1| **Mass:** 75100 **Score:** 898 **Queries matched:** 60 **emPAI:** 1.25

transketolase TktA [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
280	826.5550	825.5477	825.4021	0.1456	0	30	0.14	1	R.FGASGPYK.Q 281
308	835.3110	834.3037	833.3767	0.9271	0	28	0.35	1	K.ADDAESVK.A
505	903.4750	902.4677	902.5073	-0.0396	0	45	0.0065	1	R.VLAVDATSK.A
940	508.8236	1015.6327	1015.5913	0.0414	1	45	0.006	1	R.KLSEAVLEK.V 941 953
975	513.1796	1024.3447	1023.5601	0.7846	0	25	0.5	1	R.LTTTIGFGSK.L 974
1342	548.8046	1095.5947	1095.5601	0.0347	0	44	0.0057	1	K.FEFTPAGISK.R 1341 1344 1346
1361	551.1846	1100.3547	1099.4678	0.8869	0	(9)	21	3	K.CAFTEDVMK.R
1391	554.1081	1106.2017	1107.6400	-1.4383	0	3	77	7	K.HTPSILALTR.Q
1450	559.0236	1116.0327	1115.4627	0.5700	0	30	0.19	1	K.CAFTEDVMK.R
1562	567.1661	1132.3177	1131.5706	0.7471	1	3	91	10	K.AIQECREVK.D
1999	610.1726	1218.3307	1217.5412	0.7896	0	64	7.1e-05	1	K.DGDNDLEAIEK.A 1995 2002
2076	617.3721	1232.7297	1233.5891	-0.8593	0	29	0.22	1	R.YAHEQFGLNR.F 2080
2464	639.6676	1277.3207	1276.6888	0.6319	0	64	7e-05	1	K.LQGTGGVHGNPLK.A
5373	797.1211	1592.2277	1591.8206	0.4072	0	52	0.0009	1	M.GYTDLDQLAINTIR.V 5376 5393 5395
5375	797.1886	1592.3627	1591.8206	0.5422	0	43	0.008	1	K.SLPTYKPTDSAVASR.K 5380
7180	870.4961	1738.9777	1738.8237	0.1541	0	66	3.2e-05	1	R.VVSVPCFEVFDAQDK.D 7186
7347	878.2961	1754.5777	1753.9210	0.6567	0	78	2.5e-06	1	R.QNLPQLENSSIEAALK.G 7353
7627	890.2731	1778.5317	1777.7995	0.7323	0	58	0.00027	1	K.FMNFNPQNPDWVNR.D 7639
8352	926.8301	1851.6457	1849.9363	1.7094	0	49	0.0018	1	K.QSFVVPQQVYDLYHK.T 8343 8344
10253	1033.2141	2064.4137	2063.9337	0.4800	0	84	5.1e-07	1	K.NAVDFQPPEYNIGDWSGR.Y 10250
10852	1073.8886	2145.7627	2145.0089	0.7538	1	59	0.00017	1	R.VVSVPCFEVFDAQDKDYK.L 10822 10850 10858 10861

11131	729.8965	2186.6677	2186.0855	0.5822	0	4	49	2	K.LGNLIAIYDDNHISIDGDTK.C 11136
11449	1114.7696	2227.5247	2226.1355	1.3893	0	80	1.2e-06	1	K.VLPDGIPVLSVEAASTMGWER.Y 11440
11510	746.5862	2236.7367	2234.0725	2.6642	0	16	3	1	K.ANSGHPGAPMGMAPVSHVLFNK.F
11547	1122.4511	2242.8877	2242.1304	0.7574	0	(41)	0.009	1	K.VLPDGIPVLSVEAASTMGWER.Y 11545
11689	756.7762	2267.3067	2266.1553	1.1514	0	66	3.4e-05	1	K.VHSVIPELLSGSADLTGSNNTR.W 11687 11691 11693
12172	777.4509	2329.3307	2331.1012	-1.7705	2	4	47	7	K.DGDNDLEAIEKAIQECREVK.D
14314	887.8259	2660.4557	2658.2861	2.1697	1	1	87	2	K.ENHNVVARVVSVPCFEVFDAQDK.D 14300
15201	958.7222	2873.1447	2873.4997	-0.3550	2	2	72	5	K.DYKLKVLPDGIPVLSVEAASTMGWER.Y

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19. gi|220701504|gb|EED57842.1| **Mass:** 57367 **Score:** 886 **Queries matched:** 61 **emPAI:** 1.73

phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
212	787.1780	786.1707	786.3946	-0.2238	0	22	1.3	1	R.DMIPSPK.V
969	511.5556	1021.0967	1020.5128	0.5840	0	36	0.046	1	K.VATYDLDPK.M 970
1493	562.4141	1122.8137	1122.5743	0.2394	0	54	0.00064	1	K.AIGVIYEACK.K
1772	588.3811	1174.7477	1174.6022	0.1455	0	45	0.0053	1	R.SPKPDFPYPK.N 1774 1776 1780
2362	634.6681	1267.3217	1266.6278	0.6939	0	(60)	0.00017	1	K.YMQQLLDQTK.E 2366
2508	642.5446	1283.0747	1282.6227	0.4520	0	62	0.0001	1	K.YMQQLLDQTK.E 2519
2768	657.5511	1313.0877	1312.7351	0.3527	0	77	3.6e-06	1	K.EIGIGEIATVVGR.Y 2779 2784
2851	661.8026	1321.5907	1321.6514	-0.0607	0	64	6e-05	1	R.EITQLLGDYDR.S 2856 2865
2985	669.1186	1336.2227	1335.6670	0.5557	0	58	0.00024	1	K.YEAAIQGVAATDK.A 2989
3473	693.8611	1385.7077	1385.7878	-0.0801	2	3	86	8	R.IDQTLKKGELNK.V
4060	727.7561	1453.4977	1451.6358	1.8620	0	7	27	2	K.DDDTLFFFNYR.S 4053
4362	745.5871	1489.1597	1488.6944	0.4653	0	80	1.8e-06	1	K.GIVSGEGEESSDPVK.T 4369
5174	525.5425	1573.6057	1573.7923	-0.1865	1	4	55	8	K.QFAGEVRDMIPSPK.V 5163
6241	831.2531	1660.4917	1658.8490	1.6427	0	51	0.0012	1	K.VPFIMANAPEGWSLK.K 6262
6475	560.0692	1677.1857	1674.8439	2.3418	0	(3)	71	6	K.VPFIMANAPEGWSLK.K
6498	840.7491	1679.4837	1678.7991	0.6846	1	85	4.3e-07	1	R.VKDDDTLFFFNYR.S 6505 6513 6520
7753	895.2521	1788.4897	1788.8968	-0.4071	1	7	29	3	R.DMIPSPKVATYDLDPK.M 7752
8876	636.1729	1905.4967	1906.9240	-1.4273	2	4	60	2	K.MSAEAVGQKMADRIAEGK.F
10768	1069.9551	2137.8957	2136.9761	0.9196	0	87	2.4e-07	1	K.FEFVMNNFAPPDMVGHTGK.Y 10773 10782 10783
10911	719.1502	2154.4287	2152.9711	1.4577	0	(1)	96	2	K.FEFVMNNFAPPDMVGHTGK.Y
11056	725.6955	2174.0647	2176.0569	-1.9922	1	2	85	7	R.VEIAMKGIVSGEGEESSDPVK.T
11651	754.3675	2260.0807	2258.0049	2.0758	0	3	62	3	K.DGDAILAAETPFMSGFAEADSK.T 11656
12368	790.1205	2367.3397	2366.1641	1.1756	1	23	0.63	1	R.YEKDETDEFLKPIIVGGEER.R
12410	791.6479	2371.9217	2370.1049	1.8168	1	50	0.0013	1	R.KDGDAILAAETPFMSGFAEADSK.T 12397
12469	794.5049	2380.4927	2381.1209	-0.6282	0	4	45	1	K.QGYVLFITADHGNAEEMLTEK.G 12482
13372	835.7689	2504.2847	2505.2726	-0.9879	1	3	62	1	R.SPKPDFPYPKNIHITTMTQYK.T
13389	836.4572	2506.3497	2505.4431	0.9066	0	39	0.015	1	R.LHLLGLVSDGGVHSNITHLIGLLK.V 13384 13396
14835	922.7792	2765.3157	2763.3367	1.9790	0	10	11	1	K.TDYTFPVAFPPQHMGNVLAEWLSK.K 14834

15977	1084.3735	3250.0987	3251.6418	-1.5430	0	(3)	51	3	K.EGGVLGDVAPTVLAAMGIEQPEEMSGQNLLVK.A
16011	1091.1765	3270.5077	3267.6367	2.8710	0	53	0.00047	1	K.EGGVLGDVAPTVLAAMGIEQPEEMSGQNLLVK.A
16035	1095.7792	3284.3157	3283.6316	0.6841	0	(22)	0.54	1	K.EGGVLGDVAPTVLAAMGIEQPEEMSGQNLLVK.A 16036 16039

20. gi|220692651|gb|EED48997.1| **Mass:** 50492 **Score:** 829 **Queries matched:** 65 **emPAI:** 1.42

translation elongation factor EF-1 alpha subunit , putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5	610.4110	609.4037	609.3122	0.0915	0	19	1.3	1	K.FQTSK.Y
348	425.1676	848.3207	848.4643	-0.1436	0	20	1.8	4	K.FAELLEK.I
487	898.5350	897.5277	897.5647	-0.0370	0	(44)	0.0059	1	R.QLIVALNK.M 488 489 492
557	914.5170	913.5097	913.5597	-0.0500	0	31	0.13	1	R.QTVAVGVIK.S 555 560 561
762	488.5776	975.1407	974.5437	0.5971	0	57	0.00035	1	R.LPLQDVYK.I 757 766
1125	528.4101	1054.8057	1054.6135	0.1922	0	51	0.0012	1	K.ISGIGTVPVGR.V 1120 1122 1123
1596	1137.6180	1136.6107	1135.5873	1.0234	1	13	7.7	2	K.EAAELGKGSFK.Y 1584 1587 1592
2142	415.0975	1242.2707	1243.6884	-1.4177	2	4	67	9	R.RTGKSVEDKPK.F
2874	663.9151	1325.8157	1325.7456	0.0702	0	63	9.3e-05	1	R.EHALLAFTLGVR.Q 2881 2886 2887 2888 2889 2893 2899 2
2955	667.5621	1333.1097	1331.7231	1.3866	1	4	72	4	R.DMRQTVAVGVIK.S 2932
3171	679.0961	1356.1777	1355.6834	0.4944	0	62	0.00011	1	K.YEVTVIDAPGHR.D 3177 3179 3182 3183 3193
4972	518.5735	1552.6987	1553.8606	-1.1619	2	10	13	6	K.GSFKYAWVLDKLK.S 4975
6958	857.1516	1712.2887	1711.9144	0.3743	2	2	94	6	R.YNEIVKETSNFIKK.V
11298	736.8465	2207.5177	2205.2997	2.2180	1	10	15	2	R.EHALLAFTLGVRQLIVALNK.M
12011	770.7245	2309.1517	2308.1054	1.0463	0	4	46	2	K.MIPSKPMCVESFTDFPPLGR.F
12252	782.4152	2344.2237	2343.3162	0.9076	0	25	0.36	1	K.TLLEAIDAIEPPVRPTDKPLR.L 12250 12251
13250	1244.4541	2486.8937	2486.3455	0.5483	0	65	3.8e-05	1	R.VETGVIKPGMVVTFAPANVTTEVK.S 13249
13393	836.5032	2506.4877	2505.1819	1.3058	0	(78)	1.7e-06	1	K.SVEMHHQQLQAGNPGDNVGFNVK.N 13390
13515	841.5909	2521.7507	2521.1768	0.5739	0	83	6.3e-07	1	K.SVEMHHQQLQAGNPGDNVGFNVK.N 13517 13529 13535
15367	986.3659	2956.0757	2954.4365	1.6392	0	45	0.0034	1	K.NMITGTSQADCAILIIASGTGEFEAGISK.D
15399	991.9489	2972.8247	2970.4314	2.3933	0	(26)	0.27	1	K.NMITGTSQADCAILIIASGTGEFEAGISK.D 15397

21. gi|220701397|gb|EED57735.1| **Mass:** 32900 **Score:** 825 **Queries matched:** 32 **emPAI:** 1.38

mitochondrial phosphate carrier protein (Mir1), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
179	385.0241	768.0337	767.4218	0.6119	0	21	0.87	1	K.FVVFEK.V
313	837.4960	836.4887	836.4392	0.0495	0	16	3.7	1	K.VSEAIYR.G
352	851.4700	850.4627	850.4297	0.0330	0	20	1.6	1	R.GSYAGIGAR.L
862	498.0806	994.1467	993.4596	0.6871	0	50	0.0015	1	K.FGGYEFFK.Q 865
1434	557.6711	1113.3277	1113.6394	-0.3116	0	20	1.5	2	R.LLGATGGVEIGK.-
1829	594.0741	1186.1337	1185.5626	0.5711	0	57	0.00035	1	K.TPGEPGEGTVSR.L
2361	634.6006	1267.1867	1266.6092	0.5775	1	65	5e-05	1	R.GFDKETLSDGAK.T 2363

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         7043   861.9651  1721.9157  1721.9352  -0.0195   0    97  2.6e-08    1    R.LVSQPTFATGLLSGFGK.I 7054 7055 7057 7059 7060 7064 7
         7894   902.0281  1802.0417  1801.9039   0.1378   0    83  6.8e-07    1    K.NEGVGAFYSGFGPILFK.Q 7896 7899 7903 7913 7916 7920
         9862  1014.2786  2026.5427  2026.0483   0.4944   0    88  1.9e-07    1    K.AESPAPAAPQQLSGLALYSR.F 9879
        11386   740.2789  2217.8147  2216.1664   1.6484   1     0  1.2e+02    1    R.LFMVGTLTAGQFAIYGDIKR.L
        12262  1174.2366  2346.4587  2345.3835   1.0752   2     1       93    4    R.IRLVSQPTFATGLLSGFGKILK.N
        12652   803.3442  2407.0107  2405.1872   1.8235   0    52  0.00077    1    R.FAFAGAVCCSVTHGALTPVDVVK.T 12648
        15193   957.7472  2870.2197  2868.4810   1.7387   0    50   0.0012    1    R.QVIANEGAGALLTGFGPTAAGYFLQGAFK.F
```

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22.     gi|220699514|gb|EED55853.1|     Mass: 43394     Score: 823     Queries matched: 21     emPAI: 0.67
        aspartic endopeptidase Pep2 [Aspergillus flavus NRRL3357]
        Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
         6044   823.7296  1645.4447  1644.7995  0.6452   0   108  2.7e-09   1   K.YGSGSLSGFVSQDTLK.I 6017
         6735   848.7581  1695.5017  1694.8880  0.6138   0    90  1.5e-07   1   R.FDGILGLGFDTISVNK.I 6738 6748 6750
         6958   857.1516  1712.2887  1711.8570  0.4318   0    85  4.3e-07   1   K.WYSVYDLGNGAVGLAK.A 6957 6962 6964 6974
        10030   681.6645  2041.9717  2039.0840  2.8877   2     1       97   7   R.KWYSVYDLGNGAVGLAKAK.-
        11607  1127.6976  2253.3807  2253.1430  0.2377   1   112  8.7e-10   1   K.VKDQLFAEATSEPGLAFAFGR.F 11611 11613 11622
        12050   771.8735  2312.5987  2311.2933  1.3054   2     6       29   2   M.KSTLVTASVLLGCASAEVHKLK.L
        12892   813.7682  2438.2827  2438.1238  0.1589   1    64  4.3e-05   1   K.EGDDSVATFGGVDKDHYTGELVK.I 12896
        15450   998.8435  2993.5087  2992.4059  1.1028   0    73  5.6e-06   1   K.VVLDTGSSNLWVPSSECGSIACYLHNK.Y 15451
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23.     gi|220700072|gb|EED56411.1|     Mass: 54581     Score: 767     Queries matched: 53     emPAI: 2.04
        6-phosphogluconate dehydrogenase Gnd1, putative [Aspergillus flavus NRRL3357]
        Query   Observed   Mr(expt)   Mr(calc)     Delta Miss Score   Expect Rank  Peptide
          351   851.1480   850.1407   849.4232    0.7175   0    17      3.2    1    R.FLENEAK.G
          357   426.9941   851.9737   851.4137    0.5600   0     7       31    9    K.DITNAYR.Q
          854   497.1876   992.3607   991.5338    0.8269   0    47   0.0032    1    K.DIFQSIAAK.S 850 852
         1430   557.5611  1113.1077  1112.5040    0.6038   0    37    0.034    1    R.DYFGAHTFR.V 1426
         2118   619.8206  1237.6267  1237.6779   -0.0511   0    40    0.015    1    R.DLPANLLQAQR.D 2119
         2728   654.9316  1307.8487  1307.6106    0.2381   0    50   0.0017    1    R.FVGSGVSGGEEGAR.Y 2731
         2916   665.2116  1328.4087  1327.7434    0.6653   0    21      1.3    1    K.LNKPSIALMWR.G
         3109   676.0666  1350.1187  1348.6147    1.5040   0    65  4.8e-05    1    R.FNDDDGTPLVEK.I 3090 3113
         3242   682.0836  1362.1527  1361.7555    0.3973   0    85  4.7e-07    1    K.GVLDSFLIEITR.D 3249 3270
         3982   723.6841  1445.3537  1444.7198    0.6339   0    67  3.4e-05    1    R.QNPDLENLLFDK.F 3978
         5434   800.3386  1598.6627  1597.7736    0.8891   0    48   0.0022    1    R.VKPEHANETYPEGK.D
         5541   804.1726  1606.3307  1603.7916    2.5391   0    71  1.3e-05    1    R.GVGMPVNEIAEVFDK.W 5515
         5655   808.3501  1614.6857  1614.8253   -0.1396   0    45   0.0048    1    R.ASSLLPGPTPQFTGDK.Q 5663
         6764   850.1696  1698.3247  1696.8308    1.4939   0    29      0.2    1    K.QAFVDDLEQALYASK.I 6771
         7771   597.6359  1789.8857  1789.9727   -0.0869   1     0  1.5e+02    6    K.WNKGVLDSFLIEITR.D
         7872   901.2686  1800.5227  1799.8950    0.6278   0    90  1.3e-07    1    K.IISYAQGFMLMQEAAK.E 7880 7886
```

8190	917.4866	1832.9587	1831.8848	1.0739	0	(3)	76	2	K.IISYAQGFMLMQEAAK.E
9503	662.5089	1984.5047	1984.0862	0.4185	1	5	47	4	K.LNKPSIALMWRGGCIIR.S
9579	665.2119	1992.6137	1991.0451	1.5687	1	9	18	1	K.EYGWKLNKPSIALMWR.G
9915	678.6955	2033.0647	2032.0088	1.0559	1	30	0.13	1	R.GVGMPVNEIAEVFDKWNK.G 9913
10112	684.4119	2050.2137	2048.0037	2.2100	1	(6)	32	1	R.GVGMPVNEIAEVFDKWNK.G 10111
11164	731.1565	2190.4477	2188.1099	2.3378	2	39	0.017	1	K.RGVGMPVNEIAEVFDKWNK.G
11436	742.7349	2225.1827	2224.8790	0.3037	0	32	0.075	1	K.SEGEACCDWVGDEGAGHYVK.M 11434
11717	758.5542	2272.6407	2270.1655	2.4752	2	4	46	8	K.DERVRASSLLPGPTPQFTGDK.Q
11754	1140.0351	2278.0557	2278.1229	-0.0672	1	3	66	2	K.DITNAYRQNPDLENLLFDK.F
12546	1195.9381	2389.8617	2389.1743	0.6874	0	81	9.2e-07	1	K.GALWGIPTPAFSTALSFYDGYR.T 12545 12548
13203	827.9122	2480.7147	2479.1915	1.5232	1	1	1e+02	4	K.IISYAQGFMLMQEAAKEYGWK.L
13288	831.7119	2492.1137	2489.2988	2.8149	0	6	27	1	K.WTAINALDLGMPVTLIGEAVFSR.C
14060	871.6115	2611.8127	2611.2120	0.6007	0	36	0.029	1	K.MVHNGIEYGDMQLICEAYDILK.R 14049
14126	877.4192	2629.2357	2627.2070	2.0288	0	(21)	0.88	1	K.MVHNGIEYGDMQLICEAYDILK.R 14123
14841	923.4399	2767.2977	2767.3131	-0.0154	1	1	93	9	K.MVHNGIEYGDMQLICEAYDILKR.G

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24. gi|220689888|gb|EED46238.1| **Mass:** 35645 **Score:** 753 **Queries matched:** 60 **emPAI:** 2.80

transaldolase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
79	694.5290	693.5217	693.4537	0.0680	0	25	0.44	1	K.ALHIIK.L
207	785.6930	784.6857	784.4555	0.2302	0	16	4.1	1	K.AAQVLQR.D
453	441.8861	881.7577	881.5586	0.1991	0	50	0.0015	1	K.ILEIIPGK.V 451 452 455
624	468.5576	935.1007	934.5124	0.5883	0	61	0.00014	1	K.FAADAVTLK.D 622 623 626
1051	522.0461	1042.0777	1041.6182	0.4595	2	12	9.5	8	K.DILKQKVQA.-
2030	613.4511	1224.8877	1223.6034	1.2843	0	62	9.2e-05	1	R.LSFDTQASIDK.A 2023 2024 2026 2034 2038
2136	621.6846	1241.3547	1240.6088	0.7459	0	45	0.0055	1	K.TYINDEALFR.F 2145
2390	636.5996	1271.1847	1270.6769	0.5079	0	45	0.0051	1	K.LDAASATGLDIPK.K
2431	638.7416	1275.4687	1274.6295	0.8392	0	58	0.00027	1	K.SVQNIFNYYK.K
3329	686.2221	1370.4297	1368.7037	1.7260	1	54	0.00067	1	K.KTYINDEALFR.F 3330
3590	700.3761	1398.7377	1398.7718	-0.0341	1	97	2.8e-08	1	K.KLDAASATGLDIPK.K 3593 3600 3602 3608 3609 3610 3614
3624	468.5575	1402.6507	1403.8024	-1.1517	1	18	2.3	1	K.FAADAVTLKDILK.Q 3626 3653
3965	722.7571	1443.4997	1442.6387	0.8610	0	(27)	0.28	2	R.FEFNEEAMAVEK.L 3967 3977
4092	729.9916	1457.9687	1458.6337	-0.6649	0	33	0.086	1	R.FEFNEEAMAVEK.L 4096 4114
4698	510.2132	1527.6177	1526.8668	0.7509	2	19	1.9	1	K.KLDAASATGLDIPKK.T
7171	870.2476	1738.4807	1736.8985	1.5823	0	85	4.4e-07	1	K.KPEYAALIDAAVEYGK.Q 7155 7157 7158 7161 7164 7166 717
7684	595.3995	1783.1767	1782.8497	0.3271	1	24	0.58	2	K.QHGSNVDEKVDATLDR.L 7686
8994	959.8036	1917.5927	1917.0207	0.5720	0	75	4.2e-06	1	K.YKPQDATTNPSLILAASK.K 8999 9003 9004
11407	741.6042	2221.7907	2223.3103	-1.5196	2	3	70	4	R.VLIKIASTWEGIKAAQVLQR.D
11553	748.8762	2243.6067	2242.0939	1.5128	2	6	29	3	R.FEFNEEAMAVEKLREGISK.F

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25. gi|220691704|gb|EED48052.1| **Mass:** 79640 **Score:** 714 **Queries matched:** 57 **emPAI:** 0.76
molecular chaperone and allergen Mod-E/Hsp90/Hsp1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
69	688.5100	687.5027	687.4167	0.0860	0	22	1.4	1	K.LVDITK.D 70
515	454.0876	906.1607	905.4858	0.6749	0	40	0.018	1	K.SPFLDSLK.Q 525
976	1025.3770	1024.3697	1024.4713	-0.1016	0	40	0.016	1	R.YESLSDPSK.L
992	515.6901	1029.3657	1028.6593	0.7064	2	6	42	7	K.SAIIKELKK.K
1175	534.2826	1066.5507	1066.5335	0.0172	0	7	29	2	R.APFDLFETK.K
1382	553.0941	1104.1737	1104.5047	-0.3310	1	3	85	8	K.KVEADGESDR.T 1397 1398
2027	613.0426	1224.0707	1222.6346	1.4361	1	28	0.27	1	K.RAPFDLFETK.K 2032
2380	635.7876	1269.5607	1269.7041	-0.1433	0	68	2.3e-05	1	K.ADLINNLGTIAR.S 2385
2443	639.2086	1276.4027	1274.6354	1.7673	0	67	3.2e-05	1	R.ELISNASDALDK.I
2602	647.6841	1293.3537	1293.6564	-0.3027	1	14	7	2	K.IRYESLSDPSK.L 2598 2607 2611 2625
3052	672.6726	1343.3307	1342.7820	0.5487	2	10	19	3	K.SLKNILGDKVEK.V
3102	675.4611	1348.9077	1347.6572	1.2506	0	17	2.9	1	K.HFSVEGQLEFR.A 3096 3098 3103 3108
3529	696.7471	1391.4797	1391.7660	-0.2863	2	11	13	2	K.EFDGKKLVDITK.D
3908	719.6901	1437.3657	1435.7194	1.6463	2	19	1.9	2	R.EKEEKEFEGLAK.S
4548	757.5611	1513.1077	1512.7784	0.3293	0	61	0.00012	1	K.GVVDSEDLPLNLSR.E 4550
4696	764.7591	1527.5037	1527.7053	-0.2016	0	91	1.4e-07	1	K.SGDEVTSLSDYVTR.M 4704 4712
4890	516.1799	1545.5177	1543.8205	1.6972	1	15	4.8	1	R.ELISNASDALDKIR.Y
4946	776.3451	1550.6757	1548.8987	1.7770	2	5	51	1	R.QTLAKLLRYQSTK.S
5508	535.4422	1603.3047	1600.7831	2.5216	1	7	30	8	K.KPKIEEVDEEEEK.K
7387	880.6751	1759.3357	1758.8100	0.5257	0	91	1.2e-07	1	R.NPADITQEEYAAFYK.S 7393
8292	616.4815	1846.4227	1844.9825	1.4402	0	44	0.0052	1	K.HSEFISYPIYLHVLK.E 8290
9454	660.2895	1977.8467	1977.1194	0.7274	2	3	61	8	K.VEKVVVSHKLVGSPCAIR.T
10214	687.9979	2060.9717	2061.1443	-0.1726	2	0	1.2e+02	8	K.LGVHEDAQNRQTLAKLLR.Y
10412	1043.4156	2084.8167	2083.0109	1.8058	1	44	0.0048	1	K.TLELFTEIAEDREQFDK.F 10406 10415
10981	722.7192	2165.1357	2166.0119	-0.8761	2	2	83	3	R.IMKAQALRDTSMSSYMSSK.K 11017
11423	1112.8391	2223.6637	2222.1511	1.5126	0	72	8.6e-06	1	R.VFITDDATDLIPEWLSFIK.G 11424
11889	765.7875	2294.3407	2294.0485	0.2922	1	44	0.0055	1	K.SGDEVTSLSDYVTRMPEHQK.Q 11881 11883
12167	777.3265	2328.9577	2326.1310	2.8267	2	4	49	4	R.TGQFGWSANMERIMKAQALR.D
12614	801.5082	2401.5027	2400.2253	1.2774	0	44	0.005	1	K.NFEVLFLVDPIDEYAFTQLK.E 12606
12962	817.7152	2450.1237	2449.2675	0.8562	2	2	79	5	R.MPEHQKQIYYITGESIKAVAK.S
14169	880.8022	2639.3847	2641.3176	-1.9329	1	51	0.00083	1	K.TKPIWTRNPADITQEEYAAFYK.S

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26. gi|220693792|gb|EED50137.1| **Mass:** 49527 **Score:** 697 **Queries matched:** 46 **emPAI:** 1.17
adenosylhomocysteinase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
433	875.2790	874.2717	873.4807	0.7910	0	24	0.78	1	R.ESLIDGIK.R 428
896	501.6816	1001.3487	1000.4866	0.8622	0	7	36	2	K.YVEFGTTGK.K

968	511.5406	1021.0667	1020.6080	0.4587	0	47	0.0032	1	R.HIILLAEGR.L 971
1357	550.6911	1099.3677	1098.6801	0.6876	0	43	0.0092	1	K.KPVGVYVLPK.V 1358
1466	560.4696	1118.9247	1118.6084	0.3163	0	84	7.2e-07	1	K.VADISLAAFGR.R 1465
1521	565.0341	1128.0537	1128.5815	-0.5278	1	3	98	5	K.KYVEFGTTGK.K
1560	566.9986	1131.9827	1131.5672	0.4155	0	66	3.9e-05	1	R.YAADQPLAGAR.I 1563
1579	568.1811	1134.3477	1133.6081	0.7396	0	70	1.6e-05	1	K.VAVVAGYGDVGK.G 1575 1577
2283	630.6516	1259.2887	1257.5706	1.7181	0	11	15	2	K.GCAQALHSMGAR.V
2517	428.9972	1283.9697	1282.6993	1.2704	0	12	11	1	K.SVQNIKPQVDR.Y 2516
4106	487.5152	1459.5237	1458.7653	0.7584	1	9	19	4	R.DILVGKHFEVMR.N
4307	741.9836	1481.9527	1481.8453	0.1074	0	39	0.018	1	K.LLVPAINVNDSVTK.S 4303 4312 4314
5366	796.7346	1591.4547	1590.8188	0.6359	0	46	0.004	1	K.AAPLGQIFVTTTGCR.D
8016	908.2136	1814.4127	1813.9317	0.4810	0	103	7.8e-09	1	R.EIELAEIEMPGLMAIR.R 8028
8242	614.5849	1840.7327	1841.9934	-1.2607	1	3	79	4	R.YLMANGRHIILLAEGR.L
8319	617.2429	1848.7067	1845.9216	2.7852	0	(1)	98	8	R.EIELAEIEMPGLMAIR.R 8302
8792	633.6945	1898.0617	1898.9196	-0.8579	1	2	87	10	K.FDNLYGCRESLIDGIK.R
9116	968.2661	1934.5177	1932.0350	2.4827	2	2	96	1	R.ESLIDGIKRATDVMIAGK.V
9250	651.7045	1952.0917	1951.0262	1.0655	0	55	0.0004	1	K.LNLILDDGGDLTSLVHEK.Y 9263
9529	663.9152	1988.7237	1986.0278	2.6960	1	3	72	3	R.EIELAEIEMPGLMAIRR.R
10374	694.5219	2080.5437	2079.1212	1.4226	1	81	1e-06	1	K.KLNLILDDGGDLTSLVHEK.Y 10383
10377	1041.3321	2080.6497	2081.1561	-0.5064	1	1	97	1	K.YVEFGTTGKKPVGVYVLPK.V
10530	701.4692	2101.3857	2100.0938	1.2919	1	4	50	5	-.MAAPAHQFKVADISLAAFGR.R
10547	702.4392	2104.2957	2104.0847	0.2110	1	5	43	4	K.SVQNIKPQVDRYLMANGR.H 10557
10579	704.0982	2109.2727	2108.9473	0.3254	0	5	44	2	K.DCYGLSEETTTGVHHLYK.M
12273	1174.8021	2347.5897	2346.0110	1.5787	0	49	0.0014	1	K.GETDEEYNWCLEQQLSAFK.D 12274
15023	940.0735	2817.1987	2815.4677	1.7310	0	88	1.9e-07	1	R.VLVTEIDPINALQAAVQGFEVTTMEK.A
15031	943.0535	2826.1387	2825.4170	0.7217	1	2	65	1	R.NDAIVCNIGHFDIEIDVAWLKANAK.S
15085	945.1589	2832.4547	2831.4627	0.9921	0	(14)	4.2	1	R.VLVTEIDPINALQAAVQGFEVTTMEK.A

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27. gi\|220690667\|gb\|EED47016.1\| **Mass:** 33878 **Score:** 675 **Queries matched:** 48 **emPAI:** 1.55

mitochondrial ADP,ATP carrier protein (Ant), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
183	771.5090	770.5017	770.4399	0.0619	0	18	2.5	1	K.GAGANILR.G 182
1392	554.1691	1106.3237	1105.4829	0.8409	0	61	0.00013	1	K.YNSSFDAFR.Q 1388 1390 1399 1403
1817	592.6811	1183.3477	1181.6081	1.7396	0	19	1.8	1	R.QFNGLVDVYK.K
2100	618.8951	1235.7757	1235.6510	0.1247	0	94	5.6e-08	1	K.TLASDGIAGLYR.G 2099 2105
2178	624.2556	1246.4967	1246.6306	-0.1339	0	68	2.5e-05	1	R.TAASEGVASLWR.G 2184
2839	660.8641	1319.7137	1318.5798	1.1339	1	9	19	2	R.KYNGIMDCFR.R 2838
3260	682.7721	1363.5297	1362.7660	0.7637	0	67	2.9e-05	1	R.GFGPSVLGIVVYR.G 3248 3254 3257 3258 3261 3262 3265
3275	683.3141	1364.6137	1363.7459	0.8678	1	23	0.78	1	K.KTLASDGIAGLYR.G 3256
3353	687.1331	1372.2517	1371.7180	0.5337	0	(50)	0.0018	1	K.LLIQNQDEMLR.A 3344

3501	695.4046	1388.7947	1387.7129	1.0818	0	61	0.00013	1	K.LLIQNQDEMLR.A 3488 3497 3498 3514 3518
3570	698.9916	1395.9687	1395.6785	0.2903	2	5	44	7	R.RRMMMTSGEAVK.Y
3683	706.8776	1411.7407	1411.6734	0.0673	2	(2)	88	2	R.RRMMMTSGEAVK.Y
4230	738.2771	1474.5397	1473.7405	0.7992	0	68	2.5e-05	1	R.YFPTQALNFAFR.D 4254 4261
5851	544.4619	1630.3637	1628.8919	1.4718	1	9	19	2	R.IKLLIQNQDEMLR.A
11031	724.5335	2170.5787	2170.9486	-0.3698	1	4	52	8	R.MMMTSGEAVKYNSSFDAFR.Q
12186	778.7265	2333.1577	2335.1051	-1.9474	0	(0)	1.2e+02	7	K.SVFGMPGFVVDFMMGGVSAAVSK.T
12202	1168.8791	2335.7437	2335.1051	0.6386	0	10	13	1	K.SVFGMPGFVVDFMMGGVSAAVSK.T
12253	782.4462	2344.3167	2343.0446	1.2721	2	3	65	1	R.RMMMTSGEAVKYNSSFDAFR.Q
13891	861.2025	2580.5857	2580.4064	0.1793	1	0	1.1e+02	9	K.TLASDGIAGLYRGFGPSVLGIVVYR.G

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28. gi|220699036|gb|EED55375.1| **Mass:** 47366 **Score:** 672 **Queries matched:** 54 **emPAI:** 1.10

aspartate aminotransferase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
243	807.3660	806.3587	806.4538	-0.0951	0	33	0.095	1	R.LAESIFK.V 245
389	431.7581	861.5017	860.4868	1.0149	0	59	0.00024	1	R.IGGAFLQR.F
1165	532.9896	1063.9647	1063.5914	0.3734	1	6	48	5	R.LAESIFKVTG.-
1443	558.6411	1115.2677	1114.6499	0.6179	0	19	2.2	1	K.GKPYVLPSVR.A
1911	602.7651	1203.5157	1202.6507	0.8651	0	70	1.8e-05	1	R.ISVAGITSDNVK.R 1903 1908
1932	604.6996	1207.3847	1206.5849	0.7998	1	9	20	4	K.GMADRIIEMR.S
2378	635.6601	1269.3057	1269.7153	-0.4096	1	14	5.7	2	R.DANLRTVVVGAR.H 2380
3313	685.6696	1369.3247	1368.6925	0.6322	0	50	0.0016	1	K.EYAGITGVPSFTK.A
3722	709.1626	1416.3107	1414.8144	1.4963	0	48	0.0027	1	R.LVITQSISGTGALR.I 3706 3707 3709 3716 3718 3720 3721
4966	777.2346	1552.4547	1551.7239	0.7308	0	85	4.8e-07	1	R.VGAFSLVCENAEEK.K 4961 4976 4984
5726	811.2751	1620.5357	1618.8454	1.6903	0	85	4.7e-07	1	K.DTIGLDFEGLIADIK.A 5699 5702 5718 5725 5729
6156	827.6961	1653.3777	1654.9227	-1.5450	2	2	99	2	K.AASRDANLRTVVVGAR.H
6720	565.6165	1693.8277	1691.8811	1.9467	2	2	93	9	K.GMADRIIEMRSLLR.K
7380	880.2941	1758.5737	1758.8829	-0.3091	1	77	2.8e-06	1	R.FDKEYAGITGVPSFTK.A 7388 7389 7406
7477	884.3446	1766.6747	1766.9315	-0.2568	2	3	79	7	K.ADSFKEKINLGVGAYR.D
8034	606.3842	1816.1307	1814.9850	1.1457	1	10	16	6	K.EDRLVITQSISGTGALR.I 8012 8039
8537	624.7092	1871.1057	1869.9526	1.1531	0	11	10	1	K.IYLPNPSWANHNAVFK.D 8546
9194	649.4035	1945.1887	1943.9312	1.2575	0	39	0.019	1	R.HFVSEGHNIALCQSFAK.N 9193
11710	1136.7686	2271.5227	2271.1205	0.4022	0	87	2.7e-07	1	R.VASTIMNDPELNQQWLGEVK.G 11712
14316	887.8535	2660.5387	2662.4819	-1.9432	2	4	49	5	K.RVDSQVKILIRPFYSNPPIHGAR.V
15099	947.1329	2838.3767	2837.2656	1.1111	1	6	26	1	K.GHFAFFDMAYQGFASGNADKDAFAPR.H
15847	1060.1672	3177.4797	3174.5267	2.9531	0	16	2.4	1	K.HDWSHITSQIGMFAYTGLKPEQMDALAK.E
15984	1085.6959	3254.0657	3253.4961	0.5696	2	2	62	8	R.QISDVMKQKGHFAFFDMAYQGFASGNADK.D 15982

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29. gi|220689985|gb|EED46335.1| **Mass:** 71678 **Score:** 666 **Queries matched:** 45 **emPAI:** 0.25

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      succinate dehydrogenase subunit Sdh1, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
       279   412.9696   823.9247   823.4777   0.4471   1     9       18    7   R.AVSHRVR.D
      1972   607.6621  1213.3097  1212.5961   0.7136   1     7       33    2   R.FMERYAPTAK.D
      2513   642.7071  1283.3997  1282.7146   0.6851   1     7       30    3   K.KPHGKIDLGYR.A
      2527   643.5826  1285.1507  1285.5799  -0.4292   1     5       45    5   R.GAHAREDYPDR.D
      2780   658.1576  1314.3007  1313.5710   0.7297   0    39    0.019    1   R.ELEGYGCPFSR.T 2778
      3013   670.7451  1339.4757  1338.6793   0.7964   0    24     0.59    1   K.AHHTVLATGGYGR.A
      3346   458.1892  1371.5457  1368.8201   2.7256   2    16        4    1   R.SLAPASKISRALR.D 3338
      4214   737.7876  1473.5607  1472.8351   0.7256   0    93  8.4e-08    1   R.LGANSLLDLVVFGR.A 4220 4222 4227 4231 4241 4244
      6242   831.2621  1660.5097  1659.8917   0.6180   2     7       34    4   R.DQRRLFSSTRPAAR.I 6239
      6434   837.9396  1673.8647  1673.8519   0.0128   0   117  2.9e-10    1   R.NLLTCATQTAVAAANR.K 6456
      7085   863.8211  1725.6277  1724.8338   0.7939   1    11       11    3   R.NAMQKAMQTDVSVFR.T 7084
      7359   586.2585  1755.7537  1756.8236  -1.0699   1   (3)       67    6   R.NAMQKAMQTDVSVFR.T
      7921   903.3841  1804.7537  1803.9618   0.7919   0   103  7.7e-09    1   R.LPGISETASIFAGVDVTK.Q 7908 7913 7917 7918 7919 7922
      8478   622.3599  1864.0577  1863.8210   0.2367   0    21      1.1    1   K.GSDWLGDQDAIHYMTR.E
      9534   995.7456  1989.4767  1989.0908   0.3859   1    13      6.2    3   R.LFSSTRPAARIFGSNPLR.A 9532
     11050  1087.4826  2172.9507  2171.1011   1.8496   0     2       80    2   K.YPIIDHEYDAVVVGAGGAGLR.A
     13270   830.7865  2489.3377  2491.2190  -1.8813   2     4       50    3   R.ELSSDAGAQSIKDLDFARTADGPK.S
     15968  1083.2042  3246.5907  3246.5768   0.0139   0    60  8.3e-05    1   R.AGLPNQDLEFVQFHPTGIYGAGCLITEGSR.G 15972 15974
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30.   gi|220691583|gb|EED47931.1|      Mass: 40278     Score: 656     Queries matched: 57     emPAI: 4.67
      60S ribosomal protein L4, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
        75   690.6440   689.6367   687.4391   2.1976   2     9       28    9   K.VAKSRK.M
        97   358.5641   715.1137   714.4640   0.6498   0    51   0.0016    1   K.AAVTLLK.A 95 100 101
       676   479.8676   957.7207   957.5131   0.2076   0    44    0.008    1   K.ALGAGDDLVK.V 669 673 675
       860   497.8271   993.6397   993.5131   0.1266   0    51   0.0011    1   K.TFENAALTK.T 858 859 863 864
      1258   541.2386  1080.4627  1080.5604  -0.0976   0    44   0.0059    1   R.LNPYAAAFSK.E 1249 1260 1264
      1306   545.5886  1089.1627  1088.5138   0.6489   0    33    0.094    1   K.EFLSTLHEN.- 1304 1318
      1794  1178.7510  1177.7437  1178.5251  -0.7814   0     0  1.6e+02    4   R.AGQAAFGNQCR.S
      3213   680.9226  1359.8307  1357.7565   2.0742   0    37    0.034    2   R.LINSSEIQSVLR.A 3203
      3475   694.0886  1386.1627  1385.7191   0.4436   0    53  0.00082    1   R.GPLVVYNPEVDGK.E
      3785   713.6656  1425.3167  1424.7446   0.5721   0    50   0.0015    1   R.LDVVQQVHTGMAK.N 3790
      3908   719.6901  1437.3657  1435.6328   1.7329   0    86  3.5e-07    1   K.AGEQTSAESWGTGR.A
      3940   721.5381  1441.0617  1440.7395   0.3222   0  (41)    0.012    1   R.LDVVQQVHTGMAK.N 3941 3942 3950
      4057   727.6941  1453.3737  1450.7503   2.6234   2     1  1.3e+02    6   R.SGRMFAPTKVWR.K
      4290   740.7336  1479.4527  1478.8344   0.6183   0    57  0.00032    1   R.VANVPEVPLVVESK.T 4287 4301 4302
      4836   771.8241  1541.6337  1541.8202  -0.1865   1    50   0.0016    1   R.RGPLVVYNPEVDGK.E 4850 4853
      6346   557.3169  1668.9287  1666.8825   2.0462   1     4       57    8   R.LDVVQQVHTGMAKNK.R 6361
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7553	887.2426	1772.4707	1770.9264	1.5443	0	82	8.6e-07	1	K.DYLLPQNVVANADLAR.L 7544
8149	914.6886	1827.3627	1825.9799	1.3828	2	8	23	3	R.QRRGPLVVYNPEVDGK.E
8482	622.4985	1864.4737	1863.0254	1.4483	0	55	0.00047	1	R.FATASALAASSVPALLFAR.G 8483
8623	628.6299	1882.8677	1883.1091	-0.2414	2	6	32	2	K.TKAAVTLLKALGAGDDLVK.V
8842	635.0112	1902.0117	1899.0214	2.9903	1	1	1.1e+02	9	K.KDYLLPQNVVANADLAR.L
14390	1336.4381	2670.8617	2669.4653	1.3964	0	77	2.2e-06	1	R.NIPGVETSPVFALNLLQLAPGGHLGR.F 14386 14394 14399
15080	944.4912	2830.4517	2828.4385	2.0132	1	5	35	2	R.FVVWTSSAFEALDQVFGSGSSPAALKK.D 15060 15063 15068

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31. gi|220698900|gb|EED55239.1| **Mass:** 36449 **Score:** 653 **Queries matched:** 69 **emPAI:** 1.84

glyceraldehyde 3-phosphate dehydrogenase GpdA [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
275	410.7816	819.5487	818.4399	1.1088	0	18	3.1	2	K.VGINGFGR.I 276
288	414.9126	827.8107	826.4912	1.3195	0	3	87	8	K.VIPSLNGK.L
1473	561.0271	1120.0397	1119.6539	0.3858	0	64	7.5e-05	1	R.VVDLIAYISK.V
1959	606.8806	1211.7467	1211.6662	0.0805	0	54	0.00054	1	K.AGIALNEHFIK.L 1965 1974
2444	639.2181	1276.4217	1275.7551	0.6667	1	43	0.0085	1	R.RVVDLIAYISK.V 2436 2441 2450
2616	648.4811	1294.9477	1295.6609	-0.7131	1	5	51	4	R.TEKAVTYEDIK.K 2617
3096	675.2066	1348.3987	1346.7129	1.6858	1	4	66	3	-.MATPKVGINGFGR.I
3816	477.2295	1428.6667	1428.7572	-0.0905	0	3	74	9	R.TAAQNIIPSSTGAAK.A
4716	765.8826	1529.7507	1529.7872	-0.0365	0	78	2.4e-06	1	R.VPTANVSVVDLTCR.T 4720 4722 4728
5516	535.6415	1603.9027	1602.8586	1.0442	1	9	20	2	K.VIPSLNGKLTGMSMR.V 5513
6440	838.1911	1674.3677	1673.7474	0.6203	0	69	2e-05	1	K.LVSWYDNEWGYSR.R 6443 6445 6454
8801	950.3241	1898.6337	1896.9469	1.6868	0	1	98	1	R.FQGTIETYEEGLIVNGK.K
9426	659.2422	1974.7047	1974.0754	0.6293	2	5	47	2	K.AVGKVIPSLNGKLTGMSMR.V 9416
9559	664.7742	1991.3007	1990.0703	1.2304	2	(3)	76	4	K.AVGKVIPSLNGKLTGMSMR.V 9577
9868	676.6395	2026.8967	2025.0419	1.8549	1	1	1.1e+02	4	R.FQGTIETYEEGLIVNGKK.I
10207	1031.2881	2060.5617	2060.0435	0.5183	0	91	1.2e-07	1	K.VIISAPSADAPMFVMGVNNK.E 10213 10215 10222
10342	693.4255	2077.2547	2076.0384	1.2163	0	(6)	34	2	K.VIISAPSADAPMFVMGVNNK.E 10349
10456	698.3402	2091.9987	2092.0333	-0.0346	0	(5)	39	1	K.VIISAPSADAPMFVMGVNNK.E
11406	741.5292	2221.5657	2220.1283	1.4375	1	44	0.0049	1	K.KVIISAPSADAPMFVMGVNNK.E 11409
13313	832.8979	2495.6717	2496.2392	-0.5675	1	(2)	79	3	K.VIISAPSADAPMFVMGVNNKEYK.T
13458	838.8202	2513.4387	2512.2342	1.2046	1	5	35	1	K.VIISAPSADAPMFVMGVNNKEYK.T
14163	880.5125	2638.5157	2637.3109	1.2049	0	74	5.2e-06	1	K.VINDNFGLVEGLMTTVHSYTATQK.T 14164 14167 14172 1417
14258	886.0669	2655.1787	2653.3058	1.8729	0	(28)	0.17	1	K.VINDNFGLVEGLMTTVHSYTATQK.T 14259 14264
15142	951.9865	2852.9377	2851.3764	1.5614	0	52	0.00069	1	K.GILGYTEDDIVSTDLIGDAHSSIFDAK.A 15134 15135 15141 1
15494	1008.9015	3023.6827	3022.4746	1.2081	0	19	1.3	1	R.NAIASGDVDVVAVNDPFIETHYAAYMLK.Y
15526	1519.9371	3037.8597	3038.4695	-0.6098	0	(11)	8.3	1	R.NAIASGDVDVVAVNDPFIETHYAAYMLK.Y

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32. gi|220692490|gb|EED48836.1| **Mass:** 232514 **Score:** 630 **Queries matched:** 68 **emPAI:** 0.23

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 fatty acid synthase beta subunit, putative [Aspergillus flavus NRRL3357]
Query   Observed    Mr(expt)    Mr(calc)     Delta Miss Score   Expect Rank  Peptide
  811   985.8130    984.8057    984.4988    0.3069    1     7       35    2   K.EAHTSKNAK.K
  851   496.6436    991.2727    990.5134    0.7593    0    43   0.0086    1   K.LALNEFER.A
  955   509.8106   1017.6067   1017.5283    0.0784    1    10       20    3   R.IKEFYYR.V
 1204  1071.5360   1070.5287   1069.4862    1.0425    1     4       63    3   K.ASFEDMRSK.G
 1387   553.7266   1105.4387   1104.6404    0.7984    2    16      4.2    2   K.KLTGDFIRR.V
 1453   559.4276   1116.8407   1118.5754   -1.7347    0     5       58    1   R.GLTMQVAVER.D 1480 1490
 1471   560.9171   1119.8197   1120.4931   -0.6734    1     1  1.3e+02    9   R.EVMEGRNDR.I
 1476   561.3091   1120.6037   1119.4873    1.1164    0    19      2.3    1   K.EYFEDVYR.L
 1852   595.7601   1189.5057   1188.5995    0.9062    0     7       38    5   R.TCILQGPMAAK.F
 2047   614.6796   1227.3447   1226.6845    0.6602    0   (0)  1.5e+02    8   R.AMAWQIPLIGK.L
 2146   622.3326   1242.6507   1242.6794   -0.0287    0     6       46    8   R.AMAWQIPLIGK.L
 2159   623.2036   1244.3927   1243.6594    0.7333    1     4       65    6   R.IMIAKEAHTSK.N
 2416   637.7356   1273.4567   1272.6979    0.7588    0    67  3.2e-05    1   K.FPVILQWTGGR.G 2415
 2450   639.2911   1276.5677   1276.6775   -0.1098    0     9       24   10   K.NQISLTLFEGR.T
 3492   695.0006   1387.9867   1387.7249    0.2619    0    19      2.1    1   R.GIDVPFHSTFLR.S
 4124   731.7926   1461.5707   1459.6732    1.8975    0     6       36    2   R.GAYLDFENTFQR.K
 4638   508.3312   1521.9717   1522.7272   -0.7555    1     4       53    6   R.MVDLMYVKHESR.W
 4940   776.2406   1550.4667   1549.8174    0.6493    0    58  0.00023    1   R.ALDCLTNLLNYLK.A 4943
 5599   537.9832   1610.9277   1611.8039   -0.8762    1     2    1e+02    4   R.KDEVPMQVHLASSR.D
 5792   542.7149   1625.1227   1622.8681    2.2546    0    10       15    1   R.HAIFLADIFVQGHR.F 5789
 6506   840.8966   1679.7787   1679.7937   -0.0150    0     0  1.4e+02    6   -.MYGTSTGPQTGINTPR.S
 6790   851.0321   1700.0497   1698.8802    1.1696    1     2       96    8   K.APTGLDQNRVPFTQR.K
 7113   577.3999   1729.1777   1728.7923    0.3854    1     2       95    5   R.SNYSMCAVNPSRISK.T
 7320   584.5839   1750.7297   1747.9581    2.7717    1     1    1e+02   10   R.GNDVHAVASALPGITAKK.T
 7815   898.2391   1794.4637   1793.9022    0.5615    0    15      4.1    1   R.HFMENYGLSIIDIVK.N
 7828   898.6956   1795.3767   1794.8934    0.4833    1     2       84    6   K.MNEKNQISLTLFEGR.T
 8308   924.7516   1847.4887   1846.8171    0.6716    0    34    0.052    1   R.FGYPPMPFDGCLFGSR.I
 8451   930.8836   1859.7527   1859.0305    0.7222    0    89  1.6e-07    1   R.NFVVTGPPLSLYGLNLR.L 8450
 9124   646.2232   1935.6477   1935.0764    0.5713    1     4       50    7   K.LVHLSNGFKMVPGAQPLK.V
 9574   665.0545   1992.1417   1993.1473   -1.0055    1     9       15    2   K.TIPPGRGITINLIYVNPR.A 9564 9570 9575 9576 9587
10367   694.2195   2079.6367   2080.1066   -0.4698    0    12      7.7    2   K.ATHIVDFGPGGISGLGVLTNR.N
10498   700.2135   2097.6187   2095.1678    2.4510    0     7       30    2   K.SVFSHVQTIGQVLLELPTK.E
10542  1052.3236   2102.6327   2102.0387    0.5940    0    68  1.9e-05    1   K.AQNIDIPALMQSMSLEDVK.A
10669   708.8435   2123.5087   2125.1102   -1.6015    1     2       88    9   R.AFMRGNDVHAVASALPGITAK.K
10888   717.4119   2149.2137   2148.2055    1.0082    0    54  0.00052    1   K.HIAFKPGSVDAIQQVINIAK.A
10989  1083.8201   2165.6257   2163.0484    2.5773    2     1       91    6   K.KAIADAPGLDDQDWEKTYK.G
11176  1096.8526   2191.6907   2189.1004    2.5903    0    19      1.6    1   R.NGTSIEQPVYFENPIPLSGK.T
11401  1110.8551   2219.6957   2219.1508    0.5450    0    90  1.3e-07    1   R.SPSGLLSATQFTQPALTLMEK.A 11402 11404 11407 11409
11865   764.0939   2289.2597   2288.1266    1.1331    0    25     0.44    1   R.FLPITAPFHSQYLYSAYDR.I 11863
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12124	775.5085	2323.5037	2324.2158	-0.7121	1	0	1.2e+02	2	K.GSAGGVVTVLSEMGEPIHKLATR.G
12571	799.1472	2394.4197	2393.0991	1.3206	1	10	11	2	K.AIRQNYMSMTFESVNADGSIK.S
12676	804.7292	2411.1657	2410.1998	0.9660	0	38	0.018	1	R.GQKPVPFVPALDENFEYWFK.K 12666
12920	815.2602	2442.7587	2442.2002	0.5585	0	25	0.42	1	R.VFSSYANLPGTITHGMYTSAAVR.S 12912
14072	872.6722	2614.9947	2612.4690	2.5257	2	1	84	9	R.FKNKSVFSHVQTIGQVLLELPTK.E
14651	906.8365	2717.4877	2719.4560	-1.9683	1	4	46	3	K.EVFAPMDFAIVAGWKAITKPIFPR.T
14688	**908.6395**	**2722.8967**	**2721.3803**	**1.5165**	**0**	**40**	**0.01**	**1**	**R.TAEGGVVPLTFLFTYHPESGYAPIR.E** 14682
14788	917.1025	2748.2857	2747.5275	0.7582	2	0	1e+02	2	R.GIDVPFHSTFLRSGVKPFRSFLLK.K
15275	**973.1775**	**2916.5107**	**2915.4414**	**1.0693**	**0**	**77**	**2e-06**	**1**	**R.ETITSQAVADFVHAVGNTGEAFVDRPGK.E** 15276

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33. gi|220696409|gb|EED52751.1| **Mass:** 17491 **Score:** 612 **Queries matched:** 21 **emPAI:** 1.88

40S ribosomal protein S15, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
6016	**549.1009**	**1644.2807**	**1641.7192**	**2.5616**	**0**	**6**	**43**	**1**	**-.MADTEYNAEEAAAIK.A** 5997
8029	**908.7506**	**1815.4867**	**1813.9421**	**1.5446**	**0**	**94**	**6.2e-08**	**1**	**R.GIDLDQLLDLSSEQLR.D** 8012 8018 8021 8034 8039
9800	**1011.7336**	**2021.4527**	**2021.0577**	**0.3950**	**0**	**110**	**1.2e-09**	**1**	**R.DMIIVPEMIGSVIGIYSGK.E** 9801 9803 9825 9827
9982	**1019.7181**	**2037.4217**	**2037.0526**	**0.3691**	**0**	**(32)**	**0.092**	**1**	**R.DMIIVPEMIGSVIGIYSGK.E** 9977
9997	**1020.1366**	**2038.2587**	**2037.0526**	**1.2061**	**0**	**(83)**	**6.8e-07**	**1**	**R.DMIIVPEMIGSVIGIYSGK.E** 9980
10144	**1028.3171**	**2054.6197**	**2053.0475**	**1.5722**	**0**	**(48)**	**0.0023**	**1**	**R.DMIIVPEMIGSVIGIYSGK.E** 10136
13302	**832.4965**	**2494.4677**	**2495.3020**	**-0.8342**	**2**	**5**	**41**	**1**	**R.KFSYRGIDLDQLLDLSSEQLR.D**
13674	848.7582	2543.2527	2544.3444	-1.0917	1	12	7	4	K.THLRDMIIVPEMIGSVIGIYSGK.E

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34. gi|220697342|gb|EED53683.1| **Mass:** 107115 **Score:** 604 **Queries matched:** 40 **emPAI:** 0.43

aminopeptidase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
395	432.7376	863.4607	863.4752	-0.0145	0	14	7.3	2	R.FSLDLAAK.T 393
988	515.3301	1028.6457	1027.5815	1.0643	0	8	25	3	K.KPPLSFPSR.S 984
1332	547.7801	1093.5457	1092.5961	0.9496	1	10	18	7	K.GSSVLRMISK.Y
1405	**554.8651**	**1107.7157**	**1107.5601**	**0.1557**	**0**	**39**	**0.019**	**1**	**K.AFDSSFPLPK.M** 1396 1399
3407	**689.3491**	**1376.6837**	**1375.6918**	**0.9919**	**0**	**(36)**	**0.044**	**1**	**K.NQDIYMPLGGLR.N**
3534	**697.0826**	**1392.1507**	**1391.6867**	**0.4640**	**0**	**47**	**0.003**	**1**	**K.NQDIYMPLGGLR.N** 3532 3552
3566	**698.7346**	**1395.4547**	**1394.7194**	**0.7353**	**0**	**60**	**0.00016**	**1**	**K.YLGEDVFIQGVR.N**
3627	702.4391	1402.8637	1402.7052	0.1585	1	19	2	2	R.NAPTSDEKTTALR.C 3636
3745	**710.7366**	**1419.4587**	**1418.7405**	**0.7182**	**0**	**32**	**0.09**	**1**	**K.FAETIPAGSSAQLK.L**
3752	474.5429	1420.6067	1421.6456	-1.0389	0	7	29	8	K.QGLDENTMLTER.E
4046	**726.8216**	**1451.6287**	**1449.7075**	**1.9213**	**1**	**2**	**94**	**1**	**R.RAFPCFDEPALK.A**
6004	**822.8691**	**1643.7237**	**1642.8930**	**0.8307**	**0**	**78**	**2.4e-06**	**1**	**K.ALLFGAAGSAEDPVVVK.A**
6625	844.2856	1686.5567	1685.8096	0.7471	1	2	1e+02	8	R.NHTAGIEARWAWMK.N
7374	**879.7761**	**1757.5377**	**1756.8342**	**0.7036**	**0**	**94**	**5.6e-08**	**1**	**R.ADEINQIFDAISYMK.G** 7368

7602	889.2576	1776.5007	1774.9326	1.5682	2	4	70	3	K.GFDRAVEQSLDAIRAK.I 7604
8184	917.1026	1832.1907	1831.8927	0.2980	0	23	0.72	1	K.LTFTGILNDNMAGFYR.S 8174 8191
8269	922.7261	1843.4377	1844.8805	-1.4428	2	0	1.4e+02	3	K.NGGEKEYNVVYDRFR.N
8729	946.2001	1890.3857	1889.9735	0.4123	0	112	8.1e-10	1	K.NVGFPVVTVAEDAASSSIK.L 8734
10771	713.6615	2137.9627	2136.0640	1.8987	1	1	99	5	K.VPDLDFYKLNADHSAIYR.T
11669	1131.8576	2261.7007	2261.1362	0.5645	0	6	30	2	R.TGDVRPEEDTTLYPVMLGLR.T
12329	1179.7621	2357.5097	2356.1733	1.3365	1	1	87	4	R.ADEINQIFDAISYMKGSSVLR.M
13211	1242.0761	2482.1377	2481.2785	0.8593	0	109	1.4e-09	1	R.AGMIADAGALASSGYQSTSGLLSLLK.G 13207 13223
13328	833.7749	2498.3027	2497.2734	1.0293	0	(35)	0.036	1	R.AGMIADAGALASSGYQSTSGLLSLLK.G 13329
14791	917.3949	2749.1627	2747.4238	1.7389	0	6	28	1	R.LPPGLGMLGTVVQLTTSSFCTEAQLK.E
16404	1164.6342	3490.8807	3492.8134	-1.9326	1	1	65	3	K.QGLLTVEDRAGMIADAGALASSGYQSTSGLLSLLK.G

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35. gi|220698109|gb|EED54449.1| **Mass:** 53195 **Score:** 580 **Queries matched:** 57 **emPAI:** 1.06

mitochondrial processing peptidase beta subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
458	884.5460	883.5387	883.4763	0.0624	0	28	0.22	1	K.LEPGAIER.E 457
497	451.0531	900.0917	899.5188	0.5729	1	30	0.18	1	R.ERDVILR.E
583	461.0651	920.1157	919.4399	0.6758	0	28	0.27	1	K.SFNNDVPK.A
670	958.3540	957.3467	957.4767	-0.1300	0	24	0.7	1	R.LSPEDIER.T
691	481.0391	960.0637	959.5036	0.5601	0	34	0.081	1	K.ENIQTISR.D 689
807	492.7546	983.4947	982.4178	1.0769	0	7	26	2	K.DVMDFANR.R
1437	557.7896	1113.5647	1113.5778	-0.0131	1	45	0.0048	1	R.RLSPEDIER.T 1438 1439
1592	1136.5540	1135.5467	1133.5717	1.9750	0	8	23	3	R.TPEFIGSEVR.L 1581
2584	646.6121	1291.2097	1289.6728	1.5369	1	34	0.062	1	K.RTPEFIGSEVR.L 2576
2646	650.1086	1298.2027	1296.7877	1.4150	2	3	81	7	R.SRAALKSIQPVK.R
3598	700.6681	1399.3217	1398.7718	0.5499	0	78	2.2e-06	1	K.AVDILADILQNSK.L 3594 3597 3605 3613 3617 3620 3621
3772	713.1076	1424.2007	1423.6766	0.5242	0	73	6.8e-06	1	R.LCFNVTSAEVER.A 3767
5288	529.3662	1585.0767	1584.8049	0.2719	0	10	16	3	K.TNGTAHFLEHLAFK.G 5293 5297
6442	838.2436	1674.4727	1674.9240	-0.4512	0	(8)	23	1	R.MVLVGAGGIPHEQLVR.L
6692	846.7881	1691.5617	1690.9189	0.6429	0	62	8.8e-05	1	R.MVLVGAGGIPHEQLVR.L 6678 6686 6689
8841	952.0016	1901.9887	1901.0106	0.9782	0	33	0.078	1	K.ASILLSLDGTTAVAEDIGR.Q 8833 8844 8846 8847 8851 885
10732	711.3279	2130.9617	2129.0542	1.9076	1	1	97	8	R.AETDKTNGTAHFLEHLAFK.G
11022	1085.6961	2169.3777	2168.0175	1.3603	0	77	2.6e-06	1	K.DDDYFTALVAQAIVGNWDR.A 11008 11014 11020
13444	838.2435	2511.7087	2512.2856	-0.5769	1	9	13	1	K.TNYTADRMVLVGAGGIPHEQLVR.L
13670	848.2575	2541.7507	2540.2077	1.5430	0	70	1.2e-05	1	R.SQHQLELEIENMGAHLNAYTSR.E 13667
14530	898.6052	2692.7937	2692.4072	0.3866	0	53	0.00063	1	R.LAEEHFGSLPSKPPTSAALALTAEQK.R 14535 14537
14627	904.7372	2711.1897	2712.3038	-1.1140	1	4	47	1	K.RSQHQLELEIENMGAHLNAYTSR.E
16366	1153.2172	3456.6297	3455.6382	0.9915	1	53	0.00048	1	R.EQEEVDKQFEEVVFDHLHATAYQNQPLGR.T 16365

36. gi|220691708|gb|EED48056.1| **Mass:** 32920 **Score:** 568 **Queries matched:** 35 **emPAI:** 1.61
ubiquinol-cytochrome C reductase complex core protein 2, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
113	723.4480	722.4407	722.3599	0.0808	0	41	0.011	1	K.NFLSDK.A
544	456.5946	911.1747	910.4701	0.7046	0	18	2	1	K.WVGQFFK.E 540 545
1831	594.3696	1186.7247	1187.6034	-0.8786	0	3	87	9	K.VAAGEVASEDIK.K
2800	659.1736	1316.3327	1315.6983	0.6344	1	72	1e-05	1	K.VAAGEVASEDIKK.A 2802
3034	671.7101	1341.4057	1339.7711	1.6346	0	67	3.3e-05	1	R.EVAGPTATLALVAK.A 3012 3024 3035
3963	722.7376	1443.4607	1443.7933	-0.3326	2	6	37	8	K.KVAAGEVASEDIKK.A 3955 3968
7709	893.1721	1784.3297	1782.8788	1.4509	0	0	1.4e+02	1	K.SHTYSDAGLFTISLSGK.A
9568	996.8356	1991.6567	1990.9465	0.7102	0	81	1e-06	1	R.YQPFPGFSDALEQFAFK.W 9561 9578 9581
10373	1041.2596	2080.5047	2079.0232	1.4815	0	66	3.1e-05	1	K.ELPSSGSSSQYQLRPGATSK.Y 10371 10375 10392
10468	1047.6651	2093.3157	2093.0694	0.2463	0	56	0.00034	1	K.WTPGFSLLAQATQGFSQVR.A 10452 10476 10477 10478 1048
11420	742.1829	2223.5267	2222.1001	1.4266	1	2	88	6	R.RSMASAATPGLQYDVTEAAGVK.L
11583	1126.3406	2250.6667	2250.1420	0.5247	0	90	1.2e-07	1	K.ASVASVGDLFQLPYGEDLGLTV.- 11586 11590 11599

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37. gi|220690088|gb|EED46438.1| **Mass:** 29318 **Score:** 543 **Queries matched:** 38 **emPAI:** 2.64
40S ribosomal protein S4, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
111	722.4360	721.4287	722.3347	-0.9060	0	12	10	4	K.TGENFR.L
185	772.5510	771.5437	771.4491	0.0947	0	38	0.028	1	R.LIQVDGK.V
329	422.8766	843.7387	841.4882	2.2505	2	7	44	2	R.RRAAAIAN.-
1112	527.5441	1053.0737	1051.5887	1.4850	1	9	18	8	R.VGVVTHRER.H
1253	541.0941	1080.1737	1079.5135	0.6603	0	38	0.025	1	R.IQAEEAEYK.L 1250
1412	555.2746	1108.5347	1108.5149	0.0198	0	60	0.00016	1	K.DAVDNTFATR.E 1414
2175	624.2216	1246.4287	1244.6951	1.7336	0	43	0.0077	1	R.DCLPLIVFIR.N 2181
2348	633.8011	1265.5877	1265.6768	-0.0891	0	46	0.0042	1	R.LSAPSHWLLDK.M
2502	642.1526	1282.2907	1281.6830	0.6077	0	53	0.00075	1	K.GGIPFLVTHDAR.T 2498 2507 2518 2521 2524
3137	676.9976	1351.9807	1350.6966	1.2841	0	2	91	2	R.FDTGVVIMVTGGR.N
4556	758.3256	1514.6367	1513.8803	0.7564	1	56	0.00034	1	K.LRDCLPLIVFIR.N 4555 4560
4773	513.0635	1536.1687	1533.8007	2.3680	1	2	88	9	K.AIMMQRLIQVDGK.V
6149	551.9042	1652.6907	1651.9158	0.7749	1	5	46	1	K.GGIPFLVTHDARTIR.Y 6153
8219	919.8276	1837.6407	1836.8968	0.7439	0	91	1e-07	1	R.TDPTFPAGFMDVIGIEK.T 8220 8226 8228
8375	927.7856	1853.5567	1852.8917	0.6650	0	(43)	0.0066	1	R.TDPTFPAGFMDVIGIEK.T 8363
9344	982.7986	1963.5827	1963.1116	0.4712	2	1	1.1e+02	9	K.RVQLGKGGIPFLVTHDAR.T
10165	1029.2826	2056.5507	2056.0993	0.4514	0	55	0.00038	1	R.ESNVFVIGQDKPWISLPK.G 10174 10177 10179 10187 10192
13674	848.7582	2543.2527	2541.2210	2.0317	1	7	26	10	R.TDPTFPAGFMDVIGIEKTGENFR.L

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38. gi|220696127|gb|EED52469.1| **Mass:** 29058 **Score:** 535 **Queries matched:** 54 **emPAI:** 4.08

60S ribosomal protein L7 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
35	665.5110	664.5037	664.3795	0.1242	0	26	0.39	1	R.ELIYK.R
80	696.4220	695.4147	695.3490	0.0657	0	12	7.2	1	R.AESYVK.E
157	378.5981	755.1817	754.5065	0.6752	0	40	0.013	1	K.ILQLLR.L 158
389	431.7581	861.5017	860.5344	0.9673	2	16	5.2	6	K.RAAIFKR.A
456	442.7121	883.4097	882.6014	0.8083	1	36	0.031	1	R.KILQLLR.L
461	443.6371	885.2597	884.5555	0.7042	2	8	29	8	R.EKIRLAR.V
1135	529.5556	1057.0967	1056.5352	0.5615	0	32	0.11	1	K.LSNPTGGFHK.R 1132
1207	536.3311	1070.6477	1070.5720	0.0757	0	29	0.2	1	R.EENINALIR.Q 1208
1544	565.9746	1129.9347	1129.6091	0.3256	2	1	1.5e+02	5	R.AVAREEAEKK.K
2126	620.6356	1239.2567	1236.7302	2.5265	2	8	22	3	K.GINKISPQPRK.I
2325	632.8566	1263.6987	1263.5632	0.1355	0	47	0.0033	1	K.HFIEGGDYGNR.E 2326
2327	633.1436	1264.2727	1263.6400	0.6327	0	45	0.0053	1	K.QANNFLWPFK.L 2336 2342 2345
2420	637.8406	1273.6667	1273.7143	-0.0475	0	54	0.00068	1	R.LLQINNGTFVR.L 2427 2428 2446
2741	655.6671	1309.3197	1307.6034	1.7164	0	38	0.023	1	K.EGNFYVPEEPK.L 2736
3882	718.8366	1435.6587	1435.6983	-0.0396	1	52	0.0011	1	R.KEGNFYVPEEPK.L 3886
6001	822.8226	1643.6307	1641.8573	1.7734	0	60	0.00016	1	R.VAISDNQIIEENLGK.Y 5976 5977 5978 5983 5986 5988 600
12092	773.6952	2318.0637	2316.1247	1.9391	1	32	0.081	1	K.HFIEGGDYGNREENINALIR.Q 12076 12087
12271	783.5085	2347.5037	2348.2951	-0.7914	1	2	85	7	M.ASTATTVPTQDHVLVPETLLKK.R
12697	805.6735	2413.9987	2412.2399	1.7589	0	79	1.6e-06	1	K.ATQEMLTIINPYIAYGYPNLK.S 12685 12687 12689
12812	1215.3506	2428.6867	2428.2348	0.4519	0	(63)	5.3e-05	1	K.ATQEMLTIINPYIAYGYPNLK.S 12824 12831
13090	1234.8756	2467.7367	2465.2301	2.5066	0	50	0.0013	1	K.YGIVCVEDLIHEIYTVGPNFK.Q 13044 13050 13051 13056 13

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39. gi|220697497|gb|EED53838.1| **Mass:** 65234 **Score:** 531 **Queries matched:** 44 **emPAI:** 0.48

phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
855	497.1986	992.3827	992.5543	-0.1715	0	15	6	1	K.TFSTIVTPK.D
879	500.5621	999.1097	998.5397	0.5701	0	17	3.6	4	R.NDVVISPQK.T 880 883
1975	607.8696	1213.7247	1213.6302	0.0945	0	17	3.6	2	K.DLQSLPDSALR.D
2000	610.1736	1218.3327	1217.6768	0.6559	0	21	1.6	2	K.LGIVFVEQGTR.L
2023	612.5291	1223.0437	1222.6346	0.4091	0	45	0.0048	1	K.QALGYPAAASFK.H 2024
4292	494.2405	1479.6997	1477.6772	2.0225	1	9	18	1	R.LAGDKADNWWMR.F
4442	751.2391	1500.4637	1499.7483	0.7154	0	54	0.00064	1	K.VDFVVCNLYPFK.E 4436
4477	502.0562	1503.1467	1500.7355	2.4113	0	7	31	6	K.ANAIDLLCSGNTPR.N
4928	517.5812	1549.7217	1548.6681	1.0537	1	5	44	4	K.ADNWWMRFHDR.V
5618	806.8191	1611.6237	1612.8130	-1.1893	1	3	80	5	-.MSQQKSAILSVYDK.T 5615 5621
6545	841.7486	1681.4827	1681.9839	-0.5011	2	0	1.4e+02	1	K.TGLLDLAKGLAKNNVR.L
6895	854.7066	1707.3987	1706.8152	0.5836	0	32	0.1	1	R.VFEEVPTPFTQEER.E 6892
7460	883.4866	1764.9587	1763.8982	1.0606	0	82	9.9e-07	1	R.VTILSDPQDYPEFLK.E 7468

8050	606.7029	1817.0867	1814.8945	2.1923	1	7	31	6	R.ADKANAIDLLCSGNTPR.N 8003 8008
10255	1033.3121	2064.6097	2064.0449	0.5648	0	89	1.5e-07	1	R.MSSFGDILALSDVVDVPTAK.I 10269
10383	1041.4721	2080.9297	2080.0398	0.8899	0	(35)	0.045	1	R.MSSFGDILALSDVVDVPTAK.I 10392
10616	705.8229	2114.4467	2116.0425	-1.5958	2	2	92	2	K.ADNWWMRFHDRVLNIK.W
10874	1074.8751	2147.7357	2147.0997	0.6360	0	73	6.3e-06	1	R.EVSDGVIAAGYSPEALEILSK.K 10869 10873 10887 10890 1
11639	753.7622	2258.2647	2258.0889	0.1758	0	2	76	2	K.VYMVDDIAGIETSGLAQAYAR.A
11925	1150.5051	2298.9957	2298.2372	0.7585	0	56	0.00035	1	K.ALNGSPGYVNLLDALNAWALVK.E 11937 11939 11941
13206	828.2562	2481.7467	2479.2265	2.5203	1	5	41	2	R.GADRMSSFGDILALSDVVDVPTAK.I 13208
13557	842.5109	2524.5107	2525.2472	-0.7364	2	2	82	2	K.KGGKYLVLQMDESYVPPAEETR.T
15775	1044.3192	3129.9357	3127.4774	2.4583	2	2	57	1	K.AEYERVFEEVPTPFTQEERESWLEK.L

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40. gi|220697614|gb|EED53955.1| **Mass:** 49531 **Score:** 528 **Queries matched:** 38 **emPAI:** 1.03

Glutamate/Leucine/Phenylalanine/Valine dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
938	508.3311	1014.6477	1014.4151	0.2327	0	9	25	7	K.GIMEDCFK.N
1049	521.6576	1041.3007	1039.6026	1.6981	0	47	0.0032	1	K.ALAVVSVPER.V 1040
1529	565.2071	1128.3997	1127.6015	0.7982	0	46	0.0045	1	K.FLGFEQIFK.N 1526
1652	574.5906	1147.1667	1147.5656	-0.3988	0	24	0.75	1	K.NALTGLNMGGGK.G
1980	608.6391	1215.2637	1214.6084	0.6553	0	44	0.0062	1	R.EVGFLFGQYR.K 1979
2022	612.4666	1222.9187	1222.6346	0.2841	0	5	49	6	R.VQFNSALGPYK.G
2243	628.2301	1254.4457	1253.7132	0.7325	0	2	99	4	R.FHPSVNLSILK.F
2828	660.6221	1319.2297	1318.6153	0.6144	0	60	0.00016	1	R.INWTSEEVDAR.L 2822
3630	468.7292	1403.1657	1402.6953	0.4704	2	2	90	10	K.HATDGKESFAGKR.V
4918	775.4086	1548.8027	1547.8307	0.9720	0	43	0.0068	1	R.VAISGSGNVAQYAALK.V 4915 4929 4930 4936
5218	790.7716	1579.5287	1579.8093	-0.2806	0	73	7.2e-06	1	K.ELASTLENSTLFQK.N 5231
7316	584.5092	1750.5057	1749.8646	0.6411	0	21	1	1	K.HIGADTDVPAGDIGVTGR.E
7366	879.2811	1756.5477	1755.9043	0.6434	1	8	22	3	K.QISEIASTEAFASKFK.Y 7356
8721	945.6476	1889.2807	1888.9061	0.3746	0	100	1.6e-08	1	K.AANAGGVAVSGLEMAQNSAR.I 8727 8732
10771	713.6615	2137.9627	2136.0270	1.9357	2	7	24	1	K.NALTGLNMGGGKGGSDFDPKGK.S
11626	1128.6706	2255.3267	2257.1565	-1.8298	1	0	1.2e+02	1	K.FLGFEQIFKNALTGLNMGGGK.G
12119	775.4089	2323.2047	2323.2284	-0.0237	2	17	2.5	1	K.ESFAGKRVAISGSGNVAQYAALK.V 12123 12131 12132 12134
12379	790.7715	2369.2927	2367.2070	2.0857	2	16	3.3	1	K.ELASTLENSTLFQKNPEYRK.A
12664	804.1882	2409.5427	2408.1067	1.4361	0	63	5.8e-05	1	K.FIAEGSNMGSTQDAIDIFEAHR.E 12670
12791	809.3639	2425.0697	2424.1016	0.9681	0	(18)	1.9	1	K.FIAEGSNMGSTQDAIDIFEAHR.E
14933	1394.0221	2786.0297	2785.3440	0.6857	0	104	4e-09	1	K.VDIALPSATQNEVSGEEAQALIDAGCK.F

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41. gi|220691727|gb|EED48075.1| **Mass:** 81578 **Score:** 518 **Queries matched:** 59 **emPAI:** 0.43

NADH-ubiquinone oxidoreductase, subunit G, putative [Aspergillus flavus NRRL3357]

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

444	440.3491	878.6837	879.4450	-0.7613	0	11	14	4	R.SFATTTPR.L
734	969.6090	968.6017	968.6131	-0.0114	1	15	4.7	4	R.LTTPLIRR.E 732 735 737 738
1395	554.2501	1106.4857	1106.5100	-0.0243	0	12	10	1	R.MEEISPVMR.R
1884	599.5761	1197.1377	1197.7193	-0.5816	1	12	9.8	3	K.TQRLTTPLIR.R 1882 1899
2297	631.5646	1261.1147	1260.5638	0.5509	1	7	34	5	R.CIHCTRCVR.F 2303
2907	664.9256	1327.8367	1328.7234	-0.8867	1	1	1.3e+02	9	K.NIGPLVKTSMNR.C
3300	684.8856	1367.7567	1367.6391	0.1176	0	5	45	7	R.GNDMQIGTYLEK.N
3649	703.7666	1405.5187	1403.7772	1.7415	2	2	1e+02	3	R.QKLQLKENEFK.A
3912	719.7571	1437.4997	1437.7147	-0.2150	2	8	22	2	K.SRFACDGLKTQR.L 3900
4056	485.4405	1453.2997	1450.6228	2.6770	1	4	59	9	K.TSMNRCIHCTR.C
4429	500.6079	1498.8017	1496.8423	1.9594	1	11	11	3	R.VQVTRAATSLPGAAR.D 4428
5064	522.0459	1563.1157	1560.7817	2.3340	0	9	18	2	K.VSVEAGSALIQACEK.A
5530	803.6986	1605.3827	1604.7617	0.6210	0	52	0.001	1	R.FMNDVAGAPELGTAGR.G 5543
5760	812.5346	1623.0547	1620.7566	2.2981	0	(6)	38	1	R.FMNDVAGAPELGTAGR.G
6625	844.2856	1686.5567	1685.8988	0.6579	0	100	1.4e-08	1	R.GAQLADVVLPGAAFTEK.S
8882	954.0136	1906.0127	1904.9632	1.0495	0	66	3.2e-05	1	K.FVPATWEQALTEISSAR.Q 8877 8880 8884
9532	995.6631	1989.3117	1989.0830	0.2288	2	10	13	4	R.FACDGLKTQRLTTPLIR.R 9534
10971	1082.8971	2163.7797	2163.0735	0.7062	0	64	5.6e-05	1	R.ATSEFLDVPLPYDDIEALR.D 10976
11191	731.7142	2192.1207	2191.1161	1.0046	0	45	0.0042	1	R.AAAYEVGFTTPSPEVAQTKPK.M 11187
11410	741.7275	2222.1607	2222.1841	-0.0234	1	4	52	4	K.LASAKRPMIIVGSAAAEHADAK.A 11412
12437	792.6655	2374.9747	2374.1877	0.7870	0	35	0.039	1	K.LGSDNLALDQPGGSSPIAHGVDVR.S
12861	812.7009	2435.0807	2434.2016	0.8791	1	28	0.19	1	R.ATSEFLDVPLPYDDIEALRDR.M 12881
14383	1335.8946	2669.7747	2667.4166	2.3581	2	10	12	1	K.FGEKLASAKRPMIIVGSAAAEHADAK.A 14349 14362
14743	913.1652	2736.4737	2738.3619	-1.8882	2	17	2.1	1	R.MEEISPVMRRYDVVEPTSLGSLSK.I
14760	914.2485	2739.7237	2738.3619	1.3618	2	(4)	40	1	R.MEEISPVMRRYDVVEPTSLGSLSK.I 14744 14746 14748 1474
15318	979.9725	2936.8957	2935.4749	1.4208	0	106	2.5e-09	1	K.NLDSELSGNVIDLCPVGALTSKPYAFR.A 15316
15551	1016.3752	3046.1037	3043.5801	2.5237	1	5	36	2	K.RPMIIVGSAAAEHADAKAIFETVGSFVEK.H
15611	1021.5755	3061.7047	3059.5750	2.1297	1	(2)	67	4	K.RPMIIVGSAAAEHADAKAIFETVGSFVEK.H

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42. gi\|220693675\|gb\|EED50020.1\| **Mass:** 21942 **Score:** 518 **Queries matched:** 35 **emPAI:** 2.11

60S ribosomal protein L6 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
535	910.8100	909.8027	909.4920	0.3108	0	32	0.085	1	R.YVIATSTR.I 533
1137	529.5761	1057.1377	1056.5128	0.6249	0	23	0.92	1	K.VSTPDYFTK.E 1139
1200	535.7456	1069.4767	1067.6927	1.7840	2	10	14	5	R.KAVRPTKLR.E 1183 1191
1641	573.2896	1144.5647	1143.6499	0.9148	0	61	0.00014	1	K.AIDQSILASVK.K 1637
1693	580.2206	1158.4267	1159.6309	-1.2042	2	1	1.3e+02	6	K.KVASARASDQK.A
3118	676.3086	1350.6027	1349.7415	0.8612	1	4	66	3	R.VNARYVIATSTR.I
3366	687.8106	1373.6067	1373.7038	-0.0971	0	77	3.2e-06	1	R.IDISGVDAQTVEK.V 3370 3376 3380 3403
4672	763.3096	1524.6047	1522.8508	1.7539	0	76	3.5e-06	1	K.HLDQGVLLVTGPFK.I 4642 4662

5228	790.9141	1579.8137	1579.9297	-0.1160	0	74	5.8e-06	1	R.ESLQPGTILILLAGR.F 5209 5213 5234 5235 5238 5241 5262
6405	837.0396	1672.0647	1672.8995	-0.8348	1	1	1.1e+02	4	R.ASDQKAIDQSILASVK.K
8187	917.2371	1832.4597	1831.9468	0.5129	1	46	0.0037	1	K.KENFLGSYLASTFSLR.N 8165 8179
8338	926.0856	1850.1567	1849.1149	1.0418	1	29	0.2	1	K.LRESLQPGTILILLAGR.F
10905	718.8369	2153.4887	2152.2844	1.2043	2	2	73	5	K.LRESLQPGTILILLAGRFR.G
15192	957.7245	2870.1517	2868.4228	1.7289	2	4	42	7	K.KENFLGSYLASTFSLRNGDKPHEMK.W

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43. gi|220697586|gb|EED53927.1| **Mass:** 37155 **Score:** 504 **Queries matched:** 61 **emPAI:** 2.30

outer mitochondrial membrane protein porin [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
113	723.4480	722.4407	721.4123	1.0285	0	16	3.3	10	K.IFLSSR.I
163	379.5366	757.0587	756.4283	0.6305	0	32	0.13	1	K.VNLHFK.Q 162
382	430.1451	858.2757	857.4606	0.8151	0	61	0.00016	1	K.AANDLLNK.D 374 376 380
401	432.8291	863.6437	863.4389	0.2049	0	33	0.077	1	R.LDPSSFAK.A 396 397 402
817	493.8641	985.7137	985.5192	0.1945	0	66	5.1e-05	1	R.VNAQVEAGAK.A 813 815 820 822 826 834 836
1063	523.5981	1045.1817	1045.5556	-0.3739	0	25	0.52	1	K.APNGVTFNVK.G 1080 1082 1083
1714	581.6906	1161.3667	1160.6037	0.7630	0	59	0.00021	1	K.TGNSVGLEVASK.Y 1711 1712 1713
2307	631.7026	1261.3907	1260.6826	0.7081	1	24	0.66	1	K.SKAPNGVTFNVK.G 2313
2456	639.3406	1276.6667	1276.6663	0.0004	0	38	0.028	1	K.AEILTQYQPSK.Q 2452 2453 2458 2484
2770	657.6026	1313.1907	1312.6986	0.4921	0	75	4.9e-06	1	K.LELDNNIANGLK.A 2772 2781 2783 2794
3544	697.6631	1393.3117	1392.6997	0.6120	0	63	7.9e-05	1	K.NAHEGPIAGSLEAK.Y 3538 3553 3555 3564 3567
4169	734.6446	1467.2747	1466.7041	0.5706	0	59	0.00018	1	K.DFYHTSAASLEVK.S 4172 4173 4177 4179 4182 4185
8241	921.1871	1840.3597	1840.8600	-0.5003	0	0	1.4e+02	10	R.SMFAFSCGQVLSHNIK.I
11996	770.1469	2307.4187	2306.1542	1.2645	1	29	0.16	1	K.AANDLLNKDFYHTSAASLEVK.S
16339	1148.9105	3443.7097	3441.6629	2.0468	0	32	0.058	1	K.YSAAIGYSVPQYSAAITASNNLSVFAASYYHR.V 16335 16336 16

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44. gi|220699460|gb|EED55799.1| **Mass:** 60491 **Score:** 500 **Queries matched:** 31 **emPAI:** 0.89

phosphoglucomutase PgmA [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
398	432.7596	863.5047	862.4661	1.0386	0	14	6.3	3	K.QGVYGLAR.S 399
1421	556.2841	1110.5537	1110.5306	0.0231	0	43	0.0083	1	K.DSFVGSTVSGR.K
1546	566.0566	1130.0987	1127.5863	2.5125	0	8	27	1	K.FGLTASEYLK.D
1609	570.4266	1138.8387	1138.5910	0.2477	0	35	0.051	1	K.EIFDFDLIK.E 1611
2591	431.5535	1291.6387	1290.6490	0.9898	0	12	10	10	R.SMPTSGAVDLVAK.A 2571 2583
2946	666.6691	1331.3237	1331.6332	-0.3095	1	11	15	1	K.FFCNLFDNKK.I
3734	709.7171	1417.4197	1416.7976	0.6221	0	102	9e-09	1	K.DNVALALSLLNFK.E 3741
4862	773.0296	1544.0447	1544.7619	-0.7171	1	2	92	7	K.MMKEIFDFDLIK.E
5066	782.6336	1563.2527	1562.7729	0.4798	0	60	0.00017	1	K.AQGLQSYEVPTGWK.F
5318	794.8286	1587.6427	1586.9104	0.7323	1	4	57	2	R.IIVRLSGTGSSGATIR.L

6466	839.0966	1676.1787	1674.8213	1.3574	0	45	0.0048	1	K.YNLSNGAPAPETVTNK.I
8465	621.7109	1862.1107	1862.8581	-0.7474	0	2	81	10	K.ISICGEESFGTGSNHIR.E
9148	970.3336	1938.6527	1936.1105	2.5422	0	38	0.022	1	K.LLVGQNGILSTPAASNLIR.V 9144
9816	675.2065	2022.5977	2021.9946	0.6031	0	12	8.4	1	K.TYGPLEVEVVHSTSDYVK.M
9904	678.1889	2031.5447	2030.9797	0.5650	1	21	0.94	1	R.KVTDVGNFSYTDLDGSVSK.N
11439	743.0779	2226.2117	2226.2048	0.0069	2	5	37	3	R.YYNPEAIQKIAKISAAYGVK.K
11940	1151.3846	2300.7547	2300.1423	0.6124	0	83	7e-07	1	K.TLTSYNYAEIPELDLSSIGSK.T 11950 11952 11958
13676	848.8212	2543.4417	2542.2638	1.1779	0	53	0.00058	1	R.NMIYGANTFVSPGDSLAIISHHAK.L 13679
13711	851.1175	2550.3307	2550.2139	0.1168	0	44	0.0048	1	K.EKPDQTPSIASIQNDFWQAYGR.T 13719
14374	1335.6166	2669.2187	2667.3796	1.8392	0	47	0.0023	1	K.VFQQPNYSESFITSILLSIPEGAK.D

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45. gi|220696267|gb|EED52609.1| **Mass:** 54923 **Score:** 496 **Queries matched:** 35 **emPAI:** 0.79

dihydrolipoamide dehydrogenase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
260	816.4530	815.4457	815.4389	0.0068	0	30	0.2	1	R.GIEVGDVK.L
356	852.6610	851.6537	849.5185	2.1353	1	4	56	1	R.TKVPHIR.V
504	903.2820	902.2747	901.5498	0.7250	1	0	2e+02	8	M.FRTLLPR.A
824	987.5010	986.4937	986.4379	0.0559	0	2	1.2e+02	9	K.EAAMATYSK.A
1016	1035.5560	1034.5487	1034.5396	0.0091	0	4	68	3	R.LVIDQEYR.T
1760	586.5731	1171.1317	1170.6245	0.5073	0	53	0.00077	1	K.GTGALVDPNTVK.V
1812	592.1411	1182.2677	1181.5829	0.6848	0	7	33	8	R.VGTFPFSANSR.A
2188	416.7429	1247.2067	1247.6622	-0.4555	1	8	29	4	R.GRLVIDQEYR.T
2904	664.8441	1327.6737	1327.7096	-0.0358	0	63	7.7e-05	1	K.VNLLEGGEQTLR.G 2897 2905 2933 2939
4250	738.6541	1475.2937	1474.7272	0.5665	0	47	0.0035	1	R.LGGTCLNVGCIPSK.S 4253
4661	762.7481	1523.4817	1521.7562	1.7255	0	12	8.5	1	K.AEEEAVAAVEYITK.G 4660
4923	775.5081	1549.0017	1546.7272	2.2745	0	14	5.4	1	R.VVGDCTFGPMLAHK.A
4990	778.7491	1555.4837	1555.8821	-0.3984	0	49	0.0017	1	R.IITSTGALSLQEVPK.K 5009 5020
7590	888.5876	1775.1607	1773.9261	1.2346	0	51	0.0011	1	R.RPYTEGLGLENVGIEK.D
9212	650.2955	1947.8647	1948.0881	-0.2234	2	2	93	6	K.AKDTSVEGLTKGIEFLLK.K
9678	669.1322	2004.3747	2006.0329	-1.6582	0	3	62	10	K.MVVIGGGIIGLEMASVWSR.L
10636	1060.3036	2118.5927	2118.1330	0.4598	1	0	1.3e+02	7	K.KMVVIGGGIIGLEMASVWSR.L
11063	726.0342	2175.0807	2174.0967	0.9840	1	42	0.0087	1	R.RPYTEGLGLENVGIEKDER.G 11074
11257	1100.8251	2199.6357	2199.1423	0.4934	0	111	1.1e-09	1	K.NILIATGSEATPFPGLNIDEK.R 11258
12320	786.3455	2356.0147	2355.2434	0.7713	1	58	0.00017	1	K.NILIATGSEATPFPGLNIDEKR.I 12319
13788	853.9762	2558.9067	2557.3098	1.5969	0	28	0.17	1	R.LGAEVTVVEFLNQIGGPGMDAEIAK.Q 13786
13875	859.3862	2575.1367	2573.3047	1.8320	0	(2)	70	5	R.LGAEVTVVEFLNQIGGPGMDAEIAK.Q
16321	1144.4185	3430.2337	3429.6452	0.5885	0	2	53	3	K.GYGHVNYGVIPSVMYTHPEVAWVGQNEAEVK.A

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46. gi|220694939|gb|EED51282.1| **Mass:** 46417 **Score:** 490 **Queries matched:** 36 **emPAI:** 0.86

translation elongation factor eEF-1 subunit gamma, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
73	690.5590	689.5517	689.4225	0.1293	0	14	9.2	2	R.GVFLVR.G 72
199	782.4060	781.3987	780.3654	1.0334	0	11	11	6	K.YNDELK.L
375	858.5070	857.4997	856.5382	0.9615	0	3	97	7	R.TIAALVAAK.A
978	513.4456	1024.8767	1024.4865	0.3902	0	23	0.7	1	K.AEEYSLWK.V 973
2628	648.7461	1295.4777	1294.7397	0.7380	2	18	2.4	2	R.AFATVLDKKFR.S
2812	440.1899	1317.5477	1314.7507	2.7971	2	14	6.8	2	K.KNVEEASKVALK.N 2786
3063	673.3176	1344.6207	1343.7449	0.8759	2	10	19	10	K.YTPPKKEEKPK.K
3081	674.6966	1347.3787	1347.6248	-0.2461	0	24	0.69	1	K.EYPWADGHVFK.- 3097
3182	679.5691	1357.1237	1356.7150	0.4087	0	8	26	3	K.HLTANTFLVGER.I
4982	518.9825	1553.9257	1551.7616	2.1641	1	2	85	8	-.MAFGKIYGQPNNGR.T
6256	831.6856	1661.3567	1660.8508	0.5060	0	66	4.2e-05	1	K.LTFMANNLIGGFHAR.L 6258 6269 6288 6290
6463	559.6155	1675.8247	1676.8457	-1.0210	0	(7)	31	6	K.LTFMANNLIGGFHAR.L
9605	998.6456	1995.2767	1994.9084	0.3683	0	71	1.1e-05	1	K.YVDDMWAWDVPVTVDGK.E 9604 9624
10098	683.8792	2048.6157	2046.0745	2.5412	1	3	63	6	K.EAAPAAAAEPKPEGEQKKPK.H
10341	693.4195	2077.2367	2076.1367	1.1000	1	45	0.0045	1	K.HPLEALGKPDFILDDLKR.T 10346
10676	709.1609	2124.4607	2123.0034	1.4573	1	27	0.28	1	R.KYVDDMWAWDVPVTVDGK.E
13144	1237.8821	2473.7497	2474.1431	-0.3933	0	76	3.1e-06	1	R.GQEFKPAFDVAPDWESYDFVK.L 13142 13154 13163 13171
13465	839.3185	2514.9337	2514.1968	0.7369	0	58	0.00017	1	R.TYSNEDTRPVALPWFWQNYK.A 13462 13466 13470

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47. gi|220693036|gb|EED49382.1| **Mass:** 27511 **Score:** 465 **Queries matched:** 26 **emPAI:** 1.23

triosephosphate isomerase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
98	716.2790	715.2717	714.4024	0.8693	0	28	0.37	1	K.QLNAAAK.E
219	789.6330	788.6257	788.4644	0.1614	0	38	0.035	1	K.TIEVVTK.Q 217
1109	527.1441	1052.2737	1051.5550	0.7188	0	29	0.18	1	R.IIYGGSVSEK.N
3257	682.7076	1363.4007	1363.7017	-0.3010	0	8	24	2	K.MNGTAESITAIIK.N 3258 3260 3261 3266 3276 3280
3958	482.0992	1443.2757	1442.7129	0.5628	1	2	1.1e+02	9	-.MPRQFFVGGNFK.M
5489	802.1671	1602.3197	1601.8817	0.4380	0	102	9.6e-09	1	K.VVIAYEPVWAIGTGK.V 5495 5510 5522
5744	811.8551	1621.6957	1621.8536	-0.1579	0	78	2.4e-06	1	K.VATTQQAQEVHAAIR.K 5752 5761 5765
6242	831.2621	1660.5097	1658.7900	1.7197	0	71	1.3e-05	1	K.WLADAISPEASENTR.I 6239
9298	653.8122	1958.4147	1956.1255	2.2892	2	12	9.4	2	K.TIEVVTKQLNAAAKELTK.E
12428	792.3649	2374.0727	2373.2693	0.8035	0	64	4.4e-05	1	R.DVDGFLVGGASLKPAFVDIINAR.L 12434
13389	836.4572	2506.3497	2504.3308	2.0189	2	1	1e+02	5	R.KVKAAIDGGISVIFCIGETLEER.E

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48. gi|220690395|gb|EED46744.1| **Mass:** 29307 **Score:** 463 **Queries matched:** 27 **emPAI:** 1.63

40S ribosomal protein S3Ae [Aspergillus flavus NRRL3357]

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

413	869.8110	868.8037	867.4338	1.3699	1	11	12	2	R.KDEYSVK.A
484	449.0066	895.9987	895.5491	0.4496	0	15	4.1	3	K.LIPEVIGR.E 485
537	456.1766	910.3387	909.5324	0.8063	0	14	5.5	8	R.LFAIAFTK.R
582	460.1971	918.3797	918.4923	-0.1126	0	51	0.0017	1	K.APSTFQIR.D
610	465.6791	929.3437	929.5406	-0.1969	1	15	6.6	2	R.SSQIRAIR.K
867	499.0231	996.0317	995.4924	0.5394	0	64	6e-05	1	K.TTDDYLLR.L 866
1133	529.3736	1056.7327	1056.5927	0.1400	1	37	0.034	1	K.LRVDEIQGK.N 1136
1891	599.8401	1197.6657	1195.6053	2.0604	2	4	59	10	R.KKMTEIMQR.E
3676	706.1306	1410.2467	1408.6868	1.5599	0	76	4e-06	1	R.EAASCTLSQLTTK.L 3670 3675
4111	487.7085	1460.1037	1459.7743	0.3294	2	9	18	3	R.TSGLKNANDSLKGR.I
5584	805.8016	1609.5887	1608.8736	0.7151	0	66	4e-05	1	K.ATQGIYPLQNVHIR.K 5570 5587 5590
7674	892.2816	1782.5487	1781.8043	0.7444	0	88	2.5e-07	1	K.NCLTNFHGLDFTTDK.L 7692
9192	649.2549	1944.7427	1944.9429	-0.2002	0	17	2.6	1	K.FDLGALLNLHGESTTDDK.G
10641	1060.7316	2119.4487	2118.0018	1.4469	0	90	1.1e-07	1	R.IFEVSLADLQNDEDHAFR.K 10650 10651
11575	750.4735	2248.3987	2246.0967	2.3020	1	17	2.4	1	R.IFEVSLADLQNDEDHAFRK.V
13816	855.7022	2564.0847	2563.3031	0.7817	2	0	1.1e+02	9	K.APKFDLGALLNLHGESTTDDKGHK.V

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49. gi\|220701339\|gb\|EED57677.1\| **Mass:** 14785 **Score:** 440 **Queries matched:** 29 **emPAI:** 2.47

40S ribosomal protein S22 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
164	760.4310	759.4237	758.4003	1.0234	0	12	15	1	K.LLGFFY.-
189	388.3561	774.6977	774.4388	0.2589	0	31	0.18	1	R.YPVQLR.D
1369	551.7171	1101.4197	1100.5978	0.8219	0	40	0.018	1	K.WTTQLLPSR.Q 1367
6850	852.5461	1703.0777	1701.7383	1.3394	0	72	9.5e-06	1	K.HGYIGEFEEVDDHR.S 6823 6837 6846
7000	859.2551	1716.4957	1715.8690	0.6268	0	95	4.8e-08	1	K.TSVLNDTLNAINNAEK.A 6994 6998
9185	648.7882	1943.3427	1943.0323	0.3104	1	2	93	3	M.VKTSVLNDTLNAINNAEK.A
11839	762.7409	2285.2007	2285.3657	-0.1650	2	6	34	3	R.QVLVRPSSKVIVKFLSVMQK.H
11946	768.2169	2301.6287	2301.3606	0.2681	2	(2)	79	10	R.QVLVRPSSKVIVKFLSVMQK.H
12282	783.7769	2348.3087	2346.2213	2.0875	2	7	24	2	-.MVKTSVLNDTLNAINNAEKAGK.R
13628	845.7562	2534.2467	2535.1853	-0.9385	1	(0)	1.1e+02	10	K.FLSVMQKHGYIGEFEEVDDHR.S
13750	852.2502	2553.7287	2551.1802	2.5485	1	38	0.019	1	K.FLSVMQKHGYIGEFEEVDDHR.S
15443	998.2539	2991.7397	2990.4960	1.2437	2	0	95	1	K.VIVKFLSVMQKHGYIGEFEEVDDHR.S
16060	1096.9525	3287.8357	3289.6554	-1.8197	1	45	0.003	1	K.WTTQLLPSRQFGFVVLTTSAGIMDHEEAR.R 16056 16057 16058

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50. gi\|220701642\|gb\|EED57980.1\| **Mass:** 54187 **Score:** 435 **Queries matched:** 21 **emPAI:** 0.42

aspartyl aminopeptidase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
207	785.6930	784.6857	784.4807	0.2051	0	10	15	4	R.IKPVSNK.R
1919	603.3651	1204.7157	1206.6608	-1.9451	0	3	91	9	R.NSSTIVAFAIGK.K

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     4675   763.4206  1524.8267  1524.8260   0.0007  0   61  0.00012   1   R.TAQGADSNVLPAIIR.R 4679
     6554   841.8516  1681.6887  1680.9271   0.7616  1    2       90   4   R.TAQGADSNVLPAIIRR.L
     6945   856.6951  1711.3757  1709.8447   1.5310  0   59  0.00018   1   K.SCLGGLLEEFVFSPR.L 6948
     7117   865.9111  1729.8077  1729.9363  -0.1285  0   72  8.1e-06   1   R.YATNSPGIVLLQEVAR.K 7116
     7371   879.6986  1757.3827  1755.9156   1.4672  0   61  0.00013   1   K.AAEDGGEGVPLQLFVVR.N 7383
     8248   921.6561  1841.2977  1841.0047   0.2931  0   79    2e-06   1   K.ETQLFPIAGLVAAELNR.T 8262 8273 8276
     9895   677.6825  2030.0257  2031.1153  -1.0896  2    2       81  10   K.YYLTRNSSTIVAFAIGKK.W
    12365   789.6869  2366.0387  2367.1277  -1.0890  2    2       84   5   K.AGFQEIKEKDSWSSTCRPGGK.Y
    13856   858.5289  2572.5647  2571.3122   1.2525  0   58  0.00021   1   K.QPALDFLSFVNASPTPFHAVQSAK.E 13860
    15632  1023.7419  3068.2037  3069.4938  -1.2901  1    6       28   4   R.TLDLGNPQLSMHSIRETGGTYDVGHSIR.L 15633
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51.   gi|220699787|gb|EED56126.1|     Mass: 29357    Score: 434    Queries matched: 36    emPAI: 1.63
      cytosolic large ribosomal subunit protein L7A [Aspergillus flavus NRRL3357]
     Query   Observed    Mr(expt)    Mr(calc)     Delta Miss Score  Expect Rank  Peptide
       10   628.4500   627.4427   627.4068   0.0360  0   17      2.9   1   K.ILNLR.L
       43   674.5310   673.5237   673.4374   0.0863  0   22      1.5   1   K.LLSTIK.E 44
      861   497.9031   993.7917   992.5365   1.2552  0   22      0.9   1   K.MGVPYAIVK.G 857
     1130  1057.2290  1056.2217  1055.4407   0.7810  0   26     0.41   1   R.SEDQSEFSK.L
     1382   553.0941  1104.1737  1104.6365  -0.4628  1  (6)      41   3   R.KMGVPYAIVK.G
     1479   561.3846  1120.7547  1120.6314   0.1233  1   25     0.58   1   R.KMGVPYAIVK.G
     1634   572.5581  1143.1017  1142.6659   0.4358  0   95    6e-08   1   K.TAAVLALTEVR.S 1638
     1879   599.3251  1196.6357  1195.6197   1.0160  0    8       24   1   R.LHAEATAVAEGK.K 1873 1886
     1989   609.2716  1216.5287  1215.6248   0.9039  0   41    0.015   1   R.NFGIGQDIQPK.R 1986
     2417   637.7371  1273.4597  1270.7609   2.6989  1   10       19   5   K.KTAAVLALTEVR.S
     2935   666.2486  1330.4827  1328.7088   1.7739  1    2  1.2e+02   4   K.EDVSKKPYHVK.Y
     3397  1376.5880  1375.5807  1375.5892  -0.0084  1   15        6   2   K.EGYTDKYEESR.R 3378 3385
     3472   693.8151  1385.6157  1383.7510   1.8647  1    6       37   1   K.AAPLPYPQGKAGSK.K
     3943   721.6766  1441.3387  1440.7725   0.5662  0   56  0.00039   1   K.YGLNHVVGLVENK.K
     4109   487.6112  1459.8117  1458.7579   1.0538  1    8       23   7   R.SRNFGIGQDIQPK.R
     4474  1503.8550  1502.8477  1501.8154   1.0324  2    5       53   5   K.WPEYVRLQRQK.K
     4843   772.1856  1542.3567  1541.8202   0.5365  0   66  3.6e-05   1   K.VPPAIAQFQSTLDR.N 4841
     5123   785.7576  1569.5007  1568.8675   0.6333  1   41    0.012   1   K.YGLNHVVGLVENKK.A 5130 5132
     7691   892.6711  1783.3277  1782.9992   0.3285  1   82  8.1e-07   1   R.LKVPPAIAQFQSTLDR.N 7684 7686 7697 7712
     7845   899.4841  1796.9537  1794.9311   2.0226  2    5       48   1   R.HWGGGIMGAKAVARQEK.K
    11083   727.1052  2178.2937  2180.0961  -1.8023  1    3       71   4   K.TAAVLALTEVRSEDQSEFSK.L
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52.   gi|220696418|gb|EED52760.1|     Mass: 72424    Score: 430    Queries matched: 36    emPAI: 0.36
      mitochondrial Hsp70 chaperone (Ssc70), putative [Aspergillus flavus NRRL3357]
     Query   Observed    Mr(expt)    Mr(calc)     Delta Miss Score  Expect Rank  Peptide
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37	671.4990	670.4917	670.4377	0.0540	0	13	8.8	1	R.LVGIAAK.R
837	989.3990	988.3917	988.5488	-0.1570	1	6	51	2	-.MLPSRLTR.A
2042	614.1741	1226.3337	1225.6779	0.6559	0	71	1.3e-05	1	K.DAGQIAGLNVLR.V
3615	701.4691	1400.9237	1401.8204	-0.8967	2	10	18	6	R.LTRALPRTAFTR.A
3641	703.2716	1404.5287	1401.8344	2.6944	2	4	71	1	R.EKIAALREFVVK.N
3732	1418.3260	1417.3187	1416.7950	0.5238	2	4	70	2	R.AAGLRVPSTSFRR.W
3954	722.3236	1442.6327	1441.7776	0.8551	0	64	6.3e-05	1	R.SNLESLVDPLISR.T 3938 3952 3972
4155	733.2446	1464.4747	1462.7052	1.7695	0	89	1.9e-07	1	R.TTPSVVGFAQDGER.L 4146
4580	759.3811	1516.7477	1518.7426	-1.9949	2	1	1.3e+02	9	R.RWNSTEGGEEKVK.G
5384	797.8286	1593.6427	1593.7886	-0.1459	0	69	1.8e-05	1	K.TDELQNASLTLFDK.M 5412 5413
6056	824.2286	1646.4427	1644.8723	1.5705	0	90	1.6e-07	1	R.VVNEPTAAALAYGLEK.E 6033 6048 6054
6176	828.5896	1655.1647	1653.9162	1.2485	1	8	21	1	R.QATKDAGQIAGLNVLR.V 6160 6179
6502	840.8471	1679.6797	1679.8267	-0.1470	0	44	0.0058	1	K.NAVVTVPAYFNDSQR.Q 6544
7566	592.1409	1773.4007	1774.8996	-1.4988	2	2	1e+02	4	K.KESGLDLSGDRMAIQR.I
8287	923.7176	1845.4207	1845.9618	-0.5411	1	3	76	4	K.MTRSNLESLVDPLISR.T 8283
9548	664.4942	1990.4607	1989.9830	0.4778	1	1	1e+02	9	K.TDELQNASLTLFDKMHK.A
10206	1031.2446	2060.4747	2059.0620	1.4128	0	7	29	1	K.GQVIGIDLGTTNSAVAVMEGK.T
10214	687.9979	2060.9717	2058.9607	2.0110	0	18	2.1	1	K.STNGDTHLGGEDFDINLVR.H 10204
10859	1074.3056	2146.5967	2145.0736	1.5231	0	2	88	2	K.DANLQASEIQDVILVGGMTR.M
12829	811.2712	2430.7917	2429.2584	1.5333	1	1	92	3	K.GQVIGIDLGTTNSAVAVMEGKTPR.I
12902	814.5692	2440.6857	2441.2948	-0.6091	1	2	65	6	K.ALKDANLQASEIQDVILVGGMTR.M
15046	943.8649	2828.5727	2829.4728	-0.9001	2	2	70	2	K.ALKDANLQASEIQDVILVGGMTRMPK.V

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53. gi\|220701635\|gb\|EED57973.1\| **Mass:** 43824 **Score:** 429 **Queries matched:** 30 **emPAI:** 0.92

inorganic diphosphatase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
242	403.7141	805.4137	804.4970	0.9167	0	18	3.3	1	R.HLPGLLR.A 241
395	432.7376	863.4607	862.4912	0.9695	0	36	0.046	1	K.YALEVIR.E 392 393
1294	544.6201	1087.2257	1087.5146	-0.2888	0	68	2.9e-05	1	K.LNDVEDVER.H 1300
3338	457.9775	1370.9107	1370.6864	0.2243	0	13	8.8	2	-.MFLGSSSTSLVSR.L 3346
3536	697.2861	1392.5577	1391.8024	0.7553	0	66	4.1e-05	1	K.VIVIDVNDPLAPK.L 3537
8316	925.2056	1848.3967	1846.9023	1.4945	0	87	2.8e-07	1	K.VLGVMALLDEEETDWK.V 8329
9710	670.7529	2009.2367	2008.1541	1.0826	2	1	1.1e+02	8	R.TAPLNRLSTASPIVARVSR.T
12142	776.2859	2325.8357	2323.3223	2.5134	2	6	32	1	R.LSTASPIVARVSRTSATLAPPTK.Q 12128 12146
12430	1188.2586	2374.5027	2373.1159	1.3869	0	79	1.4e-06	1	K.GDNDPLDVCEIGELVGYPGQVK.Q 12429 12433
13842	857.7149	2570.1227	2569.2635	0.8593	2	5	35	2	R.IYKIPDGKPENQFAFSGECKNK.K 13840 13852
13863	858.8412	2573.5017	2572.2479	1.2538	1	33	0.064	1	K.AKGDNDPLDVCEIGELVGYPGQVK.Q 13873
15123	950.8869	2849.6387	2849.3085	0.3302	0	35	0.034	1	K.GYLWNYGAFPQTWEDPNTVHPETK.A
16296	1141.4909	3421.4507	3420.7024	0.7483	0	53	0.0004	1	K.DGQPVSPFHDIPLYANEEQTILNMVVEIPR.W 16303
16329	1147.1345	3438.3817	3436.6973	1.6844	0	(31)	0.078	1	K.DGQPVSPFHDIPLYANEEQTILNMVVEIPR.W 16328

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54.   gi|220697495|gb|EED53836.1|    Mass: 200523   Score: 423   Queries matched: 36   emPAI: 0.08
      clathrin heavy chain [Aspergillus flavus NRRL3357]
     Query  Observed  Mr(expt)  Mr(calc)    Delta Miss Score   Expect Rank  Peptide
       200  783.1270  782.1197  780.4316   1.6881    1     7       25    4  K.YLKMAR.K
       224  791.2860  790.2787  789.3617   0.9171    1    12       14    3  K.KDNEER.K
       298  416.3841  830.7537  829.4294   1.3244    0    11       16   10  R.TPETINR.F
      2049  614.8001 1227.5857 1226.6911   0.8947    1     5       53    9  R.KYDVVYLVTK.Y
      3246  682.2206 1362.4267 1360.7714   1.6553    1     7       34    8  R.TIQIFDLGAKQK.L
      3607  701.1296 1400.2447 1400.6130  -0.3682    0     8       26    5  K.ENDMYDTLTVGK.Y 3610
      3863  717.2616 1432.5087 1430.7015   1.8073    0     4       72    5  K.DNKPEHGHLQTR.L
      4263  739.3116 1476.6087 1476.7460  -0.1373    0    61  0.00011    1  R.LDQLSELEDFLR.S 4264
      6184  828.9726 1655.9307 1654.8249   1.1058    0     1  1.3e+02    2  K.RPINADSAIMHWTK.N
      7050  862.3331 1722.6517 1721.9240   0.7277    0    84  5.6e-07    1  K.FSDLLGPGSLISLFEK.Y 7042 7075
      8398  928.7606 1855.5067 1855.8927  -0.3860    1     0  1.3e+02    4  R.TDKLSPEWLMNYFGR.L
      8811  950.8856 1899.7567 1899.0240   0.7327    0   101  1.1e-08    1  K.AFLEADLPGELIELLEK.I 8809
      9105  645.3472 1933.0197 1930.9359   2.0838    2     1    1e+02    5  K.YCEKRDPNLAYIAYR.K
      9340  982.6856 1963.3567 1962.9422   0.4146    0    70  1.4e-05    1  R.AVNDAINDLLIEEEDYK.T 9344
      9828  675.6982 2024.0727 2021.1520   2.9207    1     8       22    2  R.QKLNEEDKPQVIIINLK.N
     10191  687.2462 2058.7167 2057.0694   1.6473    0    10       14    1  K.QVGYQPDYTQLLQHIVR.V
     10788  714.0179 2139.0317 2136.9456   2.0861    2     2       76   10  K.ENDMYDTLTVGKYCEKR.D
     11034  724.6455 2170.9147 2169.2633   1.6514    2     8       20    1  K.NIIALKAQGRTIQIFDLGAK.Q
     11368  739.2665 2214.7777 2212.0616   2.7161    1     3       70    5  K.YIEAATAMGQVTEVERICR.E
     11745  759.5129 2275.5167 2273.1085   2.4082    1     1       94    5  R.AHMGMFTELGIALSKYHPDR.V
     12201  779.5879 2335.7417 2333.1750   2.5667    1     8       18    1  R.AVNDAINDLLIEEEDYKTLR.D
     13318 1249.3991 2496.7837 2495.2155   1.5682    0    57  0.00021    1  K.AVEVYFPQEAVNDFPVAMQVSR.K
     13457  838.8082 2513.4027 2513.2294   0.1733    0     4       43    2  K.NAPQTGQQMSVILQYFGMLLDK.G
     13644  846.6769 2537.0087 2537.3159  -0.3072    1     3       61    2  R.VNPSRAPAVVGGLLDVDCEESIIK.N 13640 13650
     14083  873.4392 2617.2957 2615.3364   1.9593    1     3       62    1  R.SMVDQVIATAVPESTEPDKVSVAVK.A
     14563  901.4112 2701.2117 2701.3082  -0.0965    1     2       73    1  R.ASDPSNYLEVIETATHAGKDEDLVK.Y
     14599  902.8915 2705.6527 2703.4754   2.1773    2     7       22    1  K.RPINADSAIMHWTKNIIALKAQGR.T
     14816  920.7859 2759.3357 2756.3616   2.9741    1     2       72    4  R.VNPEKGAEFAAQLANEESGALIDLDR.V
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55.   gi|220698204|gb|EED54544.1|    Mass: 30946    Score: 417   Queries matched: 17   emPAI: 1.04
      prohibitin complex subunit Phb1, putative [Aspergillus flavus NRRL3357]
     Query  Observed  Mr(expt)  Mr(calc)    Delta Miss Score   Expect Rank  Peptide
       526  454.6286  907.2427  907.4611  -0.2184    0     6       44    8  R.NISTTTGSK.D
      1744  585.2721 1168.5297 1167.6863   0.8434    0    44   0.0055    1  R.VLPSIGNEVLK.A 1742
      1863  597.3511 1192.6877 1190.6329   2.0548    0     6       38    2  K.DLQMVSLTLR.V
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2836	660.7131	1319.4117	1318.6252	0.7865	0	72	1.1e-05	1	R.AEGEAESADIISK.A 2826
7652	891.2631	1780.5117	1779.9672	0.5445	0	64	5.8e-05	1	K.VVNEGTHFLIPWLQK.A 7653 7664 7667
7778	896.2476	1790.4807	1789.8159	0.6649	0	74	5.4e-06	1	K.LPAIYQSYGTDYDER.V
10863	1074.3881	2146.7617	2146.1786	0.5831	0	99	1.5e-08	1	R.LALPVATGALIFNNSIYDVR.G 10864 10865 10868
12387	790.9122	2369.7147	2369.2550	0.4597	2	0	1.1e+02	4	R.QANVIRAEGEAESADIISKAVAK.A
15325	981.3105	2940.9097	2939.4916	1.4181	1	2	61	1	K.LPAIYQSYGTDYDERVLPSIGNEVLK.A

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56. gi|220696972|gb|EED53313.1| **Mass:** 36717 **Score:** 414 **Queries matched:** 20 **emPAI:** 0.68

aldehyde reductase (AKR1), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
52	679.9980	678.9907	678.3734	0.6173	1	7	29	10	-.MSLGKK.V 51
875	499.6701	997.3257	996.4916	0.8341	0	20	1.3	1	R.AFEEFNIK.R 868
2850	661.7991	1321.5837	1319.6986	1.8851	0	10	14	2	R.YNVPYVANKPR.W 2853
3956	722.6081	1443.2017	1442.7518	0.4500	0	59	0.0002	1	R.HLDLATIYQNQK.E 3964
4239	492.6635	1474.9687	1475.7997	-0.8310	1	14	7.2	1	R.RYNVPYVANKPR.W
8973	958.7871	1915.5597	1914.9938	0.5659	0	85	4.5e-07	1	R.IAANFQEIELTPEEIAK.V 8970
9270	652.2309	1953.6707	1951.9064	1.7643	0	32	0.08	1	R.WNINVFGEPEEAPADHK.V 9254
11953	1151.9191	2301.8237	2301.2481	0.5756	0	76	3.3e-06	1	K.EVSPAQVILAWSQVGGHSVIPK.S 11945 11961 11964
15712	1033.4092	3097.2057	3095.4773	1.7285	0	61	6.7e-05	1	K.ALDDCLAECGLDYLDLYLVHWPVAFK.T 15713
16399	1162.8329	3485.4767	3483.6392	1.8375	0	15	3.1	1	K.TGNEYFPLVEGSTVPGGDCIIDDSISIVDTWK.A

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57. gi|220689909|gb|EED46259.1| **Mass:** 52664 **Score:** 413 **Queries matched:** 24 **emPAI:** 0.44

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1227	359.0512	1074.1317	1074.6107	-0.4789	1	10	17	4	K.IEAMNKLIK.D
1324	547.1116	1092.2087	1091.5645	0.6442	0	43	0.0085	1	K.TLQANVTSMK.S
1412	555.2746	1108.5347	1107.5594	0.9753	0	(21)	1.3	2	K.TLQANVTSMK.S 1399 1414
2100	618.8951	1235.7757	1233.6816	2.0941	0	5	49	9	K.TGIVDTSLLTSK.I 2099
3202	680.4231	1358.8317	1357.7215	1.1103	2	4	72	4	K.RWKANPTASATR.T
3566	698.7346	1395.4547	1394.7783	0.6765	1	6	34	5	R.YLHGGRVLPLDR.T
4413	748.7441	1495.4737	1493.7912	1.6826	2	5	47	8	K.FEEKIPRLSMTK.R
5427	533.7339	1598.1797	1597.8610	0.3187	1	4	65	8	K.QLHKTLQANVTSMK.S
7602	889.2576	1776.5007	1774.9829	1.5178	1	30	0.15	1	K.TGIVDTSLLTSKIWNK.V 7604
7736	894.1446	1786.2747	1785.8996	0.3751	0	129	2e-11	1	R.QDILDLTDDLLGDVNK.I 7743 7752 7753 7757
9814	675.2009	2022.5807	2021.9827	0.5980	0	4	52	9	K.SMTTILDQELGSIQDLDK.E 9805
10142	1028.2871	2054.5597	2053.9626	0.5971	0	83	6.9e-07	1	K.LFEASCQTNQSTLEGLEK.S
16030	1095.1442	3282.4107	3280.7417	1.6690	0	68	1.7e-05	1	K.YVMSYIQNAQLVVPVQVLSLEDYLQQLK.D
16094	1100.6199	3298.8377	3296.7366	2.1011	0	(53)	0.00051	1	K.YVMSYIQNAQLVVPVQVLSLEDYLQQLK.D 16095

58. gi|220699794|gb|EED56133.1| **Mass:** 86057 **Score:** 407 **Queries matched:** 50 **emPAI:** 0.51
mitochondrial aconitate hydratase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
36	666.5970	665.5897	665.3748	0.2149	0	4	58	4	R.GVSYLK.L
100	716.5640	715.5567	714.3548	1.2019	0	7	48	8	K.IQPDDK.V
582	460.1971	918.3797	918.5399	-0.1602	1	11	16	10	K.SRLFLGAR.G
713	483.7011	965.3877	962.5331	2.8546	1	21	1.2	1	-.MISTRLAR.M 716
1090	525.1766	1048.3387	1047.5601	0.7787	0	29	0.26	1	K.FNPLTDTLK.D 1087 1091 1092
1352	549.8151	1097.6157	1096.6492	0.9665	0	51	0.0012	1	K.DATNIPILIK.C
1401	554.7086	1107.4027	1105.5437	1.8590	0	25	0.49	1	K.MSENLEIVR.K 1400
1706	581.1756	1160.3367	1159.5622	0.7745	0	9	24	6	R.NTYQAPPVDR.S
1931	604.6346	1207.2547	1206.6972	0.5575	0	29	0.22	1	K.LKPPTGEGLPAK.G
2565	645.7146	1289.4147	1288.6663	0.7484	0	66	4.6e-05	1	K.LTGELSGWTTPK.D
2950	667.2506	1332.4867	1331.6681	0.8186	0	44	0.0067	1	R.STVNVAVSPTSDR.L
3446	692.2921	1382.5697	1381.8908	0.6789	1	2	89	8	K.DIILKVAGLLTVK.G 3441
3654	704.5991	1407.1837	1406.6572	0.5265	2	1	1.2e+02	10	K.DGSALNTMARKGGN.-
4019	725.2566	1448.4987	1447.7671	0.7316	0	42	0.0095	1	K.SLFTITPGSEQIR.A 4004 4028
4364	745.6646	1489.3147	1488.7725	0.5422	0	77	3.3e-06	1	R.LQVLQGFQAWDGK.D 4361
5151	525.0745	1572.2017	1569.8548	2.3469	1	10	16	3	K.DATNIPILIKCQGK.T 5113
5252	792.0556	1582.0967	1581.7423	0.3544	0	68	2.3e-05	1	K.NAFTGEYDAVPATAR.D 5254
5375	797.1886	1592.3627	1590.8253	1.5374	2	1	1.1e+02	7	K.FNPLTDTLKDKDGK.E
5852	816.1901	1630.3657	1630.9011	-0.5353	2	6	40	4	-.MISTRLARMGALAPK.S 5845
5862	544.7409	1631.2007	1630.9011	0.2997	2	(4)	57	9	-.MISTRLARMGALAPK.S
6269	555.0185	1662.0337	1662.8941	-0.8603	1	8	22	9	K.SKSLFTITPGSEQIR.A
7981	906.7686	1811.5227	1810.8447	0.6780	0	13	6.5	1	K.QGMLPLTFAEPADYDK.I 7976
8560	625.5962	1873.7667	1871.0404	2.7263	1	3	69	10	K.LTGELSGWTTPKDIILK.V 8548
9468	990.5981	1979.1817	1977.9544	1.2273	0	85	4.4e-07	1	K.ILYSHLDNPHEQDIER.G 9457 9464
9505	662.5422	1984.6047	1982.9949	1.6099	1	10	12	2	R.ANEINKEVYDFLASATAK.Y 9494 9511
12267	1174.6016	2347.1887	2346.3284	0.8603	2	0	1.2e+02	8	R.HLGGLAIITRSFARIHETNLK.K 12268
12301	1176.8506	2351.6867	2349.1358	2.5509	2	2	85	1	K.CQGKTTTDHISMAGPWLKYR.G
14680	908.2652	2721.7737	2721.3504	0.4234	1	1	79	8	R.GHLDNISNNMLIGAVNAENGEANKVK.N
15077	944.3645	2830.0717	2829.3463	0.7254	1	4	45	6	K.YRGHLDNISNNMLIGAVNAENGEANK.V
15763	1041.5439	3121.6097	3119.4441	2.1656	0	55	0.00032	1	R.DGQLQTLEEYGGVILANACGPCIGQWDR.K 15755

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59. gi|220696919|gb|EED53260.1| **Mass:** 52846 **Score:** 406 **Queries matched:** 33 **emPAI:** 0.72
ATP citrate lyase subunit (Acl), putatibe [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
237	803.0890	802.0817	802.3973	-0.3156	0	18	3.8	1	R.EWIEAR.A
1381	553.0001	1103.9857	1103.5359	0.4498	0	56	0.0004	1	R.AGPNYQEGLR.N
1586	568.5911	1135.1677	1134.6033	0.5644	0	26	0.38	1	R.EVAPVLNEHK.V

1691	579.9471	1157.8797	1157.6808	0.1989	0	37	0.039	1	K.FVAKPDQLIK.R 1689
1938	605.2431	1208.4717	1209.6030	-1.1312	0	5	48	2	R.LASLYFPEDR.A 1939
2307	631.7026	1261.3907	1259.6371	1.7537	1	6	41	6	R.RAGPNYQEGLR.N 2313
2804	659.2966	1316.5787	1314.7144	1.8644	0	22	1.1	1	K.DVQVETVTGVLR.Q 2788
3034	671.7101	1341.4057	1340.8027	0.6030	1	8	24	3	K.TGASLKLTVLNPK.G 3024 3035
4051	727.1606	1452.3067	1450.7780	1.5288	0	70	1.5e-05	1	R.SPANLGIAVAPQEGK.V
5058	782.0786	1562.1427	1561.7987	0.3440	0	25	0.57	1	K.NYPSNEEIAATLLK.K
5669	808.8391	1615.6637	1614.8590	0.8047	2	8	25	1	R.RAGPNYQEGLRNIK.S
5951	547.4375	1639.2907	1637.8890	1.4018	0	43	0.0067	1	K.VPSGVHNVLVDFISR.L 5939 5948 5961
8013	908.1831	1814.3517	1813.8821	0.4696	0	83	7.1e-07	1	K.VNIDAGPPMEFPAPFGR.E 8019 8037 8040
9283	978.8296	1955.6447	1955.0517	0.5931	0	27	0.25	1	K.VLFIGGGIANFTNVASTFK.G 9278 9287 9289
10332	1039.2891	2076.5637	2075.0575	1.5062	0	97	2.4e-08	1	K.DVLDQAEVTYPWLLASGAK.F 10331
10351	693.6289	2077.8647	2076.1480	1.7167	0	34	0.05	1	R.APVIKPTPLPPSSTHNPPAR.L
16079	1098.0149	3291.0227	3289.7203	1.3024	1	1	68	3	K.SVGEELGLNMHVYGPEMHVSGIVPLALLGKK.S

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60. gi|220699585|gb|EED55924.1| **Mass:** 22761 **Score:** 406 **Queries matched:** 22 **emPAI:** 2.00

40S ribosomal protein S7e [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
380	430.0966	858.1787	856.4766	1.7021	0	22	1.3	2	K.IALNSPSR.Q
739	485.6396	969.2647	968.5556	0.7091	0	28	0.25	1	R.HVLFVAQR.R
795	491.3631	980.7117	981.5243	-0.8126	1	5	40	9	R.EVEVGHGKK.A
1284	543.6421	1085.2697	1084.5189	0.7508	0	44	0.0067	1	R.LDAYGEVYR.R
3197	680.3151	1358.6157	1357.7830	0.8327	0	29	0.22	1	K.ATLRPLQFVSAR.E 3195
5164	787.5086	1573.0027	1573.8563	-0.8536	2	1	1.3e+02	10	K.EDGSKTLKVILDEK.E
5171	787.6491	1573.2837	1572.7097	0.5741	0	54	0.00061	1	R.NVVFEFPQSSASDF.- 5160
7628	890.3791	1778.7437	1777.0655	1.6783	0	35	0.053	1	K.AVIIFVPVPLLQGFHK.I 7615 7630 7635
10933	1079.2656	2156.5167	2156.0651	0.4516	2	3	70	1	R.RLTGRNVVFEFPQSSASDF.-
12117	1162.4141	2322.8137	2322.2835	0.5302	0	80	1.4e-06	1	R.TLTAVHDAILGDLVYPVEIVGK.R 12116 12120 12121
14640	906.6055	2716.7947	2716.3191	0.4756	0	87	2.3e-07	1	R.QNPSELENAIAGALFDLESNTQDLK.A 14641 14655 14665

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61. gi|220697966|gb|EED54306.1| **Mass:** 28784 **Score:** 403 **Queries matched:** 21 **emPAI:** 0.55

sorbitol/xylulose reductase Sou1-like, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1052	522.3061	1042.5977	1040.5979	1.9999	0	10	19	2	K.VVVVTGASGPR.G
2282	630.6151	1259.2157	1256.6765	2.5393	2	1	1.5e+02	4	K.KTYGVEAKAYK.C
5205	527.1009	1578.2807	1578.8253	-0.5446	2	4	61	7	K.NAEELKKTYGVEAK.A 5229
7454	883.3276	1764.6407	1764.0033	0.6374	0	94	5.6e-08	1	M.PIPVPSANSLTDLLSLK.G 7423 7459 7461 7467 7469 7472 7
9852	676.3089	2025.9047	2027.0946	-1.1899	2	1	92	8	K.GKVVVVTGASGPRGMGIEAAR.G
10915	1078.3716	2154.7287	2154.0481	0.6806	0	91	1e-07	1	R.VNSISPGYIDTGLSDFVDQK.I 10914 10934

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11384 1109.4721 2216.9297 2214.9562  1.9736  0   2      72   1   K.GAYVYLCSDASSYMTGSDLR.I
11756  760.3719 2278.0937 2276.1801  1.9136  1  54  0.0005   1   K.LVDDVIKDFGQIDAFIANAGR.T 11747
11918  767.0439 2298.1097 2296.0576  2.0521  0   1  1.1e+02  3   R.GCAEMGANIALTYASRPQGGEK.N
16093 1100.5492 3298.6257 3296.4966  2.1291  0   2      60   3   R.TADGGVLESTEAWMEVVQTDLNGTYHCAK.A
```

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62.   gi|220700969|gb|EED57307.1|   Mass: 32440   Score: 398   Queries matched: 26   emPAI: 0.63
      ATP synthase gamma chain, mitochondrial precursor, putative [Aspergillus flavus NRRL3357]
      Query  Observed   Mr(expt)  Mr(calc)   Delta  Miss Score  Expect  Rank  Peptide
        659  477.2296   952.4447   952.5130 -0.0683  0    15       4.3   1   K.FQILYNR.Q 662
       1006  517.2441  1032.4737  1031.5863  0.8875  0    23       0.9   1   K.TLLVVASSDK.G
       1219 1074.0120  1073.0047  1071.6651  1.3396  2     5        57   9   R.LKSIKNIEK.I
       1826  593.6431  1185.2717  1184.5972  0.6745  0    18       2.7   1   K.GLCGGIHSGLSK.A
       3052  672.6726  1343.3307  1342.8045  0.5263  2     6        48   9   K.VIASTRLTRAQK.A
       3117  676.3081  1350.6017  1349.7337  0.8681  1     2        98   6   K.ITNTMKVIASTR.L
       3372  688.0986  1374.1827  1373.6463  0.5364  0    59   0.00025   1   R.TYGQTSNTVFEK.A 3387
       6080  824.8071  1647.5997  1646.8450  0.7547  0    69    2e-05   1   R.TNPNAIVLSFANVCK.D 6085
       7312  876.0036  1749.9927  1748.9308  1.0619  0    14       5.6   2   R.ILQEHADADIVVLGEK.A
       8767  632.6792  1895.0157  1892.8832  2.1325  2     9        16   3   R.RNAMENASKNAGEMINK.F 8766 8768
       9059  643.2752  1926.8037  1926.9911 -0.1874  1     1        98   6   R.TAPPNAANFATLREIEGR.L
       9223  975.4551  1948.8957  1948.0629  0.8328  1     2        86   2   R.ILQEHADADIVVLGEKAK.A
       9342  982.7571  1963.4997  1962.9646  0.5351  0    99   1.9e-08   1   K.SANISSFEIDDQALANLR.E 9350 9353
      10215  688.0985  2061.2737  2062.9266 -1.6529  1    33     0.063   1   K.AMDESRTYGQTSNTVFEK.A 10237
      10409  695.7082  2084.1027  2084.1127 -0.0099  1     2        88   2   R.AGSAVVTRTAPPNAANFATLR.E
      13972  866.8005  2597.3797  2596.1838  1.1959  0    23      0.59   1   R.EYALANSLFWAMAEGHACEISAR.R
      14587 1352.9116  2703.8087  2702.3803  1.4284  0    69   1.5e-05   1   K.DIPTFADAQAVADQIALLPADYASVK.I 14578
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63.   gi|220701426|gb|EED57764.1|   Mass: 24023   Score: 396   Queries matched: 30   emPAI: 1.84
      40S ribosomal protein S5, putative [Aspergillus flavus NRRL3357]
      Query Observed  Mr(expt)  Mr(calc)   Delta  Miss Score  Expect  Rank  Peptide
        808 492.8936   983.7727   983.5400  0.2327  0    66    4e-05    1   R.QAVDVSPLR.R 809
       1165 532.9896  1063.9647  1063.5219  0.4428  0    35    0.056    1   K.EALAEMGTVK.L
       1438 557.8341  1113.6537  1113.5964  0.0573  1    16      4.8   10   R.KAQCPIIER.L
       1591 568.7021  1135.3897  1135.5478 -0.1581  0     7       32    4   R.LTNSLMMNGR.N
       1619 571.2691  1140.5237  1139.6411  0.8826  1    19      1.9    1   R.RQAVDVSPLR.R
       1880 599.3471  1196.6797  1195.5509  1.1288  0    30     0.15    2   K.WSYEDVEIR.D
       1942 605.6591  1209.3037  1209.6254 -0.3217  0    55  0.00049    1   R.NPVYLPHSAGR.Y 1940 1943 1951
       2983 669.1056  1336.1967  1335.7034  0.4933  0    57   0.0003    1   R.DISLTDYIQIR.N 2980 2991 2996 3001
       3167 678.7171  1355.4197  1354.7932  0.6265  0    90  1.6e-07    1   R.VNQSIALLTIGAR.E 3164
       3740 710.1326  1418.2507  1416.7660  1.4848  2    14      6.1    3   R.FRKAQCPIIER.L 3739
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4949	776.5551	1551.0957	1549.8174	1.2783	1	6	37	1	K.EALAEMGTVKLFNK.W 4958 4963
5075	522.6589	1564.9547	1564.7450	0.2098	1	5	52	6	R.LTNSLMMNGRNNGK.K
5866	816.7661	1631.5177	1630.8236	0.6942	0	81	1.2e-06	1	K.SIAECLAEELINAAK.G 5864 5873 5874 5884
10543	701.9829	2102.9267	2103.0387	-0.1120	1	0	1.3e+02	4	K.AQCPIIERLTNSLMMNGR.N

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64. gi|220690795|gb|EED47144.1| **Mass:** 35395 **Score:** 396 **Queries matched:** 37 **emPAI:** 1.45

G-protein complex beta subunit CpcB [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
118	724.4860	723.4787	723.3803	0.0984	0	29	0.15	1	K.FTITDK.G 117
167	761.5280	760.5207	759.4239	1.0968	0	24	0.92	1	R.QIVSASR.D 165
1209	536.4286	1070.8427	1069.4716	1.3711	0	25	0.53	1	R.DEQAYGYPK.R 1204 1210
1401	554.7086	1107.4027	1105.5226	1.8801	0	24	0.64	2	K.LWNTLGDCK.F 1400
1533	565.5306	1129.0467	1128.6655	0.3812	0	56	0.0005	1	K.TLIIWNLTR.D 1539
1983	608.8161	1215.6177	1215.5455	0.0722	0	46	0.0043	1	K.GHTDWVSCVR.F
2445	639.2221	1276.4297	1275.6459	0.7838	0	57	0.00035	1	R.LWELATGETTR.T 2471
3245	682.1731	1362.3317	1361.7078	0.6239	0	46	0.0044	1	K.VDELKPEYIEK.G 3246 3250 3252
3357	687.2371	1372.4597	1371.7874	0.6723	1	41	0.014	1	R.DKTLIIWNLTR.D 3340 3348
4530	756.2256	1510.4367	1508.6817	1.7550	0	68	2e-05	1	K.DGTTMLWDLNESK.H 4529 4539
8396	928.7056	1855.3967	1854.9265	0.4703	0	79	1.9e-06	1	R.FSPNPQNPVIVSAGWDK.L 8412
10273	689.6869	2066.0387	2064.9865	1.0522	0	18	2	2	R.TFVGHTNDVLSVSFSADNR.Q 10264 10276 10279 10280
11736	759.3282	2274.9627	2275.1498	-0.1871	0	3	70	2	K.HLYSLHAGDEIHALVFSPNR.Y
15330	981.9802	2942.9187	2940.4400	2.4788	0	43	0.0051	1	R.GTLEGHNGWVTSLATSLENPNMLLSGSR.D 15327 15329
15449	998.6552	2992.9437	2990.3716	2.5721	0	4	48	2	R.SLEGHSHIVSDCVISSDGAYALSASWDK.S
15574	1018.6552	3052.9437	3052.4614	0.4823	1	3	50	1	K.GHTDWVSCVRFSPNPQNPVIVSAGWDK.L

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65. gi|220691640|gb|EED47988.1| **Mass:** 17113 **Score:** 385 **Queries matched:** 28 **emPAI:** 2.54

nucleoside diphosphate kinase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
541	456.3911	910.7677	910.5600	0.2077	0	43	0.0068	1	R.GLVGPIISR.F 538 539 543 553
652	475.3541	948.6937	948.4665	0.2272	0	67	3.2e-05	1	R.GDFAIDVGR.N 650 651 654
3147	677.6826	1353.3507	1351.6197	1.7310	0	62	9.8e-05	1	K.HSQFDWIYEK.A 3139 3157
3773	713.2901	1424.5657	1422.6568	1.9089	1	45	0.0049	1	K.HSQFDWIYEKA.- 3755 3762
5876	817.2341	1632.4537	1629.8766	2.5771	0	33	0.081	1	K.EIALWFKPEELQK.Y 5845 5852 5861 5862
6148	827.3156	1652.6167	1651.9257	0.6910	0	98	2.2e-08	1	R.TILGATNPLASAPGTIR.G 6108 6115 6147 6150 6155 6160
9239	651.3292	1950.9657	1949.9517	1.0140	0	1	1.2e+02	6	-.MSDEQTFIAIKPDGVQR.G

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66. gi|220701800|gb|EED58138.1| **Mass:** 21932 **Score:** 383 **Queries matched:** 28 **emPAI:** 2.11

60S ribosomal protein L9, putative [Aspergillus flavus NRRL3357]

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

34	660.3000	659.2927	659.3126	-0.0199	0	25	0.77	1	R.GNIVEE.-
89	**707.5200**	**706.5127**	**706.3650**	**0.1477**	**0**	**27**	**0.35**	**4**	**R.NFLGEK.Y**
364	**856.5590**	**855.5517**	**855.4814**	**0.0703**	**0**	**24**	**0.72**	**1**	**R.VVTVEGPR.G** 359 360 361 365 368
531	**455.4256**	**908.8367**	**908.5331**	**0.3036**	**0**	**37**	**0.032**	**1**	**R.LPIPENVK.I** 529
2645	**649.9746**	**1297.9347**	**1297.7969**	**0.1378**	**0**	**96**	**4e-08**	**1**	**R.TIINNLIIGVTK.G** 2643 2650 2652 2657 2664
2871	**663.7471**	**1325.4797**	**1325.6979**	**-0.2182**	**1**	**24**	**0.59**	**1**	**R.KFLDGLYVSER.G**
3074	**449.7999**	**1346.3777**	**1345.7102**	**0.6675**	**0**	**13**	**8.6**	**2**	**K.DVISIELHHGAR.K**
3422	**690.1941**	**1378.3737**	**1378.6728**	**-0.2991**	**0**	**76**	**4.3e-06**	**1**	**K.NAETGLYDVEIR.N**
5118	**785.6426**	**1569.2707**	**1568.8311**	**0.4396**	**0**	**40**	**0.016**	**1**	**K.DLSHIAVTFGRPEK.D** 5113 5120 5128 5129
6324	**834.2441**	**1666.4737**	**1665.9301**	**0.5436**	**0**	**100**	**1.4e-08**	**1**	**R.ITAQPGVEIITSPNVK.D** 6327
6883	**853.9671**	**1705.9197**	**1705.8828**	**0.0370**	**0**	**14**	**6.5**	**1**	**R.YVYAHFPINVNIEK.N**
10282	**690.1942**	**2067.5607**	**2067.0273**	**0.5335**	**1**	**35**	**0.047**	**1**	**K.NAETGLYDVEIRNFLGEK.Y**

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67. gi|212283871|gb|ACJ23337.1| **Mass:** 19727 **Score:** 374 **Queries matched:** 43 **emPAI:** 1.57

glyceraldehyde-3-phosphate dehydrogenase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
288	414.9126	827.8107	826.4912	1.3195	0	3	87	8	K.VIPSLNGK.L
1959	606.8806	1211.7467	1211.6662	0.0805	0	54	0.00054	1	K.AGIALNEHFIK.L 1965 1974
2616	648.4811	1294.9477	1295.6609	-0.7131	1	5	51	4	R.TEKAVTYEDIK.K 2617
3816	477.2295	1428.6667	1428.7572	-0.0905	0	3	74	9	R.TAAQNIIPSSTGAAK.A
4716	765.8826	1529.7507	1529.7872	-0.0365	0	78	2.4e-06	1	R.VPTANVSVVDLTCR.T 4720 4722 4728
5516	535.6415	1603.9027	1602.8586	1.0442	1	9	20	2	K.VIPSLNGKLTGMSMR.V 5513
9426	659.2422	1974.7047	1974.0754	0.6293	2	5	47	2	K.AVGKVIPSLNGKLTGMSMR.V 9416
9559	664.7742	1991.3007	1990.0703	1.2304	2	(3)	76	4	K.AVGKVIPSLNGKLTGMSMR.V 9577
14163	880.5125	2638.5157	2637.3109	1.2049	0	74	5.2e-06	1	K.VINDNFGLVEGLMTTVHSYTATQK.T 14164 14167 14172 14178
14251	885.6075	2653.8007	2652.2887	1.5120	1	10	11	2	K.EYKTDINVLSNASCATNCLAPLAK.V
14258	886.0669	2655.1787	2653.3058	1.8729	0	(28)	0.17	1	K.VINDNFGLVEGLMTTVHSYTATQK.T 14259 14264
15142	951.9865	2852.9377	2851.3764	1.5614	0	52	0.00069	1	K.GILGYTEDDIVSTDLIGDAHSSIFDAK.A 15134 15135 15141 15

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68. gi|220694447|gb|EED50791.1| **Mass:** 24223 **Score:** 366 **Queries matched:** 29 **emPAI:** 1.47

ATP synthase oligomycin sensitivity conferral protein, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
886	**500.8191**	**999.6237**	**999.5964**	**0.0273**	**0**	**61**	**0.00013**	**1**	**K.ALSALGEVLK.A** 888
1215	**537.2476**	**1072.4807**	**1071.5924**	**0.8883**	**0**	**41**	**0.015**	**1**	**K.SQIVQELQK.L** 1213
1456	**559.6141**	**1117.2137**	**1116.5849**	**0.6288**	**0**	**47**	**0.0034**	**1**	**R.LGLLEGVCEK.F**
2841	**661.1161**	**1320.2177**	**1319.6469**	**0.5708**	**0**	**34**	**0.071**	**1**	**K.NFLETLAENNR.L**
4356	**744.9361**	**1487.8577**	**1486.8243**	**1.0335**	**0**	**45**	**0.005**	**1**	**K.LTGLISAPTLTASDK.S** 4342
5668	**808.7691**	**1615.5237**	**1614.9192**	**0.6045**	**1**	**80**	**1.4e-06**	**1**	**R.KLTGLISAPTLTASDK.S** 5667 5694
6038	823.6196	1645.2247	1644.8206	0.4041	0	4	56	4	R.GEIDLNITSAQELDK.K 6024 6042

6120	826.6636	1651.3127	1650.8941	0.4186	0	59	0.0002	1	K.VNPDLVGGLVVEIGDR.T 6119 6128 6129 6132 6133 6134 614
6429	837.8026	1673.5907	1672.8896	0.7011	2	4	53	5	R.LEKAVSQSHFSQGKK.L
7594	888.7181	1775.4217	1772.9156	2.5062	1	3	75	4	R.GEIDLNITSAQELDKK.T
13895	861.3982	2581.1727	2581.3963	-0.2236	1	2	69	8	K.VNPDLVGGLVVEIGDRTIDLSVSSK.I
14132	878.2962	2631.8667	2629.3170	2.5498	1	1	85	10	K.FATLMGAHRGEIDLNITSAQELDK.K
14875	925.4415	2773.3027	2773.4068	-0.1041	2	0	1e+02	1	K.FATLMGAHRGEIDLNITSAQELDKK.T

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69. gi|220692495|gb|EED48841.1| **Mass:** 40719 **Score:** 363 **Queries matched:** 23 **emPAI:** 0.87

pyruvate dehydrogenase E1 beta subunit PdbA, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1919	603.3651	1204.7157	1203.5772	1.1386	0	27	0.36	1	K.VVSPWSSEDAK.G 1910
5512	535.5685	1603.6837	1601.8447	1.8391	1	8	27	3	R.CVGLSLNAAAELKEK.Y
6174	828.5321	1655.0497	1654.9505	0.0992	0	72	8.6e-06	1	R.SVKPLDVETIVQSLK.K 6180 6183 6192 6208
7366	879.2811	1756.5477	1755.8526	0.6951	0	86	4e-07	1	R.DALNEALAEELETNPK.T 7356
7634	594.0742	1779.2007	1781.0536	-1.8529	2	9	18	7	M.AAPRLFRPAARLLSSR.L
7693	595.4992	1783.4757	1783.0455	0.4302	1	46	0.0035	1	R.SVKPLDVETIVQSLKK.T
8901	637.2899	1908.8477	1910.1326	-1.2849	2	3	73	5	R.LFRPAARLLSSRLSAPR.R
15074	944.2569	2829.7487	2831.4851	-1.7364	2	4	42	5	R.CVGLSLNAAAELKEKYGVDAEVINLR.S 15080
15132	951.4022	2851.1847	2848.3569	2.8278	0	45	0.0034	1	R.GPNGFAAGVAAQHSQDYSAWYGSIPGLK.V 15127
15167	954.7382	2861.1927	2858.4160	2.7767	0	29	0.12	1	R.DPNPVVVLENELLYGQAFPMSEAAQK.D 15168
16010	1090.9755	3269.9047	3269.6754	0.2293	1	61	6.9e-05	1	K.AAIRDPNPVVVLENELLYGQAFPMSEAAQK.D 16014
16061	1097.0072	3287.9997	3285.6703	2.3294	1	(14)	3.2	1	K.AAIRDPNPVVVLENELLYGQAFPMSEAAQK.D 16065

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70. gi|220694367|gb|EED50711.1| **Mass:** 44490 **Score:** 362 **Queries matched:** 41 **emPAI:** 0.77

60S ribosomal protein L3 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
14	635.4920	634.4847	634.3472	0.1375	0	16	4.9	1	R.VMTLR.K
27	650.4840	649.4767	649.3435	0.1332	0	25	0.51	1	R.NLFEK.T 28
124	734.8480	733.8407	732.4018	1.4390	1	8	29	5	K.KDLVTSA.-
146	749.5280	748.5207	748.4483	0.0724	0	34	0.075	1	R.AFLGTLK.K 148
712	483.5826	965.1507	964.4978	0.6529	0	19	2	1	K.TLYPQTSR.K 711
932	507.5866	1013.1587	1012.5454	0.6133	0	60	0.00015	1	R.HGSLAYLPR.K 931
1387	553.7266	1105.4387	1104.5750	0.8637	0	48	0.0025	1	K.QITPMGGFVR.Y 1384
1486	561.6296	1121.2447	1120.5699	0.6748	0	(28)	0.25	1	K.QITPMGGFVR.Y 1489
2306	631.6991	1261.3837	1262.6448	-1.2610	2	6	47	6	R.FYKNWYKSK.K 2311
2527	643.5826	1285.1507	1284.6058	0.5449	0	59	0.00022	1	K.QHAEESGASITR.E
2944	666.6096	1331.2047	1330.7067	0.4980	0	2	1e+02	5	K.KPVHLTASMGYK.A
4150	732.8716	1463.7287	1462.8395	0.8892	2	1	1.3e+02	3	R.AFLGTLKKDLVTSA.-
6044	823.7296	1645.4447	1646.8012	-1.3565	1	7	30	2	K.YAKQHAEESGASITR.E

6746	849.2041	1696.3937	1696.8607	-0.4670	1	6	38	6	K.QITPMGGFVRYGEVK.N 6749
6931	571.1635	1710.4687	1708.9294	1.5393	2	4	64	8	R.VMTLRKTLYPQTSR.K
6986	858.6311	1715.2477	1713.8574	1.3904	0	65	5.1e-05	1	R.SLTTVWAEHLSDEVK.R 6987
7852	600.2645	1797.7717	1795.9250	1.8467	1	1	1e+02	7	K.KAHLMEIQVNGGSVADK.V
7898	902.2686	1802.5227	1801.9033	0.6195	1	5	45	1	K.DDPKKPVHLTASMGYK.A
7983	906.8221	1811.6297	1811.8762	-0.2464	1	4	59	4	K.QHAEESGASITRELER.I
8265	615.3782	1843.1127	1843.0251	0.0877	2	2	93	5	K.KYCTVVRVLAHTQIR.K
10857	716.4619	2146.3637	2146.1391	0.2246	1	(1)	1e+02	8	K.KPVHLTASMGYKAGMTTVVR.D
10894	1076.6446	2151.2747	2150.9545	0.3202	0	88	1.9e-07	1	K.WVDTSSEFGHGAFQTPEEK.R 10896 10898 10907
10969	722.2192	2163.6357	2162.1340	1.5017	1	5	42	1	K.KPVHLTASMGYKAGMTTVVR.D
11551	748.7442	2243.2107	2245.1565	-1.9458	2	3	59	4	K.SFPKDDPKKPVHLTASMGYK.A 11561
11987	769.7309	2306.1707	2307.0556	-0.8849	1	7	23	1	K.WVDTSSEFGHGAFQTPEEKR.A
13682	849.2042	2544.5907	2546.2662	-1.6755	2	0	1.1e+02	7	K.QITPMGGFVRYGEVKNDFVMVK.G
14953	930.7699	2789.2877	2786.3181	2.9696	2	2	60	5	K.GSDEANASTDFDISKKQITPMGGFVR.Y 14941

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71. gi|220689219|gb|EED45570.1| **Mass:** 28314 **Score:** 357 **Queries matched:** 43 **emPAI:** 1.72
ribosomal protein S5 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
36	666.5970	665.5897	665.4224	0.1673	0	7	25	1	R.LIPAPR.G
66	687.4980	686.4907	686.4326	0.0581	0	30	0.23	2	R.AAITIAK.L 67
178	384.4386	766.8627	766.5065	0.3562	0	35	0.038	1	K.LAVLPVR.R
269	818.4440	817.4367	817.4545	-0.0178	0	22	1.4	1	K.TLENTLK.A 271
470	887.5560	886.5487	886.4549	0.0939	0	20	2.2	1	K.EWQPVTK.L
879	500.5621	999.1097	998.5761	0.5337	0	30	0.15	1	R.GTGLVASPAVK.R 877 878 880 883
2305	631.6761	1261.3377	1260.6350	0.7027	0	5	54	8	R.SPLEEFGDVLR.Q
3584	699.9946	1397.9747	1397.7231	0.2516	0	43	0.0068	1	K.EYQIVDFFLPK.L 3588 3607 3610
5995	548.7559	1643.2457	1642.9042	0.3415	1	7	29	1	K.LIRSPLEEFGDVLR.Q
6051	824.1161	1646.2177	1645.9879	0.2298	1	3	73	6	R.LIPAPRGTGLVASPAVK.R
6480	839.7666	1677.5187	1676.9461	0.5726	0	32	0.091	1	K.AVVIIGDSEGHIGLGIK.T 6469 6476 6483 6484 6485 6492 64
7231	871.3496	1740.6847	1739.8631	0.8216	0	56	0.00033	1	R.GYWGSNLGEPHSLPVK.Q 7187 7234 7235
7548	886.8741	1771.7337	1771.9542	-0.2205	0	83	6.6e-07	1	K.ITSMEQIYLHSLPIK.E 7559 7561 7576 7581
7762	597.3822	1789.1247	1787.9491	1.1756	0	(3)	69	4	K.ITSMEQIYLHSLPIK.E
9046	963.6766	1925.3387	1924.9742	0.3645	0	115	4.5e-10	1	R.LLQLAGVQDAYTSSSGSTK.T 9052 9060
9584	997.5876	1993.1607	1993.1208	0.0399	1	1	1.2e+02	2	K.AVVIIGDSEGHIGLGIKTSK.E
11304	737.1885	2208.5437	2209.2583	-0.7146	2	3	68	9	R.TRFKAVVIIGDSEGHIGLGIK.T 11305

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72. gi|220690388|gb|EED46738.1| **Mass:** 14963 **Score:** 353 **Queries matched:** 16 **emPAI:** 0.51
histone H2B [Aspergillus flavus NRRL3357]

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

663	477.7496	953.4847	952.5957	0.8890	0	29	0.17	1	R.LILPGELAK.H 661
1672	577.2411	1152.4677	1152.5339	-0.0662	0	18	2.4	1	K.ETYSSYIYK.V
2496	641.7171	1281.4197	1280.6288	0.7909	1	3	83	2	R.KETYSSYIYK.V
3934	481.0392	1440.0957	1437.7939	2.3018	2	13	7.4	8	K.LAAYNKKSTISSR.E
4918	775.4086	1548.8027	1549.8577	-1.0549	1	4	61	2	K.VLKQVHPDTGISTR.A
4965	777.2166	1552.4187	1553.8525	-1.4338	2	1	1.2e+02	6	K.AAEKKPSTGGKAPAGGK.A
7349	878.3766	1754.7387	1754.8661	-0.1274	0	(86)	3.4e-07	1	R.AMSILNSFVNDIFER.V 7365 7372 7375
7422	882.0591	1762.1037	1761.9989	0.1049	1	0	1.3e+02	5	R.LILPGELAKHAVSEGTK.A
7536	886.6126	1771.2107	1770.8611	0.3497	0	94	6.3e-08	1	R.AMSILNSFVNDIFER.V 7516 7540 7541

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73. gi|220695061|gb|EED51404.1| **Mass:** 57300 **Score:** 352 **Queries matched:** 18 **emPAI:** 0.40

4-aminobutyrate transaminase GatA [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
974	513.0636	1024.1127	1024.5665	-0.4538	0	7	31	7	R.TISTTPHLR.A
2533	643.8481	1285.6817	1285.6302	0.0515	0	62	0.0001	1	K.TGEYLYSGLQR.L 2538
2849	661.7471	1321.4797	1319.6510	1.8287	0	65	5.2e-05	1	K.GQGTFIAWDTPK.R 2844
2926	665.7946	1329.5747	1327.7208	1.8539	0	4	66	9	K.GVGVNIGGSGVSAVR.L 2898
3872	718.1776	1434.3407	1433.7514	0.5893	1	18	2.5	1	K.AATAELDKVFDVR.S
5530	803.6986	1605.3827	1603.8769	1.5058	0	3	75	5	R.LRPMLIFQQHHGK.S
5599	537.9832	1610.9277	1609.8576	1.0701	1	29	0.2	1	R.LAEKYPEHLQNLR.G
9170	971.8526	1941.6907	1941.0036	0.6871	0	67	2.8e-05	1	K.LDIPAFDWPQAPFPSLK.Y 9168
11918	767.0439	2298.1097	2299.1498	-1.0400	0	11	11	1	K.AQTAGYYYGNPALRPNKPYR.Q 11924
13011	820.7649	2459.2727	2457.1212	2.1515	0	21	0.87	1	K.FWAHDHWNLETPPDMVTFSK.K
13320	833.3335	2496.9787	2498.2111	-1.2324	1	0	1.1e+02	8	K.VAPKGLNQVFTAMAGSDANETAYK.A
15820	1054.5105	3160.5097	3159.5163	0.9935	0	75	2.8e-06	1	K.EWHNPVAAVVVEPIQSEGGDNHASPAFFR.G 15819

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74. gi|220694917|gb|EED51260.1| **Mass:** 41841 **Score:** 350 **Queries matched:** 26 **emPAI:** 0.58

actin Act1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
40	672.5430	671.5357	671.4330	0.1027	0	8	33	9	R.GILTLR.Y 42
420	872.5690	871.5617	871.5127	0.0490	1	9	24	8	R.EIVRDIK.E
938	508.3311	1014.6477	1013.4739	1.1738	0	14	7.5	2	R.DLTDYLMK.I
1555	566.6851	1131.3557	1131.5197	-0.1639	0	42	0.011	1	R.GYTFSTTAER.E 1561
1652	574.5906	1147.1667	1146.5954	0.5713	0	9	22	4	K.EITALAPSSMK.V
1720	582.8191	1163.6237	1162.5903	1.0334	0	(5)	55	1	K.EITALAPSSMK.V
4919	775.4246	1548.8347	1549.7844	-0.9496	1	4	55	6	R.MQKEITALAPSSMK.V
5992	548.5572	1642.6497	1643.7903	-1.1406	1	1	1.3e+02	9	K.QEYDESGPSIVHRK.C
7775	896.1461	1790.2777	1789.8846	0.3931	0	89	1.8e-07	1	K.SYELPDGQVITIGNER.F 7777 7799
9261	977.6231	1953.2317	1953.0571	0.1746	0	40	0.013	1	R.VAPEEHPVLLTEAPINPK.S 9269 9276

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     11434    742.6752  2225.0037  2225.1184  -0.1147   2    (1)       96    5    R.VDMAGRDLTDYLMKILAER.G
     11548    748.6749  2243.0027  2241.1133   1.8894   2     5        38    2    R.VDMAGRDLTDYLMKILAER.G
     11653    754.4299  2260.2677  2262.0297  -1.7620   0     1        91    2    K.DLYGNIVMSGGTTMYPGISDR.M
     12522    796.8322  2387.4747  2387.0998   0.3749   1     1        91    7    R.HHGIMIGMGQKDSYVGDEAQSK.R
     14219    883.6535  2647.9387  2645.2530   2.6857   0     4        46    1    K.LCYVALDFEQEIQTASQSSSLEK.S
     14903    927.6765  2780.0077  2778.2589   1.7488   1     2        72    1    M.EEEVAALVIDNGSGMCKAGFAGDDAPR.A
     15333    982.3429  2944.0067  2942.5212   1.4855   0    54   0.00039    1    R.APEALFQPSVLGLESGGIHVTTFNSIMK.C 15329
     15764   1041.7152  3122.1237  3120.6244   1.4993   0    75     3e-06    1    R.TTGIVLDSGDGVTHVVPIYEGFALPHAISR.V 15761
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75.   gi|220694374|gb|EED50718.1|     Mass: 54772     Score: 345     Queries matched: 34    emPAI: 0.42
      adenylosuccinate lyase Ade13, putative [Aspergillus flavus NRRL3357]
     Query    Observed    Mr(expt)   Mr(calc)     Delta Miss Score  Expect Rank   Peptide
       435    438.9266    875.8387   875.4348   0.4039   0    20         2    1    R.SLDDSAIR.R
      1377    552.4481   1102.8817  1102.6022   0.2795   0    18       3.2    1    K.ALEPYAAAVAK.A 1376
      2070    616.6076   1231.2007  1230.6972   0.5036   1    12        11    2    K.KALEPYAAAVAK.A
      2667    651.3521   1300.6897  1300.6874   0.0023   0    87   3.4e-07    1    K.VEQLDELVTQK.A 2674
      2729    436.9692   1307.8857  1308.7150  -0.8293   1     5        51    7    R.VLSHQAADNVKK.H 2719
      5371    531.7249   1592.1527  1590.7719   1.3809   2     7        30    9    R.NPMRSERLCSLGR.H
      5719    540.9532   1619.8377  1621.7446  -1.9069   1     5        43    6    R.YASDEMKYLFSPR.N 5723
      6059    824.2466   1646.4787  1645.8320   0.6467   0    89   2.2e-07    1    R.ACLWIQDLLMDLR.N 6073
      6257    831.7121   1661.4097  1661.8269  -0.4172   0   (78)  2.3e-06    1    R.ACLWIQDLLMDLR.N 6270 6288 6290
      7312    876.0036   1749.9927  1748.8370   1.1558   0    15       4.3    1    K.AGFDSAFIISSQTYSR.K 7311
      9725    671.2439   2010.7097  2008.9491   1.7607   0    21      0.99    1    K.GTTGTQASFLQIFDGDHSK.V 9717
      9819    675.2922   2022.8547  2023.0990  -0.2442   2     4        58    4    K.FTSTEVKKALEPYAAAVAK.A
      9858    676.4215   2026.2427  2023.9633   2.2794   1     2        75    9    R.KIDVDVGNALGSFGSTCER.I
     10769    713.6482   2137.9227  2137.0990   0.8237   0    26      0.28    1    K.DLPCLGFTHGQPAQLVTVGK.R 10784
     10938    720.1879   2157.5417  2159.0719  -1.5302   1     1        98    8    R.QDAHEEIRVLSHQAADNVK.K
     11057    725.7745   2174.3017  2174.0976   0.2041   1     1   1.1e+02    8    R.ACLWIQDLLMDLRNLER.A
     11331   1106.8056   2211.5967  2210.0421   1.5546   0    13       7.1    2    R.VNDELPFMATENIIMACVK.K
     11351    738.6195   2212.8367  2210.0421   2.7946   0    (4)       53    1    R.VNDELPFMATENIIMACVK.K
     12179    777.9422   2330.8047  2329.0896   1.7151   2     1     1e+02    2    K.EVEEPFEKDQIGSSAMAYKR.N
     12375    790.5822   2368.7247  2366.1432   2.5815   1     1   1.1e+02    5    R.RVNDELPFMATENIIMACVK.K
     14799    918.5162   2752.5267  2750.4279   2.0988   1    44     0.004    1    R.RTEFFNPILGELDTLLEPSTFVGR.A 14800
     15752   1040.6415   3118.9027  3117.5454   1.3573   2     5        33    1    R.LCSLGRHLQNLPKDALDTYSAQWFER.S
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76.   gi|220701626|gb|EED57964.1|     Mass: 58154     Score: 338     Queries matched: 28    emPAI: 0.18
      glucose-6-phosphate 1-dehydrogenase [Aspergillus flavus NRRL3357]
     Query    Observed    Mr(expt)   Mr(calc)     Delta Miss Score  Expect Rank   Peptide
      1822    593.1406   1184.2667  1183.6390   0.6277   0    69   1.8e-05    1    K.TFPALFGLYR.N 1820
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1912	602.8091	1203.6037	1204.6200	-1.0163	1	5	55	3	R.HLEDIEKGHK.E 1917
2153	622.7621	1243.5097	1241.6802	1.8296	1	(1)	1.4e+02	5	R.VLRAMDAIEPK.N
2266	629.7576	1257.5007	1257.6751	-0.1744	1	3	83	6	R.VLRAMDAIEPK.N
2487	640.8846	1279.7547	1278.6741	1.0807	0	4	57	2	-.MEISLSTIELK.D
3035	671.7551	1341.4957	1340.7088	0.7869	1	11	13	2	R.DLQKALEPNWK.E 3034
3093	450.3535	1348.0387	1347.6857	0.3531	1	4	70	8	R.IDHYLGKEMVK.N
3947	722.1126	1442.2107	1441.7098	0.5009	0	29	0.19	2	R.CPTFCALVAYIK.N 3951
4379	498.0805	1491.2197	1490.7340	0.4857	1	2	85	7	K.NERWDGVPFIMK.A
5175	787.9811	1573.9477	1573.8603	0.0874	0	92	9.3e-08	1	K.IPEAYESLILDALK.G 5177 5186 5189
5310	794.6816	1587.3487	1586.7617	0.5870	0	68	2.6e-05	1	R.GPAVLDDFTASFGYK.F 5325 5328 5330 5332
8910	637.5819	1909.7237	1911.0771	-1.3533	2	4	49	3	K.TFPALFGLYRNKFLPK.G 8906
9961	1019.0366	2036.0587	2035.0660	0.9927	0	2	85	1	K.LPGLSMQTVVTELDLTYR.R
10935	1079.4736	2156.9327	2156.1228	0.8100	0	26	0.35	1	R.VFYMALPPSVFTTVSEQLK.R
11256	734.1592	2199.4557	2200.2215	-0.7658	2	13	6.4	1	R.IIVEKPFGKDLQSSRDLQK.A
15490	1008.5355	3022.5847	3023.5102	-0.9255	1	5	35	2	R.IFTPLLHYLDDNKEIIPMEYPYGSR.G

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77. gi|220700635|gb|EED56973.1| **Mass:** 51644 **Score:** 337 **Queries matched:** 31 **emPAI:** 0.45
pyruvate dehydrogenase complex, dihydrolipoamide acetyltransferase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
505	903.4750	902.4677	902.5073	-0.0396	1	16	5.9	2	K.VLKETGEK.E
1015	518.1371	1034.2597	1033.5808	0.6789	0	51	0.0014	1	K.LSVNDFLVK.A 1014
1604	570.1371	1138.2597	1137.6645	0.5952	0	43	0.0068	1	K.VVENPLELLL.- 1606 1607 1610
1653	1148.1930	1147.1857	1146.6253	0.5604	1	10	20	3	R.MRTPSAMLIK.G
2350	633.9521	1265.8897	1265.7595	0.1303	1	32	0.091	1	K.KVVENPLELLL.- 2351
3991	724.0566	1446.0987	1446.7864	-0.6877	1	0	1.5e+02	7	R.TPSAMLIKGASSLR.R
4568	759.2261	1516.4377	1515.8257	0.6121	0	81	1.2e-06	1	K.NVQGLGLSSISNSIK.D
5419	799.4776	1596.9407	1596.9311	0.0096	2	2	88	4	K.LLKLRQALNASADGK.Y
6901	854.7931	1707.5717	1705.8676	1.7042	0	8	24	2	R.ENPHFFVSTTLSVTK.L 6889 6898
7250	871.8096	1741.6047	1740.9774	0.6273	2	1	1.2e+02	3	K.VVDGAVGAEWIKELKK.V
9050	963.8636	1925.7127	1925.0735	0.6393	0	87	2.5e-07	1	R.FTAVINPPQAGILAVGTTR.K 9048
9077	644.1609	1929.4607	1929.0531	0.4076	1	0	1.2e+02	7	K.NVQGLGLSSISNSIKDLGK.R
9126	968.8341	1935.6537	1935.1041	0.5496	0	68	2e-05	1	K.NADISVAVATPAGLITPVVK.N 9128
9820	675.3442	2023.0107	2020.0126	2.9981	0	11	11	1	K.VPAVNSSWHEENGQVVIR.Q
12154	776.7219	2327.1437	2328.3165	-1.1728	1	2	86	6	R.QHKNADISVAVATPAGLITPVVK.N
12289	784.2842	2349.8307	2351.2678	-1.4371	2	4	53	4	R.TPSAMLIKGASSLRRPQVMHR.F
14368	890.5915	2668.7527	2668.2625	0.4902	0	14	4.4	1	K.LKPEEYQGGTFTISNMGMNPAVER.F
14492	896.2475	2685.7207	2684.2574	1.4633	0	(2)	63	2	K.LKPEEYQGGTFTISNMGMNPAVER.F
15253	967.4352	2899.2837	2896.4615	2.8222	0	4	37	3	K.SFPPHTIISMPALSPTMLAGNIGAWQK.K 15254
16326	1145.8585	3434.5537	3432.9192	1.6345	1	3	43	3	K.NADISVAVATPAGLITPVVKNVQGLGLSSISNSIK.D
16405	1164.7729	3491.2967	3492.7574	-1.4606	1	1	63	9	R.YYASKSFPPHTIISMPALSPTMLAGNIGAWQK.K

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78.   gi|220689385|gb|EED45736.1|    Mass: 21866   Score: 332   Queries matched: 26   emPAI: 1.04
      cytochrome c oxidase subunit V [Aspergillus flavus NRRL3357]
     Query  Observed  Mr(expt)  Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      1008  517.4991 1032.9837 1033.5226  -0.5389  0    10      17    2   R.SSAMPTTAIR.S
      1143  530.4496 1058.8847 1058.5397   0.3451  0    22     1.3    2   K.GFVQSPPAEK.S 1146
      1922 1206.1210 1205.1137 1204.6676   0.4461  1     0 1.7e+02    7   M.FLQSVSRAAAR.S
      3699  707.9586 1413.9027 1413.6711   0.2316  0    30    0.17    1   K.VDWHQMTLQEK.K 3701
      3751  474.5035 1420.4887 1418.7300   1.7588  1    12     9.6    4   R.AAARSSAMPTTAIR.S
      3822  715.7041 1429.3937 1429.6660  -0.2723  0   (18)    2.3    1   K.VDWHQMTLQEK.K
      3967  722.7921 1443.5697 1441.7255   1.8442  0    52   0.001    1   K.AAYWIAFGPHGPR.A 3948 3958 3965
      4845  772.2251 1542.4357 1541.7660   0.6697  1     0 1.4e+02    4   K.VDWHQMTLQEKK.A
      5586  805.8901 1609.7657 1609.7988  -0.0330  0    89 1.9e-07    1   K.INPIYGISAEGYEGK.G 5563 5573 5606
     10708 1065.2951 2128.5757 2127.9870   0.5887  0    83 6.4e-07    1   R.WEAMPPQEQADLWMQLR.D 10709 10729
     10829 1073.3421 2144.6697 2143.9819   0.6878  0   (22)    0.76    2   R.WEAMPPQEQADLWMQLR.D 10828
     12366  789.9182 2366.7327 2367.2151  -0.4824  2     0 1.1e+02    5   -.MFLQSVSRAAARSSAMPTTAIR.S
     12705  805.8359 2414.4857 2415.1100  -0.6242  1     1      89    4   R.WEAMPPQEQADLWMQLRDR.M
     14173  880.8819 2639.6237 2639.5203   0.1034  0     5      38    3   K.VAQLTAVSVALFYVIHLFAKPQPK.T 14171
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79.   gi|220688985|gb|EED45337.1|    Mass: 96832   Score: 329   Queries matched: 41   emPAI: 0.18
      Hsp70 chaperone (HscA), putative [Aspergillus flavus NRRL3357]
     Query  Observed  Mr(expt)  Mr(calc)    Delta Miss Score  Expect Rank  Peptide
       110  722.3680  721.3607  720.3588   1.0019  2     9      24    1   K.KAMERA.-
       262  816.5500  815.5427  815.4865   0.0562  1    16     5.5    5   R.VQLSKGGK.E
       311  836.5020  835.4947  835.4076   0.0872  0    11      13    6   R.FEDLNAK.S
      1207  536.3311 1070.6477 1072.5625  -1.9148  1   (15)      5    3   K.DLSGDARALR.R 1208
      1219 1074.0120 1073.0047 1072.5876   0.4171  0     6      47    7   R.LNTDAIASLR.V
      1374  552.1451 1102.2757 1103.5869  -1.3112  2     4      80    3   R.LRTACERAK.R
      1774 1175.9170 1174.9097 1173.6353   1.2744  0    12      11    2   R.SANITISNAVGK.L 1772 1776
      1827  593.7601 1185.5057 1184.6513   0.8544  0    26    0.39    1   K.DAGAISGLNVLR.I
      2219  626.2816 1250.5487 1248.6747   1.8740  2     1 1.2e+02    1   K.MKEVAETKLGK.K
      2702  653.3021 1304.5897 1304.7088  -0.1191  2     6      48    6   R.EVRDLFEAAKK.A
      2969  668.2046 1334.3947 1335.6340  -1.2393  1    10      17    8   K.AQEQMEKVTEK.G
      3213  680.9226 1359.8307 1358.7266   1.1041  2     3      76    9   K.TGKDLSGDARALR.R
      4740  767.2436 1532.4727 1531.8246   0.6481  0    50  0.0016    1   K.SFSGTLEPVQQVLK.D 4737
      5558  804.7446 1607.4747 1606.8103   0.6644  0     9      18    1   K.AVITVPAYFNDNQR.Q 5555
      5613  806.7571 1611.4997 1612.8896  -1.3899  1     0 1.5e+02    5   R.QATKDAGAISGLNVLR.I
      5643  807.8811 1613.7477 1610.8048   2.9429  0    21     1.2    1   K.TFTPQEISSMVLMK.M
      6275  832.3236 1662.6327 1660.8202   1.8125  2     6      43    2   K.AQEQMEKVTEKGQR.E
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6302	833.3336	1664.6527	1663.7974	0.8553	0	70	1.5e-05	1	K.LSTTEIEQMIDDAAK.F 6306
6951	571.6045	1711.7917	1710.9853	0.8064	2	5	49	2	K.LRVGGRLNTDAIASLR.V
7286	873.8056	1745.5967	1744.9359	0.6608	0	101	1.1e-08	1	R.IINEPTAAAIAYGLGSGK.S 7294
7346	585.8459	1754.5157	1751.8685	2.6472	1	8	21	1	R.VEEIISDPTMSMKLK.R 7314
8148	610.1105	1827.3097	1824.9741	2.3357	2	2	88	6	R.GRCLLQERSLAVPNGR.V
8680	629.7755	1886.3047	1885.9352	0.3696	1	(1)	1.1e+02	9	K.TFTPQEISSMVLMKMK.E
8705	630.3349	1887.9827	1885.9352	2.0476	1	8	21	4	K.TFTPQEISSMVLMKMK.E
8850	952.2366	1902.4587	1900.0126	2.4461	1	3	71	5	R.LSSTLTNASSPVNLQRGR.C
9211	650.2899	1947.8477	1946.0255	1.8222	2	(1)	1e+02	9	R.DQTVSVAKAAMEKATAAVR.D
9297	653.6969	1958.0687	1955.1204	2.9483	1	0	1.2e+02	10	R.SLAVPNGRVGFSTSPLLLK.K
9345	655.5512	1963.6317	1962.0204	1.6113	2	2	89	6	R.DQTVSVAKAAMEKATAAVR.D
10728	1066.3191	2130.6237	2130.0957	0.5281	0	65	4.7e-05	1	K.SINPDEAVAYGAAVQAGILSGK.A 10726 10729 10730
12299	784.7372	2351.1897	2349.2216	1.9681	1	1	1.1e+02	7	R.FEDLNAKSFSGTLEPVQQVLK.D

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80. gi|220699162|gb|EED55501.1| **Mass:** 37080 **Score:** 323 **Queries matched:** 21 **emPAI:** 0.98

glycerol dehydrogenase (GldB), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
13	635.4620	634.4547	634.4054	0.0493	0	15	5.1	4	K.YVILK.E
1737	584.5296	1167.0447	1166.5754	0.4693	1	43	0.0082	1	K.REDIFVCTK.V 1734
3110	451.0529	1350.1367	1348.6735	1.4632	1	11	11	4	K.SSNPARIESNFK.S
4057	727.6941	1453.3737	1452.7249	0.6488	0	77	3.2e-06	1	K.IPGVGFGTFASEGSK.G 4069
4332	743.7646	1485.5147	1483.8035	1.7113	0	58	0.00022	1	K.AIGVSNWTIPGLEK.L 4328 4331
5101	784.6811	1567.3477	1567.8835	-0.5357	0	54	0.00064	1	K.GGNTLAQVLIAWGLR.R
5573	805.4431	1608.8717	1608.7519	0.1198	0	43	0.0071	2	K.SIELTDEDFEAVNK.V 5563 5606
6203	829.6856	1657.3567	1656.7308	0.6260	0	60	0.00015	1	K.DTFGYDVWPEETAK.N 6200
11873	764.8132	2291.4177	2292.0409	-0.6232	1	1	93	9	R.FVNMKDTFGYDVWPEETAK.N
12175	777.5619	2329.6637	2327.1169	2.5469	1	3	59	3	R.IESNFKSIELTDEDFEAVNK.V
13020	821.2569	2460.7487	2458.2142	2.5345	0	26	0.3	1	K.VWNHLHRPEDVQWSVDNSLK.R
14319	888.0205	2661.0397	2661.2421	-0.2024	2	7	21	3	R.FVNMKDTFGYDVWPEETAKNLSA.- 14315
14962	931.9599	2792.8577	2792.2541	0.6037	0	30	0.1	1	R.HLDCAWFYLNEDEVGDGIHDFLK.K

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81. gi|220699951|gb|EED56290.1| **Mass:** 73462 **Score:** 319 **Queries matched:** 26 **emPAI:** 0.19

Hsp70 chaperone BiP/Kar2, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
802	983.4760	982.4687	982.4607	0.0080	1	3	75	5	K.YDDKDVTK.D
1815	592.5971	1183.1797	1181.5823	1.5975	1	3	86	9	K.RTLSSQMSTR.I
2258	629.5096	1257.0047	1255.6521	1.3527	0	1	1.3e+02	10	K.VEILVNDQGNR.I
2529	643.5921	1285.1697	1284.6350	0.5347	0	53	0.00074	1	R.NSLENYAFSLK.N
2552	430.1202	1287.3387	1286.7194	0.6193	2	21	1.3	2	K.KNNVDITKDLK.S 2545

2666	651.3291	1300.6437	1300.6009	0.0428	0	2	1.1e+02	10	K.FEELNMDLFK.K
3000	669.8186	1337.6227	1336.7027	0.9200	0	77	3.2e-06	1	K.VQALLEEFFGGK.K 2991
3879	718.6546	1435.2947	1435.7823	-0.4876	2	5	52	10	K.DTKNFPFKVVNK.D
4695	764.7051	1527.3957	1526.7253	0.6704	0	66	4.3e-05	1	R.ITPSYVAFTDEER.L 4702
5150	524.9902	1571.9487	1573.8312	-1.8824	1	6	37	8	K.KSEVDDIVLVGGSTR.I 5169
5875	817.1796	1632.3447	1630.8566	1.4881	0	89	1.9e-07	1	R.VVNEPTAAAIAYGLDK.T 5878
6433	837.9236	1673.8327	1674.9345	-1.1018	1	5	48	2	R.IPKVQALLEEFFGGK.K
7879	601.4069	1801.1987	1798.8845	2.3142	1	1	1e+02	7	K.TFTPEEVSAMVLGKMK.E
9817	675.2079	2022.6017	2021.0277	1.5741	2	2	87	8	K.VSASDKGTGKAESITITNDK.G
10665	1062.5761	2123.1377	2122.9807	0.1570	0	7	23	1	R.IEIESFHNGEDFSETLTR.A
10697	1064.3361	2126.6577	2125.0799	1.5778	2	1	1e+02	4	K.TPKTFTPEEVSAMVLGKMK.E
12685	1207.4726	2412.9307	2410.3220	2.6087	2	1	1.1e+02	5	R.SLTKDNNLLGKFELTSIPPAPR.G
13059	822.9962	2465.9667	2467.1060	-1.1393	1	0	1.2e+02	7	R.LSQEEIDRMVAEAEEFAEEDK.A
14534	898.7249	2693.1527	2693.3660	-0.2133	1	1	94	9	R.KSQIFSTAADNQPTVLIQVYEGER.S
15065	944.1329	2829.3767	2827.3472	2.0296	1	3	51	2	K.NQVNDENGLGGQIDEDDKQTILDAVK.E 15063

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82. gi\|220691710\|gb\|EED48058.1\| **Mass:** 52223 **Score:** 319 **Queries matched:** 30 **emPAI:** 0.63

citrate synthase (Cit1), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
15	635.5770	634.5697	634.3438	0.2259	0	17	3.9	1	R.EFALR.K
394	864.4300	863.4227	863.4865	-0.0637	1	9	21	6	K.AYAKGINK.K 400 405
1011	517.7266	1033.4387	1033.5444	-0.1057	0	47	0.0034	1	K.FIEELIDR.C 1012
1101	526.5881	1051.1617	1050.6185	0.5432	0	35	0.053	1	R.ALGAPIERPK.S
1491	561.7806	1121.5467	1120.6241	0.9227	0	58	0.0003	1	K.IAPGVLTEHGK.T 1482
2271	630.0171	1258.0197	1258.7357	-0.7160	1	10	16	3	M.ASSLRIGTSVLR.S
2726	654.8531	1307.6917	1306.7973	0.8945	0	36	0.044	1	R.ALGVLPQLIIDR.A 2725
4130	732.2116	1462.4087	1461.6987	0.7100	0	66	3.5e-05	1	K.ETFADNLPGEIEK.V 4145
4931	517.7142	1550.1207	1547.7944	2.3264	0	5	46	4	K.VIGEVTLDQAYGGAR.G
5029	780.5346	1559.0547	1557.7787	1.2760	1	4	58	10	R.DLSAEWAARSDLPK.F
5178	525.8079	1574.4017	1573.8351	0.5666	1	17	3	2	R.SDLPKFIEELIDR.C
5186	789.2366	1576.4587	1573.8134	2.6454	1	5	53	7	K.MKAAIGNDLSDQAIK.D
8013	908.1831	1814.3517	1811.8764	2.4753	0	0	1.3e+02	10	K.LPDDQMFNLVSQVYK.I
8314	925.1961	1848.3777	1847.8724	0.5054	0	3	64	2	K.CLVWEGSVLDSEEGIR.F
12718	806.5669	2416.6787	2415.2335	1.4452	0	43	0.0066	1	K.DYLWSTLNAGQVVPGYGHAVLR.K 12742
13784	853.8102	2558.4087	2556.3046	2.1041	2	2	70	4	R.EFALRKLPDDQMFNLVSQVYK.I
15112	949.1819	2844.5237	2842.3782	2.1455	0	61	7.5e-05	1	R.CPSTLHPMAQFSLAVTALEHESAFAK.A 15107 15111
15357	985.5489	2953.6247	2952.3348	1.2899	1	30	0.11	1	K.DKDYSYNLANQLGFGNNNDFVELMR.L 15358
15549	1015.2145	3042.6217	3042.5848	0.0369	2	2	62	1	R.KLPDDQMFNLVSQVYKIAPGVLTEHGK.T
16125	1106.5435	3316.6087	3317.8242	-1.2154	2	1	73	10	-.MASSLRIGTSVLRSTSLAGKPVVQSVAFNGLR.C

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83. gi|220688664|gb|EED45016.1| **Mass:** 17990 **Score:** 313 **Queries matched:** 22 **emPAI:** 1.81

ribosomal protein S13p/S18e [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
752	487.5151	973.0157	972.5240	0.4917	0	29	0.24	1	R.LLNTNVDGK.Q
924	506.0671	1010.1197	1010.5219	-0.4022	1	10	14	1	R.YSNLVCKK.A
1070	524.1476	1046.2807	1045.5709	0.7098	0	40	0.018	1	K.IPTWFLNR.Q 1069 1088
1116	527.8051	1053.5957	1053.5607	0.0350	0	55	0.00047	1	K.TNFQYILR.L 1128
1256	541.2201	1080.4257	1079.6049	0.8208	0	45	0.0045	1	K.IMYALTQIK.G 1252
1337	548.5571	1095.0997	1095.5998	-0.5001	0	(19)	1.9	2	K.IMYALTQIK.G 1346
2192	624.6611	1247.3077	1246.6041	0.7036	0	79	2.2e-06	1	R.AGELTTEELER.V 2190
2706	653.5566	1305.0987	1304.6208	0.4779	0	61	0.00013	1	K.DSQVVSNNLDSK.M
3635	702.6976	1403.3807	1402.7820	0.5987	0	65	4.5e-05	1	R.VVTILQNPTQYK.I 3625 3647 3648
4145	732.6266	1463.2387	1464.8123	-1.5735	1	9	21	3	K.IMYALTQIKGVGR.R
5370	531.6992	1592.0757	1591.7624	0.3133	1	1	1.1e+02	10	K.DSQVVSNNLDSKMR.E
6852	852.5691	1703.1237	1704.9709	-1.8471	2	1	1.1e+02	7	K.QKIMYALTQIKGVGR.R
9118	646.0682	1935.1827	1933.9229	1.2598	1	15	4.5	1	R.DITDGKDSQVVSNNLDSK.M

84. gi|220692772|gb|EED49118.1| **Mass:** 23739 **Score:** 301 **Queries matched:** 10 **emPAI:** 0.14

peptidyl-prolyl cis-trans isomerase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2798	659.1081	1316.2017	1315.6732	0.5286	0	26	0.43	1	K.EIEALGSNSGALR.S
5468	801.4106	1600.8067	1600.7773	0.0294	0	107	2.8e-09	1	K.AFFDVEYAPVGTSAK.K 5466 5494 5509
8291	924.1726	1846.3307	1845.8931	0.4376	0	12	8.1	1	K.HVVFGEVADAESMNVVK.E 8295 8299 8305
15023	940.0735	2817.1987	2815.3963	1.8024	2	1	93	6	R.VIPSFMLQGGDFTRGNGTGGKSIYGEK.F

85. gi|45477378|gb|AY371490.1|_e **Mass:** 2992512 **Score:** 300 **Queries matched:** 306 **emPAI:** 0.01

Aspergillus parasiticus aflatoxin pathway gene cluster, complete sequence

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
24	649.5510	648.5437	648.3265	0.2172	0	14	6.9	2	R.QMVQK.Y 25
53	683.3690	682.3617	682.4126	-0.0509	0	5	29	9	K.GLGPLAR.E
73	690.5590	689.5517	689.4007	0.1511	1	13	10	4	R.MRLVR.V 72
79	694.5290	693.5217	694.4166	-0.8949	0	21	1.1	6	R.FLLFR.Y
121	733.1260	732.1187	731.4177	0.7010	1	11	17	3	R.QTEKVK.Q
136	744.0140	743.0067	742.3722	0.6345	0	8	32	8	R.SSHISGR.N
153	754.4440	753.4367	753.3228	0.1139	0	2	80	10	R.QCQYR.L
179	385.0241	768.0337	766.3836	1.6501	0	16	2.7	3	K.GWMFVK.R
223	790.7660	789.7587	789.4232	0.3355	2	5	63	6	K.EEKKEK.A
245	807.6060	806.5987	806.3956	0.2031	0	11	14	6	K.IEASTMR.R 243
266	817.4680	816.4607	816.4355	0.0253	1	8	35	3	R.RGQPGFR.L
278	412.8446	823.6747	823.4300	0.2447	0	3	63	7	R.HSQSIPR.Y

319	421.8941	841.7737	841.5022	0.2716	0	12	9.1	7	R.AVVLGEVR.K 333
360	428.7006	855.3867	855.4562	-0.0695	0	16	3.7	2	R.IDARPER.F
401	432.8291	863.6437	863.4535	0.1902	1	12	10	3	R.LDTTRMK.D
404	865.5240	864.5167	863.5089	1.0078	2	6	44	6	R.YRRLTR.E
427	437.7026	873.3907	873.5185	-0.1277	1	17	3.7	4	R.VIRSFPR.T
442	440.0271	878.0397	877.4691	0.5706	1	15	6	9	R.MKETTLR.A 439 441
496	450.3536	898.6927	899.5328	-0.8400	0	10	15	4	R.LLVDLEAK.D 495
517	907.4730	906.4657	907.3640	-0.8983	0	11	13	7	R.DLNCCAR.R 521 523
529	455.3336	908.6527	908.4940	0.1587	1	15	4.2	5	R.LPRSGHSR.S 531
540	911.6840	910.6767	910.5236	0.1531	0	3	66	10	K.GGQVVGVAPK.Y
585	921.4650	920.4577	920.5304	-0.0727	2	12	11	1	R.FSIRSRR.R 584
617	933.4870	932.4797	932.4352	0.0446	1	14	7.9	9	R.ERDWAEK.S 616
624	468.5576	935.1007	933.5144	1.5863	2	14	6.4	7	R.FGAERRAK.J
635	472.0851	942.1557	941.4355	0.7202	0	9	21	3	R.SFNGFGASR.F
691	481.0391	960.0637	959.5260	0.5377	2	17	3.9	8	R.RSLGERSR.R
843	495.6116	989.2087	988.5706	0.6382	0	59	0.00023	1	K.VGIDLGIFR.S 842
861	497.9031	993.7917	991.4254	2.3664	1	7	28	9	K.RSDGNCGAR.A
876	500.1451	998.2757	997.5669	0.7089	1	6	39	2	R.TPALGDRIR.J
948	1017.2320	1016.2247	1016.5549	-0.3302	1	6	48	6	K.SCGVRLLGR.S
1005	517.1206	1032.2267	1031.5472	0.6795	1	12	11	10	K.ISGRAASQSR.W
1007	517.2626	1032.5107	1033.5669	-1.0561	1	17	3.6	1	R.SSLRVGYPR.L
1008	517.4991	1032.9837	1031.5975	1.3862	1	9	24	3	R.SSGLSKVLNK.N
1019	518.4771	1034.9397	1035.5713	-0.6316	0	10	16	4	R.FVSQSLSIR.S
1084	524.6976	1047.3807	1048.4396	-1.0589	0	14	8.3	4	R.VDMDNHFR.L
1109	527.1441	1052.2737	1051.6753	0.5984	1	6	35	6	R.LLLLREAPK.S
1231	538.5126	1075.0107	1074.6033	0.4074	0	8	32	7	R.ISSSLSTKPR.A
1341	1096.5850	1095.5777	1095.5897	-0.0120	2	1	1.3e+02	10	R.TGREKVHNR.A
1416	555.6031	1109.1917	1106.6025	2.5892	1	12	11	2	K.VYLWWRGK.L
1446	1116.4860	1115.4787	1112.6189	2.8598	0	4	76	9	R.QIISLSPAER.D
1508	563.5961	1125.1777	1124.5727	0.6051	1	7	33	3	R.SALSYWSRR.Q
1511	564.1706	1126.3267	1127.6775	-1.3508	1	27	0.32	1	R.STRVGGILIGR.N 1528
1519	564.7101	1127.4057	1128.4805	-1.0747	0	3	86	4	R.GTMHHDLMR.F
1550	566.3611	1130.7077	1128.6437	2.0640	1	2	1.3e+02	3	K.MRAVVLGEVR.K
1672	577.2411	1152.4677	1150.5730	1.8947	1	5	43	3	R.GRYAELESAR.Q
1694	580.3311	1158.6477	1156.6829	1.9648	1	4	69	4	K.LKNPARPPHK.J
1716	582.6291	1163.2437	1162.5625	0.6812	2	10	16	2	R.DMGGTQRRSR.V 1717
1816	592.6776	1183.3407	1182.5265	0.8142	0	4	58	8	R.AVQAEDEHER.F 1818
1858	596.2056	1190.3967	1189.6568	0.7400	1	13	7.9	1	R.SSLVTRFQPR.Y 1854
1946	606.3316	1210.6487	1211.7350	-1.0862	1	6	35	5	R.VQSLANLLAKR.L
2034	613.7251	1225.4357	1223.6622	1.7735	2	9	19	2	K.SLRRSVSEYK.T
2042	614.1741	1226.3337	1226.7248	-0.3911	1	12	9.5	8	R.VRQTWGVLLR.H

2094	618.5981	1235.1817	1233.6731	1.5087	2	8	24	9	R.GYDLWRLRR.R	2099
2097	**412.8445**	**1235.5117**	**1233.6136**	**1.8982**	**1**	**4**	**64**	**5**	**R.ARSTTDMAPLR.A**	2101
2153	622.7621	1243.5097	1240.6169	2.8929	2	3	88	1	R.RCRGMLASFK.A	
2188	416.7429	1247.2067	1247.6696	-0.4629	0	8	25	3	R.NTIPVALSFMR.T	2185 2214
2215	**626.0501**	**1250.0857**	**1250.6367**	**-0.5510**	**1**	**2**	**95**	**7**	**R.GRNEYVSVTAR.D**	
2317	632.5626	1263.1107	1262.6619	0.4488	0	13	7.9	2	R.DSGFGLQSIIAR.J	2322
2363	634.6761	1267.3377	1267.5833	-0.2456	0	7	31	7	R.FDGAGGSGNYPVK.G	
2391	**636.6221**	**1271.2297**	**1270.6742**	**0.5555**	**1**	**3**	**87**	**3**	**R.QRAAGDGQSILR.G**	
2479	**640.4186**	**1278.8227**	**1277.6854**	**1.1374**	**2**	**4**	**71**	**3**	**R.HSVRRQWGPR.V**	
2516	428.9402	1283.7987	1282.6122	1.1866	2	14	6.5	1	R.VSDMKRMASSR.A	
2653	**650.3691**	**1298.7237**	**1297.5761**	**1.1476**	**0**	**3**	**86**	**6**	**R.YVPSFCPASDR.S**	
2669	**651.4571**	**1300.8997**	**1300.6445**	**0.2552**	**1**	**1**	**1.2e+02**	**8**	**R.EPPLVSCSKER.S**	
2697	652.7286	1303.4427	1303.6051	-0.1624	1	8	29	8	K.GAGNTGPATRCSR.R	
2723	654.6866	1307.3587	1306.7218	0.6369	2	14	6.1	2	R.SSPTHRRLTPR.V	2733
2756	**438.1199**	**1311.3377**	**1311.7147**	**-0.3769**	**0**	**13**	**8.5**	**6**	**R.IGQGTINPSLQGK.L**	
2984	**669.1121**	**1336.2097**	**1335.7003**	**0.5095**	**1**	**3**	**79**	**3**	**R.LAKGTICAMVTR.A**	
2991	669.2516	1336.4887	1335.7986	0.6901	1	8	26	4	K.NLKSVAISHVLR.S	
3006	**447.2352**	**1338.6837**	**1337.5531**	**1.1306**	**0**	**6**	**40**	**10**	**K.HDDACGSIGNHR.Q**	
3024	671.2081	1340.4017	1337.7053	2.6964	0	7	33	6	K.LLGWSLFMIDK.L	
3154	**678.0416**	**1354.0687**	**1353.7881**	**0.2807**	**1**	**1**	**1.1e+02**	**9**	**K.LALESLFHRIR.S**	
3188	679.8726	1357.7307	1355.7383	1.9924	2	4	67	7	K.RELYMFIKTR.G	
3303	**457.0392**	**1368.0957**	**1365.6567**	**2.4390**	**0**	**9**	**18**	**10**	**K.LCLCSLMAGGLR.S**	3291
3374	**688.2076**	**1374.4007**	**1373.7415**	**0.6592**	**1**	**9**	**23**	**2**	**R.ATLAASSNAWRVK.S**	
3379	**688.3016**	**1374.5887**	**1373.7626**	**0.8261**	**2**	**5**	**51**	**9**	**R.ITTSPSERLRSK.S**	
3439	**461.4752**	**1381.4037**	**1379.8725**	**1.5313**	**2**	**7**	**30**	**4**	**K.IVGNIAAARKVIR.L**	
3509	**464.0979**	**1389.2717**	**1388.7446**	**0.5272**	**1**	**7**	**35**	**6**	**R.LLGRSDINVAMGK.I**	3500
3569	**466.3235**	**1395.9487**	**1395.6929**	**0.2559**	**1**	**7**	**30**	**10**	**R.LEMLEGHGGRGPK.V**	
3573	**699.1626**	**1396.3107**	**1396.8011**	**-0.4904**	**2**	**3**	**79**	**1**	**R.KPIVNNGRTSRR.S**	
3634	**702.6811**	**1403.3477**	**1402.7456**	**0.6021**	**0**	**2**	**1e+02**	**10**	**K.LLQAFPDLETTR.R**	
3671	705.7686	1409.5227	1406.6646	2.8581	0	1	1.2e+02	7	K.MGPIQCSASTLSR.W	
3675	471.0512	1410.1317	1407.7068	2.4249	0	5	47	9	R.SDLITYAALGCPK.L	
3683	706.8776	1411.7407	1409.6933	2.0475	0	7	32	1	R.SSMISVTSRPSSR.S	
3709	708.6731	1415.3317	1415.6542	-0.3225	0	2	93	10	K.VSHSSAASGWTNGR.M	
3710	**708.6931**	**1415.3717**	**1414.6729**	**0.6989**	**0**	**82**	**9.5e-07**	**1**	**R.SGASFSDFLQQTK.G**	3713
3725	**709.2161**	**1416.4177**	**1414.7555**	**1.6622**	**0**	**51**	**0.0013**	**1**	**K.ESDTPITLAEIVK.K**	3711
3768	**712.6971**	**1423.3797**	**1422.7732**	**0.6066**	**2**	**2**	**90**	**9**	**R.FLRDRVYIADR.S**	
3973	**482.5225**	**1444.5457**	**1441.6910**	**2.8547**	**0**	**7**	**33**	**7**	**R.GGHINQTIDSGSTR.R**	
3994	**724.1981**	**1446.3817**	**1446.6773**	**-0.2956**	**0**	**11**	**13**	**2**	**K.ATVNVEEEIACGR.Q**	
4030	**1450.6890**	**1449.6817**	**1449.7616**	**-0.0799**	**1**	**5**	**51**	**6**	**K.LYPDRITGYQPK.Q**	4031
4063	**485.6399**	**1453.8977**	**1452.6966**	**1.2011**	**1**	**3**	**70**	**6**	**R.RFASCPNMTVVR.V**	
4156	**489.2695**	**1464.7867**	**1465.6481**	**-0.8613**	**1**	**(2)**	**90**	**2**	**R.KHDDACGSIGNHR.Q**	4158

4195	736.2816	1470.5487	1469.6795	0.8692	1	6	42	4	R.SWCDKMEVLFR.V	4200
4330	496.0949	1485.2627	1482.7905	2.4722	0	6	38	5	R.TMIAVLVVFGDYR.A	
4350	744.5106	1487.0067	1485.6745	1.3323	1	(2)	1.1e+02	9	R.SWCDKMEVLFR.V	
4452	501.5039	1501.4897	1498.7854	2.7043	0	(2)	95	10	R.TMIAVLVVFGDYR.A	
4544	757.3701	1512.7257	1512.8637	-0.1380	1	6	38	8	K.VELAHHVVGRQLR.H	
4568	759.2261	1516.4377	1517.6966	-1.2589	0	4	64	3	R.AQMLQSMNTVDHK.L	
4604	760.8101	1519.6057	1517.7910	1.8147	1	1	1.3e+02	9	R.TVLSRATQNTASNR.L	
4727	511.4015	1531.1827	1529.8049	1.3778	0	7	33	7	K.SSLTSITSISNPAPR.A	
4773	513.0635	1536.1687	1534.8481	1.3207	1	5	44	1	R.RPHIASGRIPEFR.E	
4896	773.8356	1545.6567	1544.8747	0.7820	2	3	80	2	R.KLTTRATSTGRPTR.F	4866 4885
4981	777.9421	1553.8697	1552.7854	1.0843	1	1	1.1e+02	5	R.SAVLLCVRMFGER.D	
5005	779.5966	1557.1787	1556.8935	0.2852	1	8	27	5	R.IMTVRWPVLMALK.I	
5105	523.5982	1567.7727	1565.8354	1.9373	1	7	31	3	R.SYGWLATKQIFPR.R	
5165	525.3512	1573.0317	1572.8884	0.1433	1	(7)	30	4	R.IMTVRWPVLMALK.I	5167 5168
5196	526.7359	1577.1857	1575.9725	1.2132	1	5	49	4	R.LPWSGRPRLLLLR.E	
5202	527.0482	1578.1227	1576.8209	1.3018	1	2	91	5	K.EIEIEHGGNGAPKVK.V	
5262	792.3481	1582.6817	1582.8184	-0.1367	1	9	17	1	R.LGGRHLMVCQQIR.S	
5359	796.2846	1590.5547	1591.8439	-1.2892	2	2	95	4	R.VVSIRMGMVSRWR.F	
5377	797.2286	1592.4427	1590.9167	1.5260	1	5	53	2	R.QLAYVEMRLILVK.L	
5393	798.1816	1594.3487	1593.7900	0.5588	1	8	21	5	R.FDGAGGSGNYPVKGLR.Q	
5407	798.8281	1595.6417	1593.8476	1.7941	0	19	2	1	R.SMGIEFLTPYVLPK.E	5406
5457	534.4892	1600.4457	1597.6937	2.7520	1	5	43	4	R.STGASLDSGQMGRCR.H	
5712	810.7801	1619.5457	1618.8315	0.7143	1	4	62	6	R.NEYVSVTARDAGIPK.L	
5762	812.5691	1623.1237	1621.9152	1.2086	1	2	85	4	K.TTVIRVSPAPTPEVR.L	
5778	542.2395	1623.6967	1621.8763	1.8205	1	5	44	4	R.VLLVLACSWRYSR.R	5731
5819	814.7676	1627.5207	1627.7413	-0.2206	1	3	74	7	R.MGRFDGAGGSGNYPVK.G	
5848	544.3449	1630.0127	1627.8967	2.1160	1	3	68	8	R.GLTVSLPISVDPMKR.L	
5870	816.9091	1631.8037	1632.8002	-0.9965	1	7	30	1	R.GIGNQRSLNGSEMVR.J	5885
5895	818.0711	1634.1277	1633.7929	0.3348	2	0	1.4e+02	7	R.QSHRYVLCCQRK.R	
5914	546.4202	1636.2387	1635.7960	0.4427	0	10	13	5	R.CSIPLSVDSMTSALR.J	
6139	551.7172	1652.1297	1651.7909	0.3388	0	(9)	19	4	R.CSIPLSVDSMTSALR.J	6135
6251	554.7192	1661.1357	1659.7715	1.3642	1	2	1e+02	8	R.SERYMIEFPFEGR.V	
6298	555.8025	1664.3857	1662.9167	1.4690	0	6	35	6	K.VMASLAFFTSVLHLK.G	
6363	557.5849	1669.7327	1668.7826	0.9501	0	7	28	5	R.IMVSCMFWPTPLR.S	
6371	557.7122	1670.1147	1671.8944	-1.7797	0	2	1e+02	8	K.IGSSVPAPGQGILSFSR.E	
6458	838.8021	1675.5897	1673.8883	1.7014	2	1	1.1e+02	6	R.SGDRIRTCTTVAIPK.F	
6628	563.2692	1686.7857	1685.8671	0.9186	0	6	41	2	R.GPQALLDCAGIRPYR.S	
6721	565.6752	1694.0037	1691.9532	2.0506	0	3	67	9	R.LYIVSSMVSLGPSVIK.V	
6748	849.2796	1696.5447	1694.8385	1.7063	1	1	1.1e+02	6	R.YRLYPALNCIPCR.D	
6860	852.8501	1703.6857	1702.8798	0.8059	2	1	1.2e+02	7	R.RHRQKPPQCQGPSK.G	
6890	569.8045	1706.3917	1705.8094	0.5824	1	5	44	3	K.AFLSYSSGGSRSSCLK.R	

6940	856.5921	1711.1697	1709.8416	1.3282	0	1	1.1e+02	4	R.TALVCLCQLGCFIR.Y	
6989	858.7501	1715.4857	1716.8617	-1.3760	2	1	1.1e+02	3	R.MSDPNWVRQTEKVK.Q	
7003	859.3861	1716.7577	1716.9457	-0.1880	1	3	65	3	R.QCQYRLINQLILR.F	
7042	861.8961	1721.7777	1722.8182	-1.0404	1	2	85	7	K.VFSSRASHMQVSPMK.T	
7051	862.3606	1722.7067	1721.7176	0.9891	1	5	43	3	R.DGGTAGSGRYHCGGEGGK.G	
7086	863.8401	1725.6657	1724.8774	0.7883	0	77	2.8e-06	1	R.QLFLFGDQTADFVPK.L	
7324	584.7689	1751.2847	1749.9751	1.3097	1	2	84	10	R.LVLHLGVQGHGHKEAR.H	
7462	883.5381	1765.0617	1766.8926	-1.8309	0	5	47	2	K.TPAPHAAISGMLYWPR.S	
7463	589.4282	1765.2627	1762.8611	2.4016	2	5	48	6	R.WHRAAAHSASSSPDKR.J	
7548	886.8741	1771.7337	1768.8600	2.8737	2	1	1.3e+02	8	R.QYALGMPRGTMKEGSK.L	
7732	893.8816	1785.7487	1782.9312	2.8176	1	3	78	1	R.GQHSQVSAIMLRWVR.W	
7810	598.9459	1793.8157	1791.0117	2.8040	1	1	1.1e+02	9	R.KVMASLAFFTSVLHLK.G	
7976	906.7431	1811.4717	1810.1040	1.3677	2	2	86	7	R.IVSAPLLATKSKRPTTK.C	
8041	909.3326	1816.6507	1817.0206	-0.3699	0	4	55	4	R.GARPPGMLQLQQLRPR.C	8042
8196	918.1231	1834.2317	1834.9036	-0.6719	1	3	79	2	R.FPVDGGTSTRMWIPAGK.H	
8230	614.0352	1839.0837	1840.9328	-1.8491	1	2	97	1	R.TCTTVAIPKFCQFIR.V	
8275	922.8376	1843.6607	1842.8465	0.8142	1	7	26	7	K.LSNTVTQMNRSCFNR.G	
8525	624.2709	1869.7907	1871.0615	-1.2708	2	4	63	9	R.SLKESDTPITLAEIVKK.T	8516
8575	626.1915	1875.5527	1873.9673	1.5854	0	1	1e+02	4	R.VDSSNLSDYPLVVLPEK.T	
8602	940.6811	1879.3477	1878.8499	0.4978	2	0	1.4e+02	2	R.GKGMVPDRMDAQVQCR.Q	
8842	635.0112	1902.0117	1903.0468	-1.0351	2	2	97	6	R.IHFTHEYIAVKVYRK.A	
8854	952.4571	1902.8997	1903.8707	-0.9710	1	3	79	2	R.NLHPCQTEQHREEAR.Y	
9061	964.7031	1927.3917	1925.9676	1.4241	2	3	62	4	R.SGRNLVPMGGIRSCPGPR.L	
9090	644.5892	1930.7457	1932.0581	-1.3124	2	1	1.1e+02	5	R.WSPLPLSKLTFSRSASR.D	
9211	650.2899	1947.8477	1949.0339	-1.1862	1	3	75	4	R.SPRATAMAAPMPRPAPVTK.A	
9260	651.9639	1952.8697	1953.0427	-0.1730	2	8	21	1	R.VTRMTGLDMETIFAKIK.E	
9265	977.7416	1953.4687	1952.9626	0.5062	1	2	77	10	R.TEAGDRAYAAAVMSQAVVK.I	9253
9331	982.3431	1962.6717	1959.9704	2.7014	1	2	81	1	R.GNAWTWEPGLYLQNRR.S	
9398	986.2966	1970.5787	1969.0376	1.5411	2	(1)	1.1e+02	5	R.VTRMTGLDMETIFAKIK.E	
9778	673.6542	2017.9407	2016.9608	0.9799	0	3	76	6	R.DPSNEMIENNRPVVMIK.N	
9987	680.2079	2037.6017	2039.1752	-1.5735	2	0	1.3e+02	10	R.AVGVTATGRVRQTWGVLLR.H	
10124	684.8855	2051.6347	2050.9491	0.6857	2	3	62	4	K.DKAQDSGGREMFQSPSGVR.T	10122
10150	685.9969	2054.9687	2054.0004	0.9684	1	2	80	5	R.MGTRDLYDLVNGFERPR.L	10140
10229	688.3972	2062.1697	2061.1153	1.0544	2	0	1.3e+02	8	R.NCIGRNLAYAEVRLTLAK.L	
10237	688.6385	2062.8937	2061.0499	1.8438	2	0	1.3e+02	8	R.LPKVFSSRASHMQVSPMK.T	
10318	692.1115	2073.3127	2071.1724	2.1403	2	3	62	3	R.QVPKSIPRVHLPMSLPTR.M	
10379	1041.3566	2080.6987	2081.0364	-0.3377	0	3	58	3	R.HIHLSELGNFIGSSMGGPTK.T	
10437	697.5029	2089.4867	2091.0834	-1.5967	1	3	60	7	R.NNHPRPAKGPHINIENAGR.E	
10439	697.5925	2089.7557	2091.1333	-1.3775	1	6	30	1	R.APVKIPELPTPAMARPTMR.T	
10520	1051.0501	2100.0857	2100.0595	0.0262	0	36	0.032	1	R.ILLDEMIMPDLLAQDSQR.F	
10747	1068.3386	2134.6627	2133.0974	1.5653	2	1	97	8	R.GLRAPGDNVQCLHLQSRGR.F	10744

10814	715.2352	2142.6837	2140.0657	2.6181	1	2	79	1	R.FMNQIDMTVVLTLNGKER.S
10828	1073.3201	2144.6257	2145.0315	-0.4058	1	1	99	7	K.LCLCSLMAGGLRSPTPPCR.A
11058	725.7855	2174.3347	2174.1776	0.1571	1	0	1.3e+02	10	R.LTLAKLLWHFDFTLDVDK.T
11118	729.1789	2184.5147	2184.1109	0.4038	1	2	78	5	R.KTAEILQASAYICGAAQHPR.K
11267	734.8899	2201.6477	2199.0711	2.5766	2	1	1.1e+02	8	R.MIKLSNTVTQMNRSCFNR.G
11320	737.9142	2210.7207	2208.1321	2.5886	2	2	74	4	R.VRTEAGDRAYAAAVMSQAVVK.I
11369	739.2875	2214.8407	2216.1670	-1.3263	1	4	50	8	R.LRGFTTYDIPYLYAIPWK.A 11368
11388	740.2889	2217.8447	2219.1568	-1.3121	2	3	65	7	K.IALLRGTMHHDLMRFHQK.Y
11414	741.9132	2222.7177	2223.1834	-0.4657	1	6	35	3	R.VGGSGAVGRTMIAVLVVFGDYR.A 11417
11420	742.1829	2223.5267	2222.1518	1.3750	1	4	44	3	R.KAPPSTPMIFPLTHSAVSDAR.K
11515	1119.5021	2236.9897	2238.1864	-1.1967	1	6	33	4	R.ATAMAAPMPRPAPVTKATLPSK.R
11784	761.2552	2280.7437	2278.2407	2.5031	2	2	70	4	K.LQGRHILPTNVPRTAHPSER.L
11835	762.6319	2284.8737	2282.0936	2.7801	1	4	45	6	R.SINTRAPVAITMHGSCNFYK.F
11889	765.7875	2294.3407	2295.1165	-0.7758	0	5	44	4	R.STGLMTAHDIIAETVEEHGIR.T
11990	769.8089	2306.4047	2307.1807	-0.7760	2	7	25	1	K.GWPALGLGDGHRRQYALGMPR.G
12042	771.6852	2312.0337	2311.2001	0.8336	2	2	83	4	K.VKQMSAQGRGQHSQVSAIMLR.W
12146	776.3945	2326.1617	2324.2616	1.9001	2	4	48	5	R.CVIAAIFGPGIFLRGWKYTR.J
12148	776.5552	2326.6437	2326.1793	0.4644	2	3	69	5	R.SWIVQPMPRQAQGFPWKDR.I 12157
12161	776.9305	2327.7697	2326.2968	1.4729	2	3	60	9	R.LLLEGGARVLVTTSREPATTSR.Y 12165
12166	777.2345	2328.6817	2330.1478	-1.4660	2	8	22	1	R.FPVDGGTSTRMWIPAGKHETK.G
12178	777.6699	2329.9877	2329.2754	0.7124	2	1	91	4	R.GASWAVSRSSLILETGKGNVAVK.Q
12207	779.7495	2336.2267	2337.2614	-1.0347	1	4	52	3	R.LYIVSSMVSLGPSVIKVGESTR.F 12203 12218
12385	790.8889	2369.6447	2367.1875	2.4573	2	5	39	3	R.HLMVCQQIRSPCWRPQKK.I
12437	792.6655	2374.9747	2375.1824	-0.2077	1	2	79	6	K.SRILLDEMIMPDLLAQDSQR.F
12492	795.4035	2383.1887	2382.1937	0.9950	1	5	39	1	R.MYPAVPGQPPRVVPASGATVCGR.F
12547	797.6795	2390.0167	2388.3338	1.6830	0	4	54	9	R.ECEAVIKPTILASSLYIGLIAK.R
12571	799.1472	2394.4197	2393.2015	1.2182	0	44	0.0054	1	K.ELIPHLSYFQVEPTEHDLAR.K 12572
12626	802.1672	2403.4797	2403.2369	0.2428	1	2	86	9	R.VVPASGATVCGRFVPEEVFNLR.J
12700	805.7462	2414.2167	2413.0816	1.1352	1	6	32	9	R.SSTQPKTTWAVQGSSENMSSER.F
12704	805.8019	2414.3837	2414.2158	0.1679	2	1	87	8	R.AQMLQSMNTVDHKLARTADLR.Q
12840	811.7192	2432.1357	2430.2900	1.8457	2	4	50	9	R.LTAARAAASIDLVADDIGSVKMSR.A 12814 12839
12885	813.4165	2437.2277	2437.2233	0.0045	0	5	38	1	R.GDIALQMGLPIYAVIASSAMAADK.I
12942	816.3345	2445.9817	2444.1642	1.8176	0	1	92	7	K.GESLPTAIFQAESPACSEAPNLR.V
12943	816.3905	2446.1497	2444.2383	1.9114	2	4	53	5	R.KEPTRTNQVWQLFQLCPGSR.A
12953	817.2342	2448.6807	2448.2882	0.3925	2	9	14	1	R.ASSLPWKIALLRGTMHHDLMR.F
12956	817.2935	2448.8587	2447.3020	1.5567	1	9	15	3	R.LDPVVATAVGPEDGNNRIADALLK.R 12952
12971	818.3479	2452.0217	2450.2931	1.7286	1	1	88	9	R.DLEHRPAGVIKGWPALGLGDGHR.R
13005	820.6559	2458.9457	2458.2250	0.7207	2	0	1e+02	8	R.RGVVPFSCSTYVGWMTQTKVR.E
13142	825.5289	2473.5647	2474.3555	-0.7908	2	4	47	7	R.RVPISCFIFARIVFHACLLR.S
13199	827.6962	2480.0667	2479.3416	0.7251	0	4	45	1	R.AIEHVPLTWWFLAVGGAWIVSK.I
13393	836.5032	2506.4877	2506.2989	0.1889	0	15	3.8	3	R.ISSIFGILESATAGDESPMLLALR.S 13390

13429	837.7859	2510.3357	2509.1141	1.2216	0	5	39	1	K.MCLVGGYDDLQEEASYGFAQLK.A 13445
13588	844.0282	2529.0627	2530.3696	-1.3069	1	3	62	2	R.LSAGLDAFALPRFDFIALSTHIR.Y
13710	851.0322	2550.0747	2551.2748	-1.2000	1	5	36	3	K.LLWHFDFTLDVDKTGNFLDQK.I 13723
13805	855.1692	2562.4857	2561.3135	1.1723	0	12	6.7	1	K.MTSFLAPICHSKPSVFTVTPVAR.F
13818	855.7395	2564.1967	2561.4516	2.7452	2	1	89	3	R.RESRIFVLLFSPASINVMVIVR.V
13894	861.3289	2580.9647	2579.3496	1.6151	1	2	79	3	R.YHIVHDASPRTTILEFPLVESR.S
13951	864.7872	2591.3397	2592.4500	-1.1103	1	0	1.1e+02	7	R.QSLGQVRTPQLVTGVYIHLGLSAR.Q
13987	869.3585	2605.0537	2603.4006	1.6531	1	0	1.2e+02	6	R.FLSPGTKPTLQAPVAPMHPRSSLR.V
14049	871.3725	2611.0957	2612.3421	-1.2464	0	2	65	3	K.VRPHMSPGGTVGVDLVPLASFDAYK.N 14051 14058
14118	876.6785	2627.0137	2628.3370	-1.3233	0	(1)	93	6	K.VRPHMSPGGTVGVDLVPLASFDAYK.N
14149	879.6989	2636.0747	2635.2820	0.7928	2	1	95	8	R.RPKPNTNFMGSVSGGELCRSRNR.S
14154	879.8712	2636.5917	2637.3432	-0.7515	2	1	94	4	R.AAASIDLVADDIGSVKMSRASELFR.N
14212	883.3275	2646.9607	2644.2360	2.7247	1	4	43	4	K.TPVGACATGVESIDSGYESIMAGKTK.M
14265	886.3062	2655.8967	2656.3795	-0.4828	2	3	50	2	K.VYRKAPPSTPMIFPLTHSAVSDAR.K
14340	889.3575	2665.0507	2662.4330	2.6177	1	0	99	4	R.LILPAVGPHTTITKDGTIEYAEAPR.Q
14346	889.8422	2666.5047	2668.2850	-1.7803	1	1	92	8	R.VVPCNLASAQDCEGLIRHVYDPR.G
14910	927.9889	2780.9447	2782.3279	-1.3832	2	1	85	3	K.GETGRSINTRAPVAITMHGSCNFYK.F
15017	939.0345	2814.0817	2812.3611	1.7206	1	0	96	5	R.APWSPISVCTCLACFGQRIYVATR.T
15274	971.8529	2912.5367	2912.4927	0.0441	2	2	61	5	R.NLDTLDEALRSASHLCFPTRTVQLR.E
15449	998.6552	2992.9437	2994.5285	-1.5847	2	0	1.1e+02	5	K.HISLDGSRSHRIHGDFLVSAVNGHAANK.G
15465	1002.4339	3004.2797	3003.2943	0.9854	1	1	77	7	R.TNMDGIMIEGDACVGLAASRTSYCHSR.G
15510	1011.9422	3032.8047	3030.4245	2.3803	0	3	50	3	R.MSTASLEGTLSMGSLCVPLPFMLTSPCK.W 15506 15507 15512
15712	1033.4092	3097.2057	3097.6126	-0.4069	1	3	51	2	R.SSSKVAVAIWTIFRPMAITMLSDAAMLR.A
15720	1034.8882	3101.6427	3102.3924	-0.7496	2	0	1e+02	9	R.VDMDNHFRLLSEFERGFTCQNGASEK.E
15763	1041.5439	3121.6097	3121.6171	-0.0074	0	0	94	8	R.VFPPPVRPWHLDYLETSQTIQMALQR.L
15909	1071.2992	3210.8757	3211.5779	-0.7022	2	1	80	7	R.DVLLREEGLDDSSSQPMVIVLDSGDRNPR.E
15979	1085.0352	3252.0837	3249.4706	2.6131	0	0	89	6	R.LASSSAAEEYWDNVSSMYAESCGITLRPR.Q

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86. gi|45477378|gb|AY371490.1|_b **Mass:** 2989536 **Score:** 297 **Queries matched:** 293 **emPAI:** 0.01

Aspergillus parasiticus aflatoxin pathway gene cluster, complete sequence

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
23	325.0841	648.1537	647.3351	0.8187	1	13	11	6	R.KNSGSR.N
26	650.4130	649.4057	649.3217	0.0840	0	8	29	2	R.LSAMGR.D
39	672.5100	671.5027	671.4078	0.0949	1	23	0.95	6	R.EVIRR.G
84	702.5160	701.5087	701.3457	0.1631	0	13	11	3	R.QGGVGER.R
216	789.4940	788.4867	788.4140	0.0727	1	7	41	10	R.SNPRSTK.L
314	421.0041	839.9937	840.5545	-0.5608	1	7	28	9	R.VLGVKGLR.I
346	424.8896	847.7647	848.4538	-0.6891	1	7	38	6	K.TIRANMK.Q
359	428.6501	855.2857	852.4058	2.8799	2	2	85	10	R.CMRRSK.I
369	429.0926	856.1707	857.5334	-1.3627	0	15	5.4	8	K.SVISLALR.E

408	**867.4640**	**866.4567**	**866.3440**	**0.1128**	**0**	**7**	**30**	**6**	**R.ESSEMER.I**	
412	**435.1566**	**868.2987**	**869.5195**	**-1.2208**	**2**	**10**	**13**	**2**	**R.KNLPRSR.Q**	
417	**436.1891**	**870.3637**	**870.4923**	**-0.1286**	**1**	**11**	**14**	**10**	**K.KTALGPER.I**	419
497	451.0531	900.0917	899.4899	0.6019	0	21	1.6	4	R.GMVDPLLR.S	
558	**914.5420**	**913.5347**	**913.4981**	**0.0366**	**0**	**4**	**78**	**5**	**R.ITSSHLTR.S**	
582	460.1971	918.3797	918.4705	-0.0908	1	16	4.8	4	R.SRMSGPLR.R	
701	**482.3616**	**962.7087**	**963.5250**	**-0.8163**	**2**	**2**	**1e+02**	**7**	**R.SAPRSYRK.L**	
707	965.5100	964.5027	964.5052	-0.0024	0	6	45	8	K.WLSMSTLK.C	708
734	969.6090	968.6017	967.5927	1.0091	1	7	31	10	R.NSIPILRR.T	
744	**486.3071**	**970.5997**	**969.4992**	**1.1005**	**2**	**6**	**43**	**9**	**K.RDDPPSKR.J**	
762	488.5776	975.1407	975.5066	-0.3658	0	12	14	8	R.LFVYGSYK.L	766
780	**978.6420**	**977.6347**	**977.4349**	**0.1998**	**1**	**6**	**46**	**8**	**R.RQGDDMTR.A**	
781	**489.8611**	**977.7077**	**979.5311**	**-1.8234**	**1**	**8**	**27**	**1**	**R.SPNIRTHR.S**	
792	**490.7691**	**979.5237**	**978.5471**	**0.9766**	**1**	**7**	**31**	**7**	**R.RQALQAHR.R**	
892	**501.3986**	**1000.7827**	**1001.5982**	**-0.8154**	**1**	**8**	**33**	**7**	**K.LRLTSSVAR.A**	
913	**503.6206**	**1005.2267**	**1005.4880**	**-0.2612**	**0**	**30**	**0.18**	**1**	**R.VLFDDQNR.A**	
920	**505.4151**	**1008.8157**	**1009.4981**	**-0.6824**	**0**	**5**	**49**	**1**	**R.YTVTYHAR.T**	
940	508.8236	1015.6327	1015.5913	0.0414	1	20	1.7	3	K.KSLDALLEK.V	953
948	1017.2320	1016.2247	1015.5159	0.7088	2	9	21	2	R.DDRRDLAR.I	
989	**515.4361**	**1028.8577**	**1029.5971**	**-0.7394**	**0**	**8**	**29**	**6**	**R.YLAGQLLPR.S**	
1025	**518.9821**	**1035.9497**	**1034.5066**	**1.4431**	**0**	**4**	**64**	**6**	**R.EIVASDVMR.E**	
1071	**524.1581**	**1046.3017**	**1043.5512**	**2.7505**	**0**	**9**	**25**	**7**	**K.VVVNYAHSR.E**	
1092	525.3256	1048.6367	1047.4906	1.1461	0	23	0.8	2	R.LIDQDMADK.V	1091
1173	**534.2316**	**1066.4487**	**1065.5243**	**0.9244**	**0**	**2**	**99**	**7**	**K.AGTWAASAGFK.E**	
1191	535.2076	1068.4007	1067.6927	0.7080	2	10	16	6	K.ARVLGVKGLR.I	
1232	**539.1326**	**1076.2507**	**1073.5942**	**2.6566**	**1**	**11**	**15**	**1**	**R.RTSGVGAGLTR.M**	1234
1362	**551.1976**	**1100.3807**	**1101.6618**	**-1.2811**	**2**	**2**	**1.2e+02**	**2**	**R.LASVSRVSKR.S**	1360
1571	**378.6832**	**1133.0277**	**1130.6091**	**2.4187**	**2**	**15**	**5.7**	**7**	**R.MRLAGQRGSR.H**	1567
1796	**393.6009**	**1177.7807**	**1179.7676**	**-1.9869**	**2**	**10**	**18**	**1**	**R.RTRPLRLLR.C**	
1801	**590.4196**	**1178.8247**	**1177.5397**	**1.2850**	**0**	**9**	**19**	**7**	**R.SAPSPTCTTTR.G**	
1817	592.6811	1183.3477	1183.6132	-0.2654	1	7	32	9	R.RGTMNLDHIK.S	
1875	**598.6936**	**1195.3727**	**1193.5499**	**1.8228**	**0**	**3**	**83**	**10**	**R.AGWGMSLATER.N**	
1884	599.5761	1197.1377	1196.6335	0.5042	1	3	74	9	K.LLSAMYTRSR.K	
1894	**600.2646**	**1198.5147**	**1198.6921**	**-0.1774**	**1**	**6**	**43**	**10**	**R.IKEDVQLLNK.L**	
1932	604.6996	1207.3847	1206.6608	0.7239	0	7	29	6	R.LFSIISLDGSR.D	
1958	**606.7881**	**1211.5617**	**1210.6418**	**0.9199**	**0**	**16**	**3.8**	**3**	**R.AGLSTAAQSLHR.Y**	1950 1952 1963
1987	1217.3360	1216.3287	1216.7040	-0.3753	2	5	62	3	R.VSKRSLQPFR.L	
2053	**615.2126**	**1228.4107**	**1225.7143**	**2.6965**	**1**	**6**	**43**	**10**	**R.AGVELVQKGAVR.S**	
2134	**621.6521**	**1241.2897**	**1240.5982**	**0.6915**	**2**	**9**	**19**	**3**	**R.KMGPQDEKHR.R**	2133 2138
2160	**623.2131**	**1244.4117**	**1244.5819**	**-0.1702**	**0**	**3**	**79**	**1**	**K.VESHSQLMGNK.E**	
2258	629.5096	1257.0047	1255.7248	1.2799	1	4	73	5	R.LDGKVALVTGAGR.G	

2259	629.5466	1257.0787	1256.7387	0.3400	2	6	42	3	R.RSLRIPQMLK.S	
2381	635.7971	1269.5797	1270.7496	-1.1699	0	5	49	1	R.ITLLITEQNVK.S	
2403	637.2901	1272.5657	1272.6674	-0.1017	0	11	14	2	K.GGVEISLQESVR.L	
2437	639.0671	1276.1197	1274.7241	1.3956	2	4	66	7	R.SGIIISSRRMR.D	
2438	639.1011	1276.1877	1275.6935	0.4942	0	50	0.0016	1	K.DHLEQLGIPVR.S	2455
2493	641.2681	1280.5217	1278.7673	1.7544	2	6	36	5	R.LWVPPISRRR.T	
2497	641.9446	1281.8747	1281.6929	0.1819	0	0	1.4e+02	6	K.VPSSEAVDILPR.Y	
2514	642.7886	1283.5627	1282.6414	0.9214	0	2	1e+02	4	R.SNVYCVLMLGK.C	
2556	645.1481	1288.2817	1286.6401	1.6416	1	3	77	4	R.GTMNLDHIKSR.F	
2619	432.7375	1295.1907	1293.6829	1.5078	1	5	52	8	R.SISYYHQLKR.S	
2630	648.7836	1295.5527	1294.7106	0.8422	1	9	18	4	R.HASLLRTSSPAR.R	
2645	649.9746	1297.9347	1297.7870	0.1477	1	15	5.5	2	K.TILAFLRHSLK.A	2648 2650
2722	654.6611	1307.3077	1306.6353	0.6724	1	3	83	10	R.WETRRPCFR.R	
2750	656.0041	1309.9937	1308.6245	1.3693	1	12	9.7	1	R.DQEMAVAAFRR.C	
2825	660.4796	1318.9447	1317.5983	1.3464	1	1	1.4e+02	6	R.SNTSRASSMSFK.A	
2868	663.5951	1325.1757	1324.6596	0.5161	1	11	12	3	R.GRATSQVHEANR.F	
2873	663.8056	1325.5967	1325.7377	-0.1410	0	(11)	14	5	R.SPQLLMVSGIGPK.D	
2952	667.5176	1333.0207	1332.6952	0.3255	0	7	35	10	R.FVHHHVGHVHK.A	
2992	669.4071	1336.7997	1334.6989	2.1008	2	8	25	4	R.QGMQLRAGYRR.Y	
3013	670.7451	1339.4757	1340.8140	-1.3383	2	2	95	8	K.AVVDSKARVLGVK.G	
3044	672.1071	1342.1997	1341.7326	0.4671	0	40	0.017	1	R.SPQLLMVSGIGPK.D	3056
3072	673.9986	1345.9827	1345.7354	0.2474	0	7	31	4	R.FASRPLKPSSEK.G	
3129	676.5956	1351.1767	1352.6758	-1.4991	0	3	83	7	R.MTVVFAGENTIR.G	
3148	677.7611	1353.5077	1353.5633	-0.0556	0	3	70	6	R.EGCNTHTGWHR.L	
3177	453.1842	1356.5307	1355.7898	0.7409	2	7	33	3	R.YARSPRPVRVR.W	3179
3221	454.5569	1360.6487	1357.6772	2.9715	1	10	17	7	R.IPAQSSSACGPRK.S	
3259	682.7381	1363.4617	1362.6133	0.8485	1	6	39	9	R.GPMLNGCDTSRR.S	
3273	683.2801	1364.5457	1364.6493	-0.1036	0	5	51	8	R.MLIEVSADTADGK.V	
3280	683.7936	1365.5727	1363.6956	1.8771	2	0	1.4e+02	9	K.LDGSRSAPRSYR.K	
3288	456.4792	1366.4157	1363.7459	2.6698	1	3	67	9	K.SPSITRALGATYK.N	
3294	684.6031	1367.1917	1368.6238	-1.4321	1	3	78	3	R.CSSLRTSCAATR.G	
3336	1371.7670	1370.7597	1371.7299	-0.9702	1	2	1e+02	5	K.YIWKLDELHR.K	
3356	458.4399	1372.2977	1370.6806	1.6172	0	4	69	8	R.WTLCGFVSVFR.G	
3398	459.6409	1375.9007	1374.6926	1.2082	1	2	1e+02	4	K.VMDRIIGGEVDR.A	
3406	689.3421	1376.6697	1375.6402	1.0296	2	1	1.5e+02	3	K.DSPKDRAPMESK.I	
3435	691.2706	1380.5267	1381.6085	-1.0818	0	1	1.3e+02	5	R.GWEWTCTSTVR.R	
3586	700.1756	1398.3367	1398.7440	-0.4072	2	5	51	3	R.GRANASRPAESRK.R	
3637	702.7536	1403.4927	1402.6816	0.8111	1	1	1.3e+02	4	R.CPVWRESVWGK.S	
3706	708.4281	1414.8417	1414.7065	0.1352	1	4	63	3	R.ATSQVHEANRFR.S	
3714	708.7586	1415.5027	1415.7773	-0.2745	1	5	51	9	R.GEIWSTIVEVRK.E	
3805	476.8445	1427.5117	1425.7113	1.8004	1	11	14	1	R.ELARHSSGPGYPR.S	3788

3849	716.5976	1431.1807	1429.7062	1.4745	1	2	1e+02	1	K.DSVNKGWNVGAQR.V	
3897	719.3581	1436.7017	1435.6878	1.0139	1	3	81	9	R.AGWGMSLATERNK.Q	
3971	723.2286	1444.4427	1442.7412	1.7015	2	6	38	4	R.RGTMNLDHIKSR.F	
3993	724.1831	1446.3517	1445.7198	0.6320	1	3	78	6	R.LWNVGCRSIADR.K	
4038	484.5365	1450.5877	1451.7593	-1.1716	2	6	41	4	R.STYRIQTQRGSR.R	
4062	485.5882	1453.7427	1454.7855	-1.0428	1	7	29	3	R.GFQPGSLGAGRPRR.E	
4073	486.0962	1455.2667	1456.6769	-1.4102	1	8	24	4	R.MWVLYSDTDRR.R	4078
4096	730.2456	1458.4767	1456.8362	1.6406	2	15	5.4	1	R.NVGKLSLSRLDGAK.E	4088 4100
4110	730.9926	1459.9707	1458.7263	1.2445	1	2	90	3	R.HPCGRIGQGQPPR.K	
4133	732.2791	1462.5437	1462.7602	-0.2165	1	6	43	10	K.KEPFVQSCVTIR.S	
4158	489.3892	1465.1457	1466.8867	-1.7410	1	2	90	8	R.ARILLCRPVTLR.S	
4163	489.6049	1465.7927	1464.7361	1.0566	0	12	9.2	1	R.SYITHTINPYTR.R	
4179	734.9661	1467.9177	1469.7436	-1.8258	1	2	93	6	R.LLTSMKDYASDVK.C	
4187	490.5599	1468.6577	1466.7109	1.9468	0	17	3.3	1	R.DLLGSMAVTMLER.I	4168
4188	490.7335	1469.1787	1466.8392	2.3396	2	9	20	2	R.RLVIVGDVHGMKK.S	4189
4254	738.7401	1475.4657	1473.6381	1.8276	0	6	44	7	K.SAYCTMVDSWVR.R	4230
4262	739.3061	1476.5977	1477.7963	-1.1986	0	2	1e+02	2	R.LISISPFVTVCSR.E	
4388	747.2191	1492.4237	1489.8253	2.5985	1	2	98	4	R.TGGGKTLNQFNILK.C	
4453	501.5585	1501.6537	1502.7987	-1.1450	2	10	18	8	R.SRSDGLVVMREVR.S	4452
4461	752.0116	1502.0087	1499.7555	2.2532	1	1	1.4e+02	4	K.DCLAVRSLFTYR.G	
4463	501.7009	1502.0807	1503.7715	-1.6908	2	4	68	5	R.DDARLMKGALDTAK.V	
4498	502.8982	1505.6727	1503.8661	1.8067	1	9	22	6	K.LPYTTAVIKETLR.L	
4506	754.3846	1506.7547	1505.7508	1.0039	1	2	91	4	R.NGSIMGVPTSKNASK.R	
4604	760.8101	1519.6057	1518.7937	0.8121	2	(1)	1.3e+02	8	R.SRSDGLVVMREVR.S	
4608	507.6035	1519.7887	1516.7854	3.0033	1	3	84	10	R.GSISPMVRLSPMSR.J	
4697	764.8131	1527.6117	1525.8940	1.7177	2	3	81	9	R.LSQDKTKLKPNVR.F	4681
4766	768.6211	1535.2277	1536.7752	-1.5475	2	9	19	2	R.KMISTVCSDNVKR.G	4771
4858	772.8551	1543.6957	1540.7192	2.9766	0	0	1.6e+02	2	R.SPPGCGPLSPETQSK.Q	
4894	516.1959	1545.5657	1543.8219	1.7438	1	0	1.4e+02	7	R.GQPRYGLSNQGVLR.N	
5028	520.6872	1559.0397	1558.8885	0.1513	2	20	1.5	1	R.WLAFHKIGLYRR.L	
5029	780.5346	1559.0547	1557.6651	1.3897	1	5	57	9	R.CETEIKSMSSGDAK.L	
5126	524.3715	1570.0927	1567.7599	2.3328	1	2	92	3	R.QCQMRLVSVEYR.K	
5337	530.6565	1588.9477	1587.8337	1.1140	2	1	1.2e+02	8	R.LKRCGLAPTSICGR.N	
5383	797.6791	1593.3437	1590.8558	2.4879	1	0	1.4e+02	4	K.TVWVPFAATSAWKK.R	
5437	800.6206	1599.2267	1596.6989	2.5278	1	1	1.2e+02	2	R.GSHGTRSSDHSAAGDR.Y	
5443	534.2212	1599.6417	1600.8468	-1.2050	2	12	9.9	2	K.VVSASPRTCQKNVR.R	5476
5450	534.3632	1600.0677	1598.8603	1.2075	1	9	20	1	R.AIATFHPKMEIGIR.R	
5497	802.3376	1602.6607	1599.8443	2.8165	0	5	46	8	R.IPYLGASAMHLNVAK.V	5429 5463 5477 5490
5546	536.5269	1606.5587	1606.7602	-0.2015	0	8	27	3	R.DWMYAVGPLTPWR.G	
5589	537.6929	1610.0567	1608.7613	1.2954	2	4	67	7	R.DQEMAVAAFRRCR.E	
5649	539.1479	1614.4217	1611.7689	2.6529	1	6	41	4	R.GNVHIGRFCQPDGR.T	

5665	808.7146	1615.4147	1614.8525	0.5622	1	0	1.4e+02	9	R.AHCGQLPRHASLLR.T	
5670	539.5739	1615.6997	1614.7130	0.9867	0	5	47	8	R.AFGQSATVDVMACSR.S	
5694	540.2372	1617.6897	1618.8245	-1.1348	0	6	42	1	R.VSMLIHSCLIMVGK.N	
5748	541.6912	1622.0517	1623.8151	-1.7634	0	4	60	3	R.GVGNQTSPLHCLVSR.H	5783
5778	542.2395	1623.6967	1623.8621	-0.1653	0	4	53	5	R.VYGGQSALVLANFTGK.E	
5894	545.6965	1634.0677	1631.8777	2.1900	2	10	14	2	R.DLLRSRSDGLVVMR.E	5893
6130	826.8116	1651.6087	1650.8035	0.8052	0	13	7.1	2	R.EALMESNNLNIFTR.T	
6249	554.7065	1661.0977	1660.9552	0.1425	0	2	97	7	K.LFLISAVAFSILPDR.H	
6359	835.7736	1669.5327	1669.9291	-0.3963	0	10	13	1	K.EVSWVVPAETISILK.N	
6461	559.5655	1675.6747	1673.8525	1.8222	0	2	89	7	K.NIITGFAHAAEFLDR.A	
6707	565.1749	1692.5027	1692.7638	-0.2611	0	2	83	6	R.ATGHGLEACPDGGAGAPR.G	6708
6735	848.7581	1695.5017	1694.8516	0.6502	0	9	16	3	R.VVSFLASDTAEWVSGK.I	6750
6754	566.6855	1697.0347	1696.8533	0.1815	0	5	46	3	R.GLLSHDPVDQIANYR.D	6770
6782	850.7426	1699.4707	1698.8253	0.6454	0	79	2e-06	1	K.GLLTNPGQDYFAFEK.H	6778
6888	854.1636	1706.3127	1707.7999	-1.4871	0	1	1.1e+02	8	K.ISTIHDPVSMSDNHR.L	
6938	856.5566	1711.0987	1709.8229	1.2758	0	5	42	4	R.IQMPCSASQSVSFIR.V	6937
6939	571.3845	1711.1317	1711.8141	-0.6823	1	2	88	6	R.FPVRFSAGWEMETR.G	
7064	575.5309	1723.5707	1721.7905	1.7802	0	4	60	10	K.NYFSMSAALMTPFSR.G	
7085	863.8211	1725.6277	1722.8505	2.7772	2	6	31	7	R.CESCAKRSGIIISSR.R	
7299	874.8686	1747.7227	1746.8067	0.9160	1	6	40	5	R.TGADGNGSVRMAQSPGSR.S	7300
7352	878.6021	1755.1897	1753.9951	1.1946	2	1	1.2e+02	1	R.AGVELVQKGAVRSWVR.V	
7380	880.2941	1758.5737	1758.8934	-0.3197	1	3	68	4	K.SQIDGQTIQPIRMEK.V	
7397	880.8521	1759.6897	1758.9920	0.6977	0	89	1.8e-07	1	K.VLYLGVSDTPAWLVVK.C	7399
7473	589.6162	1765.8267	1762.8613	2.9654	1	5	45	6	R.RDWMYAVGPLTPWR.G	
7536	886.6126	1771.2107	1769.8474	1.3633	1	6	39	3	R.MRDLLGSMAVTMLER.I	7541
7559	591.9542	1772.8407	1773.8679	-1.0272	1	3	75	10	R.SKNEGTAALELPQTCR.F	
7737	894.2246	1786.4347	1785.9710	0.4637	2	5	51	7	R.QGGVGERRPPAIREHK.Q	
7828	898.6956	1795.3767	1793.8519	1.5248	0	18	2.2	1	K.MGFPEAQGFSNGNLLGR.S	7816 7836
7834	599.6475	1795.9207	1795.9841	-0.0634	1	3	70	2	R.IRCPTLMLVIYVYR.C	
7951	603.5389	1807.5947	1808.0342	-0.4395	2	5	42	4	K.TRTITITFMLAGLKSR.T	
7955	603.8105	1808.4097	1809.8468	-1.4371	0	(5)	45	4	K.MGFPEAQGFSNGNLLGR.S	
7973	906.6056	1811.1967	1811.9790	-0.7823	1	(1)	1.1e+02	1	R.IRCPTLMLVIYVYR.C	
7980	906.7636	1811.5127	1812.9469	-1.4341	0	7	26	4	K.ENIEALGLVLSEEEIR.E	
8055	606.7882	1817.3427	1818.9476	-1.6048	1	5	46	8	K.VYIAELGLDTLRDDAR.L	
8240	614.4069	1840.1987	1840.7832	-0.5845	1	1	1.1e+02	8	K.SDEIPDSYGLNCRCR.S	
8513	624.1812	1869.5217	1870.9982	-1.4764	2	3	76	6	R.KPSPCCIRQTSLRLR.R	
8518	624.2215	1869.6427	1871.0013	-1.3586	1	4	54	7	R.ISPSQSWALARLQGTTR.S	
8977	639.6395	1915.8967	1915.9747	-0.0780	0	1	1.1e+02	8	R.GITLTTMTTMTPVVDAHK.I	
9141	646.7195	1937.1367	1936.9346	0.2021	0	8	24	1	K.SGVNSMAMLSAISATENVR.I	9149
9158	647.7345	1940.1817	1939.0601	1.1216	0	5	44	3	R.LLVLPNMAGLQLNVDWK.S	9150
9175	648.5755	1942.7047	1944.0932	-1.3884	1	3	78	6	K.EDVQLLNKLPYTTAVIK.E	9198

9190	649.1355	1944.3847	1944.1044	0.2803	1	1	1.1e+02	7	K.KIHNTLTTTASFAIVSLK.R	
9243	651.4569	1951.3487	1952.0163	-0.6675	2	1	1.2e+02	9	R.YVEIQDRIHMHSRLR.S	
9355	655.9339	1964.7797	1964.0513	0.7284	0	2	84	4	R.AINTGHLTVMILDPLGQR.F	
9474	661.1162	1980.3267	1980.0754	0.2513	0	2	87	9	R.TASVAFLFPEMTISVVIR.L	
9571	665.0005	1991.9797	1992.8782	-0.8985	1	8	22	2	R.MCSWTEENPSARGIPSR.E	
9665	668.6535	2002.9387	2002.0120	0.9268	1	4	55	3	R.EDASIVGFITASHSLGDRK.T	
9692	669.8185	2006.4337	2005.0541	1.3797	1	2	75	5	R.MQRGQLVIQHHIHHSGK.V	
9760	672.7395	2015.1967	2016.0462	-0.8495	1	14	5.5	2	K.VPVVGSLDYIPRDMGNIR.Y	9761
9763	1008.7861	2015.5577	2016.0752	-0.5175	1	1	1e+02	9	R.SLSGLDSRLTSSLHPPPPR.M	
9793	674.3675	2020.0807	2022.0330	-1.9523	2	1	1.1e+02	9	K.APWSLGCATSAPLRRHSR.H	
9795	1011.2791	2020.5437	2020.0445	0.4992	1	1	1e+02	4	R.LILTLPMSSATRSMDAAAR.A	
9910	678.4462	2032.3167	2034.1150	-1.7983	0	1	97	6	K.QFEGLQGIIEFLIITTGR.L	
9981	680.1329	2037.3767	2036.9951	0.3816	1	7	27	3	K.YLFMELESIYRMSPVK.Q	
10174	686.7552	2057.2437	2059.0586	-1.8149	1	6	30	5	K.GPKETDVSPHLGLQEIDPK.W	10179
10365	694.1735	2079.4987	2077.1069	2.3919	1	6	31	1	R.YSPGSHVHALPRLSLTSQK.V	
10392	1041.7811	2081.5477	2080.0484	1.4994	2	5	40	4	K.ARGDNPMHAGGITSGSAKLPK.G	
10397	695.0242	2082.0507	2081.8920	0.1587	0	3	61	4	K.VHQESNSSSLSGSMTGESSR.S	10388
10548	702.4549	2104.3427	2103.1014	1.2414	1	7	24	7	R.ARDAQLLHLHWADVAYPK.W	
10631	707.0865	2118.2377	2117.8531	0.3846	1	5	43	2	R.FRGSESEMSCPYHSTGDR.L	
10773	1069.9991	2137.9837	2138.8422	-0.8585	0	0	1.2e+02	3	R.YGMPDSSNFFCSNSSPNGR.W	
10811	715.1469	2142.4187	2140.1389	2.2798	2	1	98	7	K.GDVHIASSKIREVAVDFAAR.F	10815
11011	723.8265	2168.4577	2166.1671	2.2906	2	5	44	6	R.YGIVLHHHQNLNKARNPR.H	
11715	758.3255	2271.9547	2271.1834	0.7713	1	3	66	1	K.LFSNVPKAPWSLGCATSAPLR.R	11713
11851	1144.6306	2287.2467	2287.0799	0.1668	0	6	32	1	R.DILPMCESEGMGLAPWGVLGR.G	
11881	765.3182	2292.9327	2294.0348	-1.1020	0	6	32	5	R.GELAMAFQFEIMDIDHGPGGK.F	11889
11923	767.2472	2298.7197	2296.2361	2.4836	1	1	94	8	R.LLVLPNMAGLQLNVDWKSNR.R	
11966	768.8232	2303.4477	2301.2111	2.2367	2	3	64	9	R.TSPRLGSEQSNAIAVLVKCSGK.L	11967
12059	772.2609	2313.7607	2315.0634	-1.3027	1	4	54	5	K.QLMNITCTYSHRSSQTSTGK.T	
12139	776.2692	2325.7857	2323.0824	2.7033	1	0	1.2e+02	8	R.LDGAKEWNIVMLAGMQSGDEK.A	
12560	798.2119	2391.6137	2392.2645	-0.6508	2	1	88	9	R.RTSGVGAGLTRMTVVFAGENTIR.G	
12921	815.2799	2442.8177	2442.3417	0.4761	2	5	42	2	R.SSIRDLIQATLLAWRQISPMK.W	
13151	825.8425	2474.5057	2474.0689	0.4368	0	3	58	3	R.TSNDHDMLIDEAAEASSHISGMK.L	
13166	826.3032	2475.8877	2474.2012	1.6865	1	11	8.7	1	K.SSLTMATQHKTQSSPVNAAWWK.K	13159
13328	833.7749	2498.3027	2496.2357	2.0670	2	3	55	6	R.SGSLQGSDRDWPVSIPPTQARDK.J	
13356	835.0869	2502.2387	2502.1090	0.1298	2	1	86	1	R.FLKAGMSERMCSWTEENPSAR.G	
13417	837.3579	2509.0517	2510.1925	-1.1408	1	3	54	2	K.VPSDDPNEKSTPLAASFSASFSTR.J	
13614	844.8349	2531.4827	2533.2379	-1.7552	2	(1)	1e+02	5	R.EMPARITQMFMDVTSSKFGLTK.T	
13622	845.4382	2533.2927	2533.2379	0.0548	2	2	85	7	R.EMPARITQMFMDVTSSKFGLTK.T	13628
14003	870.3822	2608.1247	2608.4700	-0.3453	2	1	82	6	R.HANITKKIHNTLTTTASFAIVSLK.R	
14052	871.4142	2611.2207	2611.3533	-0.1326	0	7	22	2	R.NTTSSTLIYSYYLLAQHPEVLAK.I	
14217	883.4865	2647.4377	2645.2755	2.1623	1	2	70	1	R.ETASSSYLREALMESNNLNIFTR.T	

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     14249   885.4762  2653.4067  2652.3509   1.0558  0    24      0.49   1   R.IVDASIFPFAIDGQPMGTVYALAEK.I 14246
     14347   889.8975  2666.6707  2668.3458  -1.6751  0   (6)        28   3   R.IVDASIFPFAIDGQPMGTVYALAEK.I 14363
     14389   891.2629  2670.7667  2668.3405   2.4262  1     7        21   1   R.LQTVRFAGHGDTGNGGIGVMRPSWR.J 14391
     14467   895.1245  2682.3517  2684.3354  -1.9837  1   (3)        55   2   R.LQTVRFAGHGDTGNGGIGVMRPSWR.J
     14559   901.2685  2700.7837  2700.2701   0.5136  0     1        85   8   R.QPEPISASDVPLDTENMGNTFAVPR.A
     14933  1394.0221  2786.0297  2783.4184   2.6113  2     4        42   2   K.HCTRGHVVPQVSHSPLISGGRVMTR.R
     15119   950.8082  2849.4027  2848.5142   0.8885  2     0        95   6   K.TTLRDTSSLTDELSRIGALSSAVQVTK.R
     15291   975.9262  2924.7567  2923.3633   1.3934  1     4        42   5   K.AVGFDRGELAMAFQFEIMDIDHGPGGK.F
     15489  1008.3449  3022.0127  3021.6474   0.3654  2     3        50   1   R.DLIQATLLAWRQISPMKWPLSGSVAPK.A
     15873  1065.2952  3192.8637  3193.5114  -0.6476  2     3        46   4   R.GELAMAFQFEIMDIDHGPGGKFSPHKYR.M
     15996  1087.8809  3260.6207  3260.7056  -0.0849  1     0        92   5   R.GYPNMLYTPVPRGLLTPLFAAWPLTAETR.K
     16113  1104.4319  3310.2737  3310.6200  -0.3463  2     1        77   5   R.TNLVCADVGRCALHLGSAKHFQHPPSGEPR.E
     16115  1104.8045  3311.3917  3312.4072  -1.0155  1     1        79   2   R.SLFCFWCDWSRACSYSQLPMLSACHK.Q
     16147  1110.7329  3329.1767  3327.6545   1.5223  2     5        27   2   R.GNVHIGRFCQPDGRTHSGTGTAQLALWHVR.M 16146
     16209  1120.3712  3358.0917  3356.6659   1.4258  2     1        66   1   R.LFHHSMECRGGLDFGEGLLARVQLGWTVR.R
     16259  1131.4672  3391.3797  3388.8006   2.5792  2     1        66   1   R.GYPNMLYTPVPRGLLTPLFAAWPLTAETRK.S
     16306  1142.3982  3424.1727  3424.7934  -0.6207  1     6        22   1   K.GLWPFSTQYPTMSLLKTFYTIFVIITWR.L
     16386  1157.8399  3470.4977  3467.6485   2.8492  0     8        15   1   R.VYSWSIMNSMIFSSMEIVDVMLSIVEAASGR.F
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87.   gi|220690378|gb|EED46728.1|    Mass: 53164    Score: 292    Queries matched: 16    emPAI: 0.52
      glutamate carboxypeptidase, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
       579   459.7451   917.4757   918.5651  -1.0894  1     7        48   3   K.VIGKFSIR.T
      2469   639.7816  1277.5487  1277.6074  -0.0587  0    26      0.42   1   K.QVFGVEPDMTR.E
      3259   682.7381  1363.4617  1362.6779   0.7838  0    79   1.8e-06   1   K.QVDGLAESFIER.L 3271
      3772   713.1076  1424.2007  1424.7048  -0.5041  0     7        28   6   K.NTLDVWLQHDGK.W
      5284   529.2199  1584.6377  1583.8267   0.8110  1     9        20   1   K.AVAIPSVSAQDENRK.D
      7032   861.3981  1720.7817  1719.8679   0.9138  0    45    0.0043   1   R.EGGSIPVTLSFEQATGK.N
      9010   640.7325  1919.1757  1916.9632   2.2125  0    30      0.13   1   R.YPSLSLHGIEGAYSAPGAK.T
     10495  1049.7551  2097.4957  2096.0572   1.4385  0   102   9.1e-09   1   K.NVLLLPMGSSTDAAHSINEK.L
     10601   705.0895  2112.2467  2112.0521   0.1946  0  (15)         4   1   K.NVLLLPMGSSTDAAHSINEK.L
     11618   752.4715  2254.3927  2252.0783   2.3144  0    33     0.071   1   K.ALYPNISYTMDDLHQSLGSK.T 11601 11603 11617
     13306   832.6205  2494.8397  2494.3002   0.5395  0    65   4.1e-05   1   R.MAQFLASELEALGAEVHQRPLGK.Q 13314
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88.   gi|220690692|gb|EED47041.1|    Mass: 29383    Score: 289    Queries matched: 33    emPAI: 1.12
      40S ribosomal protein S3, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
        91   714.5520   713.5447   713.4436   0.1012  0    14       6.8   1   R.QGVLGIK.V
       613   466.3231   930.6317   930.5386   0.0931  0    31      0.17   1   R.ELTSLIQK.R 615
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632	470.2471	938.4797	937.4505	1.0292	0	27	0.26	1	K.EFIDSATR.H 628 629 630
841	495.5471	989.0797	990.5168	-1.4371	0	9	23	5	-.MAAVQGAISK.R 844
2050	614.8086	1227.6027	1226.7234	0.8793	0	29	0.2	1	R.VTPTVTDIIIR.A
2515	642.8956	1283.7767	1283.6582	0.1186	0	85	5.2e-07	1	K.AIAAQQAAEQQR.L
2688	652.2036	1302.3927	1302.7190	-0.3263	2	0	1.6e+02	6	-.MAAVQGAISKRR.K
2769	657.5946	1313.1747	1311.7286	1.4461	0	13	7.5	1	K.TLPDSVTIIEPK.E 2758
2873	663.8056	1325.5967	1324.6663	0.9304	0	56	0.00041	1	K.FPENSVSLYAAK.V 2876
3776	713.3751	1424.7357	1424.7008	0.0349	0	55	0.00042	1	R.ATHTQEVLGEQGR.R 3784
3900	719.4671	1436.9197	1436.6783	0.2414	0	33	0.084	1	R.ELAEEGYSGVEVR.V 3896 3897 3904 3905 3912
4764	768.5621	1535.1097	1534.7239	0.3859	0	37	0.028	1	K.FTDGFMIHSGQPAK.E 4763
5123	785.7576	1569.5007	1569.7933	-0.2926	2	8	24	4	K.IMRGSDPEGKAGPQK.T
5464	801.3546	1600.6947	1599.8297	0.8651	1	55	0.00053	1	R.FKFPENSVSLYAAK.V 5444 5467 5471
10125	1026.8516	2051.6887	2050.9789	0.7098	0	2	78	1	K.FVADGVFYAELNEFFQR.E
10347	693.5249	2077.5527	2078.0691	-0.5164	2	3	65	2	K.VQNRGLSAVAQCESLRYK.L

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89. gi|220700805|gb|EED57143.1| **Mass:** 58365 **Score:** 287 **Queries matched:** 23 **emPAI:** 0.32

acetyl-coA hydrolase Ach1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
259	408.4841	814.9537	813.4457	1.5080	1	10	18	5	R.GLSPRER.A 257
817	493.8641	985.7137	985.4651	0.2486	0	10	17	7	K.MHQNLAEK.G 820
1912	602.8091	1203.6037	1203.6182	-0.0145	1	2	1.2e+02	10	R.WARLNMIER.R
2692	652.2681	1302.5217	1301.6980	0.8238	0	29	0.22	1	R.IGTPHIPVDPEK.V 2676
3091	450.3429	1348.0067	1349.6762	-1.6694	0	7	30	2	R.MLNGLGGSADFLR.S 3093
3123	676.3916	1350.7687	1348.7575	2.0112	2	4	59	2	R.RSPHQVGKEIAK.G 3088
3181	679.5276	1357.0407	1356.6997	0.3410	0	66	4.3e-05	1	R.SQQVSNSPEIIR.R
4700	510.3142	1527.9207	1526.8569	1.0639	1	8	22	3	R.RKPYLILQPEDR.I
12584	800.1282	2397.3627	2395.2035	2.1593	0	57	0.00023	1	K.HLSMFPSDLVYGWYTLNKPK.N 12568 12588
13259	1245.0406	2488.0667	2486.4220	1.6447	0	89	1.4e-07	1	R.LPQNLLPIQSGIGNIANAVIGGLSK.G 13257 13266 13267 132
16123	1106.2262	3315.6567	3313.6812	1.9755	2	4	38	3	K.LAKAEDLIEFFPHGSYIGWSGFTGVGYPKK.V
16300	1141.8959	3422.6657	3422.7491	-0.0833	0	1	72	6	R.LDVAVIEASAITEDGGIIPGASVGASPELVQMADK.V

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90. gi|220701506|gb|EED57844.1| **Mass:** 52230 **Score:** 282 **Queries matched:** 30 **emPAI:** 0.44

serine hydroxymethyltransferase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
548	912.9320	911.9247	911.3695	0.5552	0	1	1.1e+02	7	R.GMGEEDFK.R
702	482.5226	963.0307	962.4709	0.5598	0	20	1.9	1	K.QVDTPEFK.Q 703
2928	444.2385	1329.6937	1326.7772	2.9166	2	2	1e+02	10	K.RIAHYIDKAIK.I
2954	667.5561	1333.0977	1332.6786	0.4191	0	5	58	6	K.QYQQQVLNNAK.A
3619	701.7361	1401.4577	1400.7340	0.7237	0	9	19	1	K.EIAAWASTFPLPV.- 3628

3855	716.7251	1431.4357	1430.7617	0.6741	0	63	8.4e-05	1	K.VASETVSDILELR.K
5463	801.2826	1600.5507	1599.8290	0.7217	0	13	7.5	2	R.VEAVLEQINIACNK.N 5470
6510	841.1291	1680.2437	1679.8195	0.4242	0	79	1.8e-06	1	K.ISAVSTYFETFPYR.V 6506 6534 6572
6838	852.2506	1702.4867	1701.8495	0.6373	0	61	0.00011	1	K.TLVESDPEIAQIMEK.E 6835
7016	860.2046	1718.3947	1717.8444	0.5503	0	(60)	0.00015	1	K.TLVESDPEIAQIMEK.E 7012
9493	992.2211	1982.4277	1981.9350	0.4928	2	4	54	3	R.IGAPAMTTRGMGEEDFKR.I 9487 9494
11634	753.6309	2257.8707	2256.1222	1.7485	0	(3)	66	1	R.LMGLDLPHGGHLSHGYQTPAR.K
11737	759.3292	2274.9657	2272.1171	2.8486	0	25	0.43	1	R.LMGLDLPHGGHLSHGYQTPAR.K
13995	869.6545	2605.9417	2606.3227	-0.3810	0	32	0.065	1	R.VNLETGIIDYDALEANAELYRPK.C 14001 14002 14007 14008
14834	922.7262	2765.1567	2765.3299	-0.1732	2	2	73	8	K.SALTPCGIRIGAPAMTTRGMGEEDFK.R 14835

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91. gi|220697596|gb|EED53937.1| **Mass:** 14407 **Score:** 273 **Queries matched:** 10 **emPAI:** 0.89

ubiquinol-cytochrome c reductase complex 14 kDa protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
687	480.5211	959.0277	958.5335	0.4942	0	59	0.00027	1	R.ADLDSLVVK.R 688
2158	623.1881	1244.3617	1243.6772	0.6845	1	5	57	2	K.ERADLDSLVVK.R
8415	929.3481	1856.6817	1855.9415	0.7403	0	84	6.1e-07	1	K.ADDLIPEESEVVQTAIK.R 8414
9196	973.8201	1945.6257	1944.8651	0.7606	0	80	1.3e-06	1	R.WMMPIANWYTDAAGYR.R 9197
9344	982.7986	1963.5827	1960.8600	2.7227	0	(14)	5	2	R.WMMPIANWYTDAAGYR.R 9340
11709	758.1139	2271.3197	2273.0622	-1.7425	2	4	50	2	K.RWMMPIANWYTDAAGYRR.L

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92. gi|220699315|gb|EED55654.1| **Mass:** 33949 **Score:** 262 **Queries matched:** 14 **emPAI:** 0.45

60S ribosomal protein L15, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2236	627.7271	1253.4397	1253.6339	-0.1942	0	22	0.87	1	R.INWICNAVHK.V 2233 2249
3658	470.1829	1407.5267	1407.8099	-0.2832	2	2	93	10	K.QGYVVYRIRVR.R
4360	745.3891	1488.7637	1486.7820	1.9817	0	31	0.14	1	K.YFEVILVDPQHK.A 4349
6094	550.6922	1649.0547	1649.7872	-0.7324	1	11	13	2	K.TRFYDYILEMGAR.I 6093
6658	845.4381	1688.8617	1688.8846	-0.0228	0	81	1.1e-06	1	K.GATYGKPTNQGINQLK.Y 6665
7121	866.2731	1730.5317	1729.8311	0.7006	0	88	2.3e-07	1	R.VLNSYWINQDSTYK.Y 7108 7127
8843	952.0456	1902.0767	1900.9854	1.0913	1	0	1.4e+02	1	R.LAAATPGSSTTPRATGDTVK.R

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93. gi|220699334|gb|EED55673.1| **Mass:** 28662 **Score:** 260 **Queries matched:** 26 **emPAI:** 0.93

Ribosomal L18ae protein family [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
562	457.9776	913.9407	913.5385	0.4022	0	60	0.00017	1	R.FGSIHILK.V 564
1149	530.6971	1059.3797	1058.6124	0.7673	0	38	0.032	1	R.IFAPNTVVAK.S 1142 1147 1156
1248	540.5811	1079.1477	1077.5818	1.5659	0	78	2.8e-06	1	R.LTEYQVIGR.H 1233 1241 1242 1243
1912	602.8091	1203.6037	1203.6248	-0.0210	0	42	0.011	1	R.HLPTEANPTPK.L 1917

1994	609.6351	1217.2557	1215.6095	1.6462	0	77	3.3e-06	1	K.VVEVDNADSIR.R 1983 1986 1991
2424	638.2766	1274.5387	1272.6655	1.8732	0	21	1.4	2	R.FWYFLTQLR.K 2400 2425
3240	681.7616	1361.5087	1361.7489	-0.2402	1	3	80	5	R.MRIFAPNTVVAK.S
4240	738.5156	1475.0167	1473.6307	1.3861	1	4	66	1	R.YDSRSGTHNMYK.E
4327	743.3076	1484.6007	1481.8089	2.7918	0	6	43	1	K.ANGEIVSLNVIPEK.R
5248	528.1865	1581.5377	1582.7297	-1.1920	0	7	28	2	R.TEAVEALYQDMAAR.H
6131	826.8116	1651.6087	1652.8787	-1.2700	2	0	1.3e+02	3	K.VKNFGIWIRYDSR.S
8234	614.1739	1839.4997	1837.0673	2.4325	2	8	21	8	K.VKKANGEIVSLNVIPEK.R

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94. gi|220692437|gb|EED48784.1| **Mass:** 54626 **Score:** 258 **Queries matched:** 21 **emPAI:** 0.42

hexokinase Kxk, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
526	454.6286	907.2427	906.4811	0.7617	0	28	0.25	1	K.YDIIIDR.D
2002	1219.5550	1218.5477	1217.6074	0.9403	0	(17)	3.6	1	K.ATQQELEMIR.R
2087	618.1966	1234.3787	1233.6023	0.7764	0	37	0.037	1	K.ATQQELEMIR.R
2527	643.5826	1285.1507	1284.6462	0.5045	1	6	36	4	K.GAFDITQSKYR.M
3489	694.8071	1387.5997	1385.7013	1.8984	0	29	0.22	1	K.MTAGLYLGEIFR.L
6609	843.7926	1685.5707	1685.9134	-0.3427	1	(2)	92	10	K.LNIKATQQELEMIR.R 6630
6865	853.1851	1704.3557	1701.9083	2.4474	1	3	79	8	K.LNIKATQQELEMIR.R
11036	724.7319	2171.1737	2169.2079	1.9659	0	1	1.2e+02	6	K.VVIMAAEDGSGVGAALIAALTLK.R
11323	1106.5436	2211.0727	2210.1471	0.9256	0	64	4.9e-05	1	K.GFDIDGVEGQDVVPPLEAILK.K 11331
11575	750.4735	2248.3987	2247.1284	1.2704	1	6	32	9	K.YDIIIDRDSPRPGQQAFEK.M
12122	775.4849	2323.4327	2325.3090	-1.8762	1	10	12	1	K.VVIMAAEDGSGVGAALIAALTLKR.V 12127
13838	857.2332	2568.6777	2568.4673	0.2105	2	1	92	2	K.VVIMAAEDGSGVGAALIAALTLKRVK.A
13930	863.2615	2586.7627	2584.4258	2.3369	2	1	81	5	K.DKVVIMAAEDGSGVGAALIAALTLKR.V
14243	885.2109	2652.6107	2651.3384	1.2723	0	73	6.4e-06	1	K.LPLGFTFSYPATQEYIDHGVLQR.W 14252
14547	900.3149	2697.9227	2696.4861	1.4366	0	78	1.7e-06	1	R.LALLDLLETRPGLIFQGQDTSQLR.K 14549
15812	1052.3135	3153.9187	3152.5311	1.3876	0	24	0.34	1	K.NLPPDMPVAINCEYGAFDNEHVVLPLTK.Y

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95. gi|220699731|gb|EED56070.1| **Mass:** 23272 **Score:** 257 **Queries matched:** 20 **emPAI:** 0.96

Mn superoxide dismutase MnSOD [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
216	789.4940	788.4867	788.4644	0.0224	0	33	0.12	1	K.LEIVSTK.D 214 222
835	495.1251	988.2357	986.5396	1.6961	0	26	0.45	1	K.NGVEGSALLK.L 825 828 833
1108	527.1006	1052.1867	1051.5338	0.6529	0	43	0.0085	1	K.ASYVEGIWK.V 1115
2344	633.7166	1265.4187	1264.6299	0.7888	0	88	2.5e-07	1	K.AAIEAQYGSVEK.F 2331 2340 2341
5643	807.8811	1613.7477	1612.7899	0.9578	0	2	87	3	K.FNGGGHINHSLFWK.N
8405	619.6589	1855.9547	1853.9689	1.9858	1	2	95	5	K.IKFNGGGHINHSLFWK.N
10423	1044.3191	2086.6237	2085.0854	1.5383	0	62	7.7e-05	1	K.NLAPHASPETNIDQAAPVLK.A 10413 10418 10420 10422

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96. gi|220693932|gb|EED50277.1| **Mass:** 56506 **Score:** 257 **Queries matched:** 28 **emPAI:** 0.33

UTP-glucose-1-phosphate uridylyltransferase Ugp1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
86	704.5610	703.5537	701.4072	2.1465	0	8	36	5	K.SVIEVR.E
273	410.5556	819.0967	818.4763	0.6205	0	12	13	1	K.HIPSIPR.I
923	506.0506	1010.0867	1009.6172	0.4696	0	46	0.0042	1	R.LLEIAQVPK.E 925
1092	525.3256	1048.6367	1047.5634	1.0733	0	27	0.36	1	K.TCSDLLLVK.S 1087 1090 1091
2114	619.6586	1237.3027	1236.7554	0.5474	1	5	48	3	K.ARLLEIAQVPK.E
4148	488.9002	1463.6787	1464.7460	-1.0673	1	5	47	5	K.ADVKGGTIIDYEGK.A
4154	733.2316	1464.4487	1462.6909	1.7579	0	4	60	1	K.LNGGLGTSMGCVGPK.S
5031	780.7331	1559.4517	1557.7398	1.7119	0	51	0.0014	1	K.YFNTNNIWMSLR.A 5018
5909	818.7666	1635.5187	1635.7392	-0.2204	0	(1)	1.2e+02	5	R.FEAEMDNFFALFR.R
6128	826.7936	1651.5727	1651.7341	-0.1613	0	15	4.5	1	R.FEAEMDNFFALFR.R
7762	597.3822	1789.1247	1788.0332	1.0916	2	1	1.1e+02	8	R.RFLPVKTCSDLLLVK.S
7800	897.3716	1792.7287	1791.8403	0.8885	1	3	76	8	K.RFEAEMDNFFALFR.R
8083	607.6825	1820.0257	1820.0156	0.0101	0	6	34	6	R.IVELDHLTITGAVNLGR.N 8089
8326	925.6796	1849.3447	1848.8981	0.4466	1	3	62	4	K.FKYFNTNNIWMSLR.A
9017	641.1762	1920.5067	1918.9650	1.5418	1	19	1.7	1	K.KYQGHNVDILTFNQSR.Y
10440	1045.9436	2089.8727	2089.0804	0.7924	1	114	5.4e-10	1	K.KGDADQAIYQLETAVGAAIR.H 10446 10448
10962	721.8565	2162.5477	2161.1142	1.4335	2	8	21	8	K.FKYFNTNNIWMSLRAIK.R
12137	776.1942	2325.5607	2326.0708	-0.5101	0	2	77	5	R.ILQHMVDTESEYIMELTDK.T
15207	958.8519	2873.5337	2871.4113	2.1224	0	3	50	1	R.TFNVNVPFVLMNSFNTDQDTQSIIK.K
15986	1085.9675	3254.8807	3254.4833	0.3974	0	14	3.7	1	K.SFDAPLQDWYPPGHGDVFESLYNSGTLDK.L

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97. gi|220692491|gb|EED48837.1| **Mass:** 205077 **Score:** 257 **Queries matched:** 58 **emPAI:** 0.10

fatty acid synthase alpha subunit FasA [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
38	672.4050	671.3977	669.3810	2.0168	0	14	7.8	4	R.VVAEPR.A 41
225	791.5420	790.5347	789.3868	1.1479	0	14	7	1	R.IGSEADAK.A
278	412.8446	823.6747	825.4821	-1.8073	1	6	37	4	K.RVVAEPR.A
381	430.1201	858.2257	859.3923	-1.1666	0	19	2.6	6	K.TGEPVDDK.D
395	432.7376	863.4607	863.4899	-0.0291	1	9	22	6	K.SLMTKLR.T
661	477.3661	952.7177	953.5004	-0.7827	1	9	19	7	R.YLKMDLR.A
807	492.7546	983.4947	983.5076	-0.0129	0	10	13	1	K.YLYAALDR.T
909	502.8981	1003.7817	1003.5121	0.2697	0	16	4.3	1	R.EIVSQCIR.I
972	512.1531	1022.2917	1022.5185	-0.2268	0	26	0.4	1	K.VFLNPDYR.V 977
995	515.9291	1029.8437	1028.5906	1.2531	0	9	23	1	K.FPSPLLDIK.Y 993
1130	1057.2290	1056.2217	1054.5883	1.6334	1	0	1.5e+02	10	K.QDSRIAPLR.G

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     1162    532.6421  1063.2697  1061.5254   1.7443  0     7        33   5   K.AASPQASFAGR.W
     1298    544.7511  1087.4877  1086.5822   0.9056  0    22       1.2   2   K.YILEHSGIR.L 1299
     1708    581.2081  1160.4017  1161.5965  -1.1947  0    40      0.02   1   K.MPGGFNITAVR.K
     1795    589.8866  1177.7587  1179.5441  -1.7854  0    13       9.1  10   R.TDIMETSDIR.Q 1806
     2945    666.6601  1331.3057  1331.6391  -0.3334  0    28      0.26   1   K.ELGEQLIENCK.E
     3033    671.7071  1341.3997  1340.7089   0.6909  0     7        35   2   R.LVAGQVPTGWDAK.R
     3145    677.6256  1353.2367  1352.7412   0.4955  0    40     0.013   1   R.SVPAPGQGVLTTAR.E 3148
     4802    770.4031  1538.7917  1539.7893  -0.9976  0     1   1.2e+02   7   K.DVAIPTGPQTTVDAR.G
     4961    777.0546  1552.0947  1553.6780  -1.5833  0     8        21   5   K.QMAEGGPISEYSNR.A
     6426    558.8552  1673.5437  1670.8774   2.6663  1     8        21   3   R.IVEIGPADTLGGMARR.T
     6696    846.9241  1691.8337  1690.8025   1.0312  0    57   0.00031   1   R.QDALSMYYDIIFGR.L 6713
     6892    854.5736  1707.1327  1708.9108  -1.7780  1     1   1.2e+02   2   R.QVVESLAKAHAVENSK.V
     6949    571.5562  1711.6467  1712.9131  -1.2664  0     5        48   2   R.QDGVLLLALTMEPASR.I 6961
     7597    888.9276  1775.8407  1772.9210   2.9197  0     2        92   1   K.VVVVTGFAEVGPWGNSR.T
     7974    604.7735  1811.2987  1810.8638   0.4349  1     2        87   5   R.QEKDAQFSLGNNFWK.Q
     8552    625.3582  1873.0527  1872.9217   0.1310  1     4        50  10   R.TLASKYEAYDAATSVQR.Q 8559
     8711    630.4502  1888.3287  1889.0556  -0.7269  2     0   1.4e+02   3   K.QQLEIIARYLKMDLR.A
     9421    659.1082  1974.3027  1975.9826  -1.6798  1     4        49   4   R.QDALSMYYDIIFGRLR.V
     9891    677.2719  2028.7937  2030.0698  -1.2761  1     7        23   1   K.VVVVTGFAEVGPWGNSRTR.W 9900 9907
    10427   1044.7756  2087.5367  2088.0456  -0.5089  1     1   1.1e+02   1   R.GTGLMGGNNMVAEGVEKLGVR.T
    11404    741.4625  2221.3657  2222.0889  -0.7231  1     5        37   4   R.GETYQLAKELGEQLIENCK.E
    11735    759.3235  2274.9487  2275.2114  -0.2626  1     5        40   3   K.AFSVTSFGFGQKGAQVIGIHPK.Y 11730
    12408    791.4452  2371.3137  2370.2577   1.0560  0    78     2e-06   1   K.NVLMTGAGAGSIGAEVLQGLISGGAK.V 12413
    12518    796.6485  2386.9237  2386.2526   0.6711  0  (50)    0.0013   1   K.NVLMTGAGAGSIGAEVLQGLISGGAK.V 12521 12525 12526
    13124    824.6832  2471.0277  2472.1597  -1.1320  2     3        63  10   R.ALSMNENQIMPPENGNGKRSNR.S 13135
    13691    850.0829  2547.2267  2546.2952   0.9315  1     4        50   1   K.GMVNLDKVVVVTGFAEVGPWGNSR.T
    14988    935.8599  2804.5577  2802.3825   2.1752  0     2        74   2   R.GALATWGLTVDDIGVASFHGTSTVANDK.N
    15551   1016.3752  3046.1037  3046.4865  -0.3828  2     3        48   3   K.YVHLSEVGNCIGSGIGGTHALRGMYKDR.Y
    15970   1083.4942  3247.4607  3245.5669   1.8938  0     1        68   2   R.ALQAQIDLWQAEHGDFYASGIEPSFDPLK.A
    16194   1118.7202  3353.1387  3354.5649  -1.4262  1     0        79   5   R.SNPLLLDFMQYHIDNCPTDRGETYQLAK.E
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98.   gi|220699092|gb|EED55431.1|      Mass: 55140     Score: 257     Queries matched: 24    emPAI: 0.50
      NADH-ubiquinone oxidoreductase, subunit F, putative [Aspergillus flavus NRRL3357]
     Query   Observed    Mr(expt)   Mr(calc)    Delta Miss Score    Expect Rank  Peptide
        60   684.6450    683.6377   684.3126  -0.6749  0     3        59   7   R.HCGGVR.G
        72   690.5210    689.5137   689.3708   0.1429  0    11        18   6   K.STDIVR.A 73
      1361   551.1846   1100.3547  1100.5040  -0.1492  0    12        13   1   R.GASWFSSFGR.E
      1510   563.7046   1125.3947  1125.5931  -0.1983  0    30      0.15   1   R.HFRPELEAK.I
      2253   629.2391   1256.4637  1256.6051  -0.1413  1     1   1.4e+02   8   R.RGASWFSSFGR.E
      3099   675.2921   1348.5697  1347.7034   0.8663  0    72   9.6e-06   1   R.AINEAYEAGLIGK.N
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3319	685.9826	1369.9507	1369.6812	0.2695	0	6	46	3	R.AMNANAAYIYIR.G
4025	725.6956	1449.3767	1448.7048	0.6719	0	52	0.0011	1	R.GEFYHEATVLQR.A 4038
4499	754.0776	1506.1407	1503.7603	2.3805	1	3	79	3	R.EREIDMLQELTK.Q
4503	754.2261	1506.4377	1506.7249	-0.2872	1	5	51	5	R.EGSKWTQQIMQR.M 4493
6144	827.1736	1652.3327	1650.7559	1.5768	0	3	78	9	R.YLVVNADEGEPGTCK.D
10359	1040.3516	2078.6887	2077.1208	1.5679	0	40	0.011	1	R.GGWDNLLAVIPGGSSTPVIPK.S 10360
10721	1066.0211	2130.0277	2128.9657	1.0621	0	86	3.2e-07	1	R.GMGAYVCGEETSLIESIEGK.A 10722
11893	765.9392	2294.7957	2293.1042	1.6915	2	(0)	1.2e+02	8	R.METGQAREREIDMLQELTK.Q
11896	766.0475	2295.1207	2293.1042	2.0165	2	6	32	5	R.METGQAREREIDMLQELTK.Q
13830	856.7945	2567.3617	2565.3162	2.0455	0	25	0.36	1	K.QVEGHTICALGEAFAWPIQGLIR.H
16224	1124.7312	3371.1717	3369.7829	1.3888	0	38	0.014	1	R.LKPPFPAAVGLFGCPSTVTNVETVAVTPTIMR.R 16226
16250	1129.8895	3386.6467	3385.7778	0.8689	0	(17)	1.9	1	R.LKPPFPAAVGLFGCPSTVTNVETVAVTPTIMR.R

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99. gi|220692461|gb|EED48808.1| **Mass:** 56705 **Score:** 248 **Queries matched:** 23 **emPAI:** 0.66

protein disulfide isomerase Pdi1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
54	683.3780	682.3707	682.4377	-0.0670	0	10	10	4	K.NIPLVK.V 53
1544	565.9746	1129.9347	1129.6343	0.3004	0	4	82	1	K.GSINIVTIDAK.L
1590	568.6766	1135.3387	1134.5921	0.7466	0	43	0.0082	1	R.TVEDLANFVK.E
1926	603.8866	1205.7587	1205.5928	0.1659	0	53	0.00076	1	R.DQGVEGYPTLK.I 1933
2323	632.7161	1263.4177	1261.6343	1.7834	0	42	0.0099	1	K.FPAFAIQDPEK.N
2423	638.2361	1274.4577	1273.6779	0.7799	0	31	0.13	1	R.GLDAVKPYQGAR.Q 2419
6472	839.4046	1676.7947	1677.8686	-1.0739	2	3	66	3	K.ENGKHKVDALEVDPK.K
6671	846.0321	1690.0497	1689.9315	0.1183	1	11	12	3	K.IFRGLDAVKPYQGAR.Q
7276	873.6186	1745.2227	1744.9247	0.2980	1	82	9.7e-07	1	K.FIQDVLDDKVEPSIK.S 7293 7297
9146	970.1611	1938.3077	1936.9418	1.3659	0	37	0.028	1	K.ATYDGEIEQDALLSWVK.T 9147
9243	651.4569	1951.3487	1950.0309	1.3178	0	4	63	3	K.QSLPAVSPVTPENLEEIK.T
11382	739.8375	2216.4907	2214.9979	1.4928	0	42	0.008	1	K.EHDLVLAEFFAPWCGHCK.A 11368 11387
15026	941.4882	2821.4427	2820.3251	1.1176	1	58	0.00017	1	K.DLVLDNEKDVLLEFYAPWCGHCK.A
15932	1073.8885	3218.6437	3215.6635	2.9802	1	1	77	1	R.QTEAIVSYMVKQSLPAVSPVTPENLEEIK.T
16324	1144.7462	3431.2167	3429.7595	1.4572	0	6	23	1	K.TASTPLVGELGPETYSGYITAGIPLAYIFAETK.E

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100. gi|220693825|gb|EED50170.1| **Mass:** 43780 **Score:** 246 **Queries matched:** 16 **emPAI:** 0.24

GTP-binding protein YchF [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
403	865.5160	864.5087	864.4011	0.1076	0	15	5	1	R.GGQSLEMK.K 404
2068	616.4051	1230.7957	1231.6958	-0.9001	1	3	93	2	K.SALPKVITTMR.T
3845	716.4311	1430.8477	1428.7824	2.0653	1	15	5.7	1	R.DLDIISEELRVK.D
7674	892.2816	1782.5487	1782.8822	-0.3334	2	5	46	5	R.EYGDEAAVKAAGKVMTK.G

7719	596.0702	1785.1887	1786.0135	-0.8247	2	2	92	3	K.NLNTKSALPKVITTMR.T
8058	909.7796	1817.5447	1816.9683	0.5764	0	105	5e-09	1	K.SQVPANLTVYDIAGLTR.G 8050 8054 8057 8062 8066
8162	915.7941	1829.5737	1827.9003	1.6734	0	84	5.7e-07	1	R.TSLNLASFFTTGADEVR.Q 8154
9123	968.7556	1935.4967	1934.8833	0.6135	0	53	0.00065	1	K.NSPGDPIIPFSACFEER.L
11071	726.4999	2176.4777	2175.0232	1.4545	0	2	85	6	K.SNLGNPANFPYATIDPEEAR.V

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101. gi|220698459|gb|EED54799.1| **Mass:** 32383 **Score:** 243 **Queries matched:** 27 **emPAI:** 0.98
40S ribosomal protein S0 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
31	656.3770	655.3697	655.4381	-0.0683	0	17	2.2	2	K.ILLAAR.I 32
595	463.8621	925.7097	925.5597	0.1501	0	37	0.025	1	R.LIIVTDPR.T 606
3445	692.1416	1382.2687	1381.7678	0.5010	0	18	2.3	1	K.TRPDGVNVINIGK.T
3823	715.8146	1429.6147	1429.6990	-0.0843	0	49	0.0021	1	R.FTPGNFTNYITR.S 3854 3863 3864
4179	734.9661	1467.9177	1467.7809	0.1368	0	1	1.3e+02	8	R.HSIGLVWWMLAR.E
6787	567.6119	1699.8137	1696.8984	2.9153	1	12	10	1	K.GRHSIGLVWWMLAR.E 6752
6865	853.1851	1704.3557	1702.7533	1.6024	1	47	0.0029	1	R.DPEAEENKEIADESK.V 6851
7813	898.0391	1794.0637	1791.8944	2.1693	1	2	86	2	R.FTPGNFTNYITRSFK.E 7805
8174	916.7716	1831.5287	1830.8465	0.6823	0	63	7.3e-05	1	R.ETEWDVVPDLYFYR.D 8173
9045	642.7072	1925.0997	1926.0323	-0.9326	1	2	78	8	K.TRPDGVNVINIGKTWEK.I 9038
15894	1068.3385	3201.9937	3200.6288	1.3649	0	29	0.13	1	M.APSQLPPIFNPTQQDIEQLLAAQCHLGSK.N 15891 15892 15896
16241	1127.6335	3379.8787	3377.6337	2.2450	0	48	0.0013	1	K.EASYVNIPVLALCDTDSPTDFVDVAIPTNNK.G 16236 16238

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102. gi|220698200|gb|EED54540.1| **Mass:** 39044 **Score:** 243 **Queries matched:** 15 **emPAI:** 0.50
spermidine synthase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1484	561.5856	1121.1567	1120.6029	0.5538	0	41	0.014	1	R.ASFVLPNFAR.K 1487
1950	606.4181	1210.8217	1210.7034	0.1183	0	72	9.7e-06	1	K.VLVIGGGDGGVLR.E 1952 1956 1958
2857	441.9845	1322.9317	1324.6960	-1.7642	2	8	25	7	K.DANRNVREPVR.S
4581	759.4236	1516.8327	1514.8126	2.0201	1	63	7.5e-05	1	K.KAILCDIDEAVIR.V 4569
4898	774.1546	1546.2947	1544.7260	1.5688	0	36	0.039	1	K.THPTIQDGWFSEK.S 4859 4887 4901
6296	833.0161	1664.0177	1665.9778	-1.9601	1	1	1.2e+02	3	K.VLVIGGGDGGVLREVVK.H
16369	1153.6715	3457.9927	3455.6773	2.3155	0	58	0.00015	1	K.NEFDVIITDSSDPEGPAESLFQKPYFELLR.D

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103. gi|220700955|gb|EED57293.1| **Mass:** 14138 **Score:** 239 **Queries matched:** 16 **emPAI:** 3.55
60S ribosomal protein L22, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
125	736.2080	735.2007	735.3915	-0.1908	0	11	13	3	K.GVYELR.F
895	501.6046	1001.1947	1000.5553	0.6394	0	46	0.0046	1	K.VVISQVGDGK.I 889 890 897
1198	535.5691	1069.1237	1068.5491	0.5746	0	46	0.0038	1	K.IFDLSAFEK.F 1192 1194 1199

2709	**653.8121**	**1305.6097**	**1305.6565**	**-0.0468**	**0**	**56**	**0.00039**	**1**	**K.FTINASQPVSDK.I** 2720
3038	**671.8121**	**1341.6097**	**1339.7248**	**1.8849**	**0**	**49**	**0.0019**	**1**	**K.IEVVSHIPFSGR.Y** 3015 3023 3026
12132	776.0495	2325.1267	2322.2696	2.8571	1	3	75	2	K.VVISQVGDGKIEVVSHIPFSGR.Y

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104. gi|220698263|gb|EED54603.1| **Mass:** 99949 **Score:** 235 **Queries matched:** 36 **emPAI:** 0.17
glycogen phosphorylase GlpV/Gph1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1403	554.7316	1107.4487	1106.5390	0.9098	2	8	28	7	K.SMSPEERKK.V
1443	558.6411	1115.2677	1114.4931	0.7746	0	12	11	2	K.ASSGEFDFQK.F
1882	599.5156	1197.0167	1196.6401	0.3766	0	8	24	7	K.SVEASIPEPLR.E 1886
2738	**655.5111**	**1309.0077**	**1307.6213**	**1.3864**	**0**	**23**	**0.86**	**2**	**R.ALDNAMLNVGMK.D**
2868	663.5951	1325.1757	1324.7027	0.4730	0	68	2.8e-05	1	K.VIFIQDYNVSK.A
4187	490.5599	1468.6577	1468.7231	-0.0654	1	10	16	7	R.YLTIKSMSPEER.K
4930	776.0496	1550.0847	1548.8381	1.2466	1	3	69	4	K.MVRMAHIAIVGSHK.V 4948
6277	**555.2745**	**1662.8017**	**1663.8756**	**-1.0739**	**1**	**5**	**51**	**10**	**R.VSIIGGKAAPGYWMAK.T**
6458	838.8021	1675.5897	1674.8981	0.6916	0	1	1.2e+02	8	K.LGGYHFLTDLALLDK.L
6607	562.8589	1685.5547	1684.9009	0.6538	2	2	88	10	R.DRLIIDWNKTQQR.Q
6687	846.6811	1691.3477	1689.8145	1.5333	1	1	1.1e+02	4	K.SITSVARMGFFSTDR.V
6861	**852.9151**	**1703.8157**	**1704.8287**	**-1.0130**	**1**	**1**	**1.3e+02**	**3**	**R.ALDNAMLNVGMKDAAR.D**
6943	**856.6636**	**1711.3127**	**1710.7597**	**0.5530**	**0**	**98**	**2.5e-08**	**1**	**K.FNAGDYENAVAEQQR.A**
8459	**621.4819**	**1861.4237**	**1862.0162**	**-0.5925**	**1**	**2**	**94**	**7**	**R.WLHQANPRLSDLIATK.L**
9515	**663.1269**	**1986.3587**	**1984.0629**	**2.2958**	**0**	**40**	**0.014**	**1**	**K.VNGVAELHSDLLQTTLFK.D**
10366	**694.1942**	**2079.5607**	**2078.0029**	**1.5579**	**0**	**3**	**59**	**3**	**R.IEDVIDQEHDAALGNGGLGR.L**
10687	**709.6185**	**2125.8337**	**2124.1361**	**1.6976**	**2**	**3**	**69**	**6**	**R.DLLSRVSIIEESHPKMVR.M**
10758	**713.3189**	**2136.9347**	**2134.0510**	**2.8837**	**2**	**9**	**17**	**1**	**R.ALDNAMLNVGMKDAARDGLK.N**
10838	1073.6321	2145.2497	2144.0790	1.1708	1	53	0.00059	1	R.VINEYADGIWNVEPLAVKD.-
11492	1118.5146	2235.0147	2232.1573	2.8575	0	11	10	1	K.FVLNGGLIIGTCDGANIEITR.E
12456	**793.6842**	**2378.0307**	**2379.2661**	**-1.2353**	**1**	**6**	**29**	**2**	**R.HMQIIFDINLFFLQTVEKK.F** 12466 12468 12473
12883	**813.2992**	**2436.8757**	**2434.2016**	**2.6741**	**0**	**3**	**61**	**3**	**R.EIGEQNIFLFGNLAEDVEELR.H**
12895	**813.8395**	**2438.4967**	**2437.2464**	**1.2504**	**0**	**56**	**0.00027**	**1**	**R.LAACLLDSLATLNYPAWGYGLR.Y** 12894
13619	**845.2705**	**2532.7897**	**2531.3595**	**1.4302**	**0**	**16**	**3.3**	**1**	**K.TVIHLVNSVASVVNNDPDIGDLLK.V** 13607 13624 13627
14284	**886.6499**	**2656.9277**	**2658.4381**	**-1.5104**	**2**	**0**	**1.1e+02**	**4**	**R.LAKHIKDTTGYSVNPTALFDIQVK.R**
14484	**895.8642**	**2684.5707**	**2684.4254**	**0.1453**	**2**	**4**	**43**	**1**	**R.VSIIEESHPKMVRMAHIAIVGSHK.V**
15167	954.7382	2861.1927	2858.5881	2.6047	2	3	53	10	K.LLPRHMQIIFDINLFFLQTVEKK.F

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105. gi|220693543|gb|EED49888.1| **Mass:** 29437 **Score:** 232 **Queries matched:** 12 **emPAI:** 0.24
mitochondrial hypoxia responsive domain protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
131	**742.4640**	**741.4567**	**742.5065**	**-1.0498**	**2**	**3**	**76**	**7**	**K.GKGILKK.K**

6180	828.8126	1655.6107	1655.8227	-0.2120	1	6	35	5	K.EGQQQQQQAKEVK.E 6174 6208
7278	**582.7869**	**1745.3387**	**1743.7920**	**1.5467**	**1**	**3**	**68**	**3**	**R.LREESLQGMSFMER.S**
9663	**1002.4336**	**2002.8527**	**2002.1211**	**0.7316**	**0**	**120**	**1.5e-10**	**1**	**K.GGTIGTVLGLIGGYAGVLAASR.R** 9664 9668 9679
10930	**719.7572**	**2156.2497**	**2158.2222**	**-1.9725**	**1**	**2**	**78**	**3**	**K.GGTIGTVLGLIGGYAGVLAASRR.Y**
12695	**805.6495**	**2413.9267**	**2412.1678**	**1.7589**	**2**	**3**	**61**	**4**	**R.LREESLQGMSFMERSLAWAR.K** 12702

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106. gi|220688653|gb|EED45005.1| **Mass:** 58964 **Score:** 231 **Queries matched:** 28 **emPAI:** 0.39

glutamate decarboxylase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
670	958.3540	957.3467	956.4239	0.9228	0	8	30	5	R.YFDVEER.Y
1128	528.7416	1055.4687	1055.5975	-0.1287	0	33	0.07	1	K.AINDLLIER.N 1140 1141
1187	**534.7106**	**1067.4067**	**1065.6084**	**1.7984**	**0**	**23**	**0.68**	**1**	**R.GHGLPLVAFR.L** 1172
1350	**549.6431**	**1097.2717**	**1097.5362**	**-0.2644**	**0**	**10**	**15**	**10**	**K.MGFIIMSQR.R**
2469	639.7816	1277.5487	1276.6445	0.9042	1	6	42	8	K.SRCDALLSDIK.L
3981	**723.6671**	**1445.3197**	**1444.7959**	**0.5238**	**1**	**7**	**33**	**7**	**R.CDALLSDIKLGLK.T**
5641	**807.7896**	**1613.5647**	**1612.8031**	**0.7616**	**0**	**58**	**0.00021**	**1**	**K.GASQVIGQYYQMIR.L** 5637 5652 5665
6132	826.8216	1651.6287	1649.8719	1.7569	0	14	6.6	2	K.YGLVYPGVGWVVWR.S
6226	**830.7006**	**1659.3867**	**1659.8005**	**-0.4138**	**0**	**79**	**1.9e-06**	**1**	**R.EGQFDEFALAHQLR.E** 6240 6244 6246
6465	**559.7225**	**1676.1457**	**1675.7876**	**0.3582**	**0**	**4**	**60**	**9**	**R.FATEQLPQTEMPER.E**
7439	588.8105	1763.4097	1763.9161	-0.5064	2	4	59	3	K.LGLKTLGDMDKAMLDK.Y 7421 7451
9194	649.4035	1945.1887	1944.9442	0.2445	1	2	87	7	R.EGQFDEFALAHQLRER.G
10305	**691.2709**	**2070.7907**	**2072.1239**	**-1.3332**	**2**	**1**	**1.1e+02**	**8**	**M.VHLAQVHRNADLDSTIKR.V**
10685	**709.3819**	**2125.1237**	**2123.0820**	**2.0417**	**0**	**32**	**0.087**	**1**	**R.SIMTNITVTADFLAQELEK.M** 10688
11453	**743.7645**	**2228.2717**	**2226.1181**	**2.1536**	**1**	**2**	**84**	**9**	**R.LPAEREGQFDEFALAHQLR.E**
16388	**1158.1929**	**3471.5567**	**3470.6520**	**0.9047**	**0**	**64**	**3.3e-05**	**1**	**R.LFNAPVHSEDEHPMGTSTIGSSEAIMLGTLAMK.R**

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107. gi|220701216|gb|EED57554.1| **Mass:** 19753 **Score:** 231 **Queries matched:** 11 **emPAI:** 0.17

TCTP family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
35	665.5110	664.5037	666.3774	-1.8737	0	17	2.8	3	-.MIIYK.D
2483	**640.6976**	**1279.3807**	**1277.6615**	**1.7192**	**1**	**4**	**62**	**3**	**K.EFKENAQTALK.R**
7441	**882.7491**	**1763.4837**	**1762.8989**	**0.5848**	**0**	**91**	**1.1e-07**	**1**	**K.DILTGDEIISDAFNLK.E** 7425 7437 7438 7444 7445 7449 747
11776	**760.9799**	**2279.9177**	**2280.2253**	**-0.3076**	**1**	**12**	**8.4**	**2**	**M.IIYKDILTGDEIISDAFNLK.E**

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108. gi|220695209|gb|EED51552.1| **Mass:** 58541 **Score:** 230 **Queries matched:** 15 **emPAI:** 0.24

myo-inositol-phosphate synthase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
736	**485.4406**	**968.8667**	**968.4604**	**0.4064**	**0**	**27**	**0.29**	**1**	**K.AFIGGDDFK.S** 747
803	**492.5746**	**983.1347**	**983.5651**	**-0.4304**	**0**	**8**	**23**	**8**	**R.AQVLEPSLK.Q**

3241	681.8566	1361.6987	1359.7762	1.9225	0	64	6.8e-05	1	K.SALVDFLINAGIK.L 3227
5235	791.2911	1580.5677	1579.8432	0.7245	0	26	0.39	1	K.GFHSVLSVLSYMLK.A
5319	794.9256	1587.8367	1587.8984	-0.0617	0	58	0.00023	1	K.APLTPPGTPVVNALNK.Q 5350 5359
5718	810.8976	1619.7807	1618.9116	0.8691	1	12	9.8	6	K.MKSALVDFLINAGIK.L 5726
10730	1066.4086	2130.8027	2131.0797	-0.2770	0	67	2.9e-05	1	R.YADIVPGVNDTADNLLNSIK.T 10735 10740
13886	860.6999	2579.0777	2580.2359	-1.1582	1	4	48	2	K.VGMMMVGWGGNNGSTVTAGIIANRR.G

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109. gi|220694293|gb|EED50637.1| **Mass:** 52402 **Score:** 228 **Queries matched:** 26 **emPAI:** 0.28

secretory pathway gdp dissociation inhibitor [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
658	476.8966	951.7787	952.4800	-0.7013	0	13	7.5	7	R.LYVNSMAR.Y 657
967	511.4011	1020.7877	1020.4658	0.3219	0	16	4.6	1	K.SGMAADAINR.I
1205	536.2781	1070.5417	1070.5356	0.0061	0	7	31	10	K.VPSDANEALR.S
2106	619.4111	1236.8077	1236.6390	0.1687	0	55	0.00044	1	K.ILADPSYFPSK.A 2110
3194	680.2076	1358.4007	1356.6642	1.7365	2	6	41	3	R.SSLMGMFEKRR.A
5839	815.6186	1629.2227	1628.7682	0.4545	1	3	78	4	K.EVYDKFSLEENTR.D
7871	601.1735	1800.4987	1799.9013	0.5974	1	6	37	7	R.ATGEELVVEGLREDQR.L
7878	601.3649	1801.0727	1799.7962	1.2765	0	3	78	8	K.SYDATSHFETTTADVR.D
8361	618.5165	1852.5277	1853.0006	-0.4729	2	1	1e+02	4	K.SPKATVAKVPSDANEALR.S
8942	638.9455	1913.8147	1912.9854	0.8293	0	2	94	5	K.TDGSDSLQLIIPQSQVGR.K
9291	653.5459	1957.6157	1956.0024	1.6133	2	4	59	10	R.RATGEELVVEGLREDQR.L
10219	1031.7861	2061.5577	2059.0983	2.4594	0	19	1.6	2	K.LLMANGELTNILVSTDVTR.Y 10201
10481	699.2495	2094.7267	2092.0225	2.7042	1	3	73	2	R.NDHYGGEAASVNIETLFKK.Y
10795	1071.3851	2140.7557	2140.0993	0.6564	0	83	6.6e-07	1	K.SPYIYPLYGLGELPQGFAR.L 10804 10805 10807 10816
14687	1362.3656	2722.7167	2722.3530	0.3637	0	30	0.12	1	K.FFGPPIPLYEPLESGENDNIFISK.S
15034	943.3162	2826.9267	2825.4460	1.4807	2	6	31	3	K.VLHIDRNDHYGGEAASVNIETLFKK.Y 15033
16147	1110.7329	3329.1767	3330.5761	-1.3994	2	0	82	9	R.DFIGHSMALYQSDDYIGKSGMAADAINRIR.L 16146

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110. gi|220695019|gb|EED51362.1| **Mass:** 17018 **Score:** 226 **Queries matched:** 20 **emPAI:** 1.97

ribosomal protein L14 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
64	686.5530	685.5457	685.4123	0.1335	0	26	0.54	1	K.LVEIGR.V
517	907.4730	906.4657	906.4195	0.0462	0	40	0.018	1	K.NLNDFER.F 516 521 522 523
1107	527.0886	1052.1627	1051.5087	0.6540	0	44	0.0062	1	K.WAQSSFAQK.T 1106
2068	616.4051	1230.7957	1232.6401	-1.8444	1	1	1.4e+02	4	K.LWQKSEIDSK.W
2346	633.7606	1265.5067	1264.7139	0.7928	0	42	0.0092	1	K.LATIVEIVDHR.R 2349 2353 2360
2549	644.6191	1287.2237	1286.6354	0.5883	0	69	2.2e-05	1	R.VLVDGPSTEENK.I 2550 2557
8531	624.6025	1870.7857	1868.0156	2.7701	1	13	7.5	1	R.GPYTGKLATIVEIVDHR.R
11651	754.3675	2260.0807	2259.3004	0.7803	0	54	0.00046	1	R.HVLPLAHATLTHFVIPQLPR.A 11656 11669

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111.  gi|220693633|gb|EED49978.1|    Mass: 24321    Score: 218    Queries matched: 31    emPAI: 1.46
      60S ribosomal protein L1 [Aspergillus flavus NRRL3357]
     Query  Observed    Mr(expt)    Mr(calc)     Delta Miss Score   Expect Rank  Peptide
        96  715.5640    714.5567    714.4388    0.1179    0    11       18    1  K.ITVAGVR.Q 94
       206  392.9781    783.9417    783.4854    0.4563    0    31     0.12    1  R.LLGPGLSK.A 201 202 205
      1904  601.4066   1200.7987   1199.6663    1.1325    0    44   0.0061    1  K.GWQNVGSLVLK.A
      4483  752.7616   1503.5087   1502.8344    0.6743    0    29     0.19    2  R.NFLETVELQIGLK.N 4464 4472 4476 4480 4484 4491
      5005  779.5966   1557.1787   1556.7293    0.4494    0    52   0.0011    1  K.FPTPISHAEDMANK.V 5012
      5168  787.5946   1573.1747   1572.7242    0.4505    0  (48)   0.0026    1  K.FPTPISHAEDMANK.V 5165 5166 5167
      5422  533.3979   1597.1717   1596.7566    0.4151    1     1  1.2e+02    7  K.HHGIDAMSTEDLKK.L
      7026  861.1501   1720.2857   1719.8427    0.4430    0    79  1.9e-06    1  R.QNIQQLLDYSQNEK.K 7020 7037
      8169  611.2225   1830.6457   1828.8778    1.7680    1     2       84    3  K.AGKFPTPISHAEDMANK.V
      9867  676.5959   2026.7657   2026.1033    0.6624    2     2       85    7  K.KGWQNVGSLVLKASMSPPK.R 9850 9852
     13590  844.0989   2529.2747   2528.2945    0.9803    2     3       61    5  K.FPTPISHAEDMANKVTDVKSTIK.F
     13801  854.9689   2561.8847   2562.2683   -0.3836    0    31    0.088    1  K.LPSVPRPNMTICILGDQHDLDR.A 13798
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112.  gi|220700819|gb|EED57157.1|    Mass: 26441    Score: 217    Queries matched: 17    emPAI: 0.43
      mitochondrial ATPase subunit ATP4, putative [Aspergillus flavus NRRL3357]
     Query  Observed    Mr(expt)    Mr(calc)     Delta Miss Score   Expect Rank  Peptide
       405  865.5530    864.5457    866.4167   -1.8710    1     9       20    4  R.IMSSSKAQ.-
       643  473.6161    945.2177    944.5178    0.6999    0    23      1.1    1  R.ELAESVIGK.I
      2251  628.8206   1255.6267   1253.7092    1.9176    0     1  1.3e+02    3  R.NVAPIANLTVSR.S
      3606  701.0621   1400.1097   1399.7307    0.3790    2     1  1.3e+02    8  R.SASNVPTEDPKKK.A
      5613  806.7571   1611.4997   1611.8832   -0.3834    0     0  1.4e+02    3  K.AQSILDALPGNSLVSK.T
      5880  817.3081   1632.6017   1630.8236    1.7781    0  (44)   0.0067    1  R.MDNVQELAGVVEVTK.Q 5879
      6087  825.2571   1648.4997   1646.8185    1.6812    0    83  8.4e-07    1  R.MDNVQELAGVVEVTK.Q 6095
      7085  863.8211   1725.6277   1724.9421    0.6856    0    89  1.6e-07    1  K.VLQQILQQSVADVER.I 7084 7103
      7613  889.8421   1777.6697   1777.8482   -0.1785    0    21      1.3    1  K.ETAQLEAQAYELEQR.T 7612
      9829  675.7392   2024.1957   2024.1153    0.0804    2     5       40    3  R.ELAESVIGKIQKELENPK.V 9828
     12855  812.4765   2434.4077   2435.3020   -0.8942    1     1  1.1e+02    5  K.ELENPKVLQQILQQSVADVER.I
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113.  gi|220701753|gb|EED58091.1|    Mass: 58506    Score: 216    Queries matched: 33    emPAI: 0.39
      pyruvate kinase [Aspergillus flavus NRRL3357]
     Query  Observed    Mr(expt)    Mr(calc)     Delta Miss Score   Expect Rank  Peptide
        74  690.6400    689.6327    689.3596    0.2732    0    32     0.15    1  K.DISDLK.F 71
       539  911.6280    910.6207    910.5025    0.1183    0     4       58    8  K.WAISHGIK.L
       819  494.0206    986.0267    985.5808    0.4459    0    37    0.037    1  R.TSIIGTIGPK.T 818
      1410  555.1711   1108.3277   1108.6128   -0.2851    0    29     0.18    1  R.GDLGIEIPAK.V 1419
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1637	572.6926	1143.3707	1141.6819	1.6888	1	10	18	2	R.RTSIIGTIGPK.T
2707	653.6971	1305.3797	1302.6139	2.7658	0	19	2	1	K.GDNIVCVQGWR.G 2702
3335	686.3781	1370.7417	1368.6860	2.0557	0	54	0.00066	1	K.NGVDMIFASFIR.R
3466	693.6211	1385.2277	1384.6809	0.5468	0	(5)	52	3	K.NGVDMIFASFIR.R
4314	495.2162	1482.6267	1481.8566	0.7702	0	4	61	1	R.VQTGRPLAIALDTK.G
4564	759.0391	1516.0637	1515.7463	0.3174	1	8	27	1	M.AASSSLDHLSNRMK.L
4929	776.0486	1550.0827	1548.9140	1.1687	1	2	92	2	K.WAISHGIKLGIINK.G 4912 4941
8357	618.3802	1852.1187	1851.9942	0.1245	1	6	34	2	R.KGVNLPGTDVDLPALSEK.D
8536	624.6612	1870.9617	1871.0022	-0.0405	1	7	31	5	K.YRPVCPILMVTRNPR.A 8534
8666	629.6875	1886.0407	1886.9971	-0.9564	1	(6)	37	7	K.YRPVCPILMVTRNPR.A 8662
8915	637.7372	1910.1897	1909.0745	1.1152	1	2	92	4	R.EAARVQTGRPLAIALDTK.G
9924	1017.7996	2033.5847	2033.0411	0.5436	0	46	0.0034	1	R.GVWPFLFPENKPDFNVK.I 9925 9930 9935 9954
10182	687.1332	2058.3777	2057.0438	1.3340	2	4	50	3	R.MKLEWHSKLNTEMVPAK.N
12635	802.3682	2404.0827	2401.3113	2.7714	2	1	1.1e+02	2	R.GDLGIEIPAPKVFIAQKMMIAK.C
13531	1262.2081	2522.4017	2521.1676	1.2341	0	75	3.9e-06	1	R.AEVSDVANAVLDGADCVMLSGETAK.G 13509
13810	855.4685	2563.3837	2565.2502	-1.8664	0	2	72	4	K.GKPVICATQMLESMTYNPRPTR.A

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114. gi|220690678|gb|EED47027.1| **Mass:** 16670 **Score:** 215 **Queries matched:** 18 **emPAI:** 0.74
40S ribosomal protein S12 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1333	548.1411	1094.2677	1093.6244	0.6433	0	54	0.00057	1	R.ISLIHDGLAR.G 1338
1595	1136.6510	1135.6437	1134.4578	1.1860	0	18	2.5	1	K.DWGEESQER.S
1722	1164.7460	1163.7387	1162.5839	1.1548	0	17	2.9	1	K.VVNCSCVVVK.D
1744	585.2721	1168.5297	1168.6274	-0.0977	0	10	17	8	K.LVIALCSEHK.I
2570	646.0681	1290.1217	1290.6788	-0.5571	1	7	33	2	R.KVVNCSCVVVK.D 2592
3045	672.1581	1342.3017	1340.6612	1.6405	0	12	12	2	R.SVLLNYFQTEQ.- 3036
5185	789.1341	1576.2537	1575.7538	0.5000	0	73	7.3e-06	1	K.MLGEWVGLCQLDR.E 5191 5197 5206 5208
8060	606.8805	1817.6197	1819.0428	-1.4230	2	7	29	2	R.ISLIHDGLARGLREAAK.A 8081
10437	697.5029	2089.4867	2088.0132	1.4735	1	3	62	8	K.VPDGKMLGEWVGLCQLDR.E 10441

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115. gi|220692700|gb|EED49046.1| **Mass:** 60045 **Score:** 213 **Queries matched:** 26 **emPAI:** 0.24
fumarate hydratase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
651	949.5220	948.5147	950.4644	-1.9496	0	14	7.1	10	-.MLAPSNFR.A 650
1463	560.1881	1118.3617	1116.5346	1.8272	0	5	56	10	R.SMASLAHAASR.A
2236	627.7271	1253.4397	1253.6326	-0.1928	1	3	68	7	R.ILSDGMKSFEK.N 2251
3020	670.9901	1339.9657	1339.6442	0.3215	1	0	1.6e+02	4	K.MTGTEFKTAPNK.F
3090	674.9986	1347.9827	1347.6895	0.2932	0	51	0.0014	1	K.NLVHGLEANEPR.I 3082
3993	724.1831	1446.3517	1444.8402	1.5116	2	3	78	7	K.VENFEKIIKIGR.T

4482	752.7106	1503.4067	1502.7114	0.6954	0	40	0.017	1	R.SLGNFDINQPQDR.M 4468
4787	769.7306	1537.4467	1534.7814	2.6654	1	3	74	2	K.GAAATVNMKFGLDPK.I
5299	529.5762	1585.7067	1585.8246	-0.1179	1	7	30	6	R.NLLHSSRILSDGMK.S 5301
5712	810.7801	1619.5457	1618.7726	0.7731	0	11	11	3	R.VETDAFGEIEVPADK.Y
10235	688.6165	2062.8277	2059.9772	2.8505	1	2	84	7	K.GFDEAIAAEVTKMTGTEFK.T 10239
11462	744.2969	2229.8687	2231.2170	-1.3483	2	1	98	5	R.MPEGVVKAFGILKGAAATVNMK.F 11481
11955	768.3372	2301.9897	2299.1967	2.7930	2	5	38	4	M.LAPSNFRAAVRSMASLAHAASR.A 11948
12690	805.4039	2413.1897	2411.2451	1.9446	2	3	60	6	R.AAVRSMASLAHAASRASASSPAVAR.S
14315	887.8272	2660.4597	2659.3242	1.1355	0	75	3.8e-06	1	R.THLQDATPLTLGQEFSGYVAQLDR.N 14319
16021	1092.8492	3275.5257	3273.6703	1.8554	1	54	0.00039	1	K.TAPNKFEVLAAHDAIVEASGSLNTLACSLFK.I 16018

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116. gi|220696367|gb|EED52709.1| **Mass:** 16028 **Score:** 212 **Queries matched:** 16 **emPAI:** 2.17

40S ribosomal protein Rps16, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
191	389.3446	776.6747	776.4181	0.2566	0	48	0.0033	1	K.FAGVDIR.V
743	971.5100	970.5027	970.5124	-0.0096	0	32	0.11	1	K.SLVAYYQK.Y
853	496.9296	991.8447	991.5087	0.3360	0	60	0.00017	1	K.QALVQYDR.T
2714	654.2921	1306.5697	1306.6704	-0.1006	1	3	93	7	M.ASVPSVQCFGKK.K
2790	658.7271	1315.4397	1315.7387	-0.2990	0	37	0.031	1	K.VYEPLLIVGADK.F
3851	716.6331	1431.2517	1430.7266	0.5251	0	60	0.00018	1	R.VSGGGHTSQVYAIR.Q 3852
5240	791.5671	1581.1197	1581.8007	-0.6810	2	6	35	6	-.MASVPSVQCFGKKK.T
6288	832.7456	1663.4767	1661.9464	1.5303	0	55	0.00049	1	K.VNGQPLSLVQPEILR.F 6256 6290 6291 6292 6302
11240	733.2445	2196.7117	2197.2080	-0.4963	2	8	21	2	R.VRVSGGGHTSQVYAIRQAIAK.S
12520	796.7349	2387.1827	2386.4060	0.7767	2	1	1e+02	4	K.QGKGLIKVNGQPLSLVQPEILR.F

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117. gi|45477393|gb|AAS66016.1| **Mass:** 43286 **Score:** 209 **Queries matched:** 24 **emPAI:** 0.67

methyltransferase B [Aspergillus parasiticus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
649	474.9836	947.9527	947.5440	0.4087	0	45	0.0053	1	R.TQAAFGLIK.E
843	495.6116	989.2087	988.5706	0.6382	0	59	0.00023	1	K.VGIDLGIFR.S 842
1185	534.6666	1067.3187	1066.6386	0.6801	0	39	0.02	1	K.EQAILVAVPK.R 1186
1968	607.3511	1212.6877	1212.7078	-0.0201	0	45	0.0056	1	R.LSSGPLQVALTK.V
2033	613.6811	1225.3477	1224.6060	0.7417	0	23	0.7	2	M.TGLDMETIFAK.I
3725	709.2161	1416.4177	1414.7555	1.6622	0	51	0.0013	1	K.ESDTPITLAEIVK.K 3711
4777	769.3351	1536.6557	1534.7814	1.8743	0	14	5.7	1	K.VLMVDIGGGFGQQSK.A 4744 4770 4784
8525	624.2709	1869.7907	1871.0615	-1.2708	2	4	63	9	R.SLKESDTPITLAEIVKK.T 8516
8760	632.3142	1893.9207	1890.9986	2.9221	1	2	77	9	K.VLMVDIGGGFGQQSKALR.A
9813	675.0902	2022.2487	2020.9175	1.3312	0	54	0.00056	1	K.AFGSDLTMFEWMPQHPK.H 9804 9815
10446	697.8545	2090.5417	2090.1306	0.4111	2	6	32	6	K.VLMVDIGGGFGQQSKALRAK.F

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   10544  1052.5286  2103.0427  2103.0194   0.0233  0    21      1.1   1   R.AEWDDLMEQVGLEIIQSK.V
   12434   792.5785  2374.7137  2376.1631  -1.4494  1     2       76   9   R.TRAEWDDLMEQVGLEIIQSK.V
   13437   837.9532  2510.8377  2511.4788  -0.6411  2     0  1.1e+02   3   R.LSSGPLQVALTKVGIDLGIFRSLK.E
   15011   938.8859  2813.6357  2814.2604  -0.6247  1     2       70   2   K.DCVFQKAFGSDLTMFEWMPQHPK.H
```

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118.  gi|6177971|dbj|BAA86103.1|     Mass: 43298    Score: 209    Queries matched: 25   emPAI: 0.67
      O-methyltransferase [Aspergillus parasiticus]
   Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
     649   474.9836   947.9527   947.5440   0.4087  0    45   0.0053   1   R.TQAAFGLIK.E
     843   495.6116   989.2087   988.5706   0.6382  0    59  0.00023   1   K.VGIDLGIFR.S 842
    1185   534.6666  1067.3187  1066.6386   0.6801  0    39     0.02   1   K.EQAILVAVPK.R 1186
    1968   607.3511  1212.6877  1212.7078  -0.0201  0    45   0.0056   1   R.LSSGPLQVALTK.V
    3725   709.2161  1416.4177  1414.7555   1.6622  0    51   0.0013   1   K.ESDTPITLAEIVK.K 3711
    4777   769.3351  1536.6557  1534.7814   1.8743  0    14      5.7   1   K.VLMVDIGGGFGQQSK.A 4744 4770 4784
    5794   813.6756  1625.3367  1624.8568   0.4799  1     3       70   8   -.MTGLDMEIIFAKIK.E
    8525   624.2709  1869.7907  1871.0615  -1.2708  2     4       63   9   R.SLKESDTPITLAEIVKK.T 8516
    8760   632.3142  1893.9207  1890.9986   2.9221  1     2       77   9   K.VLMVDIGGGFGQQSKALR.A
    9813   675.0902  2022.2487  2020.9175   1.3312  0    54  0.00056   1   K.AFGSDLTMFEWMPQHPK.H 9804 9815
   10446   697.8545  2090.5417  2090.1306   0.4111  2     6       32   6   K.VLMVDIGGGFGQQSKALRAK.F
   10544  1052.5286  2103.0427  2103.0194   0.0233  0    21      1.1   1   R.AEWDDLMEQVGLEIIQSK.V
   11743   759.4955  2275.4647  2273.1435   2.3212  2     2       81   7   -.MTGLDMEIIFAKIKEEYAR.T
   12434   792.5785  2374.7137  2376.1631  -1.4494  1     2       76   9   R.TRAEWDDLMEQVGLEIIQSK.V
   13437   837.9532  2510.8377  2511.4788  -0.6411  2     0  1.1e+02   3   R.LSSGPLQVALTKVGIDLGIFRSLK.E
   15011   938.8859  2813.6357  2814.2604  -0.6247  1     2       70   2   K.DCVFQKAFGSDLTMFEWMPQHPK.H


      Proteins matching the same set of peptides:
      gi|6177973|dbj|BAA86104.1|     Mass: 43298    Score: 209    Queries matched: 25
      O-methyltransferase [Aspergillus parasiticus]
```

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119.  gi|220695964|gb|EED52306.1|     Mass: 150551    Score: 208    Queries matched: 40    emPAI: 0.07
      hydantoin utilization protein A, putative [Aspergillus flavus NRRL3357]
   Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
     360   428.7006   855.3867   855.5290  -0.1423  1    15      4.7   4   K.VALEIRR.K 368
     446   881.4950   880.4877   880.3926   0.0951  0     7       26   7   R.EVGEYER.T
    1576   567.9981  1133.9817  1134.5894  -0.6077  1     1  1.3e+02   5   R.GGNAQRTLYR.F
    2150   415.4062  1243.1967  1243.6885  -0.4917  1     3       77   9   R.RETVVGDLTVR.S
    2974   668.6181  1335.2217  1333.7098   1.5120  1     7       30   5   R.TMDVMQALIGKK.N
    3008   670.4551  1338.8957  1338.6754   0.2203  2     3       69   7   R.DWFTRMKEVK.G
    3240   681.7616  1361.5087  1360.6987   0.8101  1     4       63   3   K.TLEATLWDREK.I
    4175   734.8896  1467.7647  1464.7936   2.9711  1     0  1.4e+02   7   K.SRENPPVEILPSK.C
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4620	761.2316	1520.4487	1518.7534	1.6953	0	47	0.0033	1	K.GVMNTDLVELLCR.N
5296	793.8016	1585.5887	1583.7476	1.8411	0	9	17	1	K.YCLPNFELELMR.L 5283
5374	531.7742	1592.3007	1591.8426	0.4582	2	9	20	2	R.TMDVMQALIGKKNK.L
6153	552.0962	1653.2667	1654.9002	-1.6335	1	2	90	8	R.SPAVDIRTVGAGGGSIAK.Y
6915	855.4481	1708.8817	1709.0087	-0.1270	0	55	0.0005	1	R.STPLIPTLVASALASIR.S 6923 6935 6937 6938
6984	858.6241	1715.2337	1714.9117	0.3221	0	94	5.6e-08	1	K.MLVGQFGSFITQFLK.A
8053	606.7615	1817.2627	1817.9305	-0.6678	1	5	48	8	R.MSVNGESVIAVNKDALR.A
8152	610.1735	1827.4987	1825.9898	1.5089	1	9	19	1	R.ETVVGDLTVRSPAVDIR.T
8172	916.5801	1831.1457	1828.9849	2.1608	1	7	28	3	R.WFTKPWGIRGGKPGSR.S
8251	614.8089	1841.4047	1839.9553	1.4494	0	4	55	8	R.FGSQIYLAACSELLLR.N
8811	950.8856	1899.7567	1899.0070	0.7497	1	4	60	7	R.THLLGRTMDVMQALIGK.K
9478	661.2739	1980.7997	1982.0909	-1.2912	2	4	50	4	R.RETVVGDLTVRSPAVDIR.T 9485
10313	691.6225	2071.8457	2071.0487	0.7970	0	1	94	4	K.FQFIHHGTTTATNAVLEGK.G
10838	1073.6321	2145.2497	2144.1241	1.1256	1	4	50	3	K.MLVGQFGSFITQFLKAWR.G
12087	773.6155	2317.8247	2319.1284	-1.3037	0	5	44	3	R.ETGLPAPSAQWELDPYGPHVR.L 12092
12318	786.3162	2355.9267	2355.2084	0.7183	1	4	44	1	K.FQFIHHGTTTATNAVLEGKGAR.T
12365	789.6869	2366.0387	2367.2039	-1.1651	2	1	92	8	K.LYSKGVMNTDLVELLCRNSR.Q
12493	795.4075	2383.2007	2381.1322	2.0685	0	9	16	3	R.LGADVGGTFTDICAFTPDGQIAR.A 12484 12501
13905	861.8962	2582.6667	2583.2322	-0.5655	2	3	57	3	R.QPDWYRSDLMAIIAACRTASSR.V
14121	876.8559	2627.5457	2626.3907	1.1550	0	9	14	1	R.SQIPGGLGAWLHYTPPEPIVPLER.V
14425	892.8212	2675.4417	2673.1985	2.2432	1	6	28	1	K.YMGITETMRVGPESAGASPGPACYR.K
15023	940.0735	2817.1987	2817.4980	-0.2992	1	4	41	2	R.STPLIPTLVASALASIRSEMDTLMLR.C

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120. gi|220695968|gb|EED52310.1| **Mass:** 46106 **Score:** 207 **Queries matched:** 12 **emPAI:** 0.32

flavohemoprotein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
19	646.3760	645.3687	645.3334	0.0354	0	20	2.6	1	K.EGDVVK.V
1027	519.1646	1036.3147	1035.4985	0.8162	0	38	0.025	1	R.QYSLSDAPR.S
1337	548.5571	1095.0997	1094.4781	0.6216	0	11	13	6	K.QADGWTDFR.H 1348
2359	634.3261	1266.6377	1264.7391	1.8987	0	4	68	2	M.PLSPEQIQLIK.A
3095	675.2011	1348.3877	1349.7191	-1.3313	2	8	23	1	R.AFKKDVDSLAEK.Y 3088
12836	811.5615	2431.6627	2431.2522	0.4105	0	61	8.9e-05	1	K.VPESSEITSFYLEPVDGKPLPK.F 12841
13793	854.5739	2560.6997	2559.3472	1.3525	1	29	0.14	1	K.KVPESSEITSFYLEPVDGKPLPK.F
15395	991.4799	2971.4177	2969.5320	1.8857	0	82	7.2e-07	1	R.ALAGALFAYASHIDDLGALGPAVELICNK.H 15396

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121. gi|220700137|gb|EED56476.1| **Mass:** 23161 **Score:** 205 **Queries matched:** 21 **emPAI:** 0.50

14-3-3 protein sigma, gamma, zeta, beta/alpha, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
523	454.5191	907.0237	906.5174	0.5063	0	8	25	6	R.NLLSVAYK.N

575	917.6150	916.6077	916.5229	0.0848	0	30	0.23	2	R.IISSIEQK.E 576
919	505.3621	1008.7097	1009.4498	-0.7401	1	10	16	1	-.MTSERENK.T 920
1358	550.6921	1099.3697	1098.5345	0.8352	0	20	1.7	2	R.YLAEFASGNK.R 1357
1509	563.6361	1125.2577	1124.5938	0.6639	0	87	2.8e-07	1	K.GSEQHVSIIR.D 1510 1516 1517
2281	630.4501	1258.8857	1258.6669	0.2188	1	1	1.2e+02	10	R.KVAATAAHEAYK.N
3516	696.1961	1390.3777	1389.7351	0.6426	1	38	0.029	2	R.IISSIEQKEESK.G
4451	751.7161	1501.4177	1500.7420	0.6757	0	5	58	1	K.EVANIGGELTVDER.N
8258	922.3011	1842.5877	1841.9445	0.6433	0	88	2.1e-07	1	K.VCQDVLDVLDESLIPK.A 8256 8257 8281
9539	664.2909	1989.8507	1988.9197	0.9311	1	4	49	3	R.DPELSRSCLPPCQAGFR.- 9547
9912	678.6132	2032.8177	2031.9973	0.8204	2	1	1.1e+02	3	K.EESKGSEQHVSIIRDYR.Q

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122. gi|220690102|gb|EED46452.1| **Mass:** 22217 **Score:** 205 **Queries matched:** 20 **emPAI:** 1.68

40S ribosomal protein S9 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
474	888.5170	887.5097	887.4712	0.0385	0	47	0.0049	1	R.IGVLDESR.M
512	453.7811	905.5477	905.4971	0.0507	0	31	0.13	1	K.IVGEYGLR.N 514
524	454.5571	907.0997	906.4447	0.6550	0	45	0.0058	1	R.VEDFLER.R 518 520 522
1005	517.1206	1032.2267	1031.5764	0.6504	0	51	0.0014	1	R.LFEGNALIR.R 1004
1841	1189.3780	1188.3707	1187.6775	0.6933	1	3	98	6	K.RLFEGNALIR.R
1910	602.5241	1203.0337	1201.7043	1.3294	1	1	1.4e+02	7	K.LGLAKSIHHAR.V
2573	646.2231	1290.4317	1288.6962	1.7355	0	37	0.031	1	K.QIVNVPSFMVR.L 2566
2665	651.1496	1300.2847	1299.6922	0.5926	1	49	0.0021	1	R.ELLTLDEKDPK.R 2663
2708	436.1892	1305.5457	1303.7360	1.8097	2	3	87	6	K.IVGEYGLRNKR.E
5430	800.1711	1598.3277	1597.8675	0.4602	2	4	58	8	R.AARELLTLDEKDPK.R
7884	601.5439	1801.6097	1799.9067	1.7030	0	59	0.00018	1	K.HIDFALTSPYGGGRPGR.V 7878
9610	998.8436	1995.6727	1995.1200	0.5527	2	4	60	7	R.HIRVGKQIVNVPSFMVR.L

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123. gi|220691722|gb|EED48070.1| **Mass:** 99216 **Score:** 201 **Queries matched:** 27 **emPAI:** 0.18

aminopeptidase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
15	635.5770	634.5697	634.3438	0.2259	0	17	3.9	1	K.EFALR.L
1170	533.7336	1065.4527	1065.4978	-0.0451	0	6	39	3	K.AEIFGEDGTK.I
1235	1077.3320	1076.3247	1075.6026	0.7221	0	2	1.3e+02	9	R.ASHPIEVPVK.N
1670	576.8456	1151.6767	1149.6063	2.0704	1	2	84	10	R.STKEIMLNSK.E
2545	429.9452	1286.8137	1286.6904	0.1233	0	23	0.75	1	K.LLIGMAGLAGDEK.V 2537 2552
3363	687.6366	1373.2587	1372.6775	0.5812	0	31	0.15	1	K.SVLEWLQAHGYA.-
3576	466.6292	1396.8657	1395.6882	1.1776	0	16	3.9	1	K.ITQASEITYDQK.S 3569
3707	708.4396	1414.8647	1414.7854	0.0794	1	4	65	9	R.KLLIGMAGLAGDEK.V
3926	480.5212	1438.5417	1435.7307	2.8110	0	7	33	5	R.SVFSQNESVAAGLK.E

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   4373    746.3891  1490.7637  1492.7133  -1.9495   1      0  1.4e+02   8   R.RAFPCFDEPNLK.A
   5086    784.1451  1566.2757  1565.7474   0.5283   0      1  1.1e+02   5   K.TDTIHGVGQNSFYK.I
   8872    636.0619  1905.1637  1903.9680   1.1958   0     40    0.014   1   K.NALEVDQIFDHISYLK.G
   8982    959.0931  1916.1717  1915.8952   0.2765   0     72    9e-06   1   K.FADQSIGEDIASFFQNK.D 8983
   9173    648.4579  1942.3517  1944.0601  -1.7084   1      2       84   3   K.LLIGMAGLAGDEKVITEAK.R 9176
   9281    978.6871  1955.3597  1955.0728   0.2870   0     75  4.1e-06   1   K.IGFPVITVAEEPSQISIR.Q
  10177   1029.7346  2057.4547  2056.1602   1.2946   2      1       94   3   R.KLLIGMAGLAGDEKVITEAK.R
  10325    692.5235  2074.5487  2072.1551   2.3936   2    (1) 1.2e+02   8   R.KLLIGMAGLAGDEKVITEAK.R
  11745    759.5129  2275.5167  2274.1274   1.3893   2      2       74   4   K.GQTALSNMPVKSERDGSSPGLK.V
  12123    775.4999  2323.4777  2321.1950   2.2827   2      1  1.1e+02   7   R.MLSDHLGRDTFLRGVANYLK.T
  14113    876.2999  2625.8777  2625.2356   0.6422   0      0  1.1e+02   9   K.ADLLAVHEFAMGAMENWGLVTYR.T
  14144    879.2085  2634.6037  2632.3061   2.2976   0     27     0.23   1   R.FLSTGDAKPEEDETTWWIPLGIK.S 14143
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124.   gi|220701627|gb|EED57965.1|     Mass: 12422     Score: 199     Queries matched: 18    emPAI: 2.38
       60S ribosomal protein L35Ae [Aspergillus flavus NRRL3357]
      Query  Observed    Mr(expt)    Mr(calc)    Delta Miss Score   Expect Rank   Peptide
        127  737.5570    736.5497    736.3868   0.1629   0    13      6.8   1    K.SFGATVR.V
        156  378.1656    754.3167    753.4174   0.8994   0    31    0.099   1    K.VAFVYR.A 153 154 155
        720  966.5710    965.5637    965.4137   0.1500   0     8       21   4    -.MPSEHGHR.L
       1427  557.3166   1112.6187   1112.6190  -0.0002   0    44   0.0064   1    R.QVNPNTSLIK.I 1431
       2473  639.9976   1277.9807   1277.6953   0.2854   0    22      1.1   2    K.VTRPHGNSGVVR.A
       6509  561.0272   1680.0597   1681.8471  -1.7874   2     2    1e+02   8    -.MPSEHGHRLYVKGR.H
       7091  864.2296   1726.4447   1725.8210   0.6238   0    78  2.1e-06   1    K.IDGVDNTEAANFYLGK.K 7090 7095 7096 7101
      13042  822.5949   2464.7627   2466.3469  -1.5842   2     4       51   1    K.VTRPHGNSGVVRAQFRHNLPPK.S
      13941  864.1509   2589.4307   2589.3227   0.1080   2    42   0.0077   1    K.IDGVDNTEAANFYLGKKVAFVYR.A 13942
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125.   gi|220700627|gb|EED56965.1|     Mass: 118573    Score: 198     Queries matched: 20    emPAI: 0.11
       translation elongation factor eEF-3, putative [Aspergillus flavus NRRL3357]
      Query  Observed    Mr(expt)    Mr(calc)    Delta Miss Score   Expect Rank   Peptide
         50  678.5450    677.5377    677.3279   0.2099   1    14      7.3   2    K.ERMAR.K
        291  415.1411    828.2677    829.4154  -1.1477   1     7       37   6    K.DANARQR.A 288
        376  858.5550    857.5477    858.5215  -0.9737   0     8       33   9    R.FIPELIK.C
        631  470.1831    938.3517    936.5617   1.7900   1     5       43   2    R.RVIGIHSR.R
        705  964.6570    963.6497    963.4444   0.2054   1     8       26   6    R.ETMDRANK.I
       2313  632.2296   1262.4447   1263.6315  -1.1868   1     6       46   8    R.KSAVIVDNMCK.L
       3373  688.1651   1374.3157   1372.7020   1.6137   0     2  1.2e+02   2    -.MPAAAASSVPAVSSK.E 3361
       4980  518.9242   1553.7507   1554.6548  -0.9041   0     2       85   4    R.SYYELGASDMEFK.F
       5084  783.9576   1565.9007   1564.8865   1.0142   0    71  1.1e-05   1    K.LVEDPQIVAPFLPK.L 5074
       5164  787.5086   1573.0027   1570.8943   2.1084   1     2       99   8    K.EALASGQFRPLVRK.E
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6087	825.2571	1648.4997	1646.9032	1.5965	2	3	80	10	K.FPEPGFLEGVKTKAK.A
7098	864.7376	1727.4607	1726.8964	0.5643	0	57	0.00027	1	R.VPALIPAVSEAMWDTK.A
7715	893.3631	1784.7117	1783.9931	0.7186	0	61	0.00012	1	K.IPEISTAGDISTVAGILK.E
14157	880.2259	2637.6557	2637.2269	0.4289	0	2	76	7	K.TVYVEHDLDSADTEQTVIGWTMK.K
14808	919.7319	2756.1737	2755.2727	0.9010	1	3	56	4	R.SYYELGASDMEFKFPEPGFLEGVK.T
14857	924.5392	2770.5957	2768.4345	2.1612	0	43	0.0059	1	K.STLVNVLTGELIPTTGDVYQHENIR.I 14855

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126. gi|220690663|gb|EED47012.1| **Mass:** 16599 **Score:** 197 **Queries matched:** 22 **emPAI:** 3.40

40S ribosomal protein S19 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
262	816.5500	815.5427	815.4752	0.0675	0	16	4.9	2	K.VIQSLEK.I 271
805	492.6636	983.3127	984.6192	-1.3065	2	9	19	9	R.KTVGVGRLR.K
1648	573.8831	1145.7517	1145.6121	0.1396	0	50	0.0018	1	K.FISAYSAFLK.R 1647 1651
1745	1169.9070	1168.8997	1167.5771	1.3226	0	30	0.16	1	K.IGVLEHDEEK.G
2029	613.2091	1224.4037	1223.6914	0.7123	0	49	0.0021	1	K.LPIPGWVDTVK.T 2026 2033
2748	655.9086	1309.8027	1309.4681	0.3346	0	75	5.3e-06	1	K.TTVDEEEEDDE.- 2743 2747
3569	466.3235	1395.9487	1397.8255	-1.8768	2	10	16	3	R.HIYLRKTVGVGR.L
5649	539.1479	1614.4217	1614.8882	-0.4665	2	5	47	6	K.FISAYSAFLKRQGK.L
6691	846.7836	1691.5527	1689.7932	1.7596	0	60	0.00015	1	R.GSRPNHHVDASGSVDR.K 6671 6672 6684
8067	910.1356	1818.2567	1817.8881	0.3686	1	21	1.3	1	R.GSRPNHHVDASGSVDRK.V 8087
11259	1101.0466	2200.0787	2198.9691	1.1096	0	26	0.34	2	K.TSCSNELPPQNADWYYVR.A

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127. gi|220690399|gb|EED46748.1| **Mass:** 54426 **Score:** 195 **Queries matched:** 26 **emPAI:** 0.12

seryl-tRNA synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
397	864.5030	863.4957	863.4348	0.0609	1	7	36	8	K.DSTSQKAK.G
1484	561.5856	1121.1567	1119.5295	1.6272	0	9	20	4	K.EDASSLLEEK.A
1547	566.1836	1130.3527	1129.5979	0.7549	1	12	12	2	K.KDAEDLALQK.E 1548
2489	641.0266	1280.0387	1280.6071	-0.5684	0	1	1.3e+02	4	-.MLDIADFVSDR.G
2670	651.6081	1301.2017	1300.6663	0.5354	0	13	9.5	2	K.TWVPENVTVEK.R
3242	682.0836	1362.1527	1361.6674	0.4853	1	10	15	5	K.NKEDASSLLEEK.A 3249
3555	465.8935	1394.6587	1391.6640	2.9947	1	5	53	7	K.QSSKAASGAEEATR.K
4423	749.3591	1496.7037	1494.7758	1.9279	0	19	1.8	1	K.YIPGAPEFLPYTK.E
6868	853.5061	1704.9977	1706.8661	-1.8684	0	(2)	98	4	R.YEVMQIGSQLNGLQK.E
6964	857.7146	1713.4147	1714.8962	-1.4814	2	2	89	3	K.AASGAEEATRKIQDLR.V
7058	862.7051	1723.3957	1722.8611	0.5347	0	3	75	4	R.YEVMQIGSQLNGLQK.E 7041 7062
8994	959.8036	1917.5927	1917.8791	-0.2864	2	9	19	2	K.YAGYSTCYRKEAGAHGK.D 9004
9027	641.7172	1922.1297	1919.9094	2.2203	1	1	1.2e+02	7	K.KYDLEAWFPFQGEYK.E
10906	718.8502	2153.5287	2155.0264	-1.4977	1	5	42	2	K.GYKPNQPPQFMLKDMMAK.T 10937

11375	1108.7701	2215.5257	2215.2212	0.3045	0	93	6.2e-08	1	K.SLGLPYQIVTIVSGALNNAASK.K 11376 11380 11385
12051	771.9475	2312.8207	2311.0651	1.7556	1	0	1.2e+02	7	R.DCLSHHEVLTRLDGYDPER.G
14985	935.7739	2804.2997	2804.4028	-0.1031	2	1	92	9	K.TWVPENVTVEKRDCLSHHEVLTR.L

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128. gi|220690053|gb|EED46403.1| **Mass:** 57832 **Score:** 191 **Queries matched:** 30 **emPAI:** 0.18

ATP sulphurylase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1245	540.1241	1078.2337	1077.6070	0.6267	0	20	1.6	1	R.IAFVASELTK.A
1413	555.3251	1108.6357	1107.6189	1.0168	0	9	21	9	R.EAIWHAIIR.K 1406
1734	584.4016	1166.7887	1167.5745	-0.7857	1	9	19	4	R.EDRHTNIQR.I
1829	594.0741	1186.1337	1185.6982	0.4355	1	6	44	8	R.VRAYQALLPR.Y
2295	631.5491	1261.0837	1260.6098	0.4739	0	4	69	5	R.HELSSELGFSR.E
2339	633.6191	1265.2237	1262.6407	2.5830	0	0	1.5e+02	8	K.LNHYDYVALR.Y
2512	642.7016	1283.3887	1283.6946	-0.3059	0	7	34	6	R.ALQVTLNQQGGR.A 2521
3748	710.9846	1419.9547	1418.7769	1.1778	0	71	1.1e-05	1	R.NLAILTIDDIYR.A 3746
5744	811.8551	1621.6957	1621.8511	-0.1554	1	10	14	3	R.MGGPREAIWHAIIR.K 5745 5765
6469	839.2366	1676.4587	1674.8949	1.5638	0	36	0.036	1	R.YPNGMAVLGLLGLAMR.M 6439 6457 6472 6476 6478 6483 648
6688	846.7061	1691.3977	1690.8898	0.5079	0	(2)	89	3	R.YPNGMAVLGLLGLAMR.M
6695	846.8921	1691.7697	1690.8898	0.8799	0	(5)	49	2	R.YPNGMAVLGLLGLAMR.M
6728	565.8189	1694.4347	1692.8947	1.5400	0	38	0.023	1	K.AGAAVIAAPIAPYEHSR.K 6730
6927	570.8542	1709.5407	1706.8848	2.6560	0	(7)	29	5	R.YPNGMAVLGLLGLAMR.M
8200	918.3351	1834.6557	1834.9485	-0.2928	2	0	1.4e+02	9	R.VVAFQTRNPMHRAHR.E
8826	634.6682	1900.9827	1898.9949	1.9878	1	5	44	2	K.DEVPAGVKTLDISGTELR.N
11298	736.8465	2207.5177	2205.1221	2.3957	1	3	72	6	R.YPNGMAVLGLLGLAMRMGGPR.E

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129. gi|220692783|gb|EED49129.1| **Mass:** 58156 **Score:** 188 **Queries matched:** 19 **emPAI:** 0.12

IMP dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1147	530.6561	1059.2977	1058.6448	0.6529	1	7	36	8	R.SKLVGIVTSR.D
1504	1125.6090	1124.6017	1124.4842	0.1175	0	6	35	9	R.GMGSIAAMEDK.K
2888	664.4331	1326.8517	1328.6870	-1.8353	1	4	60	2	M.PISNGDALGRAMK.A 2887 2890 2894 2903
4058	727.7386	1453.4627	1451.7732	1.6895	0	66	4.1e-05	1	R.EQAAPLIAAGADGLR.I 4052 4072
4271	739.7751	1477.5357	1475.7224	1.8133	1	2	88	9	-.MPISNGDALGRAMK.A
4910	774.8266	1547.6387	1547.7652	-0.1264	2	3	79	3	K.AGAGSKDSKASNAGTAR.Y
6229	830.7866	1659.5587	1658.7756	0.7831	2	8	23	3	K.AYRGMGSIAAMEDKK.A 6263
6675	846.3061	1690.5977	1689.8978	0.7000	0	5	51	3	R.YENGFILDPVVLSPK.A
8556	625.4719	1873.3937	1871.0477	2.3461	1	5	46	3	R.VLVAQGVSGSVLDRGSVTK.F
14431	893.0702	2676.1887	2674.3353	1.8534	0	56	0.00025	1	R.IGMGSGSACITQEVMAVGRPQAISVR.S 14423
16163	1113.5005	3337.4797	3334.7126	2.7672	0	18	1.3	1	K.HGALTYNDFLILPGYIGFPASDVTLDTPVTK.R

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130. gi|220695604|gb|EED51947.1| **Mass:** 28984 **Score:** 187 **Queries matched:** 7 **emPAI:** 0.24
HAD superfamily hydrolase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1142	1059.5770	1058.5697	1058.5971	-0.0274	2	6	52	6	K.KEEDKVIAK.L
2689	652.2311	1302.4477	1301.7092	0.7386	0	5	59	2	K.YHLAVVSSSALR.R
3218	681.2291	1360.4437	1358.7843	1.6594	1	5	48	6	K.LLKELGAEVIMK.D
8946	958.1541	1914.2937	1913.9272	0.3665	0	87	2.7e-07	1	R.YTGEQLIQDFVGQNFR.G 8960 8969 8974

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131. gi|220690412|gb|EED46761.1| **Mass:** 16949 **Score:** 187 **Queries matched:** 19 **emPAI:** 1.07
60S ribosomal protein L23 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
105	718.5250	717.5177	717.4021	0.1156	0	20	2.5	1	K.TLELSR.S 104
657	476.8446	951.6747	951.4913	0.1834	0	41	0.012	1	K.LYDVDTVK.V 658
1130	1057.2290	1056.2217	1055.5723	0.6494	2	6	39	3	M.APKADNKQGK.T
3949	722.2026	1442.3907	1441.7664	0.6243	0	67	3.2e-05	1	R.LTPDVDALDIAATK.L 3957 3971
4271	739.7751	1477.5357	1477.7850	-0.2493	0	(43)	0.0085	1	K.VILYPLNTESAMK.K 4289
4413	748.7441	1495.4737	1493.7799	1.6938	0	44	0.0061	1	K.VILYPLNTESAMK.K 4404 4407 4412 4421
5285	793.3386	1584.6627	1582.9155	1.7473	2	6	40	1	K.TKPSDRAGAAAKAVLK.G
5787	813.2991	1624.5837	1621.8749	2.7088	1	2	1e+02	9	K.VILYPLNTESAMKK.I
5882	817.6506	1633.2867	1631.8770	1.4097	0	2	96	3	K.IEENNTLVFIVDVK.A
7409	881.3021	1760.5897	1759.9720	0.6177	1	4	65	1	K.KIEENNTLVFIVDVK.A

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132. gi|220700002|gb|EED56341.1| **Mass:** 58413 **Score:** 187 **Queries matched:** 36 **emPAI:** 0.32
14-alpha sterol demethylase Cyp51A [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
443	440.1896	878.3647	878.4749	-0.1102	0	12	12	10	K.EVLDYLK.T
2739	655.5511	1309.0877	1308.6463	0.4415	0	32	0.086	1	K.GTSSPYLPFGAGR.H 2738
4743	767.4426	1532.8707	1530.8770	1.9938	0	36	0.04	1	R.DLDLLPLHQNLIK.E
5212	527.2382	1578.6927	1576.9235	1.7692	2	2	86	6	R.LHLSIHSLMRKVK.N 5211
5241	528.0642	1581.1707	1581.7643	-0.5936	1	12	8.2	3	R.MREIYMDIINER.R 5271
5384	797.8286	1593.6427	1594.8137	-1.1710	2	6	33	4	R.EIYMDIINERRK.N
5946	547.1579	1638.4517	1639.8756	-1.4239	0	6	39	3	K.FAYVNLGVIVATMAR.H
7210	871.1876	1740.3607	1737.8654	2.4953	2	4	63	3	R.MREIYMDIINERR.K
7362	586.4289	1756.2647	1753.8603	2.4044	2	(4)	65	6	R.MREIYMDIINERR.K
7506	885.6076	1769.2007	1769.8552	-0.6545	2	(3)	82	10	R.MREIYMDIINERR.K
8383	619.0132	1854.0177	1852.0094	2.0083	0	44	0.0055	1	K.FGLTQAALESHVPLIEK.E
8388	619.1629	1854.4667	1852.9241	1.5427	0	4	58	4	R.VEITDAMAEITIFTAGR.A
8418	929.4246	1856.8347	1855.9807	0.8540	0	(69)	1.7e-05	1	R.GFTPINFMLPWAPLPR.N 8406 8428

8549	937.4641	1872.9137	1871.9756	0.9381	0	72	8.2e-06	1	R.GFTPINFMLPWAPLPR.N
9978	1019.4761	2036.9377	2036.0699	0.8678	1	2	85	3	K.FAYVNLGVIVATMARHMK.L
10367	694.2195	2079.6367	2078.0241	1.6126	0	20	1.4	1	R.LASEPAVMEELYQEQITK.L
11396	740.7102	2219.1087	2219.0575	0.0512	2	4	47	3	R.DAAHARMREIYMDIINER.R
11456	743.8942	2228.6607	2227.1493	1.5114	1	1	1e+02	4	R.CIGEKFAYVNLGVIVATMAR.H 11455
11503	1119.1916	2236.3687	2235.0524	1.3163	2	(2)	77	7	R.DAAHARMREIYMDIINER.R
11575	750.4735	2248.3987	2247.2991	1.0997	2	7	27	8	R.KITVYLGIQGNEFILNGKLK.D
11630	753.3509	2257.0307	2254.2197	2.8110	2	4	48	6	R.GFTPINFMLPWAPLPRNRK.R 11623
12022	771.1362	2310.3867	2311.1478	-0.7611	1	1	1e+02	4	K.GTSGRVEITDAMAEITIFTAGR.A
12679	804.9729	2411.8967	2410.0504	1.8463	1	5	39	3	K.NPDRETSDMIWNLMHCTYK.N 12660
13517	841.6595	2521.9567	2520.3093	1.6474	2	1	85	9	R.HRCIGEKFAYVNLGVIVATMAR.H
15032	943.2272	2826.6597	2825.4721	1.1877	2	9	14	2	K.FAYVNLGVIVATMARHMKLFNVDGK.K 15034
15147	952.0922	2853.2547	2852.4279	0.8268	2	1	87	2	K.KGVPATDYSSMFSGPSKPAIIGWERR.F
15660	1026.8582	3077.5527	3077.4806	0.0721	0	8	18	1	K.EIAHMMITLLMAGQHSSSSISSWIMLR.L

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133. gi|414296|gb|AAA32699.1| **Mass:** 46710 **Score:** 186 **Queries matched:** 14 **emPAI:** 0.31

O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3710	708.6931	1415.3717	1414.6729	0.6989	0	82	9.5e-07	1	R.SGASFSDFLQQTK.G 3713
5076	783.5086	1565.0027	1562.7253	2.2774	0	7	28	1	K.GLFDYYSTVDEVR.G
6072	824.6816	1647.3487	1645.7947	1.5540	1	0	1.5e+02	3	R.YLATAGETKSPEDHK.L
7885	901.8376	1801.6607	1801.8958	-0.2351	2	4	53	5	K.RYLATAGETKSPEDHK.L
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M 10286
10520	1051.0501	2100.0857	2100.0595	0.0262	0	36	0.032	1	R.ILLDEMIMPDLLAQDSQR.F
10814	715.2352	2142.6837	2140.0657	2.6181	1	2	79	1	R.FMNQIDMTVVLTLNGKER.S
10974	722.3702	2164.0887	2165.2532	-1.1644	2	3	60	4	M.ALPSKAALVGLANTLSEQVKR.Y 10983
11043	725.0985	2172.2737	2171.1051	1.1686	0	51	0.00098	1	K.GKPPSWNVPSPFSLAFDPTK.G 11051
12437	792.6655	2374.9747	2375.1824	-0.2077	1	2	79	6	K.SRILLDEMIMPDLLAQDSQR.F

Proteins matching the same set of peptides:

gi|456284|gb|AAA32697.1| **Mass:** 46710 **Score:** 186 **Queries matched:** 14

O-methyltransferase [Aspergillus parasiticus]

gi|2498702|sp|Q12120.1|OMTA_ASPPA **Mass:** 46710 **Score:** 186 **Queries matched:** 14

RecName: Full=Sterigmatocystin 8-O-methyltransferase; Flags: Precursor

gi|45477394|gb|AAS66017.1| **Mass:** 46710 **Score:** 186 **Queries matched:** 14

methyltransferase A [Aspergillus parasiticus]

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134. gi|220695029|gb|EED51372.1| **Mass:** 62126 **Score:** 184 **Queries matched:** 15 **emPAI:** 0.17

2-methylcitrate dehydratase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
20	648.5020	647.4947	647.3602	0.1345	0	12	14	8	R.ISSVSR.I
1237	539.5736	1077.1327	1077.6546	-0.5219	0	15	5.8	3	K.VGLDHVVLVK.V 1236
1345	1096.8880	1095.8807	1095.5084	0.3723	0	6	38	5	K.SALEGYDVDK.Y
1688	579.5506	1157.0867	1156.6313	0.4555	1	6	44	6	R.AVNSTAPRVSR.F
2109	619.5846	1237.1547	1235.6159	1.5388	0	32	0.1	1	R.HLQAHFEQAR.I
5567	805.3651	1608.7157	1606.8539	1.8618	2	1	1.1e+02	7	R.SPRTFQSRISSVSR.I
6086	825.2481	1648.4817	1647.8906	0.5911	0	116	4e-10	1	R.LVFLDTLGCGLEALK.F 6089
8256	615.1499	1842.4277	1840.9214	1.5064	2	8	25	5	K.DIKEVTNRTHEACIR.I
11057	725.7745	2174.3017	2174.9698	-0.6681	2	7	27	1	R.HSPNTMSRKSWAAGDACQR.A
12562	798.4762	2392.4067	2391.2263	1.1804	0	29	0.17	1	K.GEGGLHTVLSAPVWGFYDVLFK.G
13804	855.1205	2562.3397	2564.2904	-1.9507	1	0	1.1e+02	4	K.MLGLSEKQTADAISQAFVDGQSLR.T
14549	900.3315	2697.9727	2698.3999	-0.4272	1	4	47	10	K.EVLEAMIKAHEIQGVLALENSYNK.V
16302	1142.1169	3423.3287	3420.7923	2.5365	2	1	71	10	K.VATTAVVAKMLGLSEKQTADAISQAFVDGQSLR.T

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135. gi|220699808|gb|EED56147.1| **Mass:** 43546 **Score:** 181 **Queries matched:** 19 **emPAI:** 0.55

NADH-ubiquinone oxidoreductase 39 kDa subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
270	818.4940	817.4867	817.3930	0.0938	1	10	20	4	R.ERQEEK.K
1524	565.1146	1128.2147	1127.5135	0.7012	0	38	0.031	1	R.DSPSEFFATK.A 1521
1733	1167.7650	1166.7577	1167.5924	-0.8347	0	8	22	1	R.VNFLEYDLR.N 1739
2417	637.7371	1273.4597	1271.6622	1.7975	0	43	0.0093	1	R.HSDIVYNLVGR.Q
4409	748.6326	1495.2507	1494.7202	0.5306	0	64	6e-05	1	K.EYSTAEIAELVDR.E 4423
5965	820.9701	1639.9257	1638.7274	1.1983	0	58	0.00024	1	K.NFSYTDVHVDGTER.I
7071	863.2341	1724.4537	1722.8478	1.6059	0	10	15	2	R.YWPVHAPDVGNALER.M 7036
7335	877.3016	1752.5887	1751.9246	0.6641	0	48	0.0022	1	K.LLWWPIISPDEVER.E 7340
7485	884.7786	1767.5427	1766.0414	1.5013	1	1	1.3e+02	9	R.NLQDVAITRTGKPILK.V
8210	613.0085	1836.0037	1834.9326	1.0711	0	3	75	4	R.SSLGGHTATVFGATGFLGR.Y
10395	695.0005	2081.9797	2083.0078	-1.0281	1	6	37	2	R.LASQGCTVVVPYREEMTK.R
14889	926.6642	2776.9707	2774.4102	2.5606	0	31	0.079	1	R.SIYPETTIVRPAPMFGFEDNLLHK.L 14883
14951	930.7325	2789.1757	2790.4051	-1.2294	0	(0)	1e+02	1	R.SIYPETTIVRPAPMFGFEDNLLHK.L

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136. gi|1293655|gb|AAC49318.1| **Mass:** 70341 **Score:** 179 **Queries matched:** 29 **emPAI:** 0.31

versicolorin B synthase [Aspergillus parasiticus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
314	421.0041	839.9937	840.5545	-0.5608	1	7	28	9	R.VLGVKGLR.I
913	503.6206	1005.2267	1005.4880	-0.2612	0	30	0.18	1	R.VLFDDQNR.A
1025	518.9821	1035.9497	1034.5066	1.4431	0	4	64	6	R.EIVASDVMR.E
1191	535.2076	1068.4007	1067.6927	0.7080	2	10	16	6	K.ARVLGVKGLR.I
2160	623.2131	1244.4117	1244.5819	-0.1702	0	3	79	1	K.VESHSQLMGNK.E

2438	639.1011	1276.1877	1275.6935	0.4942	0	50	0.0016	1	K.DHLEQLGIPVR.S 2455
2750	656.0041	1309.9937	1308.6245	1.3693	1	12	9.7	1	R.DQEMAVAAFRR.C
2873	663.8056	1325.5967	1325.7377	-0.1410	0	(11)	14	5	R.SPQLLMVSGIGPK.D
3013	670.7451	1339.4757	1340.8140	-1.3383	2	2	95	8	K.AVVDSKARVLGVK.G
3044	672.1071	1342.1997	1341.7326	0.4671	0	40	0.017	1	R.SPQLLMVSGIGPK.D 3056
4163	489.6049	1465.7927	1464.7361	1.0566	0	12	9.2	1	R.SYITHTINPYTR.R
5589	537.6929	1610.0567	1608.7613	1.2954	2	4	67	7	R.DQEMAVAAFRRCR.E
6130	826.8116	1651.6087	1650.8035	0.8052	0	13	7.1	2	R.EALMESNNLNIFTR.T
6782	850.7426	1699.4707	1698.8253	0.6454	0	79	2e-06	1	K.GLLTNPGQDYFAFEK.H 6778
7064	575.5309	1723.5707	1721.7905	1.7802	0	4	60	10	K.NYFSMSAALMTPFSR.G
7828	898.6956	1795.3767	1793.8519	1.5248	0	18	2.2	1	K.MGFPEAQGFSNGNLLGR.S 7816 7836
7955	603.8105	1808.4097	1809.8468	-1.4371	0	(5)	45	4	K.MGFPEAQGFSNGNLLGR.S
13543	**841.9519**	**2522.8337**	**2521.2754**	**1.5583**	**1**	**28**	**0.2**	**1**	**K.VKNPLFDWYQYTTPQPGLAQR.E** 13551
14217	883.4865	2647.4377	2645.2755	2.1623	1	2	70	1	R.ETASSSYLREALMESNNLNIFTR.T
14249	885.4762	2653.4067	2652.3509	1.0558	0	24	0.49	1	R.IVDASIFPFAIDGQPMGTVYALAEK.I 14246
14347	889.8975	2666.6707	2668.3458	-1.6751	0	(6)	28	3	R.IVDASIFPFAIDGQPMGTVYALAEK.I 14363

Proteins matching the same set of peptides:

gi|1293657|gb|AAC49319.1| **Mass:** 70341 **Score:** 179 **Queries matched:** 29
versicolorin B synthase [Aspergillus parasiticus]
gi|45477389|gb|AAS66012.1| **Mass:** 70341 **Score:** 179 **Queries matched:** 29
versicolorin B synthase [Aspergillus parasiticus]

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137. gi|220701430|gb|EED57768.1| **Mass:** 71526 **Score:** 179 **Queries matched:** 23 **emPAI:** 0.09
2-isopropylmalate synthase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1610	1139.8910	1138.8837	1137.5852	1.2985	1	0	1.4e+02	10	R.IVFNMDKQK.S
2447	**639.2606**	**1276.5067**	**1277.6914**	**-1.1847**	**2**	**13**	**9.1**	**3**	**R.RIVFNMDKQK.S** 2440
2671	**651.6116**	**1301.2087**	**1301.7303**	**-0.5216**	**2**	**2**	**1e+02**	**10**	**K.IVQKKSEEVSR.E**
4576	**759.3236**	**1516.6327**	**1516.8977**	**-0.2650**	**2**	**2**	**90**	**4**	**R.ALQVEFSKIVQKK.S** 4571
5864	816.6971	1631.3797	1629.6941	1.6857	0	7	32	9	R.DGNQSLPDPMDGEQK.F
5987	**548.4649**	**1642.3727**	**1641.8951**	**0.4776**	**1**	**7**	**27**	**2**	**R.VNSQSGKGGAAWVILR.S**
6509	561.0272	1680.0597	1678.8905	1.1692	2	1	1.1e+02	9	K.FRFFKMLVDIGYK.E
6871	**853.6666**	**1705.3187**	**1703.8083**	**1.5104**	**0**	**43**	**0.0077**	**1**	**R.GCAIAAAELAQMAGAQR.V**
8494	**623.1882**	**1866.5427**	**1865.0523**	**1.4904**	**1**	**2**	**83**	**1**	**K.GGAAWVILRSLELDLPR.A**
9040	**963.2351**	**1924.4557**	**1923.9910**	**0.4647**	**2**	**2**	**84**	**9**	**R.IVFNMDKQKSLEMAVR.C**
9125	**646.2249**	**1935.6527**	**1932.8636**	**2.7891**	**1**	**1**	**97**	**3**	**R.DGNQSLPDPMDGEQKFR.F** 9108
11548	748.6749	2243.0027	2244.2531	-1.2504	2	1	96	5	R.FKPLHLPDRQWPNKVIEK.A 11549
12460	**1190.4281**	**2378.8417**	**2378.2305**	**0.6113**	**0**	**91**	**8.6e-08**	**1**	**R.LVETPGVVPDDVWLQVLSPCR.E** 12462 12463 12465
13343	**834.3119**	**2499.9137**	**2501.1493**	**-1.2355**	**1**	**0**	**1.1e+02**	**4**	**R.WLATDLRDGNQSLPDPMDGEQK.F**

13833	856.9165	2567.7277	2565.4027	2.3250	2	5	39	1	R.VNSQSGKGGAAWVILRSLELDLPR.A
16004	1089.2619	3264.7637	3262.6087	2.1550	2	3	53	2	R.EKYVVSIHPHNDRGCAIAAAELAQMAGAQR.V

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138. gi|220695168|gb|EED51511.1| **Mass:** 53246 **Score:** 176 **Queries matched:** 18 **emPAI:** 0.27

aldehyde dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
902	502.0561	1002.0977	1002.5458	-0.4481	0	15	6	2	M.ASITVTGAAGR.Q
2541	644.1981	1286.3817	1284.6608	1.7209	0	41	0.013	1	K.GMNIPQAVGNLR.Y 2530
3305	1369.3660	1368.3587	1367.8248	0.5339	2	8	24	3	K.NTSGPARAKLLLK.L
4414	748.7571	1495.4997	1494.9497	0.5500	2	5	49	2	R.AKLLLKLADLIER.D
4947	776.3946	1550.7747	1550.6923	0.0825	0	16	4	1	R.DMGEEALEGWTSVK.S 4944
7553	887.2426	1772.4707	1770.9952	1.4756	2	10	16	2	K.TAASTNLKRVNLELGGK.G 7544
11204	1097.3796	2192.7447	2192.0208	0.7239	0	73	6e-06	1	K.GPSIVFDDCDLDNAVLWTR.I 11217
11275	1102.2916	2202.5687	2201.0012	1.5675	0	10	13	1	R.DADDFASLEAVDAGVLYTDSK.G
12264	1174.2571	2346.4997	2346.1995	0.3003	0	57	0.00028	1	K.EEIFGPVASIAPFETEAEVIAK.A 12262
13054	1233.8146	2465.6147	2464.3011	1.3137	0	23	0.72	1	R.EPLGVCGAIVPWNAPLMITIWK.L
13831	856.8099	2567.4077	2564.4577	2.9500	0	39	0.016	1	K.LAPALAAGNSLIIKPSELSPLYAQK.L
14221	883.7049	2648.0927	2647.3567	0.7360	2	2	76	10	R.DMGEEALEGWTSVKSVKYAILPPK.L
15816	1053.4612	3157.3617	3158.5819	-1.2202	2	1	80	3	K.RVNLELGGKGPSIVFDDCDLDNAVLWTR.I

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139. gi|220688456|gb|EED44809.1| **Mass:** 25719 **Score:** 176 **Queries matched:** 26 **emPAI:** 1.08

60S ribosomal protein L13 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
285	827.5390	826.5317	826.4912	0.0405	0	30	0.16	1	R.ANATLPIK.N 286 289
442	440.0271	878.0397	877.4909	0.5488	0	50	0.0019	1	R.GFTLAELK.E 439 441 443
901	501.8581	1001.7017	1001.5142	0.1876	0	27	0.43	1	K.ESLVANVDR.L 896 898 899
1038	520.3916	1038.7687	1036.5124	2.2563	1	4	59	6	R.CPTVKYNR.R
1929	1208.0730	1207.0657	1205.5775	1.4882	0	21	1.3	1	K.LDSSAEEVSAAK.A
2008	611.1711	1220.3277	1219.6421	0.6856	2	6	47	9	K.GEEAAYRRLR.E
2969	668.2046	1334.3947	1333.6725	0.7222	1	100	1.5e-08	1	K.KLDSSAEEVSAAK.A 2962
3442	461.6342	1381.8807	1379.7885	2.0922	1	25	0.44	1	K.KLASTIGIAVDHR.R 3439
3660	470.2682	1407.7827	1407.7946	-0.0119	1	4	63	6	K.LASTIGIAVDHRR.V
3752	474.5429	1420.6067	1419.7120	0.8948	0	49	0.002	1	K.HNNQILNQHFR.K 3751
4237	492.6309	1474.8707	1472.8239	2.0469	1	3	73	4	R.GFTLAELKEAGIPK.K
6129	826.8066	1651.5987	1648.8784	2.7203	2	0	1.3e+02	7	K.ESLVANVDRLKDYK.A
7375	879.7861	1757.5577	1756.9883	0.5695	2	4	62	4	K.LRPVVRCPTVKYNR.R
8033	606.3662	1816.0767	1814.1002	1.9765	1	5	45	5	K.AAAVAPRPVDKLRPVVR.C
9426	659.2422	1974.7047	1975.1214	-0.4167	2	2	88	9	K.EAGIPKKLASTIGIAVDHR.R

140. gi|220693734|gb|EED50079.1| **Mass:** 42627 **Score:** 176 **Queries matched:** 11 **emPAI:** 0.35

S-adenosylmethionine synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1701	580.7771	1159.5397	1158.6244	0.9153	0	13	9.3	5	K.SSEELVQIVR.N
2370	635.0111	1268.0077	1267.6772	0.3305	0	31	0.14	1	K.QVIPAELLDDR.T 2368
3970	723.2241	1444.4337	1443.7471	0.6867	0	74	5.6e-06	1	R.FVIGGPQGDAGLTGR.K
5155	787.2581	1572.5017	1571.8420	0.6597	1	1	1.2e+02	10	R.FVIGGPQGDAGLTGRK.I
12901	814.5199	2440.5377	2442.1604	-1.6227	1	3	55	1	K.IIVDTYGGWGAHGGGAFSGKDYSK.V
13860	858.6879	2573.0417	2570.2554	2.7863	2	7	27	2	R.KIIVDTYGGWGAHGGGAFSGKDYSK.V 13855
15011	938.8859	2813.6357	2812.3569	1.2788	2	1	82	6	K.IIVDTYGGWGAHGGGAFSGKDYSKVDR.S
15539	1014.5835	3040.7287	3040.4811	0.2476	0	48	0.0015	1	K.TCNVLVAIEQQSPDIAQGLHYDEALEK.L
15860	1063.3369	3186.9887	3185.6319	1.3569	0	92	5.7e-08	1	K.LGAGDQGIMFGYATDETPELLPLTVILSHK.L

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141. gi|220688462|gb|EED44815.1| **Mass:** 53555 **Score:** 174 **Queries matched:** 22 **emPAI:** 0.20

succinyl-CoA synthetase beta subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1418	555.7696	1109.5247	1106.5278	2.9970	0	5	47	3	K.SLGNDDMVIK.A
1746	585.6301	1169.2457	1168.5149	0.7308	0	68	2.5e-05	1	K.LGFDDNADFR.Q 1752
1932	604.6996	1207.3847	1206.6132	0.7715	0	62	9.7e-05	1	K.SAFELITSDPK.V 1930
3381	688.3971	1374.7797	1375.7460	-0.9662	1	18	2.6	2	K.GGVRVIYSPTEAK.M 3400
3410	460.0165	1377.0277	1378.7755	-1.7478	2	9	21	6	K.SVQFSKVVKMAR.E
4269	739.6666	1477.3187	1476.7460	0.5727	0	89	1.8e-07	1	K.IFSIEDLQNAAEK.S
4330	496.0949	1485.2627	1485.8528	-0.5901	1	6	39	7	R.SRPIAAAFRAATVR.F
4810	770.9481	1539.8817	1539.8396	0.0422	0	0	1.3e+02	3	K.ETPEAIITTPIDIK.V
5533	803.8431	1605.6717	1605.8371	-0.1654	1	2	1e+02	9	K.MFAGQMIGHKLITK.Q
6220	830.4321	1658.8497	1657.8749	0.9748	2	4	63	5	K.DTIQKLYKVFMEK.D
7798	897.2271	1792.4397	1791.8713	0.5684	0	6	39	3	K.IATELGFSEQCIPEAK.D
8462	621.6522	1861.9347	1858.9571	2.9776	1	12	8.2	2	K.SLGNDDMVIKAQVLAGGR.G 8451
9528	995.3141	1988.6137	1987.9819	0.6318	0	1	98	2	R.CDAIAQGLINVVNEMGLR.T
10060	1023.4541	2044.8937	2044.0735	0.8202	2	3	69	1	K.SLGNDDMVIKAQVLAGGRGK.G
10677	709.1625	2124.4657	2123.0544	1.4114	1	0	1.2e+02	6	R.VIYSPTEAKMFAGQMIGHK.L
12028	1156.3491	2310.6837	2310.0764	0.6073	2	0	1.2e+02	5	R.QKEVFSWRDTTQEDADEVK.A
14119	876.7075	2627.1007	2625.3731	1.7277	1	3	58	2	R.CDAIAQGLINVVNEMGLRTPIVAR.L 14118

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142. gi|220697094|gb|EED53435.1| **Mass:** 47231 **Score:** 174 **Queries matched:** 21 **emPAI:** 0.31

argininosuccinate synthase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
370	857.8760	856.8687	857.4607	-0.5919	0	9	23	5	R.IDIVENR.F
627	468.7291	935.4437	936.5181	-1.0744	2	1	1.3e+02	8	R.DPKFFKR.F
774	977.6210	976.6137	976.6069	0.0068	2	8	29	7	R.LKKYGLQK.A 771

906	502.4806	1002.9467	1002.5532	0.3935	1	11	15	7	K.KMVIEDLR.R
3471	693.7151	1385.4157	1382.6322	2.7835	0	(3)	79	8	R.GCYDSPAMTILR.A
3595	700.5941	1399.1737	1398.6272	0.5466	0	39	0.018	1	R.GCYDSPAMTILR.A
4690	764.3006	1526.5867	1525.8180	0.7687	0	66	3.5e-05	1	R.FELAFYAIQPSIK.I 4681 4697
5665	808.7146	1615.4147	1613.7937	1.6210	0	46	0.0034	1	K.TYTDSVELFNALNK.L 5637 5641 5681
6231	830.8386	1659.6627	1658.9468	0.7160	2	4	64	5	R.IDIVENRFIGLKSR.G
7713	893.2786	1784.5427	1783.8597	0.6830	0	4	59	5	R.VCLAYSGGLDTSCILR.W
12936	1223.5011	2444.9877	2444.1140	0.8737	0	56	0.00029	1	R.EFVEELCFPAIQCNAIYEGR.Y
15934	1074.3055	3219.8947	3221.6721	-1.7773	2	3	49	3	K.LVTPEKTYTDSVELFNALNKLGYTHGVGR.I 15936
16146	1110.7322	3329.1747	3328.6656	0.5091	2	0	83	9	K.SRGCYDSPAMTILRAAHLDLEGLVLDGQVR.S 16147

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143. gi|220701357|gb|EED57695.1| **Mass:** 46653 **Score:** 173 **Queries matched:** 8 **emPAI:** 0.23

adenylosuccinate synthetase AdB [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
106	720.5980	719.5907	719.3272	0.2635	0	7	41	5	R.DDMIAR.E
4711	765.7236	1529.4327	1528.7620	0.6707	0	21	1.2	1	R.TENTIPADAEVLEK.V
7005	573.5045	1717.4917	1715.9053	1.5864	2	2	80	9	K.ELASLEEKGLEGASKR.I
7006	859.8226	1717.6307	1716.9814	0.6493	0	72	8.3e-06	1	K.LLGPYIVDQLAFLQK.Y 7008
9089	966.2781	1930.5417	1929.8996	0.6421	0	68	2e-05	1	R.FGDLEYNVEEELAQFK.E 9080
14857	924.5392	2770.5957	2770.4389	0.1569	1	2	78	2	K.VGVAYILPDGTRTENTIPADAEVLEK.V

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144. gi|220689982|gb|EED46332.1| **Mass:** 52101 **Score:** 173 **Queries matched:** 32 **emPAI:** 0.63

argininosuccinate lyase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
991	515.6721	1029.3297	1029.5454	-0.2157	0	28	0.27	1	K.NADSLELLR.G
2732	655.2951	1308.5757	1309.7215	-1.1457	2	9	21	5	K.EIGGKLHTGRSR.N
3066	673.6541	1345.2937	1344.7435	0.5502	1	49	0.0023	1	R.RLDSILCDLIK.V
3599	700.6766	1399.3387	1398.8194	0.5193	2	12	9.8	4	R.RLSEIIGKEIGGK.L
3699	707.9586	1413.9027	1413.6818	0.2209	0	6	45	4	R.AFGQMAGLMMTIK.G
3822	715.7041	1429.3937	1429.6768	-0.2830	0	(3)	87	3	R.AFGQMAGLMMTIK.G
3827	715.9921	1429.9697	1429.6768	0.2930	0	(4)	71	2	R.AFGQMAGLMMTIK.G
5217	790.7626	1579.5107	1576.8018	2.7089	0	2	96	1	K.TSVPMDTLSLEQLK.T
5482	534.8449	1601.5127	1599.7450	1.7677	0	8	26	1	R.LSDAYSTGSSLMPQK.K 5481
6093	550.6912	1649.0517	1646.8199	2.2319	1	5	51	4	R.NEQVATDMRLWLR.D
6098	825.6691	1649.3237	1648.8672	0.4566	0	76	4.2e-06	1	K.DLQESIEPLLDHIK.T 6111 6114
6108	826.1626	1650.3107	1649.8260	0.4847	0	45	0.0045	1	K.TGILTQQEFSEIER.G 6115
6647	844.8351	1687.6557	1688.6988	-1.0431	0	4	55	4	R.FDEDVQTCLDYER.A
8953	639.2185	1914.6337	1914.9478	-0.3141	2	12	9.2	1	R.GKAGRAFGQMAGLMMTIK.G 8958
9611	666.2489	1995.7247	1993.9455	1.7792	0	22	0.78	1	R.AEAELDYLMPGYTHLQK.A

10790	1071.1341	2140.2537	2139.0650	1.1887	0	71	9.4e-06	1	R.WSHWILSHATAFASELQR.L
11232	1098.7676	2195.5207	2194.1013	1.4194	0	(27)	0.24	1	K.MTAALAPEMLATEIADYLVR.K
11234	732.8909	2195.6507	2194.1013	1.5494	0	36	0.033	1	K.MTAALAPEMLATEIADYLVR.K
11717	758.5542	2272.6407	2271.2574	1.3834	0	8	18	2	K.TVSDSIQIATGVLSTLTVIPEK.M 11710 11712
11785	761.2769	2280.8087	2280.0377	0.7710	1	0	1.2e+02	9	R.DFAMETMQWGSSFMLKISR.W
12593	800.6205	2398.8397	2400.2478	-1.4080	1	1	95	4	K.ISRWAEDLIIYSSLEFGFVR.L
13560	842.7692	2525.2857	2523.3220	1.9637	1	2	74	8	K.GLPTTYNKDLQESIEPLLDHIK.T
13875	859.3862	2575.1367	2572.2964	2.8403	2	1	99	8	K.AGRAFGQMAGLMMTIKGLPTTYNK.D
13938	863.7809	2588.3207	2590.2043	-1.8836	1	4	46	1	R.ESMAKELGFEGLLYNSMNTVADR.D 13939

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145. gi|220689851|gb|EED46201.1| **Mass:** 40859 **Score:** 171 **Queries matched:** 6 **emPAI:** 0.17

isoflavone reductase family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
9253	977.1696	1952.3247	1951.9262	0.3985	0	85	4.3e-07	1	K.TQNEIYDLLEEISEEK.I 9257 9264 9265
14321	888.1169	2661.3287	2661.3560	-0.0273	2	2	72	2	K.RFVPCGFITVAPPGGIMWLRDEK.E
16410	1165.8202	3494.4387	3491.7341	2.7046	0	62	4.8e-05	1	K.GPEESLTEALEGIDVVISCVGPAEQQDQIPLAK.A

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146. gi|220699072|gb|EED55411.1| **Mass:** 27262 **Score:** 171 **Queries matched:** 20 **emPAI:** 0.26

40S ribosomal protein S6 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
446	881.4950	880.4877	880.3926	0.0951	0	7	25	6	R.EAANDYAK.L
1461	560.0691	1118.1237	1118.6924	-0.5687	2	7	38	8	K.FVIRRTVTK.E
3540	697.5026	1392.9907	1394.6426	-1.6518	1	3	73	8	R.SEAAREAANDYAK.L
3654	704.5991	1407.1837	1407.6817	-0.4979	1	3	68	4	K.ITGGNDKQGFPMK.Q
4970	518.5642	1552.6707	1549.7922	2.8785	1	5	41	7	-.MKLNISYPANGSQK.I 4923 4929
5003	779.5871	1557.1597	1556.7882	0.3716	0	5	47	3	R.LLLADGHSCYRPR.R
5273	792.6671	1583.3197	1582.7185	0.6012	0	59	0.0002	1	R.MGTEVVGDSLGDEFK.G
5304	529.7645	1586.2717	1586.8603	-0.5886	1	4	65	10	K.QGFPMKQGVLLPTR.T
5959	820.7676	1639.5207	1638.8465	0.6742	0	88	2.3e-07	1	K.QGEGELPGLTDTVVPK.R 5957 5976 5978
7370	586.6845	1757.0317	1754.8145	2.2172	1	14	5.9	1	K.RMGTEVVGDSLGDEFK.G
7842	599.8402	1796.4987	1794.9476	1.5511	1	7	25	5	K.QGEGELPGLTDTVVPKR.L
8032	606.3315	1815.9727	1813.9370	2.0358	1	4	62	2	R.TRLLLADGHSCYRPR.R
9342	982.7571	1963.4997	1961.9918	1.5079	2	4	49	4	R.SEAAREAANDYAKLLANR.V
10298	690.9605	2069.8597	2070.0493	-0.1896	2	3	61	4	R.EAANDYAKLLANRVHEEK.A 10302

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147. gi|220700172|gb|EED56511.1| **Mass:** 28769 **Score:** 170 **Queries matched:** 7 **emPAI:** 0.25

proteasome component Prs3, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1258	541.2386	1080.4627	1081.5842	-1.1214	1	4	63	9	R.LDAVVKMYK.Y

10470	1047.8006	2093.5867	2093.0615	0.5252	0	85	4.1e-07	1	R.AAGSAASLIMPFLDNQVNFK.N 10471 10477 10482
15230	963.0692	2886.1857	2884.2909	1.8948	0	4	42	1	M.MSFMGHQPQSQAVGYTFSQPTNAPNK.E 15229

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148. gi|220696535|gb|EED52877.1| **Mass:** 11403 **Score:** 169 **Queries matched:** 19 **emPAI:** 1.20

60S ribosomal protein L30, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
697	481.8136	961.6127	961.5630	0.0497	1	4	77	1	R.LALVMKSGK.V
915	503.9706	1005.9267	1003.5046	2.4221	1	7	32	5	K.KNADSINSR.L
2821	660.1596	1318.3047	1316.6322	1.6725	0	(57)	0.0003	1	K.SELEYYAMLAK.A 2810
2956	667.5656	1333.1167	1332.6271	0.4896	0	58	0.00026	1	K.SELEYYAMLAK.A 2954 2960 2970
4254	738.7401	1475.4657	1475.9187	-0.4530	1	17	3.2	2	K.AKLVIIAANTPPLR.K 4230 4261 4270
5587	537.6095	1609.8067	1606.9480	2.8587	2	1	1.1e+02	10	R.LALVMKSGKVTLGYK.S
9712	670.7969	2009.3687	2007.9585	1.4102	0	61	0.00011	1	K.APVHHFSGNNIELGTACGK.L 9698 9699 9704
11536	747.8132	2240.4177	2240.0995	0.3183	1	(5)	42	6	K.LFRTSTMAVLDAGDSDILTSQ.-
11618	752.4715	2254.3927	2256.0944	-1.7017	1	6	34	4	K.LFRTSTMAVLDAGDSDILTSQ.-

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149. gi|220693968|gb|EED50313.1| **Mass:** 56416 **Score:** 168 **Queries matched:** 27 **emPAI:** 0.49

UDP-N-acetylglucosamine pyrophosphorylase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1322	546.6921	1091.3697	1090.5771	0.7926	0	51	0.0016	1	K.SLFQIQAER.I 1315
1345	1096.8880	1095.8807	1096.6492	-0.7684	1	5	52	7	R.EIKAPAVIEK.E
1469	560.7176	1119.4207	1119.5560	-0.1353	1	28	0.3	1	R.REDEFSPLK.N
2271	630.0171	1258.0197	1257.6864	0.3334	0	10	18	4	K.VAVVLMAGGQGTR.L
2414	637.7276	1273.4407	1271.7085	1.7322	0	20	1.8	2	R.NATESVGLILQK.N
3626	468.5912	1402.7517	1402.7932	-0.0415	1	3	77	8	K.SLFQIQAERIAK.L
4071	728.2331	1454.4517	1453.7102	0.7415	0	40	0.014	1	R.AANIVNHYYSFR.F
6633	844.4526	1686.8907	1685.8274	1.0633	0	37	0.029	1	K.AQLFHQLSNFDPNR.I 6621
7018	860.4726	1718.9307	1719.8654	-0.9347	0	1	1.1e+02	2	K.EAIIPWYVMTSGPTR.K
8790	633.6385	1897.8937	1898.0408	-0.1470	1	(4)	56	3	K.VAVVLMAGGQGTRLGSSAPK.G
8978	639.6675	1915.9807	1914.0357	1.9450	1	7	27	2	K.VAVVLMAGGQGTRLGSSAPK.G 8933 8936
9029	962.3016	1922.5887	1921.0237	1.5650	0	74	5.3e-06	1	K.LEQFVFDVFPLTPLEK.F 9025
9306	654.2525	1959.7357	1956.9186	2.8171	0	20	1.5	1	R.GIEHIHTYCVDNCLVK.V
9901	1016.3751	2030.7357	2029.0593	1.6765	0	44	0.0047	1	K.AAVAPDGNGGIYQALITSGVR.E
11407	741.6042	2221.7907	2221.0750	0.7157	1	3	59	2	K.NGKPDVVEYSEIDKETAEAK.D
11546	748.6329	2242.8767	2244.1862	-1.3095	1	2	82	9	K.SKAAVAPDGNGGIYQALITSGVR.E
12344	787.6045	2359.7917	2361.1859	-1.3942	1	5	39	6	-.MAAAIKETVSNLLHGHSDNTPR.Q
14053	871.4162	2611.2267	2610.2735	0.9533	0	5	33	1	K.TQDGPVTLEPLPEVATASIMDSDPK.D 14019
14701	909.3325	2724.9757	2723.4574	1.5183	1	3	53	6	K.LEQFVFDVFPLTPLEKFASIEVR.R 14682
15227	961.8249	2882.4527	2879.5585	2.8942	2	10	11	1	K.LEQFVFDVFPLTPLEKFASIEVRR.E

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150.  gi|220696166|gb|EED52508.1|     Mass: 14207     Score: 167     Queries matched: 8    emPAI: 0.54
      small nuclear ribonucleoprotein (LSM7), putative [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
      5113  523.9252  1568.7537  1567.6169   1.1369   1     6       37    6   K.ESMRDDEGNENTR.S
      5547  804.3386  1606.6627  1605.8073   0.8555   0    74    6e-06    1   K.GFDQLMNLVLDDVK.E 5534 5560 5567
      5757  812.4766  1622.9387  1621.8022   1.1366   0  (56) 0.00034    1   K.GFDQLMNLVLDDVK.E
      8355  926.8821  1851.7497  1851.9400  -0.1903   2     4       53    1   K.ENILDLSKYMDKEVR.V
      9691  669.8015  2006.3827  2007.0246  -0.6419   2     2       82    5   R.GGHAKSGGASGGAQQQEKPKK.E
```

```
151.  gi|220690751|gb|EED47100.1|     Mass: 62152     Score: 166     Queries matched: 13    emPAI: 0.11
      calnexin [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
       599   463.9866   925.9587   923.5076   2.4511   0     4       63    8   K.ASSPAPAPVK.K
      1736   584.5091  1167.0037  1166.5608   0.4430   0    43   0.0076    1   K.IANPAYFEDK.T 1738
      2121   620.1291  1238.2437  1236.5834   1.6603   0     2       98    6   K.VSEAVSSSADTGK.G
      2135   621.6811  1241.3477  1241.6768  -0.3291   1    13      7.2    2   R.EKVDHFVGLAK.Q
      4102   730.6596  1459.3047  1458.7103   0.5945   2     6       41    9   R.HKNPKTGEYEEK.H
      4366  1490.7590  1489.7517  1487.7997   1.9520   1     4       61    2   K.NPAAHHAISAKFPK.K
      6546   841.7496  1681.4847  1680.6695   0.8153   0     2    1e+02    4   K.CNDVSGCGPWSAPMK.K 6517
      7216   871.2581  1740.5017  1739.7791   0.7226   0    84  5.7e-07    1   K.APFLEQFTDDWESR.W 7248
     10470  1047.8006  2093.5867  2093.1269   0.4598   2     3       68    5   R.EKVDHFVGLAKQDPVNAVK.Q
     10546   702.3525  2104.0357  2102.0044   2.0314   1     1    1e+02    9   K.WTAPMIDNPAYKGPWSPR.K
```

```
152.  gi|220697491|gb|EED53832.1|     Mass: 20218     Score: 166     Queries matched: 26    emPAI: 0.59
      60S ribosomal protein L11 [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
        88  706.4780   705.4707   705.3810   0.0897   0    17      3.5    1   R.FDGIVR.-
       383  859.5140   858.5067   858.4447   0.0621   0    23      1.1    1   K.AEEILER.G 384
      2351  633.9931  1265.9717  1264.7252   1.2466   1    14      6.6    2   R.NEKIAVHVTVR.G 2350
      2373  635.5011  1268.9877  1267.7149   1.2728   2     6       37    1   R.YTVRTFGIRR.N
      2933  666.1076  1330.2007  1331.6615  -1.4608   2     1  1.4e+02   10   K.DKSANPMRELR.I
      3202  680.4231  1358.8317  1357.7201   1.1116   0    28     0.26    1   K.LVLNISVGESGDR.L 3180 3190 3196 3203
      4912  775.1651  1548.3157  1547.8195   0.4962   0    73  7.3e-06    1   K.VLEQLSGQTPVYSK.A 4911 4941 4945
      7087  576.2405  1725.6997  1726.9577  -1.2580   1     5       41    8   R.IQKLVLNISVGESGDR.L
     12012  770.8062  2309.3967  2308.1124   1.2843   0    26      0.3    1   R.NFSETGNFGFGINEHIDLGIK.Y 12009 12010 12015 12019 120
     14301  887.2652  2658.7737  2657.1171   1.6566   0    22     0.76    1   K.YDPGIGIYGMDFYCCMTRPGER.V
```

```
153.  gi|220698179|gb|EED54519.1|     Mass: 124619    Score: 165    Queries matched: 40    emPAI: 0.11
      isoleucyl-tRNA synthetase ,cytoplasmic [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
        68  687.8570   686.8497   686.4439   0.4058   1    10      24    7  R.RTLGLK.T
       113  723.4480   722.4407   722.3963   0.0444   1    24     0.6    4  K.KFVSDK.K
       750  325.0842   972.2307   972.5352  -0.3045   1    14     8.3    3  R.ETIERLGR.W
       888  501.1101  1000.2057   999.5964   0.6093   1    11      13    8  K.VDKITIPSK.Q
      1479  561.3846  1120.7547  1120.5733   0.1815   1     9      22    9  R.MQKVIEMAR.V 1476
      1661  575.6806  1149.3467  1150.6386  -1.2919   0     9      22    9  K.FFEGQVALLK.K
      2469  639.7816  1277.5487  1276.6697   0.8791   1    10      16    3  K.KLGMSGLEAVEK.L 2464 2474 2475
      2672  651.6126  1301.2107  1300.6928   0.5179   0     9      20    7  R.SVHFLAFPEVR.E
      3701  708.1756  1414.3367  1415.7984  -1.4616   2     0  1.5e+02    4  K.KSLPSLTSNDVKK.F
      4151  488.9232  1463.7477  1462.7748   0.9729   2     7      35    5  R.VSRMQKVIEMAR.V
      4291  740.8136  1479.6127  1478.7697   0.8430   2     3      71    2  R.MQKVIEMARVSR.E
      5654  539.2192  1614.6357  1615.9886  -1.3528   2     7      28    5  K.AADKPIIKHLKGIGR.L 5686
      6146  827.2071  1652.3997  1651.7842   0.6155   0    29    0.19    2  K.SFPGDFIAEGLDQTR.G 6120
      7186  870.6581  1739.3017  1739.0094   0.2924   1     7      26    3  R.LYLINSPVVRAEPLR.F
      7478  884.3486  1766.6827  1764.9886   1.6941   1    19     1.8    2  R.DFVGQHVKAADKPIIK.H 7455 7485
      7984  906.8366  1811.6587  1810.9505   0.7082   0    77 2.5e-06    1  R.GLAPFTPFLTDTIYQK.L 7980
      8058  909.7796  1817.5447  1816.9968   0.5479   2     8      23    4  K.KLGMSGLEAVEKLGIEK.Y 8062
      8201  612.6679  1834.9817  1834.9498   0.0319   2     2      80    5  -.MSIDFPKEEELTLKR.W
     10000  680.5342  2038.5807  2036.1994   2.3814   2     3      64    7  K.KILVDGIELVEGDLIVRR.G
     10207 1031.2881  2060.5617  2060.9956  -0.4339   1     4      51    4  R.RFGWDTHGVPIEYEIDK.K
     11346  738.5195  2212.5367  2210.1735   2.3632   2     0  1.2e+02    3  K.YNVQYSVTADWPTLGKKLK.K
     12631  802.2445  2403.7117  2404.2110  -0.4993   1     0  1.2e+02   10  K.GIGRLIVDSQITHSYPFCWR.S
     13141  825.4632  2473.3677  2472.1227   1.2450   1     3      55    2  K.SQGVDYVFDPKAEATNTNVMDR.W
     13470  839.6719  2515.9937  2514.3159   1.6779   2     2      71    4  K.FFEGQVALLKKSQGVDYVFDPK.A
     13654  846.9472  2537.8197  2536.2414   1.5784   1     0  1.1e+02    5  K.AEATNTNVMDRWILASCQSLLK.F
     14156  880.2102  2637.6087  2636.3495   1.2592   0    48  0.0021    1  K.IPCIIPQMLEGIEGSHWVPSFVK.E 14157
     14257  885.8392  2654.4957  2652.3444   2.1513   0  (32)   0.076    1  K.IPCIIPQMLEGIEGSHWVPSFVK.E 14255
     15890 1067.8582  3200.5527  3201.5304  -0.9777   2     2      63    7  K.TMNTSFMESVWWVFKQLFDKDLVYR.G
```

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154.  gi|220698604|gb|EED54944.1|     Mass: 45594    Score: 165    Queries matched: 19    emPAI: 0.23
      pyruvate dehydrogenase E1 component alpha subunit, putative [Aspergillus flavus NRRL3357]
     Query Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
       668 479.3491   956.6837   956.5655   0.1183   0    56 0.00047    1  R.SIIGELLGR.R 672
      1154 531.7251  1061.4357  1060.5077   0.9281   0    19     2.6    3  R.SSALTEYYK.R 1155
      1162 532.6421  1063.2697  1062.5379   0.7318   0     7      38    6  K.VNGMDVLATK.A 1165
      3031 671.6086  1341.2027  1340.6871   0.5157   1     3      89    8  R.MRSTHDPIAGLK.Q
      3671 705.7686  1409.5227  1406.6963   2.8264   1     1 1.3e+02   10  K.VMTEDELKALDK.A 3650
```

4333	743.7826	1485.5507	1483.7163	1.8345	2	1	1.2e+02	3	R.MEMAADRLYKEK.K
5909	818.7666	1635.5187	1634.8225	0.6962	1	1	1.1e+02	4	K.ILDWKVMTEDELK.A
6854	852.6761	1703.3377	1702.8501	0.4876	0	71	1.2e-05	1	K.LWNLPVLFGCENNK.Y 6859 6873
7745	894.7536	1787.4927	1786.9777	0.5150	2	2	96	9	-.MLFRTAWARQAAPLR.R
10086	683.3149	2046.9227	2047.9673	-1.0446	0	0	1.2e+02	9	K.NYAVSGNGPLVMEYVTYR.Y
11630	753.3509	2257.0307	2258.9653	-1.9346	2	2	75	10	K.QMYHDMVSTRRMEMAADR.L
12212	780.1839	2337.5297	2335.0638	2.4659	0	2	71	3	R.AFVDEEVSIAENMPVPDNSTR.I
12321	786.5015	2356.4827	2354.1437	2.3390	0	55	0.00035	1	R.GFCHLSTGQEAVATGIEHAITR.D

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155. gi\|220689889\|gb\|EED46239.1\| **Mass:** 52539 **Score:** 164 **Queries matched:** 19 **emPAI:** 0.13

autophagic serine protease Alp2 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
653	475.5266	949.0387	948.4341	0.6046	0	14	7.5	1	R.AYFSNYGK.C
1444	558.6681	1115.3217	1114.5295	0.7922	0	43	0.0095	1	R.DSLSFGTFNK.Y
2990	669.2466	1336.4787	1335.6565	0.8222	1	18	2.5	3	K.GSVANMSLGGGKSR.T 2986 2992 2996
3769	475.5265	1423.5577	1424.7082	-1.1505	1	10	16	1	K.GFKGSVANMSLGGGK.S
5936	819.6591	1637.3037	1635.8767	1.4271	2	5	43	4	K.VKGFKGSVANMSLGGGK.S
10393	1041.8631	2081.7117	2080.0299	1.6818	0	72	8.1e-06	1	K.CTDIFAPGLNILSTWTGSK.H 10368 10390 10394 10399
12424	792.3065	2373.8977	2373.1635	0.7342	0	16	3.3	1	R.SSGSGTMSDVVLGVEWAVQSHLK.K 12419 12426
12550	797.8412	2390.5017	2389.1584	1.3433	0	(9)	16	1	R.SSGSGTMSDVVLGVEWAVQSHLK.K
13488	840.8545	2519.5417	2517.2534	2.2884	1	0	1e+02	10	R.SSGSGTMSDVVLGVEWAVQSHLKK.A
14818	920.9092	2759.7057	2757.4120	2.2937	1	1	86	6	K.VLRSSGSGTMSDVVLGVEWAVQSHLK.K

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156. gi\|220695424\|gb\|EED51767.1\| **Mass:** 44509 **Score:** 164 **Queries matched:** 18 **emPAI:** 0.33

Ketol-acid reductoisomerase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2065	615.7411	1229.4677	1229.5564	-0.0887	0	17	3.3	1	K.EVYSDLYGER.G
2323	632.7161	1263.4177	1262.6507	0.7671	0	23	0.8	2	K.NLFDVNTAIEK.G
4713	765.8176	1529.6207	1528.7715	0.8493	0	46	0.0041	1	K.TLYFSHGFSPVFK.E 4705 4709 4714
6039	823.6246	1645.2347	1644.7743	0.4604	2	10	17	1	R.SLDYNSQKDYREK.Y
7081	576.1295	1725.3667	1722.9740	2.3927	1	3	62	8	K.AAANALPRVTLSSTPVR.G
7325	876.6661	1751.3177	1749.8897	1.4280	0	3	70	3	R.GINSSIAVYQDVTGQAK.E
10029	681.6545	2041.9417	2038.9782	2.9635	2	3	72	6	K.YEKEMQDIRDLEIWR.A
10504	700.4442	2098.3107	2097.0895	1.2213	1	50	0.0014	1	R.FKDNLKPLFNELYDSVR.D 10501
13947	864.7132	2591.1177	2591.2040	-0.0863	2	3	55	6	K.NISFAGHEETVYEREDWPREK.L 13956
15066	944.1335	2829.3787	2826.5201	2.8586	0	55	0.00034	1	K.GTIVMNLLSDAAQSETWPTIKPLITK.G 15068
15109	948.9422	2843.8047	2842.5150	1.2897	0	(33)	0.05	1	K.GTIVMNLLSDAAQSETWPTIKPLITK.G
16150	1111.7692	3332.2857	3333.5751	-1.2894	1	0	82	6	K.AIAMGVAVGSGYLYETTFEKEVYSDLYGER.G

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157.  gi|220693676|gb|EED50021.1|     Mass: 41507    Score: 162    Queries matched: 8    emPAI: 0.08
      adhesion regulating molecule, putative [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      2413  637.5896  1273.1647  1274.6554  -1.4906   1     3       93   10  K.IPVENGGFMRR.G 2422
     10155  686.1912  2055.5517  2053.1320   2.4197   0     5       46    7  K.VLHSPQFSQSLASLTVAIR.D 10133 10156 10157
     14818  920.9092  2759.7057  2758.4137   1.2920   0    99  1.5e-08    1  K.LGDIVNTLLQGEDVDVEHEIANLPR.G 14820

158.  gi|220699147|gb|EED55486.1|     Mass: 93932    Score: 162    Queries matched: 19    emPAI: 0.11
      iron superoxide dismutase A, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
       191   389.3446   776.6747   776.4214   0.2533   0    20        2    5  -.MAASLIR.T
      1015   518.1371  1034.2597  1032.5716   1.6881   0     6       44    5  K.AAGVAGLTFAR.G
      1261   541.4061  1080.7977  1080.4580   0.3397   0     6       34    9  R.DGELMNVCK.C
      1384   553.3781  1104.7417  1102.5804   2.1613   1     8       30   10  R.ILSMNPKER.S
      1466   560.4696  1118.9247  1118.6019   0.3228   0    11       15    4  K.CALGHIPVPR.T 1465
      2248   628.6296  1255.2447  1254.6204   0.6243   0    44   0.0062    1  K.SQGGGEPPSGALAK.A
      3686   707.2681  1412.5217  1409.6721   2.8496   0     7       32    1  R.EHNPNALASLCGK.C
      3773   713.2901  1424.5657  1423.7532   0.8126   1     6       39    4  R.TTNGLQGLEHRAK.D
      4676   763.4736  1524.9327  1524.7685   0.1642   1     6       35    3  R.FGPRYGISADSLSR.R
      5659   808.5931  1615.1717  1613.7573   1.4144   0    26     0.38    1  K.AIDESFGSLGEFQSK.M
      8553   937.5671  1873.1197  1871.9716   1.1481   0    30     0.16    1  K.MNAALAGIQGSGWAWLVK.D
      8727   630.9705  1889.8897  1887.9665   1.9232   0   (1) 1.2e+02    6  K.MNAALAGIQGSGWAWLVK.D
     10379  1041.3566  2080.6987  2080.0364   0.6623   0    90  1.2e-07    1  K.ATLPDLAYDYGALEPSISGK.I 10376
     10943   720.3012  2157.8817  2157.2018   0.6799   2     0  1.3e+02    8  R.TALRAGASATPKAAGVAGLTFAR.G
     11353   738.6379  2212.8917  2211.1661   1.7256   2     4       49   10  R.NLFRHAIVVTRWSDLGDGR.S
     12645   802.8109  2405.4107  2406.1849  -0.7742   1     3       56    1  K.EGLQSKDDVPAMPSLTPLEAHR.L
     14882   926.0502  2775.1287  2773.4320   1.6967   1     0       99    4  R.AISGIFESAITDDTLPGQRILSMNPK.E

159.  gi|220698234|gb|EED54574.1|     Mass: 10101    Score: 161    Queries matched: 5    emPAI: 0.80
      DUF543 domain protein [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      1882  599.5156  1197.0167  1196.5098   0.5069   0    26     0.38    2  R.AWEEADSSFR.R
      3586  700.1756  1398.3367  1398.7718  -0.4351   0    45   0.0045    1  R.ATKPVSEALLNEK.W 3599
      3989  723.8786  1445.7427  1443.7412   2.0016   0    83  8.2e-07    1  R.AWPAWVGLGFGAGR.A 3974

160.  gi|220698203|gb|EED54543.1|     Mass: 10741    Score: 160    Queries matched: 6    emPAI: 1.30
      ubiquinol-cytochrome C reductase complex subunit UcrQ, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      1393   554.1731  1106.3317  1106.5720  -0.2403   0    53  0.00078    1  R.IASYSLSPNR.Q 1411
```

8879	636.2372	1905.6897	1903.9805	1.7092	0	64	5.3e-05	1	R.QRPLAGTAHAAFFNTFR.R 8883
9721	1006.2466	2010.4787	2007.9262	2.5525	0	42	0.0088	1	K.NGVFLGTWGDFGCPTPQR.I 9722

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161. gi\|220690400\|gb\|EED46749.1\| **Mass:** 54446 **Score:** 159 **Queries matched:** 22 **emPAI:** 0.12

D-3-phosphoglycerate dehydrogenase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
152	753.0710	752.0637	752.3123	-0.2486	0	11	10	2	K.QMTDSR.G
514	454.0421	906.0697	907.5240	-1.4542	0	24	0.72	2	R.DVHVIGIR.S 512
1339	548.7561	1095.4977	1094.5356	0.9621	0	21	1.3	2	R.DGSYLINASR.G
1888	599.7531	1197.4917	1197.6717	-0.1800	0	4	58	1	R.AIGVEVGDALVR.Y
2271	630.0171	1258.0197	1257.6452	0.3745	0	13	9.9	2	K.SSLPEDQLIEK.I
2651	650.2956	1298.5767	1297.7030	0.8737	0	20	1.5	1	K.HLKPFATEDIK.V
2671	651.6116	1301.2087	1300.5717	0.6370	0	25	0.6	1	R.SLTMDEPEHAR.V
3160	678.4461	1354.8777	1354.7569	0.1209	0	64	6.3e-05	1	K.VLLLENVNQTGR.D 3168
6515	841.2901	1680.5657	1680.9087	-0.3429	1	8	24	2	R.DILTKQGYQVEFLK.S 6514 6523 6533 6541 6580
7466	883.7046	1765.3947	1765.9509	-0.5562	1	1	1.1e+02	7	R.GSVVDIPALIHAMRSGK.V
9070	643.8479	1928.5217	1929.9003	-1.3786	1	1	1.1e+02	9	R.QFEQMRDGSYLINASR.G 9075
9763	1008.7861	2015.5577	2015.0687	0.4890	0	79	1.5e-06	1	R.YVNEGTTLGAVNLPEVALR.S
10772	713.6659	2137.9757	2136.2266	1.7491	1	6	30	3	R.SVAELVIAEIIALARQLGDR.S
15365	986.2965	2955.8677	2953.4743	2.3934	0	11	9.1	1	R.QVPTLESLLSQSDFVTCHVPELPETK.N

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162. gi\|220697509\|gb\|EED53850.1\| **Mass:** 56414 **Score:** 158 **Queries matched:** 22 **emPAI:** 0.33

translation initiation factor EF-2 gamma subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
625	936.1460	935.1387	934.4872	0.6515	1	12	11	4	R.FKNELER.N
890	1001.4650	1000.4577	1000.5917	-0.1340	1	3	92	9	R.LLGVKTADGK.Q
1783	588.8671	1175.7197	1175.6233	0.0964	0	19	2	1	K.IQCRPIFSR.V
2058	615.3781	1228.7417	1227.7187	1.0230	0	8	24	1	K.GGVAGGSILTGVLK.L 2054
2136	621.6846	1241.3547	1242.7085	-1.3538	0	7	35	7	K.FAVPGGLIGVGTR.V 2145
2880	664.2276	1326.4407	1327.7823	-1.3416	2	6	47	6	R.LLGVKTADGKQAK.V
3185	679.7031	1357.3917	1358.6136	-1.2219	1	6	37	7	K.SEKEIDPPCER.D
3339	686.5621	1371.1097	1370.7194	0.3903	0	38	0.03	1	R.VVSLFAEHNDLK.F
4488	502.6092	1504.8057	1503.8409	0.9648	2	6	42	6	R.FKNELERNITIK.L
4492	753.6306	1505.2467	1504.7443	0.5024	0	10	14	1	K.LSLTSPACTEIGEK.I
4569	759.2431	1516.4717	1515.8621	0.6097	1	10	15	4	K.STVVKAISEVQTVR.F 4581
6255	831.6676	1661.3207	1660.8308	0.4899	0	65	5.4e-05	1	R.SFDVNKPGAEIDELK.G
6319	834.0436	1666.0727	1665.9301	0.1426	0	20	1.6	1	R.GTVADGSPIIPISAQLK.Y
10395	695.0005	2081.9797	2082.1837	-0.2040	1	7	29	1	K.FIRGTVADGSPIIPISAQLK.Y
11247	733.8409	2198.5007	2197.1531	1.3476	0	66	3.1e-05	1	K.YNIDAVNEYLVSHIPVPVR.D 11250

```
      13870   859.2129  2574.6167  2574.3509   0.2658   2     0  1.1e+02  10   K.NEVLMVNIGSTATGAKVMGVKADAAK.L
      15203   958.7752  2873.3037  2870.5389   2.7648   1    24     0.46   1   R.SFDVNKPGAEIDELKGGVAGGSILTGVLK.L 15191
```

```
163.  gi|220692416|gb|EED48763.1|     Mass: 25380     Score: 155     Queries matched: 5    emPAI: 0.13
      conserved hypothetical protein [Aspergillus flavus NRRL3357]
     Query  Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect  Rank   Peptide
       7746  894.7706  1787.5267  1785.9373    1.5894    0     1  1.2e+02    6   K.YDQGGLILVLNSANGPR.R
       8217  919.7316  1837.4487  1836.9774    0.4713    0    91  1.2e-07    1   R.FNAPILYQSVPLNSFK.R 8222
      13334  834.0362  2499.0867  2500.2052   -1.1184    1     4       53    7   R.VMTVMIKYSIMSTFAFANSSEK.V 13336
```

```
164.  gi|220694880|gb|EED51223.1|     Mass: 38139     Score: 154     Queries matched: 19    emPAI: 0.39
      mitochondrial import receptor subunit (tom40), putative [Aspergillus flavus NRRL3357]
     Query  Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect  Rank   Peptide
        671  958.3960   957.3887   957.5647   -0.1760    1     7       34   10   R.WSPKLVTK.T
       1114  527.5971  1053.1797  1052.5477    0.6320    0    32    0.084    1   K.VFGMSPLFR.V 1113
       1719  582.7866  1163.5587  1161.5567    2.0020    1     5       54    8   K.YDFRASTFR.A
       2979  668.7716  1335.5287  1336.6735   -1.1448    1     0  1.6e+02    2   R.ASTFRAQVDSAGK.V
       4544  757.3701  1512.7257  1511.7806    0.9451    0    85    5e-07    1   K.EVLLSNFMFSGLR.A 4543
       5216  790.7471  1579.4797  1577.8525    1.6272    0    35    0.052    1   R.AALGLPNPGTVDNIAR.E 5203
       5226  527.5972  1579.7697  1580.8385   -1.0688    1    21      1.3    1   R.ADLTKVFGMSPLFR.V 5223
       7151  579.8092  1736.4057  1733.9536    2.4521    1    10       13    2   R.RAALGLPNPGTVDNIAR.E
       7919  903.3591  1804.7037  1803.9440    0.7597    0    24     0.54    1   R.IAMPISLTFAGEIDQAK.Q 7922
      10182  687.1332  2058.3777  2056.0663    2.3114    1     1  1.2e+02    9   K.EVLLSNFMFSGLRADLTK.V
      10449  698.0855  2091.2347  2088.9687    2.2660    0     1  1.1e+02    7   K.VFMQGNFGSDGALAAVGNYR.W
      12529  797.1885  2388.5437  2390.2627   -1.7190    2     2       73    8   K.RIAMPISLTFAGEIDQAKQSAK.L
      13236  829.5632  2485.6677  2486.2046   -0.5369    0     1    1e+02    4   R.VEAGVDMNLQFAPNAAAALMGGPSR.D
      13480  840.3822  2518.1247  2518.1944   -0.0697    0   (0)  1.1e+02    9   R.VEAGVDMNLQFAPNAAAALMGGPSR.D
```

```
165.  gi|220701104|gb|EED57442.1|     Mass: 34750     Score: 154     Queries matched: 26    emPAI: 0.58
      cytochrome C1/Cyt1, putative [Aspergillus flavus NRRL3357]
     Query    Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect  Rank   Peptide
        610   465.6791   929.3437   929.4719   -0.1282   0    46   0.0047    1   K.TFDHAALR.R 614
        955   509.8106  1017.6067  1016.5655    1.0412   0    21      1.4    1   K.IVYSPPVSR.R 950
       1644   573.5956  1145.1767  1144.6604    0.5163   1    37    0.042    1   R.KIVYSPPVSR.R 1646
       1730   584.0706  1166.1267  1165.6019    0.5248   0    45   0.0051    1   K.LSDYIPAPYK.N 1741
       2839   660.8641  1319.7137  1318.5758    1.1379   0     5       51    4   R.EVCASCHSLTR.V
       4540   756.8726  1511.7307  1510.6796    1.0511   0    36    0.038    1   R.SFVGVMHTVDEMK.A 4537
       4774   769.1146  1536.2147  1534.8719    1.3429   0    12      9.9    1   R.AANGGALPPDLSLIVK.G 4775 4789
       9930   679.0669  2034.1787  2032.9863    1.1924   1     7       28    2   R.VPWRSFVGVMHTVDEMK.A 9935
```

9949	1018.6816	2035.3487	2034.8993	0.4494	0	73	6.5e-06	1	K.DVVEFLNWAAEPEMDDR.K 9947 9984
10126	1026.8581	2051.7017	2050.8942	0.8075	0	(17)	2.9	1	K.DVVEFLNWAAEPEMDDR.K 10123 10136
10635	1060.2886	2118.5627	2118.2275	0.3352	1	0	1.3e+02	6	K.MGVKAIALLTGLFAVSVWVK.R
12141	776.2855	2325.8347	2326.9383	-1.1036	0	3	61	5	K.AMAEENEYDTEPNDQGEIEK.R 12138 12172

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166. gi|220692849|gb|EED49195.1| Mass: 36696 Score: 153 Queries matched: 19 emPAI: 0.19

hydroxymethylbilane synthase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
64	686.5530	685.5457	685.4374	0.1083	0	9	23	8	R.DVLVIK.Q 65
506	904.0040	902.9967	903.4086	-0.4119	1	7	39	8	R.DPRGYPAE.-
8033	606.3662	1816.0767	1817.9458	-1.8691	0	5	47	7	K.NGGMLYAVGQGALGIEIR.K
8217	919.7316	1837.4487	1837.0322	0.4165	2	5	43	3	K.YPHLKVIDVRGNIGTR.L 8219
9345	655.5512	1963.6317	1962.0357	1.5961	1	3	73	4	K.NGGMLYAVGQGALGIEIRK.D
9658	668.3265	2001.9577	2000.9370	1.0208	0	0	1.3e+02	9	K.DVPTTLPPACTLGPMMER.E
10785	713.8812	2138.6217	2135.9542	2.6675	0	4	50	2	R.DMLNNIGHNETTFASTAER.S
10958	1081.9201	2161.8257	2161.1089	0.7169	0	106	2.9e-09	1	K.LDAEDSPYTCIILAAAGLLR.L 10953 10962 10965
12992	819.4645	2455.3717	2457.2646	-1.8928	1	0	1.2e+02	6	K.QGLPNMSLSDLPAGSVVGTSSIRR.T
13136	825.2125	2472.6157	2473.3250	-0.7093	1	13	5.4	1	R.LAKLDAEDSPYTCIILAAAGLLR.L 13131 13167
15254	967.4399	2899.2977	2896.5116	2.7861	2	7	21	2	R.ISQYLDSKNGGMLYAVGQGALGIEIRK.D 15253

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167. gi|220689951|gb|EED46301.1| Mass: 56683 Score: 153 Queries matched: 20 emPAI: 0.33

woronin body major protein precursor, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
563	458.1261	914.2377	913.4981	0.7396	0	28	0.28	1	R.ALVINDGGR.E 556
1271	542.6031	1083.1917	1082.5760	0.6157	0	56	0.00036	1	R.YLGVDLFTR.Q 1272
3784	713.6616	1425.3087	1424.6684	0.6403	1	6	35	2	R.ERYQEPTSYPR.F
4397	747.7491	1493.4837	1491.8046	1.6792	0	0	1.4e+02	3	K.VLSTTTVVDHPPAR.K
4427	750.2351	1498.4557	1497.8191	0.6366	0	30	0.16	1	K.QGIPVVPQGELFSK.I
4517	754.8236	1507.6327	1506.8042	0.8285	0	1	1.1e+02	7	R.QVSVEPVNPPSQVK.V
4615	761.0221	1520.0297	1519.7188	0.3109	0	(36)	0.035	1	R.DNQIVAMTETGDVK.Q
4794	769.8886	1537.7627	1535.7137	2.0490	0	47	0.0027	1	R.DNQIVAMTETGDVK.Q 4780 4781 4787
6077	824.7556	1647.4967	1644.8406	2.6561	1	9	19	1	R.RSADTVPIPCNFIR.I
7393	880.8021	1759.5897	1759.9468	-0.3571	1	11	12	2	R.ALVINDGGRELVVDYK.V 7387 7415
8357	618.3802	1852.1187	1850.0560	2.0627	0	13	7.7	1	R.IGDILILQGRPCQVIR.I
13784	853.8102	2558.4087	2559.2618	-0.8531	1	(3)	65	2	R.YQQQDRFQQEKPYPEVHLAR.E 13790

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168. gi|220696373|gb|EED52715.1| Mass: 15921 Score: 152 Queries matched: 23 emPAI: 0.79

40S ribosomal protein S11 [Aspergillus flavus NRRL3357]

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

1118	528.1031	1054.1917	1053.5567	0.6350	0	67	3.3e-05	1	K.TPGPGAQSALR.A 1119
1399	554.6956	1107.3767	1106.6448	0.7320	0	35	0.05	1	K.ELGINALHIK.I 1403 1419
1637	572.6926	1143.3707	1143.6434	-0.2726	2	8	29	5	-.MAPKQKTAAAK.E
1718	582.6501	1163.2857	1160.6336	2.6521	2	1	1.3e+02	9	R.VTGGMKVKADR.D
1912	602.8091	1203.6037	1202.6666	0.9371	2	8	31	2	R.ALARSGMRIGR.I 1917
3730	709.6186	1417.2227	1416.6733	0.5495	0	58	0.00024	1	R.IEDVTPTPSDSTR.R 3733
4407	748.2291	1494.4437	1493.7694	0.6743	2	6	40	7	R.ETICRVTGGMKVK.A
8945	639.1012	1914.2817	1912.0061	2.2756	2	6	36	2	K.TPGPGAQSALRALARSGMR.I
9844	676.1889	2025.5447	2024.9956	0.5491	0	20	1.2	1	R.IFASFNDTFVHVTDLSGR.E 9854 9855 9861
11004	723.6425	2167.9057	2168.9830	-1.0773	1	4	45	1	R.DESSPYAAMLAAQDVAARCK.E 11035
11158	730.9925	2189.9557	2190.0699	-0.1142	2	3	67	10	R.SGMRIGRIEDVTPTPSDSTR.R
11303	737.1152	2208.3237	2207.0276	1.2961	1	15	4.4	1	K.ADRDESSPYAAMLAAQDVAAR.C 11302
13435	837.9235	2510.7487	2511.1482	-0.3995	2	3	60	1	K.ADRDESSPYAAMLAAQDVAARCK.E

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169. gi|220691267|gb|EED47615.1| **Mass:** 10350 **Score:** 152 **Queries matched:** 5 **emPAI:** 0.34

60S ribosomal protein L37a [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1307	545.6311	1089.2477	1089.5277	-0.2800	0	8	31	6	R.QAVGIWECK.G
1639	572.7536	1143.4927	1142.5832	0.9095	1	6	46	10	K.YGTRYGASLR.K
2402	425.1675	1272.4807	1270.6782	1.8025	2	9	20	8	K.YGTRYGASLRK.Q
6300	833.2531	1664.4917	1663.8530	0.6388	0	102	9.9e-09	1	K.TVAGGAYTVSTPAAAATR.S 6307

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170. gi|220690482|gb|EED46831.1| **Mass:** 38935 **Score:** 151 **Queries matched:** 10 **emPAI:** 0.08

adenosine kinase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1630	1142.5190	1141.5117	1141.6203	-0.1086	0	12	9.4	1	K.LIAGGAAQNTAR.G
2048	614.7091	1227.4037	1226.6659	0.7378	0	6	43	1	K.QPQIWSLVEK.A
10479	1048.2606	2094.5067	2094.0568	0.4499	0	94	6e-08	1	R.GAQYILPDNSVLYIGCVGR.D 10480
10724	1066.2841	2130.5537	2131.0190	-0.4653	1	5	43	3	R.SMCTHLAAANEYKLEHLK.Q 10723
13527	841.7499	2522.2277	2520.4163	1.8114	0	4	51	3	R.VAIVTQGTLPTVAATVKPNGEVEVK.E 13512
14093	873.8055	2618.3947	2618.2152	0.1795	1	2	79	2	K.CGVIITGHNRSMCTHLAAANEYK.L 14099

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171. gi|220700314|gb|EED56652.1| **Mass:** 59238 **Score:** 151 **Queries matched:** 13 **emPAI:** 0.11

cyclopropane-fatty-acyl-phospholipid synthase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1310	545.6966	1089.3787	1089.5414	-0.1627	1	10	19	7	R.KAGIEDSQSR.I
3204	680.5581	1359.1017	1357.6851	1.4166	1	6	43	2	R.NQTAWGNNGLRK.A 3201
3344	686.7266	1371.4387	1369.6951	1.7436	1	4	70	3	K.SKIPMEVFYEK.Y 3320
7790	896.7361	1791.4577	1791.9268	-0.4691	0	1	1.1e+02	2	K.YASVHYGAQVTGITLGR.N

8887	636.6305	1906.8697	1906.9222	-0.0525	0	8	22	2	K.HFLFGFIPEMLMHTR.S
9040	963.2351	1924.4557	1923.9731	0.4826	0	82	8.7e-07	1	K.YIFPGADASTPLGFVVDR.L 9051
10057	682.5445	2044.6117	2043.9506	0.6611	2	6	32	2	R.IMCLDYRDAPRVDGGYK.K
11038	724.9139	2171.7197	2170.1456	1.5741	0	52	0.00078	1	K.IGLKPGDTVLDLGCGWGTLAK.Y 11045
11761	760.4992	2278.4757	2277.1246	1.3512	2	1	1.1e+02	5	R.VDGGYKKITCLEMAEHVGVR.H

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172. gi|220689529|gb|EED45880.1| **Mass:** 12588 **Score:** 149 **Queries matched:** 22 **emPAI:** 3.26

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1179	534.4891	1066.9637	1065.4913	1.4724	0	5	47	10	K.QDFCIVER.Y
1255	541.1806	1080.3467	1079.5862	0.7605	0	57	0.00034	1	K.LLEASAVYSK.D 1249 1258
1561	567.0876	1132.1607	1132.6063	-0.4456	0	10	18	8	M.VYTIVVHMR.A
2207	625.5961	1249.1777	1248.5927	0.5850	0	31	0.12	1	K.YHLENPYWK.T 2202
2703	653.4241	1304.8337	1304.6136	0.2201	0	22	1.1	1	R.FEELVPEGEEK.K
2866	663.3161	1324.6177	1322.7081	1.9096	1	1	1.1e+02	1	K.LLEASAVYSKDK.E
3870	478.6799	1433.0177	1432.7085	0.3092	1	22	0.91	1	R.FEELVPEGEEKK.-
3881	718.7836	1435.5527	1433.7806	1.7721	0	40	0.017	1	K.TFDPYVIPLLEK.D 3877 3880
4941	776.2691	1550.5237	1551.8256	-1.3019	1	3	80	6	R.AKPDEESISKLHAK.L
5348	795.6386	1589.2627	1588.8096	0.4531	2	46	0.0038	1	R.RFEELVPEGEEKK.- 5342 5347 5349
10388	694.8075	2081.4007	2080.0551	1.3457	1	7	24	1	K.TFDPYVIPLLEKDMDLR.R
11382	739.8375	2216.4907	2217.1463	-0.6556	1	13	6.7	2	M.VYTIVVHMRAKPDEESISK.L 11387
11494	1118.5306	2235.0467	2236.1562	-1.1095	2	0	1.2e+02	2	K.TFDPYVIPLLEKDMDLRR.F

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173. gi|220695409|gb|EED51752.1| **Mass:** 15120 **Score:** 149 **Queries matched:** 8 **emPAI:** 0.84

ribosomal protein L26 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
213	787.5430	786.5357	786.4235	0.1122	0	18	3.4	1	R.EQILER.I
692	481.2821	960.5497	960.5314	0.0183	0	36	0.055	1	R.VIMSAPLSK.E
1223	537.7881	1073.5617	1073.5717	-0.0100	1	63	9.2e-05	1	R.KDDEVTIVR.G 1225
1898	600.4766	1198.9387	1198.6054	0.3333	0	69	2.2e-05	1	M.TVQNHSLASSR.R 1897
3757	474.7729	1421.2967	1419.7470	1.5497	0	57	0.0003	1	K.SNGQSVPLGIHPSK.V
10815	715.2842	2142.8307	2143.0956	-0.2649	2	0	1.2e+02	9	K.AHFNAGSGERRVIMSAPLSK.E

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174. gi|46370542|gb|AAS90074.1| **Mass:** 44093 **Score:** 148 **Queries matched:** 12 **emPAI:** 0.07

NorA [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2134	621.6521	1241.2897	1240.5982	0.6915	2	9	19	3	R.KMGPQDEKHR.R 2133 2138
2660	650.7046	1299.3947	1298.6004	0.7944	1	6	40	2	R.GQFRSAEDFSR.E 2662
7397	880.8521	1759.6897	1758.9920	0.6977	0	89	1.8e-07	1	K.VLYLGVSDTPAWLVVK.C 7399

7980	906.7636	1811.5127	1812.9469	-1.4341	0	7	26	4	K.ENIEALGLVLSEEEIR.E
8741	**631.6272**	**1891.8597**	**1891.0026**	**0.8571**	**0**	**6**	**37**	**2**	**-.MVLPTAPEPPTLLGYHR.I** 8745 8755
11851	1144.6306	2287.2467	2287.0799	0.1668	0	6	32	1	R.DILPMCESEGMGLAPWGVLGR.G

Proteins matching the same set of peptides:
gi|46370627|gb|AAS90094.1| **Mass:** 44093 **Score:** 148 **Queries matched:** 12
NorA [Aspergillus flavus]
gi|220694822|gb|EED51166.1| **Mass:** 44093 **Score:** 148 **Queries matched:** 12
aflE/ norA/ aad/ adh-2/ NOR reductase/ dehydrogenase [Aspergillus flavus NRRL3357]

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175. gi|220699220|gb|EED55559.1| **Mass:** 32741 **Score:** 148 **Queries matched:** 11 **emPAI:** 0.21
conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2657	650.5141	1299.0137	1298.7962	0.2175	0	31	0.12	2	K.ALIPAVVNIVYK.K
2886	664.4051	1326.7957	1325.7707	1.0250	0	6	42	6	K.IIWIQNDLIAK.W 2874
6248	**554.6955**	**1661.0647**	**1662.7970**	**-1.7323**	**1**	**7**	**32**	**4**	**R.YLNKVGMMHAAQER.M**
6797	851.3341	1700.6537	1698.7180	1.9357	0	2	1e+02	3	K.ILGDSSSTSASSSDDDR.S
10103	**683.9949**	**2048.9627**	**2047.7986**	**1.1641**	**0**	**3**	**69**	**7**	**R.DGEEYAEEMSQMTLDER.E**
11496	**746.1379**	**2235.3917**	**2233.3674**	**2.0243**	**2**	**5**	**40**	**3**	**K.VALVRAIGKIIWIQNDLIAK.W**
12188	**778.7612**	**2333.2617**	**2332.9787**	**0.2830**	**1**	**1**	**99**	**8**	**R.IRDGEEYAEEMSQMTLDER.E**
13794	**1281.4516**	**2560.8887**	**2560.2333**	**0.6554**	**0**	**108**	**1.6e-09**	**1**	**R.INYLQDFLDFNSADVEALTTGSK.Y** 13803 13808

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176. gi|220696700|gb|EED53042.1| **Mass:** 20770 **Score:** 146 **Queries matched:** 18 **emPAI:** 0.35
60S ribosomal protein L18 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
49	**678.4570**	**677.4497**	**677.3609**	**0.0888**	**1**	**22**	**1.2**	**1**	**K.FERAR.G**
55	**683.3920**	**682.3847**	**682.4377**	**-0.0530**	**0**	**27**	**0.18**	**2**	**R.LLNVPK.L** 56 57
70	689.4530	688.4457	687.3551	1.0906	0	12	14	3	M.GIDLDR.H
1516	564.6586	1127.3027	1125.6506	1.6521	0	52	0.0012	1	R.APTGANTLLLR.G 1514
1602	**569.9046**	**1137.7947**	**1137.6618**	**0.1329**	**0**	**24**	**0.59**	**1**	**R.INRPPVSLSR.I** 1605
2573	646.2231	1290.4317	1290.7183	-0.2866	0	16	4.5	2	K.SENVYLQVLVK.L 2583
3551	**465.6792**	**1394.0157**	**1392.8816**	**1.1341**	**1**	**7**	**32**	**8**	**R.LLNVPKLSVAALR.F**
4083	**729.3076**	**1456.6007**	**1456.7885**	**-0.1878**	**0**	**78**	**2.6e-06**	**1**	**K.AGGETLTLDQLALR.A** 4084 4103 4105
5496	**535.2075**	**1602.6007**	**1602.9318**	**-0.3311**	**2**	**8**	**23**	**4**	**K.LSVAALRFTATARAR.I**
7583	**888.3331**	**1774.6517**	**1771.9879**	**2.6638**	**1**	**2**	**88**	**8**	**R.LFMSRINRPPVSLSR.I**

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177. gi|46370464|gb|AAS89999.1| **Mass:** 232840 **Score:** 145 **Queries matched:** 44 **emPAI:** 0.04
PksA [Aspergillus flavus]

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

24	649.5510	648.5437	648.3265	0.2172	0	14	6.9	2	R.QMVQK.Y 25
103	**717.4400**	**716.4327**	**716.3566**	**0.0762**	**1**	**12**	**16**	**6**	**R.DRVDGR.S**
897	501.7006	1001.3867	1000.6281	0.7586	1	17	3.9	4	R.VVLQSTVKK.A 889 890 895
1617	571.2136	1140.4127	1140.5710	-0.1582	0	7	29	6	R.HTVDMAQALR.S
2034	613.7251	1225.4357	1223.6622	1.7735	2	9	19	2	K.SLRRSVSEYK.T
2335	633.5566	1265.0987	1262.6407	2.4580	1	11	14	1	K.KYHAPFASSQK.V
2801	659.2111	1316.4077	1315.7096	0.6982	0	28	0.25	1	K.NAITLSGSPSTLR.A
3061	**673.1676**	**1344.3207**	**1341.6889**	**2.6319**	**0**	**4**	**77**	**6**	**R.AGLVPDTTPSTQR.D**
3326	**686.1251**	**1370.2357**	**1370.6911**	**-0.4554**	**1**	**3**	**84**	**3**	**R.CQRGTHAMLAVK.A**
3591	**700.4056**	**1398.7967**	**1397.8718**	**0.9249**	**2**	**1**	**1.3e+02**	**3**	**R.GALRVVLQSTVKK.A**
3631	**702.6071**	**1403.1997**	**1403.6755**	**-0.4758**	**1**	**0**	**1.5e+02**	**7**	**K.SYEVYTKMGQAK.E**
4161	**489.5759**	**1465.7057**	**1463.6108**	**2.0949**	**0**	**12**	**8.9**	**1**	**R.AFCAMPEMAQHR.T** 4162
4167	**489.8612**	**1466.5617**	**1463.6094**	**2.9523**	**0**	**4**	**56**	**5**	**R.MALMSTYEAMER.A**
4340	**496.4349**	**1486.2827**	**1486.8872**	**-0.6044**	**1**	**4**	**57**	**9**	**R.QVKSVTIVPFLTR.M**
4568	759.2261	1516.4377	1517.6966	-1.2589	0	4	64	3	R.AQMLQSMNTVDHK.L
6940	856.5921	1711.1697	1709.8416	1.3282	0	1	1.1e+02	4	R.TALVCLCQLGCFIR.E
6960	**571.9085**	**1712.7037**	**1712.8767**	**-0.1730**	**1**	**9**	**19**	**1**	**K.EHVSIISDLIDRVMA.-**
7086	863.8401	1725.6657	1724.8774	0.7883	0	77	2.8e-06	1	R.QLFLFGDQTADFVPK.L
9218	**650.5109**	**1948.5107**	**1946.9594**	**1.5513**	**1**	**1**	**1.1e+02**	**8**	**R.MPKVGIVWAAETVMDER.D**
9311	**981.1061**	**1960.1977**	**1958.9302**	**1.2675**	**0**	**91**	**1.1e-07**	**1**	**R.FPESPTTESFWDLLYK.G** 9315
10554	**702.6782**	**2105.0127**	**2102.0143**	**2.9984**	**0**	**5**	**45**	**4**	**K.TLFMLPDGGGSAFSYASLPR.L**
11640	**753.8102**	**2258.4087**	**2256.2213**	**2.1874**	**0**	**2**	**72**	**7**	**R.VVEETTKPLGATLVVETDISR.K**
12378	**790.7629**	**2369.2667**	**2370.2179**	**-0.9512**	**0**	**1**	**88**	**4**	**R.VLINNFSAAGGNTALIVEDAPER.H** 12414
12438	**792.6672**	**2374.9797**	**2374.1661**	**0.8136**	**2**	**3**	**56**	**2**	**R.MPKVGIVWAAETVMDERDAPK.M**
12660	803.8829	2408.6267	2408.1473	0.4794	0	2	72	5	K.VLMMMQHDTIPPHCGIKPGSK.I
12704	805.8019	2414.3837	2414.2158	0.1679	2	1	87	8	R.AQMLQSMNTVDHKLARTADLR.Q
12981	**818.7969**	**2453.3687**	**2454.3053**	**-0.9366**	**2**	**3**	**61**	**2**	**K.GPQLLRTTLTMEWPPKAAATTR.S**
13112	**824.2465**	**2469.7177**	**2469.3950**	**0.3227**	**1**	**2**	**73**	**7**	**K.TLVIELGPKPLISGMVKMTLGEK.I**
13132	**824.8125**	**2471.4157**	**2469.3950**	**2.0207**	**1**	**(0)**	**1.1e+02**	**8**	**K.TLVIELGPKPLISGMVKMTLGEK.I**
13664	**847.8485**	**2540.5237**	**2540.0188**	**0.5049**	**0**	**4**	**47**	**1**	**R.DPENMNCTHGAMIESFCNEIR.R** 13667 13670
13850	**858.2382**	**2571.6927**	**2571.1225**	**0.5702**	**1**	**(1)**	**93**	**3**	**K.EAPQMDPAQRMALMSTYEAMER.A**
13991	**869.5172**	**2605.5297**	**2603.1124**	**2.4173**	**1**	**7**	**21**	**1**	**K.EAPQMDPAQRMALMSTYEAMER.A**
14986	**935.7805**	**2804.3197**	**2803.2827**	**1.0371**	**1**	**0**	**1e+02**	**10**	**R.MALMSTYEAMERAGLVPDTTPSTQR.D**
16307	**1142.4669**	**3424.3787**	**3421.8107**	**2.5681**	**2**	**2**	**53**	**5**	**K.ENDLVHGDVVVLDGEQVVAFFRGLSLRSVPR.G**
16386	1157.8399	3470.4977	3470.6210	-0.1233	2	1	67	9	K.GMHFMIQKRTEFGPDGWDTIMPGASFDIVR.A

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178. gi|1081987|gb|AAC41674.1| **Mass:** 232793 **Score:** 145 **Queries matched:** 42 **emPAI:** 0.04
polyketide synthase

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
24	649.5510	648.5437	648.3265	0.2172	0	14	6.9	2	R.QMVQK.Y 25

579	459.7451	917.4757	915.4774	1.9983	0	2	1.3e+02	7	R.TTNVPQTR.R
937	**1015.6040**	**1014.5967**	**1014.6437**	**-0.0470**	**1**	**4**	**81**	**6**	**R.VVLQTTVKK.A**
1617	571.2136	1140.4127	1140.5710	-0.1582	0	7	29	6	R.HTVDMAQALR.S
2034	613.7251	1225.4357	1223.6622	1.7735	2	9	19	2	K.SLRRSVSEYK.T
2335	633.5566	1265.0987	1262.6407	2.4580	1	11	14	1	K.KYHAPFASSQK.V
2801	659.2111	1316.4077	1315.7096	0.6982	0	28	0.25	1	K.NAITLSGSPSTLR.A
3061	673.1676	1344.3207	1341.6889	2.6319	0	4	77	6	R.AGLVPDTTPSTQR.D
3316	**457.6419**	**1369.9037**	**1368.7296**	**1.1741**	**1**	**4**	**64**	**8**	**R.AIPASGRPGAGKCK.L**
3326	686.1251	1370.2357	1370.6911	-0.4554	1	3	84	3	R.CQRGTHAMLAVK.A
4167	489.8612	1466.5617	1463.6094	2.9523	0	4	56	5	R.MALMSTYEAMER.A
4293	494.3592	1480.0557	1479.7425	0.3132	1	1	1.1e+02	7	R.AMTDNGIKCTLLK.L
4340	496.4349	1486.2827	1486.8872	-0.6044	1	4	57	9	R.QVKSVTIVPFLTR.M
4568	759.2261	1516.4377	1517.6966	-1.2589	0	4	64	3	R.AQMLQSMNTVDHK.L
5374	531.7742	1592.3007	1593.8297	-1.5290	0	7	30	4	R.SSHIVALSAHVGASMK.T
6940	856.5921	1711.1697	1709.8416	1.3282	0	1	1.1e+02	4	R.TALVCLCQLGCFIR.E
6960	571.9085	1712.7037	1712.8767	-0.1730	1	9	19	1	K.EHVSIISDLIDRVMA.-
7075	863.3661	1724.7177	1723.0468	1.6709	2	1	1.1e+02	7	R.SVPRGALRVVLQTTVK.K
7086	863.8401	1725.6657	1724.8774	0.7883	0	77	2.8e-06	1	R.QLFLFGDQTADFVPK.L
7318	**876.3001**	**1750.5857**	**1750.8863**	**-0.3006**	**2**	**0**	**1.4e+02**	**5**	**R.RWDINTHVDPSGKAR.N**
9311	981.1061	1960.1977	1958.9302	1.2675	0	91	1.1e-07	1	R.FPESPTTESFWDLLYK.G 9315
10554	702.6782	2105.0127	2102.0143	2.9984	0	5	45	4	K.TLFMLPDGGGSAFSYASLPR.L
10561	**1054.1901**	**2106.3657**	**2105.0398**	**1.3259**	**2**	**4**	**51**	**1**	**R.RMPKVGIVWAADTVMDER.D** 10560
11640	753.8102	2258.4087	2256.2213	2.1874	0	2	72	7	R.VVEETTKPLGATLVVETDISR.K
11665	**754.8075**	**2261.4007**	**2260.1667**	**1.2340**	**2**	**0**	**1.2e+02**	**9**	**K.NVAEVQRAMTDNGIKCTLLK.L**
12257	**782.6335**	**2344.8787**	**2344.1555**	**0.7232**	**2**	**4**	**50**	**2**	**R.MPKVGIVWAADTVMDERDAPK.M**
12378	790.7629	2369.2667	2370.2179	-0.9512	0	1	88	4	R.VLINNFSAAGGNTALIVEDAPER.H 12414
12660	803.8829	2408.6267	2408.1473	0.4794	0	2	72	5	K.VLMMMQHDTIPPHCGIKPGSK.I
12704	805.8019	2414.3837	2414.2158	0.1679	2	1	87	8	R.AQMLQSMNTVDHKLARTADLR.Q
12981	818.7969	2453.3687	2454.3053	-0.9366	2	3	61	2	K.GPQLLRTTLTMEWPPKAAATTR.S
13664	847.8485	2540.5237	2540.0188	0.5049	0	4	47	1	R.DPENMNCTHGAMIESFCNEIR.R 13667 13670
13850	858.2382	2571.6927	2571.1225	0.5702	1	(1)	93	3	K.EAPQMDPAQRMALMSTYEAMER.A
13991	869.5172	2605.5297	2603.1124	2.4173	1	7	21	1	K.EAPQMDPAQRMALMSTYEAMER.A
14698	**909.2912**	**2724.8517**	**2722.5091**	**2.3426**	**2**	**1**	**80**	**3**	**K.MTLGDKISTLPTLAPNKAIWPSLQK.I**
14986	935.7805	2804.3197	2803.2827	1.0371	1	0	1e+02	10	R.MALMSTYEAMERAGLVPDTTPSTQR.D
16386	1157.8399	3470.4977	3470.6210	-0.1233	2	1	67	9	K.GMHFMIQKRTEFGPDGWDTIMPGASFDIVR.A

Proteins matching the same set of peptides:

gi|1081989|gb|AAC41675.1| **Mass:** 232793 **Score:** 145 **Queries matched:** 42
polyketide synthase
gi|1584702|prf||2123354A **Mass:** 232793 **Score:** 145 **Queries matched:** 42

```
        polyketide synthase
        gi|2492660|sp|Q12053.1|PKSL1_ASPPA    Mass: 232793   Score: 145    Queries matched: 42
        RecName: Full=Aflatoxin biosynthesis polyketide synthase; Short=PKS
        gi|45477381|gb|AAS66004.1|       Mass: 232793   Score: 145    Queries matched: 42
        polyketide synthase [Aspergillus parasiticus]
```

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179.    gi|46370488|gb|AAS90022.1|       Mass: 233156   Score: 145    Queries matched: 43   emPAI: 0.04
        PksA [Aspergillus flavus]
       Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
          24  649.5510   648.5437   648.3265   0.2172   0    14      6.9   2   R.QMVQK.Y 25
         937 1015.6040  1014.5967  1014.6437  -0.0470   1     4       81   6   R.VVLQTTVKK.A
        1617  571.2136  1140.4127  1140.5710  -0.1582   0     7       29   6   R.HTVDMAQALR.S
        2034  613.7251  1225.4357  1223.6622   1.7735   2     9       19   2   K.SLRRSVSEYK.T
        2801  659.2111  1316.4077  1315.7096   0.6982   0    28     0.25   1   K.NAITLSGSPSTLR.A
        3061  673.1676  1344.3207  1341.6889   2.6319   0     4       77   6   R.AGLVPDTTPSTQR.D
        3316  457.6419  1369.9037  1368.7296   1.1741   1     4       64   8   R.AIPASGRPGAGKCK.L
        3326  686.1251  1370.2357  1370.6911  -0.4554   1     3       84   3   R.CQRGTHAMLAVK.A
        4167  489.8612  1466.5617  1463.6094   2.9523   0     4       56   5   R.MALMSTYEAMER.A
        4293  494.3592  1480.0557  1479.7425   0.3132   1     1  1.1e+02   7   R.AMTDNGIKCTLLK.L
        4340  496.4349  1486.2827  1486.8872  -0.6044   1     4       57   9   R.QVKSVTIVPFLTR.M
        4568  759.2261  1516.4377  1517.6966  -1.2589   0     4       64   3   R.AQMLQSMNTVDHK.L
        5374  531.7742  1592.3007  1593.8297  -1.5290   0     7       30   4   R.SSHIVALSAHVGASMK.T
        6940  856.5921  1711.1697  1709.8416   1.3282   0     1  1.1e+02   4   R.TALVCLCQLGCFIR.E
        7075  863.3661  1724.7177  1723.0468   1.6709   2     1  1.1e+02   7   R.SVPRGALRVVLQTTVK.K
        7086  863.8401  1725.6657  1724.8774   0.7883   0    77  2.8e-06   1   R.QLFLFGDQTADFVPK.L
        7318  876.3001  1750.5857  1750.8863  -0.3006   2     0  1.4e+02   5   R.RWDINTHVDPSGKAR.N
        9311  981.1061  1960.1977  1958.9302   1.2675   0    91  1.1e-07   1   R.FPESPTTESFWDLLYK.G 9315
       10554  702.6782  2105.0127  2102.0143   2.9984   0     5       45   4   K.TLFMLPDGGGSAFSYASLPR.L
       10561 1054.1901  2106.3657  2105.0398   1.3259   2     4       51   1   R.RMPKVGIVWAADTVMDER.D 10560
       11665  754.8075  2261.4007  2260.1667   1.2340   2     0  1.2e+02   9   K.NVAEVQRAMTDNGIKCTLLK.L
       12257  782.6335  2344.8787  2344.1555   0.7232   2     4       50   2   R.MPKVGIVWAADTVMDERDAPK.M
       12378  790.7629  2369.2667  2370.2179  -0.9512   0     1       88   4   R.VLINNFSAAGGNTALIVEDAPER.H 12414
       12660  803.8829  2408.6267  2408.1473   0.4794   0     2       72   5   K.VLMMMQHDTIPPHCGIKPGSK.I
       12704  805.8019  2414.3837  2414.2158   0.1679   2     1       87   8   R.AQMLQSMNTVDHKLARTADLR.Q
       12883  813.2992  2436.8757  2437.3866  -0.5108   1     1       89   5   K.GLIDDKSLVIELGPKPLISGMVK.M
       12919  815.2245  2442.6517  2441.3637   1.2880   1     4       46   2   K.SLVIELGPKPLISGMVKMTLGDK.I 12930
       12981  818.7969  2453.3687  2454.3053  -0.9366   2     3       61   2   K.GPQLLRTTLTMEWPPKAAATTR.S
       13004  820.5772  2458.7097  2457.3586   1.3511   1   (2)       69   6   K.SLVIELGPKPLISGMVKMTLGDK.I
       13664  847.8485  2540.5237  2540.0188   0.5049   0     4       47   1   R.DPENMNCTHGAMIESFCNEIR.R 13667 13670
       13850  858.2382  2571.6927  2571.1225   0.5702   1   (1)       93   3   K.EAPQMDPAQRMALMSTYEAMER.A
       13991  869.5172  2605.5297  2603.1124   2.4173   1     7       21   1   K.EAPQMDPAQRMALMSTYEAMER.A
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14698	909.2912	2724.8517	2722.5091	2.3426	2	1	80	3	K.MTLGDKISTLPTLAPNKAIWPSLQK.I
14986	935.7805	2804.3197	2803.2827	1.0371	1	0	1e+02	10	R.MALMSTYEAMERAGLVPDTTPSTQR.D
16152	**1112.2992**	**3333.8757**	**3334.7198**	**-0.8440**	**0**	**2**	**52**	**2**	**R.ADVTVGHSLGEFAALYAAGVLSASDVVYLVGQR.A**
16386	1157.8399	3470.4977	3470.6210	-0.1233	2	1	67	9	K.GMHFMIQKRTEFGPDGWDTIMPGASFDIVR.A

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180. gi|40054456|gb|AAR32704.2| **Mass:** 233115 **Score:** 145 **Queries matched:** 37 **emPAI:** 0.04

PksA [Aspergillus sp. L]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
24	649.5510	648.5437	648.3265	0.2172	0	14	6.9	2	R.QMVQK.Y 25
937	1015.6040	1014.5967	1014.6437	-0.0470	1	4	81	6	R.VVLQTTVKK.A
1617	571.2136	1140.4127	1140.5710	-0.1582	0	7	29	6	R.HTVDMAQALR.S
2034	613.7251	1225.4357	1223.6622	1.7735	2	9	19	2	K.SLRRSVSEYK.T
2801	659.2111	1316.4077	1315.7096	0.6982	0	28	0.25	1	K.NAITLSGSPSTLR.A
3061	673.1676	1344.3207	1341.6889	2.6319	0	4	77	6	R.AGLVPDTTPSTQR.D
3316	457.6419	1369.9037	1368.7296	1.1741	1	4	64	8	R.AIPASGRPGAGKCK.L
3326	686.1251	1370.2357	1370.6911	-0.4554	1	3	84	3	R.CQRGTHAMLAVK.A
4167	489.8612	1466.5617	1463.6094	2.9523	0	4	56	5	R.MALMSTYEAMER.A
4293	494.3592	1480.0557	1479.7425	0.3132	1	1	1.1e+02	7	R.AMTDNGIKCTLLK.L
4340	496.4349	1486.2827	1486.8872	-0.6044	1	4	57	9	R.QVKSVTIVPFLTR.M
5374	531.7742	1592.3007	1593.8297	-1.5290	0	7	30	4	R.SSHIVALSAHVGASMK.T
6940	856.5921	1711.1697	1709.8416	1.3282	0	1	1.1e+02	4	R.TALVCLCQLGCFIR.E
7075	863.3661	1724.7177	1723.0468	1.6709	2	1	1.1e+02	7	R.SVPRGALRVVLQTTVK.K
7086	863.8401	1725.6657	1724.8774	0.7883	0	77	2.8e-06	1	R.QLFLFGDQTADFVPK.L
7318	876.3001	1750.5857	1750.8863	-0.3006	2	0	1.4e+02	5	R.RWDINTHVDPSGKAR.N
8549	937.4641	1872.9137	1871.9346	0.9792	1	2	88	4	R.AQMLQSMNTIDHKLAR.T
9311	981.1061	1960.1977	1958.9302	1.2675	0	91	1.1e-07	1	R.FPESPTTESFWDLLYK.G 9315
10554	702.6782	2105.0127	2102.0143	2.9984	0	5	45	4	K.TLFMLPDGGGSAFSYASLPR.L
10561	1054.1901	2106.3657	2105.0398	1.3259	2	4	51	1	R.RMPKVGIVWAADTVMDER.D 10560
11640	753.8102	2258.4087	2256.2213	2.1874	0	2	72	7	R.VVEETTKPLGATLVVETDISR.K
11665	754.8075	2261.4007	2260.1667	1.2340	2	0	1.2e+02	9	K.NVAEVQRAMTDNGIKCTLLK.L
12257	782.6335	2344.8787	2344.1555	0.7232	2	4	50	2	R.MPKVGIVWAADTVMDERDAPK.M
12660	803.8829	2408.6267	2408.1473	0.4794	0	2	72	5	K.VLMMMQHDTIPPHCGIKPGSK.I
12981	818.7969	2453.3687	2454.3053	-0.9366	2	3	61	2	K.GPQLLRTTLTMEWPPKAAATTR.S
13664	847.8485	2540.5237	2540.0188	0.5049	0	4	47	1	R.DPENMNCTHGAMIESFCNEIR.R 13667 13670
13850	858.2382	2571.6927	2571.1225	0.5702	1	(1)	93	3	K.EAPQMDPAQRMALMSTYEAMER.A
13991	869.5172	2605.5297	2603.1124	2.4173	1	7	21	1	K.EAPQMDPAQRMALMSTYEAMER.A
14698	909.2912	2724.8517	2722.5091	2.3426	2	1	80	3	K.MTLGDKISTLPTLAPNKAIWPSLQK.I
14986	935.7805	2804.3197	2803.2827	1.0371	1	0	1e+02	10	R.MALMSTYEAMERAGLVPDTTPSTQR.D
16152	1112.2992	3333.8757	3334.7198	-0.8440	0	2	52	2	R.ADVTVGHSLGEFAALYAAGVLSASDVVYLVGQR.A
16386	1157.8399	3470.4977	3470.6210	-0.1233	2	1	67	9	K.GMHFMIQKRTEFGPDGWDTIMPGASFDIVR.A

Proteins matching the same set of peptides:

gi|46370626|gb|AAS90093.1| **Mass:** 233115 **Score:** 145 **Queries matched:** 37
PksA [Aspergillus flavus]

gi|220694831|gb|EED51175.1| **Mass:** 233116 **Score:** 145 **Queries matched:** 37
aflC / pksA / pksL1 / polyketide synthase [Aspergillus flavus NRRL3357]

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181. gi|220696379|gb|EED52721.1| **Mass:** 55053 **Score:** 144 **Queries matched:** 16 **emPAI:** 0.12
eukaryotic translation initiation factor 3 subunit EifCl, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1317	546.5186	1091.0227	1090.5771	0.4456	0	33	0.097	1	K.NTLYNPTIR.S
1532	565.3721	1128.7297	1127.5533	1.1765	0	9	21	2	K.LYTTMDLQK.L 1518 1522
2071	616.7276	1231.4407	1230.6496	0.7911	0	24	0.7	1	K.LAGFLEVEPEK.L 2073
3453	692.6871	1383.3597	1381.7792	1.5806	0	1	1.2e+02	4	K.MLGYFSIIGLLR.V
4538	756.7761	1511.5377	1511.7368	-0.1991	1	1	1.2e+02	5	K.NFQKGGNSYDAIAK.K
9267	652.1742	1953.5007	1952.0156	1.4851	0	49	0.0019	1	R.LQHGGPEALPLFEELFR.S 9255
10837	716.0802	2145.2187	2143.0156	2.2031	1	(1)	1.1e+02	3	K.RGEDPMAFAGEYGSRPLYK.M
10948	720.9349	2159.7827	2159.0106	0.7722	1	3	67	3	K.RGEDPMAFAGEYGSRPLYK.M
13093	823.6359	2467.8857	2468.0826	-0.1968	0	(0)	1.2e+02	4	R.VMAAHFTTYYYVGFSYMMMR.R
13476	840.0769	2517.2087	2516.0673	1.1414	0	0	1.1e+02	2	R.VMAAHFTTYYYVGFSYMMMR.R
16411	1166.6499	3496.9277	3495.7045	1.2232	0	62	4.8e-05	1	R.WVEGGLLEGEPVAANDLDYALENDLIHVSETK.A 16412

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182. gi|220692565|gb|EED48911.1| **Mass:** 41921 **Score:** 143 **Queries matched:** 14 **emPAI:** 0.08
actin Act1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5992	548.5572	1642.6497	1643.7903	-1.1406	1	1	1.3e+02	9	K.QEYDESGPSIVHRK.C
7775	896.1461	1790.2777	1789.8846	0.3931	0	89	1.8e-07	1	K.SYELPDGQVITIGNER.F 7777 7799
9166	648.1062	1941.2967	1941.8118	-0.5151	0	3	74	6	-.MDDETAAIVIDNGSGMCK.A 9183
11357	738.7129	2213.1167	2214.0627	-0.9460	0	2	77	2	K.DLYGNIVMSGGSTLYPGIADR.L
12522	796.8322	2387.4747	2385.1383	2.3364	1	2	80	5	R.HHGIIIGMGQKDSYVGDEAQSK.R
14751	913.9399	2738.7977	2737.3282	1.4695	1	1	89	6	K.RGVLSLHYPIEHGIVNNWDDMEK.I
14841	923.4399	2767.2977	2768.2018	-0.9041	1	1	93	10	M.DDETAAIVIDNGSGMCKAGFAGDDAPR.A
15686	1030.8272	3089.4597	3086.4801	2.9796	2	1	78	2	K.CDVDVRKDLYGNIVMSGGSTLYPGIADR.L
16033	1095.3632	3283.0677	3282.6457	0.4220	0	(2)	68	1	K.MTQIMFETFNVPAFYVSIQAVLSLYASGR.T
16094	1100.6199	3298.8377	3298.6406	0.1971	0	14	4	4	K.MTQIMFETFNVPAFYVSIQAVLSLYASGR.T
16095	1100.6592	3298.9557	3298.6406	0.3151	0	(11)	8	3	K.MTQIMFETFNVPAFYVSIQAVLSLYASGR.T

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183. gi|220692810|gb|EED49156.1| **Mass:** 14839 **Score:** 141 **Queries matched:** 22 **emPAI:** 1.28

alkaline serine protease [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
52	679.9980	678.9907	678.3231	0.6676	1	8	25	2	-.MSGRGR.G
480	894.6300	893.6227	892.4324	1.1903	0	4	57	3	R.IASNSGVVM.- 477
746	486.3901	970.7657	970.4872	0.2785	0	42	0.012	1	K.EAAELWPR.I 747
879	500.5621	999.1097	997.6107	1.4991	1	12	10	7	K.KVMPAVVVR.Q 871
934	507.6281	1013.2417	1013.6056	-0.3639	1	(2)	1e+02	9	K.KVMPAVVVR.Q
1947	606.3661	1210.7177	1208.5680	2.1497	2	11	13	5	-.MSGRGRGSSGNK.L 1955 1957
3524	696.4766	1390.9387	1390.7932	0.1455	1	6	45	7	R.NLYIISVKGTGAR.L
4113	731.1471	1460.2797	1458.7575	1.5223	0	(28)	0.24	1	R.LPAAGVGDMVMATVK.K
4252	738.7131	1475.4117	1474.7524	0.6593	0	(42)	0.0093	1	R.LPAAGVGDMVMATVK.K
4383	746.7241	1491.4337	1490.7473	0.6864	0	47	0.0029	1	R.LPAAGVGDMVMATVK.K 4378 4394
5316	794.7901	1587.5657	1586.8524	0.7133	1	3	73	4	R.LPAAGVGDMVMATVKK.G
6158	827.7191	1653.4237	1651.9344	1.4893	1	4	51	7	K.VMPAVVVRQSKPWR.R
7654	891.3261	1780.6377	1780.0294	0.6083	2	7	31	1	K.KVMPAVVVRQSKPWR.R
11131	729.8965	2186.6677	2184.8843	1.7834	0	3	71	6	K.MSLGLPCGAVMNCCDNSGAR.N
12084	773.4669	2317.3787	2316.2042	1.1745	2	1	1.1e+02	9	K.GTGARLNRLPAAGVGDMVMATVK.K

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184. gi\|220693799\|gb\|EED50144.1\| **Mass:** 30406 **Score:** 141 **Queries matched:** 21 **emPAI:** 0.11

TIM-barrel enzyme family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
312	837.1880	836.1807	836.4280	-0.2472	0	29	0.2	1	K.DAEYVLK.R 313
2132	621.4821	1240.9497	1239.7551	1.1947	0	8	25	2	K.IIVGAGAGIGLTAK.F
2643	649.7981	1297.5817	1296.6496	0.9321	1	5	49	5	R.DMRTFLTELR.R
6871	853.6666	1705.3187	1704.8392	0.4795	0	18	2.5	2	R.LPVEMAIQENAEAFK.K
7363	586.4675	1756.3807	1757.0451	-0.6644	1	2	89	8	K.IIVGAGAGIGLTAKFIEK.G 7380 7388
8073	607.2639	1818.7697	1816.9393	1.8305	1	16	3.8	1	R.LPVEMAIQENAEAFKK.L
8489	623.0425	1866.1057	1867.0210	-0.9153	2	2	78	7	-.MPRPTTRQEVLDRLR.K
8568	938.2771	1874.5397	1874.0302	0.5095	0	86	3.5e-07	1	R.LGFIGVQNFPTVGLIDGK.F 8577 8587
12409	791.5672	2371.6797	2370.2617	1.4181	2	6	32	1	R.LPVEMAIQENAEAFKKLQVNV.-
12573	799.2449	2394.7127	2396.3250	-1.6123	1	2	74	9	R.DAVVKINPEIIVLCHGGPLAGPK.D
12677	804.7449	2411.2127	2409.1158	2.0969	0	3	61	1	R.IAHEMDLVTTPYAFTVDEGER.M
13361	835.3485	2503.0237	2504.1424	-1.1187	2	4	51	2	K.FRQNLEETGMGYDREVEMIR.I
14838	922.9215	2765.7427	2767.2945	-1.5518	1	0	1.1e+02	10	R.IAHEMDLVTTPYAFTVDEGERMAR.A
15164	953.9659	2858.8757	2858.5476	0.3281	2	2	72	6	K.INPEIIVLCHGGPLAGPKDAEYVLKR.T
15923	1073.1612	3216.4617	3214.7424	1.7193	2	1	78	3	R.DAVVKINPEIIVLCHGGPLAGPKDAEYVLK.R 15924

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185. gi\|220690459\|gb\|EED46808.1\| **Mass:** 34616 **Score:** 140 **Queries matched:** 14 **emPAI:** 0.44

succinyl-CoA synthetase alpha subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
868	499.0586	996.1027	995.5440	0.5587	0	25	0.45	1	K.VIFQGFTGK.Q
1355	1099.9410	1098.9337	1099.5444	-0.6107	0	3	89	2	R.MGHAGAIVSGGK.G
2264	629.7411	1257.4677	1255.6455	1.8222	1	2	1.1e+02	6	R.RMGHAGAIVSGGK.G
2509	428.7005	1283.0797	1283.7172	-0.6375	1	12	8.9	2	K.IGIMPGFIHKR.G
2884	1327.7010	1326.6937	1326.7507	-0.0570	0	4	73	4	K.ISALEAAGVIVER.S
3822	715.7041	1429.3937	1429.8253	-0.4315	2	6	36	2	R.ITDILKTQNKTR.L
5152	787.1736	1572.3327	1572.8875	-0.5548	1	5	53	5	R.SPASLGKALLNEFVK.R 5148
5950	547.4122	1639.2147	1638.8590	0.3557	0	38	0.026	1	K.AGSTHLDRPVFANVR.D 5960
6519	841.3281	1680.6417	1679.8487	0.7930	0	45	0.0046	1	R.LVGPNCPGIIAPGQCK.I
7210	871.1876	1740.3607	1739.9458	0.4150	0	88	2.4e-07	1	K.ETGATASAIFVPPPLAAK.G 7204
15291	975.9262	2924.7567	2923.5185	1.2382	2	4	42	4	R.MGHAGAIVSGGKGGADSKISALEAAGVIVER.S

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186. gi|220694688|gb|EED51032.1| **Mass:** 80166 **Score:** 139 **Queries matched:** 21 **emPAI:** 0.17

arginyl-tRNA synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1821	593.0581	1184.1017	1182.5815	1.5202	1	6	39	4	K.ARMALYESAR.Q
4353	744.7526	1487.4907	1485.7609	1.7298	1	4	60	4	K.ITELMGHKDLASR.C
4537	756.7096	1511.4047	1510.7337	0.6710	0	1	1.2e+02	10	K.MTHTLSSSYEVLK.V 4540
5392	798.1466	1594.2787	1593.8362	0.4425	1	0	1.4e+02	10	K.LGAATGIDSEKIYTR.L
5807	814.4741	1626.9337	1624.8535	2.0803	0	26	0.37	1	R.TLEPCTILQYLFK.M 5787
6429	837.8026	1673.5907	1672.8607	0.7301	0	51	0.0012	1	R.MLAQWPDVLLNTTR.T
7465	883.6596	1765.3047	1764.8835	0.4212	0	70	1.5e-05	1	K.FPNSFPSLNPVDIYR.E 7431 7466
10731	1066.4171	2130.8197	2129.1117	1.7080	2	0	1.3e+02	1	K.AGVSEKSEGAVIVDFTKHGAK.K
11084	727.1609	2178.4607	2179.1170	-0.6562	0	2	79	3	K.MIYVVAMQQDLHLAQLFK.I 11083
11924	767.2632	2298.7677	2297.2130	1.5547	0	1	1.1e+02	7	R.STIIGGFLANLYTVMGWDVIK.M
12361	789.4542	2365.3407	2363.3464	1.9943	1	19	1.7	1	R.LQWSSTLDKGDLLLPVPALGIK.G 12356
13812	855.4999	2563.4777	2562.2754	1.2023	1	16	3	1	K.QFGSEEALNKDPINHLFDVYVK.I
13876	859.8229	2576.4467	2577.3360	-0.8893	2	1	85	4	K.MTHTLSSSYEVLKVVGSEPELKK.A
14361	890.2732	2667.7977	2665.3136	2.4841	2	0	1.1e+02	4	K.YRQTYARLNIDFDVYSGESQIK.N
15420	995.3139	2982.9197	2981.3998	1.5199	0	6	26	1	K.YQQVENPEETADILGITSVMVQDMSGK.R

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187. gi|220696155|gb|EED52497.1| **Mass:** 26272 **Score:** 137 **Queries matched:** 25 **emPAI:** 1.05

60S ribosomal protein L17 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
297	831.5010	830.4937	830.4320	0.0617	0	32	0.17	1	K.LEAVPMR.R 295 298 302
387	431.4556	860.8967	860.5371	0.3596	0	50	0.0021	1	K.FLIDLLK.N 386 388 390
946	509.0671	1016.1197	1014.5710	1.5488	0	44	0.0068	1	K.GLDTGNLVVK.H 937
1013	517.7741	1033.5337	1033.5669	-0.0331	0	53	0.001	1	K.HIQVNQAPK.G
1081	524.6341	1047.2537	1046.5396	0.7141	0	36	0.053	1	R.YAAQDIPAAK.S 1071 1079 1085

2104	619.2881	1236.5617	1234.6557	1.9060	0	57	0.00034	1	**R.ALTFLDNVTNK.L** 2117
3853	716.6766	1431.3387	1431.7623	-0.4235	2	3	73	5	**K.QFGVSKARWPEK.S**
4744	767.4961	1532.9777	1534.8328	-1.8551	2	2	98	4	K.GPVAKEAHLSSRQR.G
8309	924.7631	1847.5117	1845.9479	1.5638	2	1	1e+02	7	**K.NTRETAQAINGMKLQR.A** 8320
8883	636.5309	1906.5707	1904.0592	2.5116	2	4	57	3	R.TTTRLAISKFQRPTER.K
10091	683.6212	2047.8417	2047.0772	0.7645	1	2	77	1	**R.ALTFLDNVTNKLEAVPMR.R**
14860	924.6752	2771.0037	2771.5069	-0.5032	2	0	1e+02	2	**K.FLIDLLKNAEANADTKGLDTGNLVVK.H**
15968	1083.2042	3246.5907	3247.6118	-1.0210	1	2	65	5	R.AHGRINPYMTNPCHIELILTEGEEVVQK.G

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188. gi|220688980|gb|EED45332.1| **Mass:** 41120 **Score:** 137 **Queries matched:** 11 **emPAI:** 0.26
acetyl-CoA acetyltransferase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1203	536.2056	1070.3967	1069.7111	0.6856	0	57	0.00034	1	**R.ILTTLLGVLK.A** 1202
1536	565.6751	1129.3357	1128.6543	0.6814	0	44	0.0077	1	**K.FTTAPALAIPK.A** 1535
2233	627.6711	1253.3277	1251.7914	1.5363	1	7	32	3	K.LKELNLKPVAK.I 2228
3311	685.6541	1369.2937	1369.6990	-0.4053	0	20	1.6	1	**K.ILGWGDAAQQPSK.F**
10504	700.4442	2098.3107	2097.0048	1.3059	1	0	1.3e+02	8	K.YGNQSLVDGIMKDGLTDAGK.Q
11295	736.7005	2207.0797	2204.9579	2.1218	0	1	99	8	**K.QELMGLQAEECAQDHGFSR.E**
15335	982.5389	2944.5947	2942.4886	2.1061	0	49	0.0012	1	**K.ADGIKPSDIQEVFFGNVISANVGQNPAR.Q** 15331

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189. gi|220691506|gb|EED47854.1| **Mass:** 17947 **Score:** 136 **Queries matched:** 17 **emPAI:** 1.36
cytochrome c oxidase subunit Va, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
461	443.6371	885.2597	884.5080	0.7518	0	15	5.7	1	R.QELGVALR.E
959	510.3016	1018.5887	1017.5244	1.0644	0	47	0.0035	1	**R.VNDFPTAVR.V** 956 958 960
1768	587.8771	1173.7397	1173.6255	0.1143	1	51	0.0013	1	**R.RVNDFPTAVR.V**
1860	596.6006	1191.1867	1190.6295	0.5572	0	39	0.02	1	**K.QYLEALEGLR.Q** 1859
5251	791.9456	1581.8767	1580.7471	1.1296	0	2	93	3	**K.EFDGVQDVFELQR.N**
13039	1232.9066	2463.7987	2464.2420	-0.4433	0	57	0.00026	1	**R.NLNNCFAYDLVPSVEVLSAALR.A** 13044 13050 13051 13054 1
15465	1002.4339	3004.2797	3002.5349	1.7449	2	1	79	8	K.QYLEALEGLRQELGVALREELYPGEQ.-

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190. gi|220691647|gb|EED47995.1| **Mass:** 84150 **Score:** 136 **Queries matched:** 27 **emPAI:** 0.08
glutamyl-tRNA synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
593	463.5481	925.0817	924.5392	0.5425	0	16	3.2	2	**K.ALDPLLQR.L** 592 594
1487	561.6826	1121.3507	1120.5665	0.7842	0	22	1	2	R.SVQIWDFAR.M 1484
2064	410.7815	1229.3227	1228.6663	0.6564	0	8	24	9	**R.QIVTDPSSGVVK.E**
2403	637.2901	1272.5657	1272.6422	-0.0765	1	9	21	5	R.RDATVEENLAR.F 2411
4511	754.6671	1507.3197	1505.7337	1.5861	0	7	30	6	R.NPQYQWMLDALK.L

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     5028    520.6872  1559.0397  1557.8086   1.2312  2    13      8.3   4   K.KGSPEGLGWCIRAK.I
     5093    523.2355  1566.6847  1565.7178   0.9670  1     7       27   5   K.ETMAAQRMDGLPSK.R
     6094    550.6922  1649.0547  1648.8362   0.2186  0     2       87  10   R.FPPEPSGYLHIGHAK.A
     6837    852.2501  1702.4857  1701.8335   0.6522  1     8       25   2   R.DPVIYRSNPDPHHR.T 6850
     7290    874.0151  1746.0157  1744.8115   1.2042  0     6       37   3   K.DTLQEDDALEDVLNR.N
     7606    889.3576  1776.7007  1776.8617  -0.1610  1     1  1.2e+02   5   R.DRNPQYQWMLDALK.L
     7806    897.6361  1793.2577  1791.9559   1.3018  0    76  3.7e-06   1   K.AYAPGQPAVLFYIPTGK.T 7799
     7879    601.4069  1801.1987  1801.9363  -0.7375  0     1  1.2e+02   8   K.NITNLDWTLIWATNK.K
    10890    717.5639  2149.6697  2148.0595   1.6102  0     9       17   5   R.IFTSGFGGIMSNMQLTLATK.A
    13024    821.6115  2461.8127  2461.2046   0.6081  0    33    0.064   1   K.ENSEFQDAIVEDLALMGIKPDK.M 13025
    13185    827.0302  2478.0687  2477.1995   0.8692  0  (18)       2   1   K.ENSEFQDAIVEDLALMGIKPDK.M
    13529    841.7582  2522.2527  2522.1595   0.0933  1     3       60   4   R.EDATADCNVAELKEGDIIQFER.K 13517
    15714   1033.7039  3098.0897  3099.7233  -1.6336  1     3       48   2   R.LNTHLLLRSFIVGYSLSTADIALWGALR.G
    15746   1039.7125  3116.1157  3114.5656   1.5502  1     1       79   3   K.QDEEITLMNWGNAIVRQIVTDPSSGVVK.E
```

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191.   gi|220690361|gb|EED46711.1|    Mass: 16817    Score: 135    Queries matched: 16    emPAI: 0.73
       60S ribosomal protein L27a, putative [Aspergillus flavus NRRL3357]
      Query  Observed    Mr(expt)    Mr(calc)     Delta Miss Score  Expect Rank  Peptide
        728  968.4610    967.4537    967.4552   -0.0015   0    21       1    1   K.YHPGYFGK.V 729
       1022  518.5736   1035.1327   1034.6488    0.4839   0    44  0.0064    1   R.IPEIPIVVR.A 1023 1029
       1893  600.2491   1198.4837   1197.6506    0.8331   0    22    0.92    1   K.LWSLVPAEQR.D 1891
       2211  625.8146   1249.6147   1247.7714    1.8433   1     9      20    1   K.GRIPEIPIVVR.A
       6840  852.3106   1702.6067   1701.9189    0.6878   0    74 5.8e-06    1   K.TDTAPVIDLLPLGYSK.V 6817 6856 6857
       7126  866.7141   1731.4137   1729.9151    1.4986   0    37    0.03    1   K.TNQQFWKPVINLDK.L 7135
       7149  579.7989   1736.3747   1734.8346    1.5401   2     8      22    1   R.KHPGGRGMAGGQHHHR.T 7156
```

```
192.   gi|220692165|gb|EED48512.1|    Mass: 59020    Score: 135    Queries matched: 9    emPAI: 0.06
       N-acetylglucosamine-phosphate mutase [Aspergillus flavus NRRL3357]
      Query  Observed    Mr(expt)    Mr(calc)     Delta Miss Score  Expect Rank  Peptide
       1578  568.1801   1134.3457   1135.6536   -1.3078   2     7      36    2   K.LAKAFKGVMR.G
       1783  588.8671   1175.7197   1174.6016    1.1181   0     8      27    5   K.LPSVCTNTGVK.H 1773
       3640  703.1851   1404.3557   1403.8024    0.5533   0    87 3.1e-07    1   R.IATLAAAFIGDLTK.N 3642
      11101  728.0915   2181.2527   2183.1732   -1.9205   2     2      75   10   K.GSLTVDCANGVGGPKLRELLK.Y 11119
      12475  794.7512   2381.2317   2381.2842   -0.0525   1     0 1.1e+02    3   K.IGIIQTAYANGASTEYIEKVLK.L
      15396  991.6642   2971.9707   2973.5559   -1.5852   1     2      65    4   K.NAGIAQHLKIGIIQTAYANGASTEYIEK.V
```

```
193.   gi|220689407|gb|EED45758.1|    Mass: 32431    Score: 134    Queries matched: 11    emPAI: 0.10
       iron-sulfur protein subunit of succinate dehydrogenase Sdh2, putative [Aspergillus flavus NRRL3357]
      Query  Observed    Mr(expt)    Mr(calc)    Delta Miss Score  Expect Rank  Peptide
```

910	503.0931	1004.1717	1003.5814	0.5903	0	20	2	2	K.SIKPYLQR.E 909
1977	608.2726	1214.5307	1213.5649	0.9659	0	11	13	6	K.MQSYSLDLNK.T
1990	609.3751	1216.7357	1216.6308	0.1049	0	87	3.6e-07	1	K.TGPMMLDALIR.I 1993
2130	621.0376	1240.0607	1238.5601	1.5006	0	0	1.4e+02	10	K.NEMDPTLTFR.R
3001	669.9466	1337.8787	1337.6867	0.1920	0	17	3	2	K.DLVPDLTQFYK.Q
3013	670.7451	1339.4757	1338.6568	0.8189	0	14	6.5	2	R.WNPDQPTEKPK.M
12581	799.7552	2396.2437	2396.1902	0.0536	1	2	72	5	K.MQSYSLDLNKTGPMMLDALIR.I
14265	886.3062	2655.8967	2653.3641	2.5326	2	1	92	4	K.MQSYSLDLNKTGPMMLDALIRIK.N
14385	891.0189	2670.0347	2669.3590	0.6757	2	(1)	97	1	K.MQSYSLDLNKTGPMMLDALIRIK.N

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194. gi|220690101|gb|EED46451.1| **Mass:** 18033 **Score:** 134 **Queries matched:** 18 **emPAI:** 0.99
60S ribosomal protein L21, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
18	643.4760	642.4687	642.3125	0.1562	0	15	6.1	1	R.YAFSR.N 17
344	848.1560	847.1487	845.4606	1.6881	2	9	28	4	K.ENAEKKK.Q
381	430.1201	858.2257	857.4858	0.7399	0	56	0.00049	1	R.VGDIVDIK.V 372 378 379
791	490.7336	979.4527	979.5339	-0.0811	0	50	0.0016	1	K.TGVVYNVTK.S 790 792 793
2573	646.2231	1290.4317	1290.6754	-0.2437	1	8	27	3	K.VNGAVQKGMPYK.V 2597
2745	437.5432	1309.6077	1310.6262	-1.0185	1	8	25	6	-.MGHSHGLRSGTR.Y 2760
3237	681.7041	1361.3937	1358.7194	2.6743	0	24	0.6	1	K.EHGQIALSTYLK.T
12435	1188.4106	2374.8067	2372.2012	2.6055	0	36	0.028	1	R.EAHVVQAAAPETITPIPYDTHI.- 12436

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195. gi|220701844|gb|EED58182.1| **Mass:** 77569 **Score:** 133 **Queries matched:** 26 **emPAI:** 0.13
glycerol-3-phosphate dehydrogenase, mitochondrial [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
168	761.5690	760.5617	760.4079	0.1538	0	7	46	4	K.SSEALVR.N 166
290	415.0976	828.1807	827.5229	0.6579	1	10	17	6	K.LVKEALR.E 289
1015	518.1371	1034.2597	1032.5426	1.7171	0	4	78	9	K.AIDAFPMLR.K
1907	1203.2690	1202.2617	1200.6211	1.6406	1	7	35	1	K.DASGNLNGARVK.D
2905	664.8541	1327.6937	1327.7459	-0.0522	2	18	2.6	3	R.DPKVKSSEALVR.N 2904 2939
3810	715.0836	1428.1527	1427.6721	0.4806	0	18	2.4	2	K.AVWELDYNQYK.L 3806
4199	736.7006	1471.3867	1470.7579	0.6288	0	0	1.4e+02	3	R.AWQVAALSSPTNAR.F
4288	740.6916	1479.3687	1478.7769	0.5918	0	60	0.00017	1	R.ISALYPFIDGEVR.Y
6997	859.1726	1716.3307	1715.9682	0.3625	2	2	87	2	K.NFLGLSRAQVEAGKVK.Q
7487	884.8016	1767.5887	1767.9195	-0.3308	1	1	1.1e+02	6	K.AVWELDYNQYKLVK.E
10190	687.2395	2058.6967	2059.8364	-1.1397	0	3	62	10	K.DNMIGAMVYYDGAHNDSR.M
10280	690.1012	2067.2817	2068.0187	-0.7370	1	2	80	5	K.DLEWKESVSFLSSMGLPK.N
10528	701.3305	2100.9697	2101.0804	-0.1106	2	1	1e+02	8	K.DIIPGKNGQEEGEFTIRAK.G
11044	1087.1871	2172.3597	2171.9364	0.4233	1	3	76	1	R.KDNMIGAMVYYDGAHNDSR.M 11046

15193	957.7472	2870.2197	2868.4184	1.8013	0	3	50	3	R.MNVSLAMTAALYGSTVVNHMQVTGLTK.D
16286	**1140.0059**	**3416.9957**	**3415.6606**	**1.3351**	**0**	**41**	**0.0071**	**1**	**K.EIVAPSSGVHVILPGYYSPSDMGLIDPSTSDGR.V** 16287
16308	**1142.5852**	**3424.7337**	**3421.7782**	**2.9555**	**2**	**2**	**58**	**9**	**R.ISALYPFIDGEVRYAVRHEYAQTAVDVIAR.R**
16345	**1149.8212**	**3446.4417**	**3444.7089**	**1.7328**	**0**	**51**	**0.00072**	**1**	**R.VIFFLPWQGNTIAGTTDQPTEITTQPEPSEK.D** 16346

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196. gi|220699161|gb|EED55500.1| **Mass:** 52977 **Score:** 133 **Queries matched:** 19 **emPAI:** 0.13
phosphatidyl synthase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
83	702.3110	701.3037	700.4595	0.8442	1	9	25	3	K.LLTRAK.D
98	716.2790	715.2717	715.4228	-0.1511	1	12	13	4	K.EKVAAAK.N
335	845.5400	844.5327	842.4610	2.0717	1	8	38	3	R.AKDPVASR.I 334
755	**487.7086**	**973.4027**	**972.5240**	**0.8787**	**0**	**30**	**0.18**	**1**	**K.ALTGVDLER.V**
2539	**644.1606**	**1286.3067**	**1287.5943**	**-1.2876**	**0**	**0**	**1.5e+02**	**7**	**K.VNPVTGGDSGSAVE.-**
3385	688.6166	1375.2187	1374.7103	0.5084	0	6	45	10	R.LASVVTADGNSVSR.D 3381
4699	**510.3019**	**1527.8837**	**1527.7755**	**0.1082**	**1**	**6**	**39**	**8**	**K.MKFDAILVFADSR.D**
6993	**858.9216**	**1715.8287**	**1716.9119**	**-1.0831**	**1**	**2**	**86**	**2**	**R.VSRLASVVTADGNSVSR.D**
7996	605.0849	1812.2327	1812.8643	-0.6315	1	9	17	4	K.WNPKVNPVTGGDSGSAVE.-
8157	**915.1171**	**1828.2197**	**1827.9704**	**0.2494**	**2**	**13**	**7.2**	**1**	**R.GSRNSFGTSLPIPRSPR.V**
8518	624.2215	1869.6427	1870.0173	-0.3746	2	7	26	2	R.NSFGTSLPIPRSPRVSR.L
8883	636.5309	1906.5707	1905.0207	1.5500	1	2	80	6	R.ISIEAQYKALTGVDLER.V
12472	**794.7049**	**2381.0927**	**2381.1838**	**-0.0911**	**0**	**88**	**1.9e-07**	**1**	**R.IPIYFSQGDLIMPTDHQGPPR.L** 12495
15352	**984.7752**	**2951.3037**	**2948.3941**	**2.9096**	**0**	**10**	**12**	**1**	**R.TGVFQGGDNDENNPANFGVFPNVLEAVK.A**
15510	1011.9422	3032.8047	3032.5561	0.2487	2	6	26	2	R.VSRLASVVTADGNSVSRDLLASQVQDMSK.E
16254	**1130.4842**	**3388.4307**	**3386.6956**	**1.7352**	**1**	**1**	**69**	**2**	**K.FDAILVFADSRDYATDMQLILDLLLAEDGK.L**

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197. gi|220695611|gb|EED51954.1| **Mass:** 28707 **Score:** 133 **Queries matched:** 8 **emPAI:** 0.12
AI-BP family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1160	**532.6081**	**1063.2017**	**1062.5822**	**0.6196**	**1**	**7**	**35**	**7**	**K.NELYQRLK.T**
1786	**589.1716**	**1176.3287**	**1174.6611**	**1.6676**	**1**	**5**	**50**	**1**	**R.HFLGGRFLTK.S**
2597	647.6176	1293.2207	1291.7282	1.4926	2	(2)	1.1e+02	6	R.TARMSLKAISSK.D
2744	**437.5199**	**1309.5377**	**1307.7231**	**1.8146**	**2**	**3**	**70**	**4**	**R.TARMSLKAISSK.D**
9718	**670.9919**	**2009.9537**	**2009.0366**	**0.9172**	**0**	**2**	**87**	**1**	**K.FMPEYLISLTAPKPCVK.Y**
10629	**1059.8606**	**2117.7067**	**2117.1409**	**0.5659**	**0**	**82**	**8.5e-07**	**1**	**K.TQLDNLSVPFITDFPVAIK.S** 10636 10644

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198. gi|220700980|gb|EED57318.1| **Mass:** 86258 **Score:** 133 **Queries matched:** 17 **emPAI:** 0.12
protein transport protein Sec23, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
19	646.3760	645.3687	645.3810	-0.0123	0	14	9.7	2	R.VTTVAR.N

1868	597.6356	1193.2567	1193.5829	-0.3262	0	3	71	3	R.LSWNTFPSSR.M
1942	605.6591	1209.3037	1206.5881	2.7157	1	5	43	6	K.DDPTSFRLEK.N 1940
2714	654.2921	1306.5697	1307.7561	-1.1864	0	4	60	3	K.VTGLIGHAVSLNK.K
2942	666.5516	1331.0887	1329.7041	1.3846	0	43	0.0084	1	R.AVLNPYANVDVR.A 2940
3327	686.1911	1370.3677	1368.8381	1.5296	0	55	0.00056	1	R.LVVPIGAVYTPLK.D 3304 3320 3333
6941	571.4265	1711.2577	1712.8497	-1.5920	0	5	43	5	K.NFTLYPQFMFHLR.R
7909	902.8496	1803.6847	1802.8700	0.8148	2	0	1.3e+02	4	R.SHHDIDRDNIKYYK.K
14129	877.7735	2630.2987	2629.2806	1.0181	0	40	0.011	1	R.NLSGPAGDPTLAQSFDQEAAAVLMAR.I
14378	890.8152	2669.4237	2668.3418	1.0819	1	3	58	3	R.IFDKDANDNLLMGFNASLEVLTTK.E
16084	1099.1385	3294.3937	3294.7441	-0.3504	0	9	11	1	K.QVQEMLGLLSAGVRPNMPQQPARPPLGPAAR.F 16085

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199. gi\|220699918\|gb\|EED56257.1\| **Mass:** 45222 **Score:** 133 **Queries matched:** 14 **emPAI:** 0.15
pyruvate dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
351	851.1480	850.1407	849.4742	0.6665	1	15	4.9	2	-.MLSRSLK.R
668	479.3491	956.6837	956.5655	0.1183	0	56	0.00047	1	K.SIIGELLGR.R 672
950	509.1746	1016.3347	1014.4440	1.8907	0	5	54	5	K.YGMGTSVER.A
1413	555.3251	1108.6357	1106.6084	2.0273	1	9	20	6	K.QDKLITAYR.S
5000	779.3946	1556.7747	1554.9206	1.8542	2	4	61	3	R.GGTVKSIIGELLGRR.D
6854	852.6761	1703.3377	1702.8501	0.4876	0	71	1.2e-05	1	K.LWNLPVIFGCENNK.Y 6859 6873
7729	596.2055	1785.5947	1782.8107	2.7840	1	4	59	3	R.YAGHSMSDPGIAYRSR.E
8967	639.4589	1915.3547	1916.8673	-1.5126	1	1	1.1e+02	10	K.VNDEVAEAEKMPEPDTK.L
10745	712.5535	2134.6387	2131.9943	2.6444	2	1	94	7	R.SKVNDEVAEAEKMPEPDTK.L
12112	775.1095	2322.3067	2324.1583	-1.8516	0	4	49	4	R.GFCHLSTGQEAVAVGIEHALTK.Q 12122

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200. gi\|220696689\|gb\|EED53031.1\| **Mass:** 76035 **Score:** 132 **Queries matched:** 14 **emPAI:** 0.09
leukotriene A4 hydrolase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1244	539.9841	1077.9537	1077.6070	0.3467	0	6	41	5	R.VLGEVYSLAK.S
1938	605.2431	1208.4717	1208.6852	-0.2135	1	10	15	1	R.MKFVRPLYR.N
3736	473.5625	1417.6657	1415.7772	1.8885	0	6	41	7	K.VNRPLAIETFEK.N
3874	718.4691	1434.9237	1432.8303	2.0934	1	1	1.3e+02	7	K.FVRPLYRNLQK.V
6338	835.0866	1668.1587	1667.7679	0.3909	1	12	9	1	K.GKDPDDAFSSIPYEK.G
10569	703.5169	2107.5287	2106.0455	1.4832	0	52	0.00077	1	K.ATMLEFFQHDLEASNLLK.N 10571
11108	1092.5281	2183.0417	2182.1998	0.8419	0	6	34	2	K.STIDFNITSPLPVVASGLPVR.G
12144	776.3452	2326.0137	2323.2113	2.8024	2	2	85	3	K.GFNFLFHLENLLAKDKFDR.F
12340	787.5089	2359.5047	2357.2631	2.2417	0	59	0.00017	1	K.LPIPSYLFALASGDISEAAIGPR.S 12331 12344
12559	798.1889	2391.5447	2390.2270	1.3177	0	15	3.8	1	K.VDGQASHWELLPPLEPYGAALK.I 12556

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201.  gi|220694934|gb|EED51277.1|    Mass: 14556    Score: 131    Queries matched: 7    emPAI: 0.23
      NADH-ubiquinone oxidoreductase B14 subunit, putative [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      1779  588.7306  1175.4467  1175.6299  -0.1831   0    23    0.87    2   M.TINPTYLAQR.T 1777
      2993  669.4431  1336.8717  1335.6207   1.2510   0    11      13    1   K.YFRPEEDPGAR.L 2994 2995
      3993  724.1831  1446.3517  1445.7667   0.5850   0    86 4.1e-07    1   R.LPPNFISGFLEGR.N 3986

202.  gi|220692152|gb|EED48499.1|    Mass: 15603    Score: 130    Queries matched: 15    emPAI: 1.67
      60S ribosomal protein L27e [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
        40  672.5430   671.5357   671.4330   0.1027   0    17     3.7    1   R.VAIITR.G 42
       139  745.5470   744.5397   744.4898   0.0499   0    16     6.1    2   R.IKPFIK.V
       722  484.0726   966.1307   965.5123   0.6184   0    29    0.19    1   R.WFFTPLR.F 721
      1169  533.3976  1064.7807  1064.5753   0.2054   0    33   0.073    1   R.YTLELEGLK.G 1167
      1435  557.7121  1113.4097  1112.5808   0.8290   1    31    0.14    1   R.WFFTPLRF.- 1440
      3047  672.3231  1342.6317  1342.6816  -0.0499   0  (38)   0.025    1   K.VVNYNHLMPTR.Y
      3206  680.5966  1359.1787  1358.6765   0.5022   0    41   0.014    1   K.VVNYNHLMPTR.Y 3199 3212
      4435  750.8941  1499.7737  1499.7885  -0.0148   0    79 2.1e-06    1   K.AHPFAYAVVAGIER.Y
      7879  601.4069  1801.1987  1802.9890  -1.7903   2     1 1.2e+02    8   R.YAGKKVVIVQPNDTGSK.A

203.  gi|220701644|gb|EED57982.1|    Mass: 39515    Score: 130    Queries matched: 11    emPAI: 0.17
      epoxide hydrolase, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      1806   590.6276  1179.2407  1178.5602   0.6806   0    11      14    4   R.DVICDTITSR.L 1801
      2491   641.2136  1280.4127  1280.6513  -0.2386   0     3      74    2   K.AQIDAFASVGFR.A 2496
      2986   669.1321  1336.2497  1335.6724   0.5773   0    44  0.0064    1   R.GWQGFLPYVNR.E 2990
      6430   837.8126  1673.6107  1673.7066  -0.0958   0    18     2.4    1   K.TVEWFDSDIAGMCK.A
      6886   569.6732  1705.9977  1705.8206   0.1771   1     2      87    4   R.AIAPDMPGYGQSTARR.V
      9007   640.6975  1919.0707  1919.9445  -0.8738   1     2      86    9   R.DVICDTITSRLVEPMR.E
     12324  1179.3991  2356.7837  2356.1416   0.6421   0    68 2.1e-05    1   R.FIVEELPSEWPGFWTAGYTK.K 12329

204.  gi|220701605|gb|EED57943.1|    Mass: 112558    Score: 129    Queries matched: 20    emPAI: 0.03
      C1 tetrahydrofolate synthase, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
       517   907.4730   906.4657   907.4222  -0.9565   0    10      18   10   -.MPFSSPAR.S 521
      3134   676.7521  1351.4897  1352.7023  -1.2126   2     5      53    6   K.REFQPVMFKR.L
      4100   730.4211  1458.8277  1460.6929  -1.8652   1     2      99    5   R.RSSYSTGTTMAATK.I
      4445   751.4816  1500.9487  1502.7664  -1.8176   1     1 1.4e+02    7   -.MPFSSPARSAALPR.C
      4694   510.1392  1527.3957  1526.8417   0.5541   1     1 1.3e+02    7   R.GITVGQAPTEKGLTR.E
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4921	775.4846	1548.9547	1548.8848	0.0699	2	3	75	10	K.VSLDVLDRLAHRR.N
5678	809.0976	1616.1807	1613.8989	2.2819	0	1	1.3e+02	2	R.SSGLTPDTVVIVATVR.A
6424	837.7606	1673.5067	1673.8737	-0.3669	1	3	77	1	K.DVDGFGAINIGELAKR.G 6432
8388	619.1629	1854.4667	1852.9570	1.5097	1	9	19	1	K.DFKLLYELEGTIQER.I 8405
9100	645.2322	1932.6747	1930.0306	2.6441	1	2	90	6	K.CRSSGLTPDTVVIVATVR.A
9914	678.6912	2033.0517	2033.9398	-0.8881	0	2	87	7	K.SGDPVTCDDIGAGGALAALMK.D 9917
10145	1028.3376	2054.6607	2053.1671	1.4937	1	0	1.3e+02	7	K.TPDVESIIKTADILVAALGK.T
10697	1064.3361	2126.6577	2125.1518	1.5059	0	99	1.7e-08	1	K.IVNLPETAIESELLQDITK.A 10686
10860	1074.3336	2146.6527	2147.0416	-0.3889	1	8	22	1	R.SSYSTGTTMAATKIDGTQIAK.N 10872

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205. gi|220697901|gb|EED54241.1| **Mass:** 47101 **Score:** 129 **Queries matched:** 14 **emPAI:** 0.15

cofactor for methionyl- and glutamyl-tRNA synthetase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1305	545.5796	1089.1447	1088.5648	0.5799	0	17	4	2	K.SAAMVLAASPR.V 1309 1321
7142	867.6431	1733.2717	1732.9359	0.3358	0	55	0.00045	1	M.AINSAPESSLLSLIYR.S 7141
7621	890.1826	1778.3507	1777.9686	0.3821	0	1	1.1e+02	2	K.AAAQNAGAPAESKPLVVGK.G
8193	612.2142	1833.6207	1831.9792	1.6416	1	13	7.4	3	K.GKPEAPKEGAAPAAEGKPK.K
8806	634.0635	1899.1687	1899.0036	0.1651	0	2	81	3	K.AKPAPAPAAPPSPCAIDLR.V
9405	658.1592	1971.4557	1972.9710	-1.5153	0	2	87	6	R.TVCSGLNGLIPLEEMQGR.K
9985	680.1715	2037.4927	2035.1062	2.3866	1	1	1.2e+02	9	K.EKAAAQNAGAPAESKPLVVGK.G
11079	726.8822	2177.6247	2175.2012	2.4236	0	19	1.5	1	K.DEKPVITTILGQLNGHLATR.T
11194	1097.0791	2192.1437	2191.0896	1.0541	0	69	1.6e-05	1	R.SYPTAVSPDATETDLLTVSPK.I
13157	826.0335	2475.0787	2473.2781	1.8006	2	2	79	8	K.TVRTVCSGLNGLIPLEEMQGRK.I
13575	843.5709	2527.6907	2526.4309	1.2599	0	14	5.1	1	R.TTILGSKPSVADIAAYALLAPVVEK.W

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206. gi|220695108|gb|EED51451.1| **Mass:** 37711 **Score:** 127 **Queries matched:** 6 **emPAI:** 0.09

nucleoside-diphosphate-sugar epimerase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3065	673.6036	1345.1927	1345.7394	-0.5467	0	2	1.1e+02	3	K.LFGWSPSKPSLK.E
3304	685.1321	1368.2497	1367.7548	0.4950	0	8	23	3	K.ELIPEIVDLEAK.N
4450	751.6521	1501.2897	1500.7759	0.5138	0	20	1.6	2	K.TAIVCPPTIYGPGR.G 4440
6797	851.3341	1700.6537	1700.9726	-0.3189	2	1	1.3e+02	7	R.ARKLFGWSPSKPSLK.E
15179	955.7929	2864.3567	2862.4049	1.9518	0	127	2.1e-11	1	K.NIWHQVHVQDLSDVYGALADAAAAGGGK.A

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207. gi|220691359|gb|EED47707.1| **Mass:** 14972 **Score:** 126 **Queries matched:** 15 **emPAI:** 0.51

60S ribosomal protein L32 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
39	672.5100	671.5027	671.4218	0.0810	0	32	0.12	2	R.VEIIAK.A
572	459.1906	916.3667	915.5178	0.8489	0	35	0.069	1	K.AFLVQNPK.D 570

2119	619.9196	1237.8247	1238.6441	-0.8194	0	(18)	2.2	2	K.DVELLLMHNR.T
2245	**628.3576**	**1254.7007**	**1254.6390**	**0.0617**	**0**	**28**	**0.27**	**1**	**K.DVELLLMHNR.T** 2254
2552	430.1202	1287.3387	1285.6601	1.6786	1	11	14	7	K.CVPESWRKPK.G
3236	**681.6961**	**1361.3777**	**1360.6735**	**0.7042**	**0**	**84**	**7e-07**	**1**	**R.TYAAEIGHAVSSR.K** 3208 3238 3258 3262
5561	**805.1611**	**1608.3077**	**1607.7977**	**0.5100**	**1**	**10**	**16**	**1**	**K.SNIPMPSIGYGSNKK.T**
8217	919.7316	1837.4487	1836.9404	0.5084	2	4	58	5	K.SNIPMPSIGYGSNKKTK.H
10786	**713.8975**	**2138.6707**	**2136.1514**	**2.5194**	**1**	**1**	**1.1e+02**	**4**	**K.AFLVQNPKDVELLLMHNR.T**

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208. gi|220700651|gb|EED56989.1| **Mass:** 30156 **Score:** 126 **Queries matched:** 5 **emPAI:** 0.23

proteasome component Pre8, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1227	359.0512	1074.1317	1072.6604	1.4713	2	11	14	3	K.KATGKTGGILK.G
2909	**665.0001**	**1327.9857**	**1326.7031**	**1.2826**	**0**	**6**	**48**	**2**	**K.SSSPLIDPPSLSK.V**
10913	**1078.2871**	**2154.5597**	**2154.0489**	**0.5108**	**0**	**106**	**3.3e-09**	**1**	**K.VSLITPDIGMVYAGMGPDYR.V**
11366	**739.1509**	**2214.4307**	**2213.2419**	**1.1888**	**0**	**42**	**0.0084**	**1**	**K.LVQIEYALNAVNQGVTALGIK.A**
14710	**909.7625**	**2726.2657**	**2724.3867**	**1.8791**	**1**	**1**	**89**	**4**	**K.VSLITPDIGMVYAGMGPDYRVLVDK.A**

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209. gi|220696408|gb|EED52750.1| **Mass:** 11080 **Score:** 125 **Queries matched:** 5 **emPAI:** 0.72

60S acidic ribosomal protein P2/allergen Asp F 8 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
428	874.4910	873.4837	873.4807	0.0030	0	34	0.093	1	K.VISELEGK.D
3218	681.2291	1360.4437	1359.6882	0.7556	0	83	8.4e-07	1	K.DLQQLITEGSEK.L 3213
11390	**740.3129**	**2217.9167**	**2215.1583**	**2.7584**	**1**	**59**	**0.00015**	**1**	**K.VISELEGKDLQQLITEGSEK.L**
13920	**862.7202**	**2585.1387**	**2584.3959**	**0.7428**	**2**	**0**	**1.1e+02**	**7**	**R.LQKVISELEGKDLQQLITEGSEK.L**

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210. gi|220690318|gb|EED46668.1| **Mass:** 58675 **Score:** 125 **Queries matched:** 16 **emPAI:** 0.06

glutaryl-CoA dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1550	566.3611	1130.7077	1129.6608	1.0470	2	1	1.6e+02	8	R.KQFKGNPLAK.Y
2178	624.2556	1246.4967	1244.6401	1.8566	0	21	1.3	2	R.DQWSPALTISK.V 2184
7144	**868.6081**	**1735.2017**	**1736.8437**	**-1.6420**	**2**	**1**	**1.1e+02**	**3**	**K.DEGKSTPEMISMIKR.Q**
8085	**607.8189**	**1820.4347**	**1821.9216**	**-1.4869**	**2**	**6**	**35**	**2**	**R.LKDEGKSTPEMISMIK.R**
8108	**608.8162**	**1823.4267**	**1821.9216**	**1.5051**	**2**	**(3)**	**74**	**8**	**R.LKDEGKSTPEMISMIK.R**
9281	978.6871	1955.3597	1956.0720	-0.7123	0	2	89	5	K.TWITNSPISDILIVWAK.L
9348	**655.6682**	**1963.9827**	**1964.9230**	**-0.9403**	**2**	**3**	**75**	**3**	**K.STPEMISMIKRQNCDR.A**
10179	686.9025	2057.6857	2059.0559	-1.3702	0	3	59	10	R.LQSASHVHNAPTASLNASVR.G 10174 10176
13206	828.2562	2481.7467	2479.1611	2.5857	0	0	1.2e+02	7	R.SGMSVQSSLAMTAIYEFGSQELK.D
13860	858.6879	2573.0417	2571.3948	1.6469	1	1	90	5	K.TWITNSPISDILIVWAKLESTGK.I
14830	**922.4435**	**2764.3087**	**2766.2840**	**-1.9753**	**1**	**1**	**95**	**10**	**R.SGMSVQSSLAMTAIYEFGSQELKDR.F**

15522	1013.3212	3036.9417	3035.5348	1.4069	0	92	5.7e-08	1	K.VLLSICSMLTDPNPDDPLVPEIAHVYK.T 15531

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211. gi|220692679|gb|EED49025.1| **Mass:** 18720 **Score:** 125 **Queries matched:** 14 **emPAI:** 0.64
allergen Asp F3 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
939	508.5816	1015.1487	1014.5498	0.5989	0	33	0.087	1	R.YAIVIDHGK.V
1158	532.1121	1062.2097	1061.5757	0.6340	0	51	0.0015	1	K.VTYAALEPAK.N 1154 1155 1157
1468	560.5121	1119.0097	1118.4992	0.5105	0	32	0.12	1	K.SLGWADEEGR.T 1461
4126	731.8361	1461.6577	1461.6987	-0.0410	0	71	1.4e-05	1	K.NDDILFLSDPDAK.F 4127
4847	772.2601	1542.5057	1542.8154	-0.3097	1	7	28	1	K.NHLEFSRAETVIK.H
5394	798.1886	1594.3627	1595.7766	-1.4139	0	4	58	2	K.FNVCGIPINYNASK.E 5392
13607	844.6389	2530.8947	2529.3090	1.5857	0	26	0.26	1	K.VILFALPGAFTPVCSANHVPEYK.E 13594

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212. gi|220701354|gb|EED57692.1| **Mass:** 37539 **Score:** 125 **Queries matched:** 17 **emPAI:** 0.40
oxidoreductase, zinc-binding dehydrogenase family, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
9	616.6210	615.6137	614.4115	1.2022	1	4	92	3	K.GKAVLK.F
5024	520.5835	1558.7287	1557.7497	0.9790	1	2	96	7	R.GFIVGDAGMGDKYTK.E 5025
5899	818.3456	1634.6767	1633.9151	0.7616	0	41	0.012	1	R.IRPLENPLGIEDIR.V 5898
6351	835.5661	1669.1177	1666.8171	2.3006	1	4	58	2	R.LTMRGFIVGDAGMGDK.Y
8238	920.9091	1839.8037	1838.9131	0.8906	2	(1)	1e+02	4	K.RLTMRGFIVGDAGMGDK.Y
8240	614.4069	1840.1987	1838.9131	1.2856	2	6	37	2	K.RLTMRGFIVGDAGMGDK.Y
9756	672.6525	2014.9357	2013.9717	0.9640	0	15	4.1	1	K.SYSPAFAMDKPIDSSSIAK.V 9737
10040	681.8565	2042.5477	2041.0013	1.5465	0	3	66	8	R.VVVCGMISQYNSAPYPIK.N
10328	692.6872	2075.0397	2075.0180	0.0217	2	4	56	2	R.LTMRGFIVGDAGMGDKYTK.E
11482	1117.0346	2232.0547	2230.2321	1.8226	1	82	7.6e-07	1	K.KGETIFVSAASGAVGQLVGQLAK.H 11480
12471	794.6819	2381.0237	2378.2230	2.8007	0	3	55	1	K.ALTHETVGIDNSADALLGIFHGK.N
13448	838.4835	2512.4287	2511.3447	1.0840	0	9	13	1	R.VFLGALGMPGLTAYSSLYEIGKPK.K
16026	1094.3209	3279.9407	3277.5349	2.4058	0	33	0.05	1	R.LAPEGIDIYYENVGGEHLEAALDAMNNFGR.V

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213. gi|220700053|gb|EED56392.1| **Mass:** 57182 **Score:** 124 **Queries matched:** 14 **emPAI:** 0.06
PH domain protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2722	654.6611	1307.3077	1305.6598	1.6479	0	8	25	2	R.ATMALIEGSLER.K
3278	683.6211	1365.2277	1363.6707	1.5570	1	6	35	9	K.WWTVIKDCTR.G
3739	710.1196	1418.2247	1417.7599	0.4649	1	16	3.9	3	R.ATMALIEGSLERK.S 3717 3740
3867	478.5692	1432.6857	1433.7263	-1.0405	0	8	29	8	K.NDNVLINPDAPPR.T
5526	803.4041	1604.7937	1604.8239	-0.0302	0	75	5.2e-06	1	K.IPPDFEWVNFITK.N 5533 5559
5633	807.2961	1612.5777	1611.8692	0.7085	2	1	1.3e+02	9	R.LNKQIIEENNNRK.D 5638

7892	901.9811	1801.9477	1801.8015	0.1462	0	6	34	1	K.HMCGYLEDYVTVTSK.V
10647	707.6702	2119.9887	2121.0677	-1.0790	2	2	84	6	K.SRAMLKGYSSGYYVVTPAR.Y
14799	918.5162	2752.5267	2752.2093	0.3174	1	1	89	6	R.RASMSDDEAIPDSDSSETTNLLNER.L

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214. gi|220690447|gb|EED46796.1| **Mass:** 26723 **Score:** 124 **Queries matched:** 8 **emPAI:** 0.26

translation initiation factor eIF-6, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5568	537.2475	1608.7207	1605.7603	2.9604	1	3	85	8	R.LGEMGPRGVGMGSTNK.E 5554
10794	1071.2991	2140.5837	2139.1172	1.4666	0	77	2.6e-06	1	R.DQDELSSLLQVPLVAGSVNR.G 10789
13871	859.2355	2574.6847	2576.1887	-1.5040	2	3	65	1	R.LGEMGPRGVGMGSTNKESIVESFY.-
14071	872.6255	2614.8547	2613.3221	1.5326	0	38	0.016	1	R.QTIADNVLTGSYMALSNQGGIVHPK.T 14068 14076

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215. gi|46370508|gb|AAS90042.1| **Mass:** 70350 **Score:** 124 **Queries matched:** 27 **emPAI:** 0.20

VBS [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
314	421.0041	839.9937	840.5545	-0.5608	1	7	28	9	R.VLGVKGLR.V
913	503.6206	1005.2267	1005.4880	-0.2612	0	30	0.18	1	R.VLFDDQNR.A
1025	518.9821	1035.9497	1034.5066	1.4431	0	4	64	6	R.EIVASDVMR.E
1191	535.2076	1068.4007	1067.6927	0.7080	2	10	16	6	K.ARVLGVKGLR.V
1575	1134.9860	1133.9787	1133.5564	0.4223	1	12	9.3	1	K.ADDSKAVVDSK.A
2160	623.2131	1244.4117	1244.5819	-0.1702	0	3	79	1	K.VESHSQLMGNK.E
2584	646.6121	1291.2097	1289.7092	1.5006	0	13	8.5	3	K.EHLEQLGIPVR.S 2576 2579
2750	656.0041	1309.9937	1308.6245	1.3693	1	12	9.7	1	R.DQEMAVAAFRR.C
2873	663.8056	1325.5967	1325.7377	-0.1410	0	(11)	14	5	R.SPQLLMVSGIGPK.E
3013	670.7451	1339.4757	1340.8140	-1.3383	2	2	95	8	K.AVVDSKARVLGVK.G
3044	672.1071	1342.1997	1341.7326	0.4671	0	40	0.017	1	R.SPQLLMVSGIGPK.E 3056
4163	489.6049	1465.7927	1464.7361	1.0566	0	12	9.2	1	R.SYITHTINPYTR.R
5589	537.6929	1610.0567	1608.7613	1.2954	2	4	67	7	R.DQEMAVAAFRRCR.E
6130	826.8116	1651.6087	1650.8035	0.8052	0	13	7.1	2	R.EALMESNNLNIFTR.T
6782	850.7426	1699.4707	1698.8253	0.6454	0	79	2e-06	1	K.GLLTNPGQDYFAFEK.H 6778
7064	575.5309	1723.5707	1721.7905	1.7802	0	4	60	10	K.NYFSMSAALMTPFSR.G
7828	898.6956	1795.3767	1793.8519	1.5248	0	18	2.2	1	K.MGFPEAQGFSNGNLLGR.S 7816 7836
7955	603.8105	1808.4097	1809.8468	-1.4371	0	(5)	45	4	K.MGFPEAQGFSNGNLLGR.S
13543	841.9519	2522.8337	2521.2754	1.5583	1	28	0.2	1	K.VKNPLFDWYQYTTPQPGLAQR.E 13551
14217	883.4865	2647.4377	2645.2755	2.1623	1	2	70	1	R.ETASSSYLREALMESNNLNIFTR.T

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216. gi|46370556|gb|AAS90088.1| **Mass:** 70334 **Score:** 124 **Queries matched:** 27 **emPAI:** 0.20

VBS [Aspergillus flavus]

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

314	421.0041	839.9937	840.5545	-0.5608	1	7	28	9	R.VLGVKGLR.V
913	503.6206	1005.2267	1005.4880	-0.2612	0	30	0.18	1	R.VLFDDQNR.A
1025	518.9821	1035.9497	1034.5066	1.4431	0	4	64	6	R.EIVASDVMR.E
1191	535.2076	1068.4007	1067.6927	0.7080	2	10	16	6	K.ARVLGVKGLR.V
1575	1134.9860	1133.9787	1133.5564	0.4223	1	12	9.3	1	K.ADDSKAVVDSK.A
2160	623.2131	1244.4117	1244.5819	-0.1702	0	3	79	1	K.VESHSQLMGNK.E
2584	646.6121	1291.2097	1289.7092	1.5006	0	13	8.5	3	K.EHLEQLGIPVR.S 2576 2579
2750	656.0041	1309.9937	1308.6245	1.3693	1	12	9.7	1	R.DQEMAVAAFRR.C
2873	663.8056	1325.5967	1325.7377	-0.1410	0	(11)	14	5	R.SPQLLMVSGIGPK.E
3013	670.7451	1339.4757	1340.8140	-1.3383	2	2	95	8	K.AVVDSKARVLGVK.G
3044	672.1071	1342.1997	1341.7326	0.4671	0	40	0.017	1	R.SPQLLMVSGIGPK.E 3056
4163	489.6049	1465.7927	1464.7361	1.0566	0	12	9.2	1	R.SYITHTINPYTR.R
5589	537.6929	1610.0567	1608.7613	1.2954	2	4	67	7	R.DQEMAVAAFRRCR.E
6782	850.7426	1699.4707	1698.8253	0.6454	0	79	2e-06	1	K.GLLTNPGQDYFAFEK.H 6778
7064	575.5309	1723.5707	1721.7905	1.7802	0	4	60	10	K.NYFSMSAALMTPFSR.G
7828	898.6956	1795.3767	1793.8519	1.5248	0	18	2.2	1	K.MGFPEAQGFSNGNLLGR.S 7816 7836
7955	603.8105	1808.4097	1809.8468	-1.4371	0	(5)	45	4	K.MGFPEAQGFSNGNLLGR.S
8054	909.6501	1817.2857	1816.8512	0.4345	1	2	98	10	R.ETASSSYLREALMESK.N
10668	**708.7585**	**2123.2537**	**2122.1456**	**1.1081**	**2**	**2**	**83**	**10**	**R.EALMESKNLNIFTRTLVK.R**
13543	841.9519	2522.8337	2521.2754	1.5583	1	28	0.2	1	K.VKNPLFDWYQYTTPQPGLAQR.E 13551

Proteins matching the same set of peptides:

gi|220694810|gb|EED51154.1| **Mass:** 70334 **Score:** 124 **Queries matched:** 27
aflK/ vbs/ VERB synthase [Aspergillus flavus NRRL3357]

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217. gi|220701100|gb|EED57438.1| **Mass:** 173645 **Score:** 123 **Queries matched:** 22 **emPAI:** 0.02
glycogen debranching enzyme Gdb1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
169	**381.3331**	**760.6517**	**761.3854**	**-0.7337**	**1**	**8**	**37**	**6**	**R.RLEGCK.R**
496	450.3536	898.6927	897.4742	1.2185	1	14	6.3	3	K.YTRLMAK.Y 484 495
1266	**542.0011**	**1081.9877**	**1080.5928**	**1.3950**	**0**	**9**	**20**	**4**	**K.LVDLVHETR.L**
2360	634.3376	1266.6607	1263.6935	2.9672	1	3	70	8	R.LPANEVTKQHK.S 2354 2358
2383	**636.0746**	**1270.1347**	**1268.6547**	**1.4800**	**0**	**2**	**99**	**2**	**K.HGMIPNLLSSGK.L**
2509	428.7005	1283.0797	1282.6670	0.4127	0	10	15	3	K.TPTHYIDIAPR.L
2951	**667.4071**	**1332.7997**	**1330.7092**	**2.0905**	**1**	**1**	**1.3e+02**	**3**	**K.GELGSEGGIGSIKK.I**
4169	734.6446	1467.2747	1464.6667	2.6080	0	8	26	3	R.EAMQAWSTGELSR.L
4312	742.1886	1482.3627	1480.6616	1.7011	0	(6)	43	2	R.EAMQAWSTGELSR.L
5683	**809.2951**	**1616.5757**	**1615.9185**	**0.6572**	**0**	**93**	**7.9e-08**	**1**	**R.DLPLNALSIFSVISK.F** 5678
6223	**554.0625**	**1659.1657**	**1657.9304**	**1.2353**	**1**	**6**	**41**	**7**	**K.FNAVRELPSFLLPR.Y**
7278	582.7869	1745.3387	1742.9349	2.4038	1	1	1.2e+02	5	K.TADDLIVVMNVLRER.V

7602	889.2576	1776.5007	1777.8417	-1.3410	2	1	1.2e+02	6	K.MGESEKAGNKGFPGTPR.D
9341	**655.5052**	**1963.4937**	**1962.0588**	**1.4349**	**1**	**2**	**92**	**5**	**R.RVPSLAAGLPHFAVDWAR.C**
10152	**686.0632**	**2055.1677**	**2056.0490**	**-0.8813**	**1**	**2**	**94**	**10**	**R.EGSLWVNIPEDRKPFNR.S**
12190	**778.7949**	**2333.3627**	**2335.1848**	**-1.8221**	**2**	**3**	**60**	**10**	**R.GIYKDLYKSGKPYEDYQLR.S**
16390	**1158.2789**	**3471.8147**	**3472.6908**	**-0.8760**	**2**	**0**	**80**	**10**	**R.LMAKYFSGFRIDNCHSTPLGVAEYLLDEAR.K**

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218. gi|46370639|gb|AAS90106.1| **Mass:** 70397 **Score:** 123 **Queries matched:** 23 **emPAI:** 0.15

VBS [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
314	421.0041	839.9937	840.5545	-0.5608	1	7	28	9	R.VLGVKGLR.V
1025	518.9821	1035.9497	1034.5066	1.4431	0	4	64	6	R.EIVASDVMR.E
1191	535.2076	1068.4007	1067.6927	0.7080	2	10	16	6	K.ARVLGVKGLR.V
1575	1134.9860	1133.9787	1133.5564	0.4223	1	12	9.3	1	K.ADDSKAVVDSK.A
2160	623.2131	1244.4117	1244.5819	-0.1702	0	3	79	1	K.VESHSQLMGNK.E
2584	646.6121	1291.2097	1289.7204	1.4893	1	13	8.5	4	K.DHLDRLGIPVR.S 2576
2750	656.0041	1309.9937	1308.6245	1.3693	1	12	9.7	1	R.DQEMAVAAFRR.C
2873	663.8056	1325.5967	1325.7377	-0.1410	0	(11)	14	5	R.SPQLLMVSGIGPK.D
3013	670.7451	1339.4757	1340.8140	-1.3383	2	2	95	8	K.AVVDSKARVLGVK.G
3044	672.1071	1342.1997	1341.7326	0.4671	0	40	0.017	1	R.SPQLLMVSGIGPK.D 3056
4163	489.6049	1465.7927	1464.7361	1.0566	0	12	9.2	1	R.SYITHTINPYTR.R
5589	537.6929	1610.0567	1608.7613	1.2954	2	4	67	7	R.DQEMAVAAFRRCR.E
6130	826.8116	1651.6087	1650.8035	0.8052	0	13	7.1	2	R.EALMESNNLNIFTR.T
6782	850.7426	1699.4707	1698.8253	0.6454	0	79	2e-06	1	K.GLLTNPGQDYFAFEK.H 6778
7064	575.5309	1723.5707	1721.7905	1.7802	0	4	60	10	K.NYFSMSAALMTPFSR.G
10901	**718.5989**	**2152.7747**	**2153.0899**	**-0.3151**	**1**	**4**	**45**	**3**	**K.VESHSQLMGNKETLPQAIR.E** 10912
13543	841.9519	2522.8337	2521.2754	1.5583	1	28	0.2	1	R.VKNPLFDWYQYTTPQPGLAQR.E 13551
14217	883.4865	2647.4377	2645.2755	2.1623	1	2	70	1	R.ETASSSYLREALMESNNLNIFTR.T

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219. gi|220690598|gb|EED46947.1| **Mass:** 23086 **Score:** 122 **Queries matched:** 21 **emPAI:** 0.72

ribosomal protein L16a [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
87	**705.5500**	**704.5427**	**704.3275**	**0.2152**	**0**	**13**	**9.7**	**2**	**R.GAAAMER.L**
267	**409.5461**	**817.0777**	**816.4031**	**0.6746**	**0**	**36**	**0.057**	**1**	**R.GGPFHFR.A** 268
450	**441.7731**	**881.5317**	**880.5494**	**0.9823**	**0**	**48**	**0.002**	**1**	**R.VVVPQALR.V** 447 448 449
2203	**625.3141**	**1248.6137**	**1246.6234**	**1.9903**	**0**	**13**	**9.3**	**1**	**K.VFEGVPPPYDK.K** 2197
2557	645.2321	1288.4497	1289.6874	-1.2376	2	2	1e+02	10	K.TARGAAAMERLK.V
3215	681.1271	1360.2397	1360.6908	-0.4511	0	4	72	7	-.MSSTEPVVVIDGK.G
3390	**688.6721**	**1375.3297**	**1374.7184**	**0.6114**	**1**	**42**	**0.011**	**1**	**K.VFEGVPPPYDKK.K** 3399
3841	**716.2496**	**1430.4847**	**1431.7160**	**-1.2313**	**1**	**1**	**1.3e+02**	**9**	**R.FNPTRGGPFHFR.A**

3960	722.6921	1443.3697	1441.6660	1.7037	0	58	0.00025	1	R.CEALNISGEFFR.A 3966
4489	502.6169	1504.8287	1502.8133	2.0154	2	8	28	4	K.VFEGVPPPYDKKK.R 4488
7100	576.8459	1727.5157	1727.8559	-0.3402	2	2	89	7	R.GMIPHKTARGAAAMER.L
9700	670.4549	2008.3427	2010.0568	-1.7141	1	4	51	2	-.MSSTEPVVVIDGKGHLLGR.L
11210	732.0455	2193.1147	2190.1143	3.0004	2	0	1.3e+02	3	R.GAAAMERLKVFEGVPPPYDK.K

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220. gi|220698656|gb|EED54996.1| **Mass:** 39682 **Score:** 122 **Queries matched:** 9 **emPAI:** 0.17
26S proteasome regulatory particle subunit Rpn8, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3071	673.8221	1345.6297	1344.7249	0.9048	0	79	2.2e-06	1	M.PATTADTLSLVTR.T
6384	836.4571	1670.8997	1670.7972	0.1025	1	6	41	1	K.IQNRQQQEENEQK.R
6744	849.1661	1696.3177	1694.9607	1.3570	0	73	6.7e-06	1	R.YTPNPLLVIVDVQPK.E 6737 6743
7342	877.8046	1753.5947	1752.9080	0.6867	0	0	1.3e+02	4	K.TNDQLMAIYLSSLIR.A
8626	942.7201	1883.4257	1882.0061	1.4197	1	3	74	8	R.AITAFHDLIENKIQNR.Q
8927	638.3085	1911.9037	1910.0626	1.8412	0	8	21	1	R.TVTVAPLVLLSVADHYGR.S 8926

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221. gi|220690852|gb|EED47201.1| **Mass:** 83225 **Score:** 122 **Queries matched:** 10 **emPAI:** 0.04
threonyl-tRNA synthetase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
208	393.6011	785.1877	785.3668	-0.1791	0	4	72	4	K.SSEPGPGR.A
1218	537.4066	1072.7987	1071.6176	1.1812	0	5	60	10	K.IDITIADALK.R
1839	595.1011	1188.1877	1187.7026	0.4851	0	82	1.2e-06	1	K.IFNALQTLLR.S 1842
2270	629.9876	1257.9607	1257.6387	0.3220	0	16	4.5	1	K.QGVMIPLEEAR.E
7580	888.2361	1774.4577	1774.8559	-0.3982	1	2	1e+02	3	K.QMQEHLKFLEEAEK.R
7713	893.2786	1784.5427	1783.9614	0.5813	2	10	13	2	K.QGVMIPLEEAREKLR.A
10032	681.6959	2042.0657	2041.1221	0.9436	2	4	48	6	R.SYRELPLRLADFGVLHR.N
11865	764.0939	2289.2597	2289.0332	0.2266	0	3	71	10	K.IMQNSSAYFLGDQSNDSLQR.I 11863

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222. gi|220700991|gb|EED57329.1| **Mass:** 17658 **Score:** 121 **Queries matched:** 8 **emPAI:** 0.19
ATP synthase delta chain, mitochondrial precursor, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2317	632.5626	1263.1107	1262.7207	0.3900	2	5	47	8	M.SSLRFARSALR.A 2324
3548	697.8546	1393.6947	1393.7612	-0.0665	2	5	56	4	-.MSSLRFARSALR.A
3683	706.8776	1411.7407	1409.7561	1.9846	2	(1)	1.3e+02	5	-.MSSLRFARSALR.A
4129	732.0531	1462.0917	1461.6947	0.3970	0	121	1.4e-10	1	K.IASGSGSEQDIAEAK.I
5918	819.1936	1636.3727	1634.9243	1.4484	0	9	20	1	K.IELEVLETLQAHLK.- 5913 5931

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223. gi|220697392|gb|EED53733.1| **Mass:** 38055 **Score:** 120 **Queries matched:** 17 **emPAI:** 0.40

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         mitochondrial peroxiredoxin Prx1, putative [Aspergillus flavus NRRL3357]
         Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
          1006  517.2441  1032.4737  1031.5651   0.9086   0     5      55    4   R.SVFIIDPNK.K
          1310  545.6966  1089.3787  1088.5714   0.8074   0    61 0.00016    1   R.VVDALQTTDK.H
          1311  545.7766  1089.5387  1088.5574   0.9813   1    10      20    3   R.RNSDETVIR.R
          1707  581.2011  1160.3877  1159.6601   0.7276   1    39   0.025    1   R.SVFIIDPNKK.I 1704
          1875  598.6936  1195.3727  1194.6067   0.7661   0   (23)   0.81    1   R.LIMSYPASTGR.N
          1953  606.6601  1211.3057  1210.6016   0.7041   0    48  0.0021    1   R.LIMSYPASTGR.N 1946
          2393  636.7241  1271.4337  1270.6921   0.7416   0    59 0.00021    1   K.LTFPIIADPER.K 2401
          3611  701.2656  1400.5167  1398.7871   1.7296   1    25    0.46    1   K.LTFPIIADPERK.V
          5554  536.7859  1607.3357  1607.8817  -0.5460   2     2      94    5   K.KIRLIMSYPASTGR.N
          9608  666.1075  1995.3007  1994.0255   1.2752   1    10      15    5   R.LIMSYPASTGRNTAEVLR.V 9591
         11249 1100.3191  2198.6237  2196.9521   1.6716   0    15     4.4    1   K.VAYAYDMVDYQDTTNVDSK.G
         15422  995.6632  2983.9677  2981.5135   2.4542   0    20    0.92    1   K.HGVTTPINWLPGDDVVIPPPVSTEDAQK.K 15423

224.    gi|220690860|gb|EED47209.1|     Mass: 24585   Score: 120   Queries matched: 9   emPAI: 0.29
         NADH-ubiquinone oxidoreductase 213 kDa subunit [Aspergillus flavus NRRL3357]
         Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
          3994  724.1981  1446.3817  1446.6950  -0.3133   0    90 1.4e-07    1   R.TSGEQTLAELGEGR.G 4026
          7319  584.5549  1750.6427  1749.7475   0.8952   0    10      13    2   -.MAETATSQNPSEPSER.L 7317 7322 7323
          8897  955.2041  1908.3937  1906.9135   1.4802   0     1 1.1e+02    5   R.SGGTIGVFAAMGGTYEFVK.T
         10778 1070.1651  2138.3157  2137.1202   1.1956   0    57 0.00025    1   K.TTMLTGGVGLFASAVQNTLTR.K 10760

225.    gi|220697217|gb|EED53558.1|     Mass: 76932   Score: 119   Queries matched: 16   emPAI: 0.13
         NADPH cytochrome P450 reductase (CprA), putative [Aspergillus flavus NRRL3357]
         Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
          1443  558.6411  1115.2677  1115.5216  -0.2538   1     8      29    6   K.GEEMVKHMR.S
          1520  564.8341  1127.6537  1129.6455  -1.9918   2     6      41    2   K.AGKTRDILEK.M
          2253  629.2391  1256.4637  1255.6384   0.8254   0    11      14    1   K.VGTTVLFFGCR.N
          3986  723.8486  1445.6827  1446.6303  -0.9476   0     5      44    5   R.NEDFLYQDEFK.A 3993
          4440  751.1881  1500.3617  1499.7984   0.5633   0    28    0.24    1   K.VPIPTPTTYDAAVR.Y 4450
          5531  536.1492  1605.4257  1603.8093   1.6164   1     5      45    3   R.YYSISSSSLVQKDK.I
          6507  841.0136  1680.0127  1680.8359  -0.8232   0     0 1.3e+02    4   R.QFVSSLAAFAPDEATK.T
          8396  928.7056  1855.3967  1854.8523   0.5444   0     8      23    3   R.EAVYEPVFNVTEDESK.S
         11628 1128.8761  2255.7377  2254.9688   0.7689   0   115   4e-10    1   R.IGSAGEGDDGAGTMEEDFLAWK.E
         11679  755.7289  2264.1647  2263.2147   0.9500   0    17     2.3    1   K.LPSDPSRPIIMVGPGTGVAPFR.G 11680 11682
         11755  760.3605  2278.0597  2279.2096  -1.1499   0   (6)      33    7   K.LPSDPSRPIIMVGPGTGVAPFR.G
         14453  894.1232  2679.3477  2678.4969   0.8509   0     4      50    6   -.MAQLDTLDLVVLVALLVGSVAYFTK.G
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226. gi|220691248|gb|EED47596.1| **Mass:** 90839 **Score:** 118 **Queries matched:** 33 **emPAI:** 0.11
cell division control protein Cdc48 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
277	822.9160	821.9087	822.3759	-0.4672	0	2	95	5	K.AFEEAEK.N
402	433.0456	864.0767	863.4501	0.6266	1	11	13	9	R.DIFDKAR.A
1336	548.4836	1094.9527	1092.4869	2.4658	0	8	21	7	K.MAGESESNLR.K 1327
1937	605.1206	1208.2267	1205.6115	2.6153	0	9	18	4	R.GILMYGPPGTGK.T 1936
2199	625.2201	1248.4257	1246.6670	1.7588	0	37	0.03	1	R.YALGVSNPSALR.E 2174
3839	716.2076	1430.4007	1429.7201	0.6806	1	1	1.3e+02	5	R.WEDIGGLEEVKR.E
4047	484.9229	1451.7467	1449.7571	1.9896	0	5	44	9	R.VVSQLLTLMDGMK.A
4109	487.6112	1459.8117	1461.7146	-1.9029	2	10	18	4	R.AHFEEAMKTARR.S
4463	501.7009	1502.0807	1500.7792	1.3015	1	2	1.1e+02	10	R.LEIMQIHTKNMK.L
5353	795.9661	1589.9177	1589.8633	0.0544	1	19	2	1	R.RVVSQLLTLMDGMK.A
6561	841.9141	1681.8137	1680.8063	1.0075	0	0	1.4e+02	2	R.VVNQLLTEMDGMTSK.K
6629	844.4026	1686.7907	1685.8988	0.8919	0	4	53	1	R.LDTLVYVPLPDQASR.E
8084	911.1716	1820.3287	1817.9233	2.4054	0	44	0.0057	1	R.AAAPCVVFLDELDSIAK.S 8063 8078
8275	922.8376	1843.6607	1841.9774	1.6833	0	98	2.2e-08	1	K.NSPAIIFIDEIDSIAPK.R 8253 8256
8356	618.2785	1851.8137	1848.9914	2.8224	2	0	1.3e+02	6	R.RVVSQLLTLMDGMKAR.S
9606	666.1019	1995.2837	1994.9486	0.3351	1	1	1.1e+02	4	R.YEAFAQSLKNSGGSSFFR.F
10081	683.2182	2046.6327	2046.0283	0.6044	2	4	54	4	R.FGRFDREVDIGIPDPTGR.L
10885	717.2829	2148.8267	2145.8896	2.9372	0	5	40	5	K.MDEDEEVDEEDPVPELTR.A 10884
11627	752.8425	2255.5057	2255.2161	0.2896	2	2	78	4	K.NSPAIIFIDEIDSIAPKREK.T 11617 11623
12084	773.4669	2317.3787	2315.2750	2.1037	2	4	50	2	K.THGFSGADLGFVTQRAVKLAIK.Q
13325	833.7012	2498.0817	2496.3199	1.7618	2	3	53	1	K.FGLSPSRGVLFYGPPGTGKTMLAK.A
14181	881.2605	2640.7597	2642.4400	-1.6803	2	0	1.1e+02	6	K.SIGIKPPRGILMYGPPGTGKTLMAR.A
14883	926.0742	2775.2007	2774.4378	0.7630	2	5	32	2	R.KAFEEAEKNSPAIIFIDEIDSIAPK.R

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227. gi|45477378|gb|AY371490.1|_f **Mass:** 3003861 **Score:** 118 **Queries matched:** 322 **emPAI:** 0.00
Aspergillus parasiticus aflatoxin pathway gene cluster, complete sequence

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
134	743.5380	742.5307	742.3973	0.1334	0	9	24	1	K.AEPIASR.N
162	757.6070	756.5997	756.4718	0.1279	2	17	3.5	2	R.RKANLR.V
184	772.2110	771.2037	772.4807	-1.2769	0	11	13	6	R.TISLALR.K
219	789.6330	788.6257	788.4504	0.1753	1	7	43	8	K.RANTTVK.H
231	400.5331	799.0517	798.4283	0.6235	1	14	6	3	K.HLMSRR.Y
235	802.4770	801.4697	800.4980	0.9717	2	6	62	1	R.AKSALRR.L 236
354	426.6781	851.3417	851.3960	-0.0542	0	7	30	1	R.APCSYVR.S
420	872.5690	871.5617	871.4949	0.0668	1	9	25	9	K.KDLMIPR.R
440	439.8106	877.6067	879.4120	-1.8053	0	9	23	4	K.STSMVSPR.W
455	441.9846	881.9547	882.5287	-0.5740	0	8	21	10	K.LLGPSIQR.V

475	**891.8930**	**890.8857**	**890.5086**	**0.3771**	**1**	**0**	**1.8e+02**	**10**	**R.TLFQARR.S**	
598	**463.9856**	**925.9567**	**926.4934**	**-0.5366**	**1**	**4**	**54**	**6**	**R.DAKLHSTR.R**	
604	**927.3700**	**926.3627**	**925.5094**	**0.8534**	**1**	**10**	**15**	**3**	**R.ANTTVKHR.S**	
615	466.6291	931.2437	931.4975	-0.2537	0	17	4.3	2	R.TDQTVLQK.I	613
646	**474.5431**	**947.0717**	**944.5053**	**2.5665**	**2**	**9**	**26**	**5**	**R.SRRSHFR.E**	644
671	958.3960	957.3887	957.4630	-0.0743	0	11	14	5	R.SFTPFMTK.L	
694	961.9170	960.9097	959.5586	1.3511	1	7	44	9	R.LATQMLKR.G	
774	977.6210	976.6137	976.4185	0.1952	0	19	2	3	R.QVCHDYR.D	771
777	**489.5991**	**977.1837**	**975.5396**	**1.6441**	**2**	**14**	**6.9**	**4**	**R.SMISRARR.Q**	
778	489.6051	977.1957	976.5375	0.6582	1	13	8.9	3	R.ILQTCKSK.D	785
805	492.6636	983.3127	983.4607	-0.1480	0	10	15	6	R.NDAVLHCR.M	
819	494.0206	986.0267	983.5400	2.4867	0	16	4.7	3	K.VSLPGDQLR.C	
829	**494.3591**	**986.7037**	**987.5396**	**-0.8359**	**2**	**1**	**1.7e+02**	**6**	**R.RLPMRSGR.S**	
852	992.5760	991.5687	991.5345	0.0342	2	(2)	1.1e+02	10	R.SMISRARR.Q	
879	500.5621	999.1097	998.5509	0.5589	0	12	11	8	R.LDLETRPR.E	
929	**507.3851**	**1012.7557**	**1013.5869**	**-0.8312**	**0**	**16**	**4.6**	**2**	**R.NIVALTVER.I**	
991	515.6721	1029.3297	1026.5611	2.7687	0	7	35	9	R.FPSLSAHLR.R	
1041	**520.5516**	**1039.0887**	**1038.4843**	**0.6045**	**1**	**4**	**66**	**2**	**R.SSSRSWSSR.D**	
1067	**1046.5950**	**1045.5877**	**1043.6101**	**1.9776**	**1**	**4**	**79**	**1**	**R.RGHGLIHVR.Y**	
1074	**524.3736**	**1046.7327**	**1044.5539**	**2.1789**	**1**	**0**	**1.8e+02**	**2**	**R.KVMPVHYR.I**	
1099	**525.8601**	**1049.7057**	**1048.5050**	**1.2007**	**1**	**7**	**32**	**2**	**R.RGNPTSDFR.Y**	
1102	**526.5926**	**1051.1707**	**1050.6410**	**0.5297**	**2**	**6**	**44**	**4**	**R.IKGARTLHR.A**	
1185	534.6666	1067.3187	1066.6386	0.6801	0	39	0.02	1	K.EQAILVAVPK.R	1186
1230	**538.3631**	**1074.7117**	**1074.6774**	**0.0343**	**2**	**10**	**18**	**5**	**R.RLGKVLHPR.R**	
1322	546.6921	1091.3697	1090.5077	0.8620	0	14	7.5	6	R.GNGVMEIAER.G	
1323	**546.7546**	**1091.4947**	**1089.5535**	**1.9412**	**1**	**10**	**17**	**3**	**R.MCANLLRGR.K**	
1333	548.1411	1094.2677	1094.5581	-0.2904	1	15	5.1	5	R.NSPAGTKHAGR.Y	1338
1345	1096.8880	1095.8807	1095.6077	0.2730	0	4	62	9	K.SRPTLFTFK.S	
1346	549.1011	1096.1877	1095.5052	0.6825	0	7	33	8	R.MLNNAGTTMK.K	
1380	**552.9826**	**1103.9507**	**1105.5484**	**-1.5977**	**1**	**(2)**	**1.1e+02**	**4**	**R.MCANLLRGR.K**	
1390	554.0626	1106.1107	1106.6461	-0.5354	2	6	42	9	R.FRRAIAAFR.J	
1435	557.7121	1113.4097	1111.5146	1.8952	0	1	1.4e+02	10	R.GTVGSEFNSSK.R	
1442	**558.2096**	**1114.4047**	**1111.5002**	**2.9046**	**0**	**(4)**	**76**	**10**	**R.MLNNAGTTMK.K**	
1451	559.1946	1116.3747	1116.6073	-0.2326	1	(7)	36	5	R.RAVTISMSPR.J	
1453	559.4276	1116.8407	1118.5754	-1.7346	0	1	1.6e+02	10	R.MLAASNVLER.E	
1494	**562.4756**	**1122.9367**	**1120.5962**	**2.3405**	**2**	**10**	**15**	**3**	**K.GTHRRQNPR.H**	
1496	**562.6756**	**1123.3367**	**1122.5101**	**0.8266**	**0**	**6**	**42**	**3**	**R.SSSRPHCHR.F**	
1574	**378.9595**	**1133.8567**	**1132.6023**	**1.2545**	**1**	**11**	**12**	**6**	**R.RAVTISMSPR.J**	1562
1581	1135.5350	1134.5277	1133.6267	0.9010	0	6	37	4	R.APLLAVMTFR.F	1594
1598	**569.5571**	**1137.0997**	**1134.5743**	**2.5254**	**0**	**3**	**72**	**4**	**K.DPFVLMLER.R**	
1599	**569.6181**	**1137.2217**	**1134.6145**	**2.6072**	**1**	**4**	**66**	**2**	**R.AETYIRINR.R**	

1602	569.9046	1137.7947	1137.5713	0.2234	1	13	6.8	3	K.GGIFSQRMSR.E	
1689	579.7991	1157.5837	1158.6067	-1.0230	0	9	22	7	K.EGLMVPVTAAR.C	
1718	582.6501	1163.2857	1163.5982	-0.3125	2	1	1.2e+02	7	R.SRQFRMPSR.T	
1761	586.6846	1171.3547	1169.6404	1.7143	0	18	2.8	2	R.LAAPESSGIAVR.V	
1858	596.2056	1190.3967	1189.6779	0.7188	1	10	18	3	R.STLITVGTRSR.S	1854
1859	596.4076	1190.8007	1189.6581	1.1426	1	4	66	8	R.VPRHSWRPR.A	
1863	597.3511	1192.6877	1192.6200	0.0677	0	7	33	1	R.NIIPLSEHDR.S	
1905	601.4506	1200.8867	1200.7342	0.1525	1	3	85	7	R.LRSAPYLLIR.Q	
1916	603.2901	1204.5657	1203.6935	0.8722	2	3	85	2	R.ISSKRANTTVK.H	
1938	605.2431	1208.4717	1208.6890	-0.2173	2	2	87	5	R.SHIRHYLKR.D	
1941	605.5966	1209.1787	1206.7019	2.4768	1	5	49	6	R.HLLKQGMKPR.T	1939
1983	608.8161	1215.6177	1215.5997	0.0181	0	9	22	4	K.LTFNGGHDTVR.N	
2053	615.2126	1228.4107	1227.6618	0.7489	2	11	13	1	R.QCGRRVSPLR.T	
2067	616.3111	1230.6077	1228.6524	1.9553	1	5	50	4	K.DAIESGVLGGRR.C	
2103	619.1626	1236.3107	1235.5968	0.7139	1	1	1.4e+02	7	R.EPNKTQFMGGK.L	
2246	628.4891	1254.9637	1253.6438	1.3200	1	2	1e+02	7	R.NTERIYMSIK.S	
2302	631.6306	1261.2467	1262.6255	-1.3788	1	8	30	3	R.DAEGDRNLFVK.A	
2343	633.7021	1265.3897	1264.6775	0.7122	2	16	3.7	1	K.KSISEYKTPGR.H	
2350	633.9521	1265.8897	1265.6914	0.1983	0	8	22	9	R.MAISSIAHPLAR.Y	
2368	634.7976	1267.5807	1265.6476	1.9331	1	8	25	3	K.YLQAGQTRSSR.F	
2405	1273.6000	1272.5927	1271.7197	0.8730	2	11	15	3	R.KNRDDIVLATK.Y	2396 2397 2406
2447	639.2606	1276.5067	1275.7147	0.7921	1	8	26	9	R.TSVITITERTR.R	
2458	1277.6880	1276.6807	1276.6385	0.0423	2	2	1.1e+02	10	K.EHRSQPPDRR.Q	
2459	639.3861	1276.7577	1276.7979	-0.0402	2	17	3.6	1	K.KVKLIPQPQAR.V	2446 2466
2474	640.0646	1278.1147	1276.6524	1.4624	0	6	42	7	R.KPNSASQFTAAR.W	
2491	641.2136	1280.4127	1279.6857	0.7270	2	1	1.1e+02	4	R.RRPSSDAKAHR.Q	
2518	643.0201	1284.0257	1282.5434	1.4823	0	13	7.4	3	R.YLGCCTGPEAR.R	2507
2577	646.2876	1290.5607	1289.7065	0.8542	1	7	36	3	K.SRVQPRPHASR.L	
2578	646.3106	1290.6067	1290.6754	-0.0687	1	12	10	4	K.DPFVLMLERR.M	
2594	647.3436	1292.6727	1291.6806	0.9921	0	3	74	7	K.TTLGSGLSGMLGAK.V	2606
2626	648.7156	1295.4167	1294.6393	0.7774	1	6	43	10	R.MLWWRNFSR.K	
2724	436.8105	1307.4097	1304.7023	2.7074	1	10	15	2	K.REFNLVQLMR.C	
2762	657.1581	1312.3017	1311.7809	0.5208	1	4	59	8	K.LICRGLKPLSR.M	
2781	658.1591	1314.3037	1314.6317	-0.3279	1	14	7.1	9	R.NQWGVDEPRSK.K	2794
2784	658.3251	1314.6357	1313.7164	0.9193	2	3	88	2	R.EESGVVLRRGGR.G	
2822	660.1951	1318.3757	1315.5946	2.7812	0	4	63	4	R.SHWTGGADNFPK.E	
2923	665.7216	1329.4287	1326.6853	2.7434	0	1	1.4e+02	5	K.FVAMAALATTTSK.C	
2943	666.6086	1331.2027	1330.6854	0.5173	2	6	48	1	R.TSHPSFRSTRR.R	
3005	670.3451	1338.6757	1336.6782	1.9975	1	3	66	7	R.RRPPAPCNNQK.T	
3010	670.6711	1339.3277	1340.7677	-1.4400	2	6	38	1	R.ATKNWPRVLTR.K	
3179	453.2799	1356.8177	1357.6851	-0.8674	1	8	23	2	K.RSPPHPTGAPGER.R	

3209	**454.2245**	**1359.6517**	**1358.7127**	**0.9390**	**2**	**9**	**19**	**7**	**R.SVAGRRASQGGASR.V**	
3269	**683.1366**	**1364.2587**	**1365.7616**	**-1.5029**	**1**	**0**	**1.4e+02**	**10**	**K.TEKVIHELIER.K**	
3283	**683.9951**	**1365.9757**	**1363.5688**	**2.4070**	**1**	**2**	**1e+02**	**9**	**R.WERGSCGGQDGR.I**	
3285	**456.3912**	**1366.1517**	**1367.6187**	**-1.4669**	**1**	**10**	**14**	**2**	**R.QANASRCMFQR.C**	
3327	686.1911	1370.3677	1369.8129	0.5549	2	1	1.2e+02	10	R.LVVRWCIRLR.R	
3374	688.2076	1374.4007	1373.6874	0.7134	1	5	61	10	K.NKIMNENGWLR.V	
3410	460.0165	1377.0277	1377.6897	-0.6620	0	5	48	10	R.CVLWVATTICR.R	
3421	690.1651	1378.3157	1376.6031	1.7127	0	5	46	8	R.AHDFDSPTICSK.R	
3500	463.9192	1388.7357	1390.6993	-1.9636	1	7	39	8	K.ESHFLQPYSKR.N	3509
3577	**699.4461**	**1396.8777**	**1396.8224**	**0.0553**	**1**	**14**	**5.9**	**2**	**R.LGEMPILLLRSR.V**	3579 3582 3583
3684	**707.0866**	**1412.1587**	**1413.6459**	**-1.4872**	**1**	**2**	**1.1e+02**	**3**	**K.ECPLEDPGRWR.A**	
3696	**707.8336**	**1413.6527**	**1414.7456**	**-1.0929**	**2**	**7**	**35**	**1**	**K.SDADPIKVEKWK.Q**	
3714	708.7586	1415.5027	1414.7641	0.7387	2	5	54	10	R.RSGETVREGGVIR.Y	
3807	**476.8969**	**1427.6687**	**1427.6979**	**-0.0292**	**0**	**9**	**18**	**2**	**R.LYACPAADAALHR.A**	3805
3831	**716.0801**	**1430.1457**	**1428.7395**	**1.4062**	**0**	**13**	**8.2**	**1**	**R.IHTMSTSAPLLSR.Y**	
3842	**716.2611**	**1430.5077**	**1429.7460**	**0.7618**	**2**	**4**	**66**	**3**	**R.LRSSMEVTAHRK.S**	
3929	**480.6205**	**1438.8397**	**1439.7707**	**-0.9310**	**1**	**5**	**44**	**9**	**R.GYQMGLLARFLR.R**	
3946	**721.9656**	**1441.9167**	**1439.6497**	**2.2670**	**0**	**4**	**61**	**4**	**R.SSNLGMNGTGLMSR.R**	
3995	**724.2381**	**1446.4617**	**1444.6538**	**1.8079**	**0**	**3**	**80**	**2**	**R.LVSSTEMSTSTMR.F**	3997
4125	**731.8126**	**1461.6107**	**1460.6487**	**0.9620**	**0**	**(0)**	**1.5e+02**	**6**	**R.LVSSTEMSTSTMR.F**	
4235	**738.4021**	**1474.7897**	**1476.7837**	**-1.9940**	**1**	**2**	**96**	**1**	**K.WGLESLFRTVNR.L**	4242
4239	492.6635	1474.9687	1472.7406	2.2282	1	4	61	8	R.GSGCKVSLPGDQLR.C	
4269	739.6666	1477.3187	1477.8252	-0.5065	2	8	26	8	R.KAFDLSISSLRNK.D	
4320	742.7346	1483.4547	1483.8471	-0.3923	1	0	1.5e+02	10	R.TVNRLSLQPTLSR.C	
4344	**744.3366**	**1486.6587**	**1485.6558**	**1.0029**	**0**	**7**	**34**	**1**	**R.YASGPTFDICAER.I**	
4370	**497.8272**	**1490.4597**	**1489.7316**	**0.7282**	**1**	**9**	**21**	**10**	**R.LCAPRMCANLLR.G**	
4432	**500.7739**	**1499.2997**	**1496.8212**	**2.4785**	**2**	**4**	**62**	**8**	**R.EKRTASAVVFPHR.V**	4433
4554	**758.2261**	**1514.4377**	**1513.7671**	**0.6706**	**1**	**6**	**37**	**5**	**R.VDNEVPRCSLLGR.F**	4553
4598	**507.3849**	**1519.1327**	**1519.7114**	**-0.5787**	**0**	**6**	**42**	**10**	**K.GSELQSGEGNTISNK.E**	
4777	769.3351	1536.6557	1534.7814	1.8743	0	14	5.7	1	K.VLMVDIGGGFGQQSK.A	4744 4770 4784
4936	776.1681	1550.3217	1548.7501	1.5716	1	2	85	3	R.SSACRIQTGCGKPK.R	4916 4925
5023	**520.5519**	**1558.6337**	**1555.7354**	**2.8983**	**1**	**7**	**34**	**5**	**R.RCGGATVWFYPSR.R**	
5068	782.8416	1563.6687	1563.8290	-0.1603	1	1	1.3e+02	10	K.QKTTLGSGLSGMLGAK.V	
5076	783.5086	1565.0027	1562.7253	2.2774	0	7	28	1	K.GLFDYYSTVDEVR.G	
5122	**524.1582**	**1569.4527**	**1567.8583**	**1.5944**	**2**	**5**	**49**	**6**	**R.GDDKVFVHQRIVR.V**	
5123	785.7576	1569.5007	1569.7423	-0.2416	0	7	30	6	K.TDPFGLGNIHGEEGK.A	
5271	528.7419	1583.2037	1580.7174	2.4863	0	5	41	10	R.DSLMLDMNNVELR.S	
5371	531.7249	1592.1527	1593.8032	-1.6505	1	19	1.8	1	R.ISESAVKSTSMVSPR.W	5382
5398	**532.6199**	**1594.8377**	**1595.7508**	**-0.9131**	**1**	**(4)**	**63**	**5**	**R.SSNLGMNGTGLMSRR.L**	
5401	**532.6612**	**1594.9617**	**1595.7508**	**-0.7891**	**1**	**8**	**21**	**1**	**K.RSSNLGMNGTGLMSR.R**	5396 5412
5403	532.8025	1595.3857	1595.7508	-0.3651	1	(3)	75	7	K.RSSNLGMNGTGLMSR.R	

5604	**538.0929**	**1611.2567**	**1611.7457**	**-0.4890**	**1**	**(2)**	**93**	**2**	**K.RSSNLGMNGTGLMSR.R**	
5610	806.7016	1611.3887	1611.7457	-0.3570	1	7	29	5	R.SSNLGMNGTGLMSRR.L	5616
5650	**539.1482**	**1614.4227**	**1615.8657**	**-1.4430**	**1**	**4**	**58**	**9**	**K.RCWIAPEFVLIGR.R**	
5739	811.7191	1621.4237	1620.8260	0.5977	0	1	1.1e+02	10	R.SLEHSPDLFPGPGIR.K	
5783	813.1726	1624.3307	1621.8280	2.5028	1	3	74	4	R.LNAMTLQSSNRLMK.R	
5829	**543.7465**	**1628.2177**	**1628.8522**	**-0.6345**	**0**	**7**	**28**	**2**	**K.ADQGVSAEPVPLPPPR.N**	
5870	816.9091	1631.8037	1632.9212	-1.1175	1	0	1.4e+02	6	R.IRAAHLTHDVVFVR.A	
5967	**547.7352**	**1640.1837**	**1641.7569**	**-1.5732**	**1**	**4**	**61**	**2**	**R.RYASGPTFDICAER.I**	
6038	823.6196	1645.2247	1642.8652	2.3596	2	7	29	2	R.SIPATSQSWRARQR.C	
6072	824.6816	1647.3487	1645.7947	1.5540	1	0	1.5e+02	3	R.YLATAGETKSPEDHK.L	
6157	**552.1452**	**1653.4137**	**1652.8100**	**0.6038**	**2**	**3**	**67**	**5**	**R.CRRRPPAPCNNQK.T**	6138
6201	**829.6016**	**1657.1887**	**1657.8107**	**-0.6220**	**2**	**4**	**61**	**2**	**R.MVWDIDPRQRNGR.S**	
6486	**560.3782**	**1678.1127**	**1676.9111**	**1.2017**	**1**	**12**	**9.5**	**2**	**R.HPSAQLVTWRVEVR.E**	6489
6782	850.7426	1699.4707	1699.8907	-0.4199	2	21	1.1	2	K.GARTLHRAGFPNFEK.I	6778
6837	852.2501	1702.4857	1701.7642	0.7216	1	0	1.4e+02	8	R.DDPVECGRHDPLHR.R	
6868	853.5061	1704.9977	1705.9475	-0.9498	1	1	1.2e+02	9	R.SVPPRLAAPESSGIAVR.V	6898
6877	**853.8056**	**1705.5967**	**1703.8856**	**1.7112**	**2**	**4**	**61**	**1**	**K.TVPWRYASVNREAR.R**	
7009	**573.6062**	**1717.7967**	**1715.8526**	**1.9442**	**2**	**6**	**37**	**2**	**R.DGLCAKWNTPTARAR.A**	
7027	**861.2026**	**1720.3907**	**1718.8376**	**1.5531**	**1**	**1**	**1e+02**	**5**	**K.YIYSPSHERDSLPR.S**	
7278	582.7869	1745.3387	1745.9359	-0.5972	2	1	1.3e+02	6	R.CGGKLQSLPVRAAAYR.C	
7282	**582.8192**	**1745.4357**	**1742.9362**	**2.4995**	**1**	**3**	**79**	**9**	**R.ATAILTRWTRPCAAR.L**	
7294	874.2596	1746.5047	1746.8173	-0.3126	0	4	63	5	R.LSSAQESFSEGGNIHGK.C	
7350	**878.4006**	**1754.7867**	**1751.8519**	**2.9348**	**2**	**3**	**64**	**1**	**K.RSSNLGMNGTGLMSRR.L**	
7373	**879.7526**	**1757.4907**	**1756.9148**	**0.5759**	**0**	**1**	**1.2e+02**	**2**	**K.VHYLGISDSPAWVVSK.A**	
7448	**883.0561**	**1764.0977**	**1762.8575**	**1.2402**	**2**	**2**	**89**	**3**	**R.IVERRCRPMQCMK.R**	
7580	888.2361	1774.4577	1773.8913	0.5664	2	2	1e+02	2	R.MCARPMPVGGVQKRR.C	
7601	**593.1409**	**1776.4007**	**1775.9107**	**0.4900**	**1**	**9**	**21**	**4**	**R.RLLWQSGPYSDLWR.J**	
7604	889.3046	1776.5947	1776.9522	-0.3575	1	8	24	2	R.QAYIWLSKISSTPQR.T	
7675	**595.1975**	**1782.5707**	**1780.9114**	**1.6593**	**2**	**5**	**42**	**10**	**R.NRDRSASPMAHSAILR.I**	
7691	892.6711	1783.3277	1782.9523	0.3754	1	4	53	10	R.ARISLLGATSGVVSHCR.R	
7806	897.6361	1793.2577	1791.0155	2.2422	2	4	57	7	R.FESARLRSAPYLLIR.Q	
7885	901.8376	1801.6607	1801.8958	-0.2351	2	4	53	5	K.RYLATAGETKSPEDHK.L	
7978	**906.7496**	**1811.4847**	**1810.9108**	**0.5739**	**2**	**1**	**1e+02**	**7**	**R.LSGDRTIQFQRSMTR.C**	
7998	605.1209	1812.3407	1810.7913	1.5494	1	12	10	4	R.YCRCGPELPLCSGSR.E	7996
8072	**607.2382**	**1818.6927**	**1817.9127**	**0.7800**	**1**	**11**	**12**	**3**	**R.LRDSLMLDMNNVELR.S**	
8125	609.5842	1825.7307	1825.9548	-0.2240	1	4	59	9	R.LAGRFTDGVHGSLGQGVR.H	
8157	915.1171	1828.2197	1827.9374	0.2824	2	5	47	3	R.GRGNQDCTSKIGAPVIR.R	
8309	924.7631	1847.5117	1845.9923	1.5194	1	2	81	4	R.WWIIVMSELTLRQR.R	
8338	926.0856	1850.1567	1849.9026	0.2541	1	(3)	73	3	R.LRDSLMLDMNNVELR.S	
8414	929.2726	1856.5307	1857.9710	-1.4403	2	15	4.6	2	K.WNNQIFGSRRAPLGSR.J	8415
8420	**620.0419**	**1857.1037**	**1856.9648**	**0.1389**	**2**	**8**	**20**	**4**	**R.VRMCARPMPVGGVQKR.R**	

8423	620.1289	1857.3647	1856.9648	0.3999	2	(5)	39	2	R.VRMCARPMPVGGVQKR.R	
8563	625.6809	1874.0207	1874.8945	-0.8738	1	1	1.1e+02	6	R.LPVSECERFDLSPGGGR.G	
8722	630.8102	1889.4087	1887.9295	1.4792	2	1	1.2e+02	5	R.LVSSTEMSTSTMRFRR.M	
8760	632.3142	1893.9207	1890.9986	2.9221	1	2	77	9	K.VLMVDIGGGFGQQSKALR.A	
8779	633.2759	1896.8057	1895.0741	1.7316	1	1	1e+02	3	R.RDHIKPLLGISSYLQR.T	
8830	634.7709	1901.2907	1900.8666	0.4242	0	2	81	3	R.LHDVFFSQETMFEAGK.H	
8867	635.6602	1903.9587	1903.9244	0.0343	2	(1)	1.3e+02	6	R.LVSSTEMSTSTMRFRR.M	
8876	636.1729	1905.4967	1902.8570	2.6397	0	1	1.1e+02	8	R.WSGSPAEYPPECPSLAR.V	
8934	638.7415	1913.2027	1912.9901	0.2126	2	4	55	6	K.DAIESGVLGGRRCTIGPR.T	
8964	639.3442	1915.0107	1916.9271	-1.9163	1	2	94	8	R.RIMHGSEVCSVMPSVTK.V	
9017	641.1762	1920.5067	1917.8785	2.6282	1	2	80	10	K.GDENGSPMIRNVNLCAR.M	
9076	965.7201	1929.4257	1929.0836	0.3421	2	1	1.2e+02	10	K.IKDFAYPVEVIPNIRR.I	
9216	650.3989	1948.1747	1946.9956	1.1791	1	4	61	4	R.GENIIQSLRPRSTSMSR.Y	9222
9264	652.1495	1953.4267	1952.0262	1.4006	1	9	16	2	K.VRAEQSLCLNASVHLAGK.I	
9298	653.8122	1958.4147	1955.9696	2.4451	0	1	1e+02	6	R.CSSIEPILIYMSATISR.L	
9348	655.6682	1963.9827	1964.0149	-0.0322	0	6	35	1	R.LMYNALILSARPDASSSR.V	
9392	657.6259	1969.8557	1967.8288	2.0269	0	15	4.5	2	R.SCCGTLATPTQQCNWGK.R	9383
9407	658.2845	1971.8317	1969.0601	2.7716	1	5	41	3	K.SCCGPLQILPISRSLIR.V	9393 9405
9436	659.6475	1975.9207	1975.0520	0.8687	1	3	62	3	K.TRSTMQGITIQEAGLTLR.D	
9559	664.7742	1991.3007	1991.0854	0.2154	2	2	85	6	R.AVGWVHPGKIRGDFIPSR.A	
9564	664.8135	1991.4187	1991.9750	-0.5563	0	5	47	7	R.WPSSCGILISLWMWTR.L	
9686	1003.6916	2005.3687	2006.0553	-0.6866	2	0	1.2e+02	3	R.FPRLNAMTLQSSNRLMK.R	
9735	671.7552	2012.2437	2014.0894	-1.8457	1	0	1.3e+02	10	R.YCRPQPTSVVRPSIRAK.L	
9772	673.1675	2016.4807	2015.8976	0.5832	0	0	1.2e+02	7	R.DTLKPQRPHGCSMDACK.Y	
9813	675.0902	2022.2487	2020.9175	1.3312	0	54	0.00056	1	K.AFGSDLTMFEWMPQHPK.H	9804 9815
9856	676.3915	2026.1527	2027.0146	-0.8619	1	7	26	2	R.ACFSVVAAVRNDETVVYK.L	9849
9921	678.8085	2033.4037	2035.0125	-1.6088	2	9	18	1	R.NVNLCARMLNNAGTTMKK.K	
10061	682.6795	2045.0167	2046.9840	-1.9673	1	0	1.3e+02	9	R.LCQMPGSSLPGRHPQGGPR.G	
10106	684.0532	2049.1377	2048.0208	1.1169	1	4	57	2	R.ITSGQDVVNLVSACKGDTGK.S	
10175	686.7855	2057.3347	2056.1218	1.2129	1	3	65	7	R.IGQRVLSFPDWQLQTLR.R	
10235	688.6165	2062.8277	2062.1047	0.7230	2	3	65	6	R.GLKPLSRMLWWRNFSR.K	
10269	1033.7701	2065.5257	2065.1102	0.4155	1	2	82	5	R.AEQSLCLNASVHLAGKIVR.C	
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M	10286
10323	692.4769	2074.4087	2075.0694	-0.6607	1	9	16	1	R.QAMPSTPHGIQPRSGNLIR.I	10324 10341
10384	694.6859	2081.0357	2078.2584	2.7773	1	(0)	1.2e+02	2	R.LMLIPRPTLMLILIRNR.I	
10386	694.7089	2081.1047	2078.2584	2.8463	1	1	1.1e+02	5	R.LMLIPRPTLMLILIRNR.I	
10446	697.8545	2090.5417	2090.1306	0.4111	2	6	32	6	K.VLMVDIGGGFGQQSKALRAK.F	
10482	699.2742	2094.8007	2093.0211	1.7796	1	1	97	7	R.MIYAHSDGISTTVAGRSAEK.T	
10527	701.3205	2100.9397	2101.1069	-0.1671	0	0	1.3e+02	8	R.WLSHHAQIVGTNTAPSLAAK.V	
10536	701.7735	2102.2987	2103.0967	-0.7980	2	1	1e+02	10	R.RGENIIQSLRPRSTSMSR.Y	
10544	1052.5286	2103.0427	2103.0194	0.0233	0	21	1.1	1	R.AEWDDLMEQVGLEIIQSK.V	

10762	713.4415	2137.3027	2138.1776	-0.8748	1	2	86	5	R.NIYFLVPGLLSGSDFKIQK.S	10759 10766
10954	721.4885	2161.4437	2162.1340	-0.6903	1	2	78	2	R.ARAVVSVPPAIMFSVSICSR.V	
11048	725.2565	2172.7477	2174.1841	-1.4364	2	14	5.9	1	K.AKTRSTMQGITIQEAGLTLR.D	11059
11141	730.4179	2188.2317	2187.9249	0.3069	1	1	1.1e+02	5	R.CGDSGGAGADVWCFIMTGRR.Q	11139
11256	734.1592	2199.4557	2199.1007	0.3550	0	0	1.3e+02	6	R.ELMGPAHSHIFQALEHNIR.J	
11308	737.3735	2209.0987	2209.3166	-0.2179	1	4	51	1	R.TQRLMLIPRPTLMLILIR.N	
11352	738.6302	2212.8687	2212.2229	0.6458	2	2	88	5	R.IGQRVLSFPDWQLQTLRR.Q	
11364	1107.9231	2213.8317	2211.0273	2.8044	2	2	83	3	R.SERSSGNTAAICPICNYRR.Q	
11469	744.5109	2230.5107	2232.0456	-1.5349	2	4	47	2	R.TYWPSACKKVETMQQGYR.R	
11629	753.2769	2256.8087	2257.1868	-0.3781	2	4	56	5	R.DHGLRQFVVYQGLWNAAKR.D	
11721	759.0565	2274.1477	2273.2170	0.9307	2	1	1e+02	3	R.STAILCGLNPMRLATQMLKR.G	
11743	759.4955	2275.4647	2276.2232	-0.7585	0	1	99	9	K.MSVALGSAIMIVASVIQAATVGR.W	
11913	766.7665	2297.2777	2295.2695	2.0083	0	1	94	3	K.ILLGITPGISPTCGLSLVPTMR.L	
12052	771.9839	2312.9297	2310.2327	2.6970	1	1	1e+02	7	R.CSSIEPILIYMSATISRLLK.H	
12107	774.6892	2321.0457	2319.1325	1.9133	2	1	96	6	R.LCQMPGSSLPGRHPQGGPRGSK.E	
12366	789.9182	2366.7327	2364.2437	2.4890	2	2	84	2	R.NNFLSNVEKKLAPSLASSNFGK.R	
12417	792.0559	2373.1457	2373.2454	-0.0997	2	2	81	8	R.RYFSPRHSLSIQGNVIWGTR.G	
12434	792.5785	2374.7137	2376.1631	-1.4494	1	2	76	9	R.TRAEWDDLMEQVGLEIIQSK.V	
12649	803.2165	2406.6277	2404.3182	2.3095	1	4	54	5	R.KMSVALGSAIMIVASVIQAATVGR.W	
12660	803.8829	2408.6267	2406.2366	2.3902	1	1	95	10	R.VRIHPEGYTPAPGTPPATASMLK.A	12652
12901	814.5199	2440.5377	2438.2331	2.3046	1	1	82	2	K.IRPMLWWWSGTRSWGHGVAR.D	
13084	823.4165	2467.2277	2468.2693	-1.0416	2	3	72	2	R.IQVNYGGTGTGTKSMRLSVDASLQK.L	
13139	825.2739	2472.7997	2470.3049	2.4948	0	15	3.9	2	R.FNFWIWLAAEGVETTIHVPLK.G	
13217	828.6342	2482.8807	2482.3056	0.5751	2	1	1.1e+02	6	R.TTSRMPPAFFSIPWHVSPRIR.R	
13225	828.9809	2483.9207	2481.3704	2.5504	2	2	70	5	R.FVVTSVLPGELRSIRVDNEVPR.C	
13257	830.3592	2488.0557	2485.2127	2.8430	2	7	23	3	R.CSRGMVDAGPKFVAMAALATTTSK.C	
13348	834.5242	2500.5507	2498.3032	2.2475	2	0	1.1e+02	4	K.SCCGPLQILPISRSLIRVCNR.H	
13364	835.4795	2503.4167	2501.2698	2.1469	2	2	75	5	R.STLIKSLSSLEMYYFKCFLR.S	
13404	836.9332	2507.7777	2507.2016	0.5761	0	2	78	5	K.TVTQGNGHVVHIYAAMDGWPPNK.S	
13593	844.2442	2529.7107	2529.0974	0.6133	1	1	82	1	R.QEPSDCDYPGSMMKAVSHLFSK.W	
13641	846.5529	2536.6367	2538.2107	-1.5740	1	7	26	2	R.LSSTRTMMSSGYSPGLSIAHWNR.S	
13699	850.6325	2548.8757	2548.3472	0.5286	0	10	13	1	R.IAMGIGLGFAQTAAPPLTTEIAHPR.H	
13761	852.6762	2555.0067	2554.2057	0.8011	1	(1)	1e+02	10	R.LSSTRTMMSSGYSPGLSIAHWNR.S	
13822	856.2899	2565.8477	2566.4530	-0.6052	2	3	58	1	R.GRLLLGGQSLSNPRAPLLAVMTFR.F	
13824	856.5565	2566.6477	2564.3614	2.2864	1	3	61	3	R.APLLAVMTFRFEGHSGWLIIYK.E	13823
13974	867.0505	2598.1297	2598.3880	-0.2583	2	5	40	2	R.SFTPFMTKLWDSTVSLLIKTQR.C	
14524	898.2885	2691.8437	2692.2884	-0.4446	2	6	31	1	K.RQLGGLMWCSALESTRTTDMHVK.S	
14626	904.7085	2711.1037	2712.2861	-1.1823	1	2	75	4	K.SNTCVAFKPRQTSGQSNWSTVMAR.I	14625
14835	922.7792	2765.3157	2765.3225	-0.0068	1	1	99	6	R.SMTRCPGSQNGAPSPPLISLSPQDPR.H	
15011	938.8859	2813.6357	2814.2604	-0.6247	1	2	70	2	K.DCVFQKAFGSDLTMFEWMPQHPK.H	
15245	965.8289	2894.4647	2892.3887	2.0761	2	1	72	4	K.GHWNTFSWTLLRFMMRMEHIQR.A	

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      15568  1018.2382  3051.6927  3051.8405  -0.1478   2     1        78   2   R.LMLIPRPTLMLILIRNRIHNLILNR.I
      15819  1054.3972  3160.1697  3158.5356   1.6341   2     1        81   7   R.MSREPRTLLNDSLGFEPFELSHFHQR.Q
      15968  1083.2042  3246.5907  3246.6352  -0.0444   2     1        70   7   R.MYPVWPVVDVARLRDSLMLDMNNVELR.S
      15991  1087.1869  3258.5387  3258.6563  -0.1176   1     7        17   1   R.INSSPNIPVEADPPICIVVCSAMIKLHER.R
      16303  1142.2029  3423.5867  3423.5815   0.0053   2     6        22   4   K.AEADADPVEEEKTDPFGLGNIHGEEGKAAGTNR.H 16308

228.  gi|220699528|gb|EED55867.1|     Mass: 17846    Score: 117    Queries matched: 34    emPAI: 1.82
      ubiquitin (UbiC), putative [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
        22  324.9441   647.8737   647.4006   0.4731   0    27     0.46    1  R.LIFAGK.Q 20 23 24
       198  781.5760   780.5687   780.4204   0.1483   0    22     0.86    1  -.MQIFVK.T 196
       702  482.5226   963.0307   963.5753  -0.5446   2    11       16    7  K.KVYTTPKK.I
       827  987.5940   986.5867   987.4985  -0.9118   1    11       15    1  K.VDGDGKIER.L
      1046  520.7191  1039.4237  1038.5094   0.9143   0    47    0.003    1  K.EGIPPDQQR.L 1030 1037 1045
      1181  534.5726  1067.1307  1066.6135   0.5172   0    46   0.0035    1  K.ESTLHLVLR.L 1191 1200
      1261  541.4061  1080.7977  1080.5451   0.2526   0    39    0.017    1  R.TLSDYNIQK.E 1257 1259 1263
      1577  568.0741  1134.1337  1133.6808   0.4529   1     1  1.5e+02    9  M.QIFVKTLTGK.T 1579
      4654  762.6321  1523.2497  1522.7740   0.4758   1    61  0.00011    1  K.IQDKEGIPPDQQR.L
      7449  883.0766  1764.1387  1762.8836   1.2551   0    30     0.13    1  K.TITLEVESSDTIDNVK.S 7433 7437 7444 7445 7447 7448 745
     10555  702.6812  2105.0217  2103.8747   1.1470   0   (7)       26    3  R.ECPAPECGAGVFMAAMHNR.Q 10554
     10655  708.2002  2121.5787  2119.8696   1.7091   0     7       22    2  R.ECPAPECGAGVFMAAMHNR.Q
     11753  760.3535  2278.0387  2275.9707   2.0680   1     2       77    2  R.RECPAPECGAGVFMAAMHNR.Q

229.  gi|220699027|gb|EED55366.1|     Mass: 34266    Score: 117    Queries matched: 30    emPAI: 0.74
      polyubiquitin UbiD/Ubi4, putative [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score   Expect Rank  Peptide
        22  324.9441   647.8737   647.4006   0.4731   0    27     0.46    1  R.LIFAGK.Q 20 23 24
       198  781.5760   780.5687   780.4204   0.1483   0    22     0.86    1  -.MQIFVK.T 196
      1046  520.7191  1039.4237  1038.5094   0.9143   0    47    0.003    1  K.EGIPPDQQR.L 1030 1037 1045
      1181  534.5726  1067.1307  1066.6135   0.5172   0    46   0.0035    1  K.ESTLHLVLR.L 1191 1200
      1261  541.4061  1080.7977  1080.5451   0.2526   0    39    0.017    1  R.TLSDYNIQK.E 1257 1259 1263
      1577  568.0741  1134.1337  1133.6808   0.4529   1     1  1.5e+02    9  M.QIFVKTLTGK.T 1579
      4654  762.6321  1523.2497  1522.7740   0.4758   1    61  0.00011    1  K.IQDKEGIPPDQQR.L
      7449  883.0766  1764.1387  1762.8836   1.2551   0    30     0.13    1  K.TITLEVESSDTIDNVK.S 7433 7437 7444 7445 7447 7448 745
     11336  738.2772  2211.8097  2212.2514  -0.4417   2     4       51    9  K.ESTLHLVLRLRGGMQIFVK.T 11359

230.  gi|220691376|gb|EED47724.1|     Mass: 24940    Score: 116    Queries matched: 4    emPAI: 0.13
      uracil phosphoribosyltransferase [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
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5857	544.5995	1630.7767	1631.9029	-1.1262	1	8	25	2	R.VVMLSVLGSETGIRR.A 5859
16374	1155.3642	3463.0707	3461.7638	1.3069	0	93	4.8e-08	1	R.QDGSDSNTAAADTAILLDPIVATGATAEAAIHLLR.E 16376

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231. gi|220698520|gb|EED54860.1| **Mass:** 47208 **Score:** 116 **Queries matched:** 19 **emPAI:** 0.14

stomatin family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
385	431.1001	860.1857	858.5035	1.6822	1	14	8.9	9	R.QSSRLLR.S
1460	559.9566	1117.8987	1116.5411	1.3576	0	20	1.7	1	R.AEILDSEGQR.Q 1463
1521	565.0341	1128.0537	1126.5659	1.4879	0	3	91	3	K.YVDAFSNLAK.E
2006	610.8511	1219.6877	1219.6230	0.0647	0	6	40	1	K.QSVILASEAMR.Q
2419	637.8131	1273.6117	1272.6422	0.9695	1	5	52	5	K.RAEILDSEGQR.Q
3489	694.8071	1387.5997	1386.7691	0.8306	2	3	96	4	M.DVASRQSSRLLR.S 3493
4233	738.3541	1474.6937	1472.7776	1.9161	0	6	40	1	R.FVPQQTAWIVER.M
6497	840.6806	1679.3467	1679.0022	0.3446	0	62	8.6e-05	1	R.ILEPGLAILIPFIDR.I 6503
9524	663.7219	1988.1437	1988.0109	0.1328	1	3	68	9	K.QSVILASEAMRQEQINR.A 9537
11984	769.6165	2305.8277	2303.0739	2.7538	0	37	0.022	1	K.ASYGVEDAEYAISQLAQTTMR.S
12562	798.4762	2392.4067	2392.3186	0.0881	1	8	19	2	R.LLQNPRLPTSALTATNNLNSVR.R 12571 12572
14309	887.6952	2660.0637	2657.3231	2.7406	0	5	34	3	R.ATLNTNITQAINEAAQDWGVVCLR.Y 14311

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232. gi|220698443|gb|EED54783.1| **Mass:** 35240 **Score:** 116 **Queries matched:** 14 **emPAI:** 0.09

translation initiation factor 2 alpha subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
464	886.7790	885.7717	885.4807	0.2910	0	11	14	4	R.VSPEDVIK.C
1413	555.3251	1108.6357	1108.5587	0.0771	0	11	12	5	K.QIAEMGAYVK.L
1516	564.6586	1127.3027	1125.7346	1.5682	2	9	22	9	R.IRSIQKLIR.I
5012	520.2449	1557.7127	1557.7385	-0.0258	0	7	32	3	K.YPEVDSYVMVNVK.Q 5002
8041	909.3326	1816.6507	1815.9805	0.6703	0	72	9.2e-06	1	K.LVAPPLYVLTSQCLDK.A 8042
8677	944.1381	1886.2617	1885.8768	0.3849	0	3	65	3	R.ADIEVTCFGYEGIDAVK.A
9387	657.5512	1969.6317	1970.9367	-1.3050	1	2	78	6	K.AVTEHDDAALQELMEKR.E 9403
11546	748.6329	2242.8767	2242.0609	0.8158	1	11	10	1	K.MAPKAVTEHDDAALQELMEK.R
12703	805.7775	2414.3107	2414.1570	0.1538	2	4	52	4	K.MAPKAVTEHDDAALQELMEKR.E
12769	808.5929	2422.7567	2421.2685	1.4882	2	11	10	1	K.LLEYDNIDGMILLSELSRRR.I
15747	1039.8675	3116.5807	3116.4293	0.1514	2	2	60	1	-.MSLTNCRFYEEKYPEVDSYVMVNVK.Q

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233. gi|220691503|gb|EED47851.1| **Mass:** 148535 **Score:** 115 **Queries matched:** 38 **emPAI:** 0.09

phosphoribosylformylglycinamidine synthase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
572	459.1906	916.3667	917.5117	-1.1449	1	15	6.9	4	K.RLVLMDR.D 570
806	492.7126	983.4107	983.6015	-0.1908	0	8	21	7	R.VLSLPAVASK.S 803

1105	**526.9226**	**1051.8307**	**1052.4523**	**-0.6215**	**0**	**7**	**34**	**10**	**R.NASEQYEGR.V**
1904	601.4066	1200.7987	1199.6258	1.1729	1	11	14	4	R.DEGAVGRGSKPK.A
2936	**666.2616**	**1330.5087**	**1329.7115**	**0.7972**	**0**	**8**	**28**	**2**	**R.TVMGGIASWLPAK.A** 2934
3079	**674.4926**	**1346.9707**	**1345.7064**	**1.2643**	**0**	**(0)**	**1.5e+02**	**9**	**R.TVMGGIASWLPAK.A**
3628	702.4546	1402.8947	1400.7511	2.1436	0	4	70	4	R.TLLTEIDIGNGQK.E 3631
5058	782.0786	1562.1427	1561.8208	0.3220	1	3	91	9	K.LGISIPVGKDSMSMK.M
5577	**805.6566**	**1609.2987**	**1607.8492**	**1.4495**	**1**	**4**	**68**	**1**	**R.SRGHAIAASIGAQDVR.A**
7431	882.5676	1763.1207	1760.9131	2.2076	0	0	1.3e+02	2	K.AGLAGYCVSDLQIPGLK.Q
7562	**887.5851**	**1773.1557**	**1773.7735**	**-0.6178**	**2**	**0**	**1.4e+02**	**1**	**K.DSMSMKMKWTDEASK.Q**
7907	**902.6591**	**1803.3037**	**1802.8331**	**0.4706**	**0**	**27**	**0.25**	**1**	**R.SDGGLFTTLAEMMFAGR.C**
8202	**612.6759**	**1835.0057**	**1836.9511**	**-1.9454**	**2**	**4**	**55**	**4**	**K.LGISIPVGKDSMSMKMK.W**
8864	**635.6022**	**1903.7847**	**1904.9335**	**-1.1488**	**0**	**6**	**37**	**3**	**R.MAVAESLMNIAAADLVDR.L**
9192	649.2549	1944.7427	1944.9033	-0.1606	0	2	85	7	R.AQEVINACTAMGDNNPIK.F
9885	**676.9975**	**2027.9707**	**2026.0081**	**1.9626**	**0**	**3**	**62**	**1**	**R.LEDVGETVLMFVDLSFGR.K** 9854
10108	**684.1649**	**2049.4727**	**2051.0575**	**-1.5848**	**0**	**3**	**66**	**2**	**K.DVVETLFTEELGAVFQVR.K**
10661	**1062.2436**	**2122.4727**	**2121.0928**	**1.3799**	**0**	**37**	**0.023**	**1**	**K.EVTAPMSLVISAFAPVGNYR.K**
11031	724.5335	2170.5787	2170.0980	0.4807	1	7	24	2	R.LEDVGETVLMFVDLSFGRK.T 11018 11040
11259	1101.0466	2200.0787	2198.0903	1.9885	0	37	0.028	1	R.TGTISPWSSQATGIAHVCGLR.K
11583	1126.3406	2250.6667	2250.1083	0.5585	2	8	19	3	K.AQEWGDIGPWGRVFYSARR.W 11586 11599
12918	**815.0875**	**2442.2407**	**2440.3253**	**1.9154**	**0**	**53**	**0.00057**	**1**	**R.DSTEYPKPIDLPLSVLFGKPPK.M** 12919
12946	**816.7075**	**2447.1007**	**2446.1911**	**0.9096**	**1**	**1**	**84**	**8**	**R.KTLGGSALAQVFNQVGDDCPDVR.D**
13067	**823.1535**	**2466.4387**	**2464.2784**	**2.1603**	**1**	**1**	**1.1e+02**	**5**	**K.QAKEVTAPMSLVISAFAPVGNYR.K**
14767	**914.6889**	**2741.0447**	**2741.5804**	**-0.5356**	**2**	**3**	**51**	**5**	**R.VLSLPAVASKSFLITIGDRTVGGLTAR.D**
14924	**929.2685**	**2784.7837**	**2785.4433**	**-0.6596**	**1**	**2**	**67**	**2**	**R.DQMVGRWQTPVSDVAVTATALLQGVK.T** 14932
16214	**1122.1752**	**3363.5037**	**3365.5002**	**-1.9965**	**0**	**0**	**95**	**3**	**K.LSANWMSASSHPGEGAAIYEAAEAIGMDLCPK.L**

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234. gi|220701006|gb|EED57344.1| **Mass:** 29127 **Score:** 115 **Queries matched:** 8 **emPAI:** 0.11

6-phosphogluconolactonase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
47	676.4920	675.4847	674.3136	1.1711	0	6	59	4	R.HDTFR.V 46
783	**978.9500**	**977.9427**	**977.5546**	**0.3882**	**1**	**13**	**7.7**	**6**	**R.IFAAKDSVK.L**
2642	**649.7966**	**1297.5787**	**1297.7606**	**-0.1818**	**0**	**85**	**5.1e-07**	**1**	**R.VAVSGGSLPTVLAK.A** 2647
3684	707.0866	1412.1587	1411.7307	0.4280	0	5	53	1	R.ELPSALVNQGAGEK.V
9086	**644.3585**	**1930.0537**	**1929.9374**	**0.1163**	**0**	**1**	**1.1e+02**	**7**	**K.VSWFTDHPAVEGVSFPR.R**
16140	**1109.0042**	**3323.9907**	**3323.6575**	**0.3332**	**1**	**2**	**51**	**2**	**R.ELPSALVNQGAGEKVSWFTDHPAVEGVSFPR.R**

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235. gi|220690479|gb|EED46828.1| **Mass:** 27419 **Score:** 114 **Queries matched:** 29 **emPAI:** 0.77

60S ribosomal protein L8, putative [Aspergillus flavus NRRL3357]

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

37	671.4990	670.4917	670.4126	0.0791	0	9	20	5	K.AGLIAAR.R
408	867.4640	866.4567	866.4134	0.0433	0	24	0.53	1	R.TLDYAER.H 409
724	**484.2881**	**966.5617**	**965.4930**	**1.0687**	**0**	**46**	**0.0034**	**1**	**R.GSIFTANTR.L** 714 717 718
844	496.0951	990.1757	988.5124	1.6633	0	45	0.0062	1	R.GMVGIVAGGGR.T 841
2723	654.6866	1307.3587	1306.7106	0.6482	2	5	49	10	R.KGRGSIFTANTR.L
3749	**710.9881**	**1419.9617**	**1419.7253**	**0.2365**	**1**	**2**	**1e+02**	**5**	**K.STSRGMVGIVAGGGR.T**
7135	578.3402	1731.9987	1729.9621	2.0366	2	(9)	17	3	K.VVKSTSRGMVGIVAGGGR.T
7268	873.3316	1744.6487	1745.9571	-1.3083	2	21	1.1	2	K.VVKSTSRGMVGIVAGGGR.T 7274 7279 7284 7285 7288 7289 72
7747	**596.8912**	**1787.6517**	**1786.8486**	**0.8031**	**0**	**51**	**0.0011**	**1**	**R.TSGNYVTVIGHNPEDGK.T** 7765
11065	**726.2189**	**2175.6347**	**2174.0188**	**1.6159**	**0**	**25**	**0.4**	**1**	**R.GVAMNPVDHPHGGGNHQHIGK.A**
13180	**826.8119**	**2477.4137**	**2476.1733**	**1.2404**	**0**	**9**	**14**	**1**	**K.HVTETFIANEGMYTGQFIYAGK.N**
14167	880.7469	2639.2187	2640.3004	-1.0817	2	1	1e+02	9	K.AGDRGALGRTSGNYVTVIGHNPEDGK.T

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236. gi|220694246|gb|EED50590.1| **Mass:** 101077 **Score:** 114 **Queries matched:** 42 **emPAI:** 0.10

Coatomer subunit gamma, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1223	537.7881	1073.5617	1074.6397	-1.0780	1	23	0.87	4	K.TGVTTKITVR.A 1225
1988	**609.1961**	**1216.3777**	**1216.6564**	**-0.2787**	**1**	**9**	**21**	**10**	**K.LFQNKDPSLR.Q**
2480	**640.4251**	**1278.8357**	**1280.7162**	**-1.8805**	**1**	**3**	**85**	**5**	**R.VAALIKMAFSSK.T** 2481
2674	651.6806	1301.3467	1301.7918	-0.4451	2	10	18	10	R.TKKLTTATPTLK.A 2692
2732	655.2951	1308.5757	1308.5867	-0.0110	1	13	7.6	2	K.KDEDADQTMIK.L
2787	**658.5616**	**1315.1087**	**1314.7143**	**0.3944**	**0**	**58**	**0.00029**	**1**	**R.IIDATTVQGIER.L**
3405	**689.3296**	**1376.6447**	**1375.7646**	**0.8802**	**0**	**5**	**54**	**3**	**K.QAGMLAFLSGILR.D**
4932	**517.7265**	**1550.1577**	**1548.7090**	**1.4488**	**1**	**9**	**17**	**7**	**K.DEDADQTMIKLDR.T** 4933
4978	**777.6381**	**1553.2617**	**1552.7200**	**0.5417**	**0**	**2**	**83**	**2**	**R.KPMMQMLDGWLR.H**
5189	789.4206	1576.8267	1576.8647	-0.0380	1	2	1e+02	9	K.DPSLRQMVYLVLK.E
6528	841.5241	1681.0337	1679.9458	1.0879	1	5	42	2	K.LTTATPTLKAPSTGPPK.S
7023	**860.8326**	**1719.6507**	**1719.8904**	**-0.2397**	**1**	**5**	**45**	**7**	**K.DTAVGSDVLYRANAIR.A**
8217	919.7316	1837.4487	1837.9794	-0.5307	1	2	88	7	R.MALVKMVQQYGAAGVIK.S 8222
8368	**618.6869**	**1853.0387**	**1851.0077**	**2.0311**	**1**	**11**	**11**	**1**	**K.FPSKQAGMLAFLSGILR.D** 8366
8536	624.6612	1870.9617	1868.0441	2.9176	2	6	40	6	R.VAALIKMAFSSKTGVTTK.I
9209	**650.2515**	**1947.7327**	**1948.8580**	**-1.1253**	**2**	**(0)**	**1.3e+02**	**6**	**-.MSYMKKDEDADQTMIK.L**
9371	**656.8725**	**1967.5957**	**1964.8529**	**2.7428**	**2**	**6**	**32**	**2**	**-.MSYMKKDEDADQTMIK.L**
9468	990.5981	1979.1817	1980.9747	-1.7930	0	7	27	8	K.ELANTAEDVIMSTSIIMK.D 9464
9622	**666.6602**	**1996.9587**	**1996.9697**	**-0.0109**	**0**	**(4)**	**58**	**3**	**K.ELANTAEDVIMSTSIIMK.D**
10302	691.0722	2070.1947	2068.1317	2.0631	0	49	0.0015	1	K.TPSVSSAALVSSYHLLPIAR.D 10298
11388	740.2889	2217.8447	2218.0081	-0.1634	2	7	27	3	R.HKHEMVNFEAAKAICDMR.D 11389
11487	**745.5132**	**2233.5177**	**2234.1616**	**-0.6439**	**1**	**2**	**81**	**5**	**R.AALNLRLMAEEDETASLFLK.N**
11920	**767.2069**	**2298.5987**	**2296.3366**	**2.2621**	**2**	**1**	**1.1e+02**	**4**	**R.IIDATTVQGIERLIKTAIVDK.T**
12493	795.4075	2383.2007	2382.2179	0.9828	0	30	0.11	1	R.DVTDAEASQAVHVLQLFLSSPR.A 12501

12994	819.6245	2455.8517	2457.2474	-1.3957	2	7	22	1	K.QAGMLAFLSGILRDEGGYEFKR.S
14824	921.6705	2761.9897	2760.3945	1.5952	2	1	99	10	K.FPSKQAGMLAFLSGILRDEGGYEFK.R
15279	973.8539	2918.5397	2918.3790	0.1607	2	2	68	4	K.TGNEASVDRLMKQISGFMADITDEFK.I
15319	980.2552	2937.7437	2939.5421	-1.7984	1	(0)	1e+02	8	R.QMVYLVLKELANTAEDVIMSTSIIMK.D
15365	986.2965	2955.8677	2955.5370	0.3307	1	(1)	80	10	R.QMVYLVLKELANTAEDVIMSTSIIMK.D 15369
15429	1494.4761	2986.9377	2987.5269	-0.5892	1	2	63	1	R.QMVYLVLKELANTAEDVIMSTSIIMK.D 15428

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237. gi\|220696195\|gb\|EED52537.1\| **Mass:** 36152 **Score:** 114 **Queries matched:** 18 **emPAI:** 0.09

glyceraldehyde 3-phosphate dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
275	410.7816	819.5487	818.4399	1.1088	0	18	3.1	2	K.VGINGFGR.I 276
1456	559.6141	1117.2137	1118.6196	-1.4059	1	3	85	10	M.TAKVGINGFGR.I
2212	625.8261	1249.6377	1249.6601	-0.0224	1	2	1e+02	2	-.MTAKVGINGFGR.I
6283	832.5116	1663.0087	1663.9032	-0.8945	1	0	1.5e+02	4	R.LEKGASYEEIITAIK.E
6440	838.1911	1674.3677	1673.7474	0.6203	0	69	2e-05	1	K.IVSWYDNEWGYSR.R 6443 6445 6454
7939	603.2995	1806.8767	1804.9512	1.9256	2	4	52	1	K.VKFYAEKDPANIPWK.E
9866	676.5872	2026.7397	2024.1127	2.6271	2	7	28	5	R.GGRAAAQNLIPSSTGAAKAVGK.V 9832
9997	1020.1366	2038.2587	2038.0194	0.2393	0	2	85	7	K.FGVVEGLMTAVHAYTATQK.L
10559	702.8109	2105.4107	2107.0329	-1.6222	0	4	55	1	K.VIISAPSADAPMYVMGVNEK.T
11406	741.5292	2221.5657	2219.1330	2.4327	1	17	2.4	2	K.KVIISAPSADAPMYVMGVNEK.T 11403
13709	851.0225	2550.0457	2548.3029	1.7428	2	8	20	1	K.GGAKKVIISAPSADAPMYVMGVNEK.T 13707

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238. gi\|220699259\|gb\|EED55598.1\| **Mass:** 17822 **Score:** 111 **Queries matched:** 24 **emPAI:** 1.38

ubiquitin UbiA, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
22	324.9441	647.8737	647.4006	0.4731	0	27	0.46	1	R.LIFAGK.Q 20 23 24
564	458.1891	914.3637	912.5280	1.8357	0	14	7.5	9	R.GGIIEPSLK.A
1046	520.7191	1039.4237	1038.5094	0.9143	0	47	0.003	1	K.EGIPPDQQR.L 1030 1037 1045
1181	534.5726	1067.1307	1066.6135	0.5172	0	46	0.0035	1	K.ESTLHLVLR.L 1191 1200
1261	541.4061	1080.7977	1080.5451	0.2526	0	39	0.017	1	R.TLSDYNIQK.E 1257 1259 1263
1871	597.9671	1193.9197	1193.6842	0.2355	1	1	1.1e+02	1	R.KIATMQIFVK.T
3004	670.1771	1338.3397	1337.6986	0.6411	1	5	45	2	K.KCGHTNQLRPK.K 2999
4654	762.6321	1523.2497	1522.7740	0.4758	1	61	0.00011	1	K.IQDKEGIPPDQQR.L
6498	840.7491	1679.4837	1677.9851	1.4986	2	(0)	1.4e+02	6	R.KIATMQIFVKTLTGK.T
6734	566.0569	1695.1487	1693.9801	1.1687	2	1	1.1e+02	7	R.KIATMQIFVKTLTGK.T
7312	876.0036	1749.9927	1748.8680	1.1247	0	7	28	3	K.TITLDVESSDTIDNVK.A
13120	824.5232	2470.5477	2468.3235	2.2243	1	2	80	2	M.VKLSVIASSDQPDLSAIVSQQQR.K

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239. gi|220694536|gb|EED50880.1| **Mass:** 56754 **Score:** 111 **Queries matched:** 21 **emPAI:** 0.25

V-type ATPase, B subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
930	**507.4951**	**1012.9757**	**1011.5025**	**1.4732**	**0**	**16**	**4**	**1**	**R.VLDEFYAR.S** 933
1181	534.5726	1067.1307	1066.4753	0.6554	0	15	5.2	4	-.MASEFVDPR.M 1176
1808	**591.7641**	**1181.5137**	**1181.5863**	**-0.0725**	**1**	**6**	**40**	**3**	**K.YAIGRDAAAMK.A**
2968	668.1916	1334.3687	1333.7136	0.6551	2	9	20	7	R.LMKSAIGEGRTR.K
3437	**691.6226**	**1381.2307**	**1381.7493**	**-0.5186**	**1**	**4**	**67**	**7**	**K.LSLEFLEKFEK.T**
6492	840.2651	1678.5157	1677.8726	0.6431	0	35	0.044	1	R.SIYDSLDIAWNLLR.I
6998	859.2126	1716.4107	1714.9254	1.4854	0	74	6.2e-06	1	R.VTLFLNLANDPTIER.I
9172	**648.3079**	**1941.9017**	**1943.8611**	**-1.9594**	**0**	**4**	**54**	**4**	**R.GYPGYMYTDLSTIYER.A**
10551	**702.6072**	**2104.7997**	**2106.0746**	**-1.2748**	**1**	**10**	**13**	**4**	**K.FPRYNEIVSLTLPDGTER.S** 10548
11230	**732.7339**	**2195.1797**	**2193.1364**	**2.0433**	**0**	**34**	**0.046**	**1**	**K.IPIFSASGLPHNEIAAQICR.Q** 11221
11329	**738.1475**	**2211.4207**	**2212.0259**	**-0.6052**	**1**	**3**	**59**	**4**	**R.GYPGYMYTDLSTIYERAGR.V**
11408	**741.6059**	**2221.7957**	**2221.1161**	**0.6796**	**2**	**0**	**1.2e+02**	**2**	**K.LGVSEDMLGRVFDGSGRAIDK.G**
11984	769.6165	2305.8277	2305.1736	0.6541	2	2	87	3	K.TKVEFSGHSLKLGVSEDMLGR.V
12600	**800.9495**	**2399.8267**	**2397.1556**	**2.6712**	**0**	**42**	**0.008**	**1**	**R.VYPEEMISTGISAIDTMNSIAR.G** 12585
13014	**820.8239**	**2459.4497**	**2458.2492**	**1.2005**	**1**	**0**	**1.1e+02**	**7**	**K.GPKVLAEDYLDINGQPINPYSR.V**
13920	862.7202	2585.1387	2582.4697	2.6691	2	5	39	3	R.IRYNTIAGINGPLVILDNVKFPR.Y

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240. gi|220698647|gb|EED54987.1| **Mass:** 33238 **Score:** 110 **Queries matched:** 15 **emPAI:** 0.46

mitochondrial GTP/GDP transporter Ggc1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
164	760.4310	759.4237	758.4360	0.9877	0	1	2.1e+02	3	K.LLMTGPK.L
2231	**627.4871**	**1252.9597**	**1252.6122**	**0.3476**	**0**	**7**	**30**	**5**	**K.IISDEGMGLYR.G**
2248	628.6296	1255.2447	1254.7370	0.5078	1	11	12	3	K.GLTPKLLMTGPK.L
4835	**771.8131**	**1541.6117**	**1540.7674**	**0.8443**	**0**	**45**	**0.0048**	**1**	**R.NAPGSFALFGGSAFAK.E**
5011	**520.2399**	**1557.6977**	**1556.8522**	**0.8455**	**2**	**10**	**15**	**1**	**M.SPAIAQAGSASKDVKK.E**
5368	**796.8321**	**1591.6497**	**1590.8082**	**0.8415**	**0**	**50**	**0.0014**	**1**	**K.FTSLFPGLGYAAGYK.V**
5738	811.6906	1621.3667	1619.8532	1.5135	2	7	28	5	R.QTNPEAFRGRGLFK.I
6184	828.9726	1655.9307	1653.8297	2.1010	1	1	1.3e+02	3	K.QVVFKEYANACLGR.K
7020	860.5981	1719.1817	1718.9032	0.2785	1	3	66	3	R.KFTSLFPGLGYAAGYK.V
8949	**639.1295**	**1914.3667**	**1913.9121**	**0.4546**	**2**	**3**	**66**	**2**	**K.RLMSNQTRITSMEGMK.Q**
9625	999.9831	1997.9517	1998.9291	-0.9774	1	2	94	4	R.NFENPESGFRIVSNMMK.N
12042	771.6852	2312.0337	2309.2631	2.7706	0	39	0.017	1	R.LLGSGTAGIAELLVFHPVDTTAK.R
12048	**771.8132**	**2312.4177**	**2311.1498**	**1.2679**	**1**	**27**	**0.23**	**1**	**R.GAGWTAARNAPGSFALFGGSAFAK.E**
15667	**1028.3375**	**3081.9907**	**3080.6618**	**1.3289**	**2**	**4**	**38**	**1**	**K.ESATARLLGSGTAGIAELLVFHPVDTTAKR.L** 15668

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241. gi|220701041|gb|EED57379.1| **Mass:** 36927 **Score:** 110 **Queries matched:** 8 **emPAI:** 0.19

ARP2/3 complex 34 kDa subunit , putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2288	**630.8176**	**1259.6207**	**1260.5921**	**-0.9714**	**0**	**16**	**4.1**	**2**	**K.EGGEVMAIHYR.E** 2291
2950	667.2506	1332.4867	1331.7310	0.7558	1	6	39	4	K.RTADFLQVLNR.A
4195	736.2816	1470.5487	1469.8354	0.7133	0	39	0.019	1	R.ALTLQNAPQVLFR.N 4200
12651	**803.2799**	**2406.8177**	**2408.1430**	**-1.3253**	**1**	**2**	**74**	**3**	**K.YSTEAAPQGVKEGGEVMAIHYR.E**
15631	**1023.4542**	**3067.3407**	**3064.4666**	**2.8741**	**0**	**64**	**4.1e-05**	**1**	**R.FSGSPPVSIDQIASDFDGVTFHLSTPESK.T** 15623

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242. gi|220699754|gb|EED56093.1| **Mass:** 24240 **Score:** 109 **Queries matched:** 12 **emPAI:** 0.68

GTP-binding nuclear protein Ran, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
429	**874.5120**	**873.5047**	**873.4960**	**0.0087**	**0**	**4**	**89**	**1**	**M.ATPIPTFK.L** 430
952	**339.9125**	**1016.7157**	**1014.5710**	**2.1447**	**0**	**11**	**16**	**10**	**K.LVLVGDGGTGK.T**
1977	608.2726	1214.5307	1213.5979	0.9329	0	36	0.045	1	K.NLQYYDISAK.S
3023	671.2071	1340.3997	1341.6928	-1.2931	1	1	1.3e+02	10	K.KNLQYYDISAK.S
4585	**759.5126**	**1517.0107**	**1514.7585**	**2.2522**	**0**	**47**	**0.0034**	**1**	**R.VCENIPIVLCGNK.V** 4558
7726	**596.1679**	**1785.4817**	**1783.9046**	**1.5772**	**0**	**50**	**0.0014**	**1**	**K.SNYNFEKPFLWIAR.K** 7713 7728
11410	741.7275	2222.1607	2223.9929	-1.8322	0	4	46	3	R.DGYYINGQCGIIMFDVTSR.I 11412

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243. gi|45477378|gb|AY371490.1|_d **Mass:** 2978547 **Score:** 108 **Queries matched:** 262 **emPAI:** 0.00

Aspergillus parasiticus aflatoxin pathway gene cluster, complete sequence

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
61	**343.0916**	**684.1687**	**682.4126**	**1.7561**	**0**	**9**	**16**	**8**	**R.IGQPLR.V**
192	**779.6050**	**778.5977**	**778.3102**	**0.2875**	**0**	**3**	**71**	**2**	**R.CAMEPR.T**
200	783.1270	782.1197	780.3766	1.7431	0	7	25	4	K.YLENSR.A
312	837.1880	836.1807	836.4174	-0.2367	1	6	38	6	R.MKGSGTTR.Y
481	**447.8351**	**893.6557**	**892.4151**	**1.2406**	**0**	**6**	**39**	**4**	**R.DTNPGPHR.A**
497	451.0531	900.0917	899.5804	0.5113	0	21	1.6	4	K.SSVLLILR.T
523	454.5191	907.0237	907.4624	-0.4387	1	7	33	8	R.ARGGYTQR.V
539	911.6280	910.6207	911.3994	-0.7786	0	8	22	4	R.MFCPVSR.G 547
543	456.4791	910.9437	911.5328	-0.5891	0	7	26	9	R.LPVDVELK.A
649	474.9836	947.9527	947.5440	0.4087	0	45	0.0053	1	R.TQAAFGLIK.E
652	475.3541	948.6937	948.5253	0.1684	2	13	8.7	7	R.FRSIRDR.M
723	**967.5480**	**966.5407**	**966.4744**	**0.0663**	**1**	**2**	**87**	**2**	**R.HGGRGPGSSR.L**
724	484.2881	966.5617	965.4640	1.0977	0	13	6.7	6	R.GETYLMPR.Q 714
788	**490.4151**	**978.8157**	**977.4600**	**1.3557**	**0**	**(7)**	**30**	**3**	**R.MGGSAGGGSGIK.V**
792	490.7691	979.5237	979.4757	0.0480	1	8	24	5	R.SGLKSSGCGK.I
862	498.0806	994.1467	993.4550	0.6918	0	16	3.4	2	R.MGGSAGGGSGIK.V 865
873	**499.3881**	**996.7617**	**995.5260**	**1.2357**	**2**	**5**	**44**	**4**	**R.KSHRESPR.K**

876	500.1451	998.2757	997.5305	0.7452	1	3	70	8	R.TPVTGPDRR.G
879	500.5621	999.1097	997.5305	1.5792	1	12	11	10	R.EPTVGPSRR.A 871 880
901	501.8581	1001.7017	1001.5328	0.1689	0	3	89	7	R.VGCIIAVDR.D
914	**503.9606**	**1005.9067**	**1006.4946**	**-0.5879**	**0**	**1**	**1.5e+02**	**8**	**R.LYYVMFR.Q**
925	506.2261	1010.4377	1010.5583	-0.1205	2	9	17	10	R.LTKKAYCK.J
937	1015.6040	1014.5967	1014.6437	-0.0470	1	4	81	6	R.VVLQTTVKK.A
963	**510.9071**	**1019.7997**	**1019.5553**	**0.2445**	**0**	**7**	**31**	**4**	**R.IFLHFTSR.R**
1004	516.8321	1031.6497	1031.5764	0.0734	0	15	5.9	5	R.GPYILSNIR.G 1005
1025	518.9821	1035.9497	1037.6233	-1.6736	0	4	66	7	R.NDVLPLVLR.S 1024
1035	**520.2396**	**1038.4647**	**1037.5407**	**0.9241**	**0**	**4**	**62**	**9**	**R.LPGHQFPSR.N**
1049	521.6576	1041.3007	1039.6654	1.6353	1	4	57	8	R.ALWRIILR.K
1128	528.7416	1055.4687	1055.5975	-0.1287	0	11	14	9	R.EVNALLEIR.Q 1141
1131	**529.2196**	**1056.4247**	**1056.5716**	**-0.1469**	**0**	**8**	**26**	**8**	**K.FPNLNIPSR.S**
1170	533.7336	1065.4527	1065.5315	-0.0788	1	9	21	2	K.SPEVHGRER.D
1208	536.3326	1070.6507	1072.4906	-1.8399	1	12	11	5	R.DPRCPCLR.E 1207
1223	537.7881	1073.5617	1073.5829	-0.0212	0	16	4.8	7	R.TLATNSGAALR.H 1225
1356	**550.6726**	**1099.3307**	**1097.6418**	**1.6890**	**2**	**2**	**1.1e+02**	**10**	**R.GPGSSRLLRR.I**
1380	552.9826	1103.9507	1105.5451	-1.5944	1	8	30	1	R.CWARLTGSR.E 1383
1424	**1113.2920**	**1112.2847**	**1111.5622**	**0.7226**	**0**	**1**	**1.3e+02**	**9**	**R.QPSAAGPSLER.E**
1468	560.5121	1119.0097	1118.5105	0.4992	1	11	14	4	R.GDRDADAPFR.S 1461 1476
1496	562.6756	1123.3367	1122.5755	0.7612	2	2	1e+02	9	R.RHGGRGPGSSR.L
1585	**1135.8250**	**1134.8177**	**1134.5153**	**0.3024**	**0**	**3**	**81**	**4**	**R.EDTGLASTDAR.R**
1617	571.2136	1140.4127	1140.5710	-0.1582	0	7	29	6	R.HTVDMAQALR.S
1757	**586.4286**	**1170.8427**	**1172.6448**	**-1.8021**	**2**	**9**	**21**	**2**	**R.IMKPKDNRR.L**
1779	588.7306	1175.4467	1174.4850	0.9617	0	12	10	4	R.GEAEQADENGR.J
1785	**392.9785**	**1175.9137**	**1175.7251**	**0.1886**	**1**	**10**	**18**	**6**	**R.VLGQRVIHVR.R** 1784
1843	**595.2571**	**1188.4997**	**1187.6775**	**0.8222**	**1**	**11**	**15**	**10**	**R.SWAVSRLLTR.Y**
1862	**597.2761**	**1192.5377**	**1193.6741**	**-1.1364**	**2**	**1**	**1.2e+02**	**6**	**K.TRGVDVVHRR.L**
1880	599.3471	1196.6797	1197.5659	-0.8862	0	5	43	5	R.SSTLCLTSSSR.S
1949	**606.3841**	**1210.7537**	**1208.7465**	**2.0072**	**1**	**19**	**1.6**	**1**	**R.ILSARPRQLR.A** 1943
2036	**613.9436**	**1225.8727**	**1225.7506**	**0.1221**	**2**	**6**	**42**	**6**	**R.RAPKTINSVLK.V**
2308	**421.5665**	**1261.6777**	**1261.7619**	**-0.0841**	**2**	**10**	**16**	**3**	**R.QSPVRKVHALK.L**
2335	633.5566	1265.0987	1262.6407	2.4580	1	11	14	1	K.KYHAPFASSQK.V
2353	423.0332	1266.0777	1265.5876	0.4901	1	11	12	3	R.WTFGCRFHR.Q
2400	425.0192	1272.0357	1270.5976	1.4382	1	5	50	5	R.NMSKSSGFEIR.J
2410	637.5166	1273.0187	1274.6289	-1.6101	0	8	25	4	R.LASSKPAPMSDR.A 2413 2422 2460
2431	638.7416	1275.4687	1276.5949	-1.1262	0	13	9.1	3	K.WQNGTFNSPAR.F 2445
2494	**641.4686**	**1280.9227**	**1279.6846**	**1.2381**	**0**	**4**	**64**	**4**	**R.TMQVYALVVEK.J**
2505	**642.4211**	**1282.8277**	**1282.6591**	**0.1686**	**0**	**5**	**49**	**9**	**R.AMVDIHDLELK.C**
2574	**646.2251**	**1290.4357**	**1289.7052**	**0.7306**	**1**	**1**	**1.2e+02**	**6**	**R.SLSSSTVLGQRR.R**
2582	**646.5446**	**1291.0747**	**1291.6772**	**-0.6025**	**0**	**12**	**9.6**	**2**	**R.AIGSFVDQITNK.Y**

2595	**647.5476**	**1293.0807**	**1291.6521**	**1.4287**	**1**	**1**	**1.3e+02**	**6**	**R.YSSPPSKQVGSR.T**	
2617	648.5756	1295.1367	1295.6002	-0.4635	0	5	46	3	K.ELSGGMAMFPTR.S	
2708	436.1892	1305.5457	1305.6612	-0.1155	1	4	67	4	K.LFPSRAACTQR.S	
2733	655.3016	1308.5887	1308.7190	-0.1303	0	8	27	5	K.FLLNQPVEPPR.N	
2801	659.2111	1316.4077	1315.7096	0.6982	0	28	0.25	1	K.NAITLSGSPSTLR.A	
2830	**660.6361**	**1319.2577**	**1320.7150**	**-1.4573**	**0**	**8**	**25**	**6**	**R.SSPGKPAASPIGPR.J**	
2894	664.6071	1327.1997	1328.6071	-1.4074	0	8	26	3	R.GWGSALMEFSTK.V	
2896	**664.6366**	**1327.2587**	**1326.6979**	**0.5608**	**2**	**4**	**64**	**6**	**R.KGFHMPERGLR.E**	
2898	664.6766	1327.3387	1325.6225	1.7162	1	3	83	8	R.LSDSHGDFHRR.R	2884
3047	672.3231	1342.6317	1343.6906	-1.0588	0	7	37	4	R.AAGSSLQSSQRPR.L	
3061	673.1676	1344.3207	1341.6889	2.6319	0	4	77	6	R.AGLVPDTTPSTQR.D	
3091	450.3429	1348.0067	1346.6718	1.3349	0	10	17	1	R.ADSPTEFTAPLAK.G	
3130	**676.6396**	**1351.2647**	**1350.7040**	**0.5608**	**0**	**5**	**47**	**8**	**K.CSPIMIQFLVK.E**	
3155	**678.1886**	**1354.3627**	**1354.5862**	**-0.2234**	**1**	**0**	**1.5e+02**	**7**	**K.QDNHSGDPSDRK.I**	
3162	452.7699	1355.2877	1356.6469	-1.3592	0	7	32	10	R.SSHPGVHHCAIR.R	
3183	679.6256	1357.2367	1355.7673	1.4694	1	0	1.6e+02	9	K.RITIALVDNWR.J	
3195	680.2316	1358.4487	1357.7024	0.7464	1	6	44	6	K.KLQAEGCQSLPK.L	
3207	**454.0879**	**1359.2417**	**1356.7765**	**2.4652**	**0**	**5**	**53**	**7**	**R.QVLTPPSLALYR.L**	
3229	**681.5501**	**1361.0857**	**1361.6986**	**-0.6129**	**1**	**0**	**1.5e+02**	**10**	**R.SCPPAPHSVRVR.Q**	
3316	457.6419	1369.9037	1368.7296	1.1741	1	4	64	8	R.AIPASGRPGAGKCK.L	
3318	**685.9786**	**1369.9427**	**1367.6140**	**2.3287**	**0**	**4**	**60**	**1**	**R.GGVQMSPDTFTGR.G**	3310
3324	**686.0786**	**1370.1427**	**1368.7586**	**1.3841**	**2**	**4**	**67**	**2**	**R.STRHRAGTAATLK.I**	
3326	686.1251	1370.2357	1370.6911	-0.4554	1	3	84	3	R.CQRGTHAMLAVK.A	
3410	460.0165	1377.0277	1377.6646	-0.6368	0	11	13	2	R.AMRPFPNTCIR.R	3425
3447	**692.3251**	**1382.6357**	**1379.7826**	**2.8531**	**2**	**2**	**95**	**7**	**R.FARFSARWVLK.M**	
3563	**698.6031**	**1395.1917**	**1395.7583**	**-0.5665**	**1**	**3**	**76**	**7**	**R.QNQSTSHLVKVR.S**	
3871	**717.5636**	**1433.1127**	**1430.7340**	**2.3787**	**1**	**3**	**76**	**1**	**R.QCLANTAPGPKFK.R**	
3892	**479.8562**	**1436.5467**	**1437.7075**	**-1.1607**	**1**	**9**	**18**	**3**	**K.YFGDSPMPKPRK.D**	
3949	722.2026	1442.3907	1441.6984	0.6924	1	8	21	4	R.LTPGGMTRSSYTR.G	3957
3951	722.2191	1442.4237	1441.7776	0.6461	0	32	0.095	1	R.VEGLQAVLEESLR.L	3947
4000	**724.5336**	**1447.0527**	**1448.7960**	**-1.7433**	**2**	**2**	**1.1e+02**	**9**	**R.LHAPRLSGAERSR.E**	
4167	489.8612	1466.5617	1463.6094	2.9523	0	4	56	5	R.MALMSTYEAMER.A	
4269	739.6666	1477.3187	1475.7692	1.5495	2	15	5.3	2	K.DGSSPSRSRSSLIK.L	
4293	494.3592	1480.0557	1479.7425	0.3132	1	1	1.1e+02	7	R.AMTDNGIKCTLLK.L	
4299	**741.6056**	**1481.1967**	**1480.7166**	**0.4801**	**0**	**1**	**1.1e+02**	**3**	**R.AVANPMPDAPPVMR.A**	
4340	496.4349	1486.2827	1486.8872	-0.6044	1	4	57	9	R.QVKSVTIVPFLTR.M	
4424	**500.1452**	**1497.4137**	**1497.7684**	**-0.3546**	**0**	**3**	**79**	**9**	**K.LNFMLGITIGMTR.L**	
4450	751.6521	1501.2897	1502.8470	-1.5573	2	4	69	4	R.RRYSGIWPLSLR.W	
4467	**501.8579**	**1502.5517**	**1502.9521**	**-0.4004**	**2**	**1**	**1.2e+02**	**8**	**K.RPIRIEVVPLRR.T**	
4649	**762.5226**	**1523.0307**	**1524.7950**	**-1.7642**	**0**	**3**	**73**	**1**	**R.AGWLLAEHGRPYR.S**	
4872	515.9292	1544.7657	1544.7446	0.0211	0	3	88	9	R.TQHVFMFSTYLR.Q	

4947	776.3946	1550.7747	1549.7527	1.0220	2	4	55	5	K.TRDLHMMRSLMK.Q
4972	518.5735	1552.6987	1549.7961	2.9026	2	8	21	10	R.LDRGEGATAYVSRR.H 4962 4967
5086	784.1451	1566.2757	1565.8348	0.4409	2	6	34	2	R.GGRVSLGASSFCKIK.K 5091
5156	**525.1765**	**1572.5077**	**1571.7878**	**0.7199**	**1**	**4**	**54**	**8**	**R.FSPPIDQSRICPR.V**
5189	789.4206	1576.8267	1574.8317	1.9950	2	2	1e+02	8	R.LTNNKYPWLRDR.C
5285	793.3386	1584.6627	1583.9049	0.7579	0	3	81	4	R.FAGRPVQLPPPHLR.I
5342	530.7162	1589.1267	1590.8783	-1.7516	1	7	32	5	R.LWIHPLRSYPGPR.W
5374	531.7742	1592.3007	1593.8297	-1.5290	0	7	30	4	R.SSHIVALSAHVGASMK.T
5713	**810.8121**	**1619.6097**	**1618.8283**	**0.7814**	**0**	**0**	**1.3e+02**	**4**	**K.TRPINTCAMLISSR.G**
5723	541.1115	1620.3127	1621.8536	-1.5409	1	3	79	9	K.AVSESELHTQIPRR.K
5755	**812.4071**	**1622.7997**	**1623.8113**	**-1.0115**	**1**	**1**	**1.2e+02**	**10**	**K.SIKELSGGMAMFPTR.S**
5847	**544.2292**	**1629.6657**	**1630.7812**	**-1.1155**	**1**	**5**	**45**	**3**	**R.DAAHVSSRAWSTSTR.G**
5862	544.7409	1631.2007	1632.8366	-1.6358	2	6	38	6	K.RQGSTSISKPECKR.J
6106	826.0336	1650.0527	1650.7647	-0.7119	0	2	87	7	R.SCVPATASAPWFMAR.F
6120	826.6636	1651.3127	1651.8682	-0.5555	1	0	1.4e+02	6	R.NTLFNSSFAPRALSK.S
6139	551.7172	1652.1297	1651.8253	0.3044	1	7	31	10	R.SPWAKLGSGCHPSLR.C
6293	**555.6029**	**1663.7867**	**1662.8438**	**0.9429**	**2**	**4**	**65**	**8**	**R.ISGGDGFTSRRGSPAAK.T**
6325	**834.2531**	**1666.4917**	**1665.8111**	**0.6807**	**0**	**3**	**71**	**2**	**R.ILHGWADEDSSALPR.C**
6477	**839.6716**	**1677.3287**	**1675.8318**	**1.4969**	**1**	**4**	**60**	**2**	**R.HADGIVYGRDFVEAK.J**
6488	**840.1981**	**1678.3817**	**1677.9124**	**0.4694**	**1**	**5**	**46**	**3**	**R.TCLPSFTELRTLIK.S**
6702	847.1501	1692.2857	1691.9220	0.3637	1	5	47	2	R.DLQRLHQQFGPVVR.I
6998	859.2126	1716.4107	1714.9828	1.4279	1	6	36	3	R.LAASSIQLLASSLDAKK.L
7075	863.3661	1724.7177	1723.0468	1.6709	2	1	1.1e+02	7	R.SVPRGALRVVLQTTVK.K
7127	866.7591	1731.5037	1730.8780	0.6257	1	9	17	3	R.GSPAAKTWSTWFPPAK.E
7308	**875.7836**	**1749.5527**	**1750.8533**	**-1.3006**	**2**	**5**	**43**	**1**	**R.RDAGDHPVMPRLTDR.V**
7318	876.3001	1750.5857	1750.8863	-0.3006	2	0	1.4e+02	5	R.RWDINTHVDPSGKAR.N
7395	**587.5502**	**1759.6287**	**1758.8748**	**0.7539**	**1**	**3**	**79**	**7**	**R.EPSGTLDKTSLSGNPTR.R**
7456	589.2249	1764.6527	1761.9229	2.7298	1	2	95	9	K.NQSIAALCMITVKAAR.L
7473	589.6162	1765.8267	1766.8760	-1.0493	0	5	48	7	R.YVELGPSSILTDMAQK.A
7556	**887.2651**	**1772.5157**	**1772.0018**	**0.5139**	**1**	**5**	**51**	**6**	**K.QGRVFQLLPLLEMTK.L** 7567
7608	**889.7021**	**1777.3897**	**1777.8240**	**-0.4342**	**0**	**3**	**85**	**2**	**R.QMLPDACFNAAAAGGIR.F**
7628	890.3791	1778.7437	1776.8438	1.8999	1	2	96	4	R.CGQTANSRPYPRASGR.L
7757	597.2762	1788.8067	1789.9363	-1.1295	0	5	45	9	K.LLGATELTAAQYTPWR.E
8100	**608.6089**	**1822.8047**	**1820.9104**	**1.8943**	**1**	**7**	**28**	**4**	**R.APPAMSGRLPGHQFPSR.N** 8102
8450	930.8016	1859.5887	1858.9286	0.6602	1	17	2.8	2	R.ASSAEDGGTVQVRQLWR.L 8451
8464	**621.6845**	**1862.0317**	**1862.9019**	**-0.8701**	**1**	**9**	**19**	**2**	**K.IKAIESMPACTGDWLR.M**
8519	**624.2242**	**1869.6507**	**1869.9043**	**-0.2536**	**0**	**12**	**8.4**	**1**	**R.TRPSVAEAAGMVTFYDR.J**
8544	937.2666	1872.5187	1874.0230	-1.5042	2	3	65	2	R.KNQSIAALCMITVKAAR.L 8590
8635	**629.2785**	**1884.8137**	**1882.9611**	**1.8526**	**1**	**4**	**57**	**9**	**R.EFAPRAMVDIHDLELK.C**
8970	958.7711	1915.5277	1914.9759	0.5518	2	8	21	2	R.EPSGTLDKTSLSGNPTRR.S 8945 8973
9069	**643.8122**	**1928.4147**	**1927.9350**	**0.4798**	**1**	**0**	**1.2e+02**	**7**	**R.GWGSALMEFSTKVDSGLK.K**

9228	**650.8225**	**1949.4457**	**1950.9087**	**-1.4630**	**0**	**4**	**54**	**4**	**R.TPFASYLGFFHMYQSR.Y**
9260	651.9639	1952.8697	1953.1272	-0.2575	2	3	71	10	K.RTTQLAGLVRNNAIWLK.L
9311	981.1061	1960.1977	1958.9302	1.2675	0	91	1.1e-07	1	R.FPESPTTESFWDLLYK.G 9315
9428	**659.2965**	**1974.8677**	**1973.0227**	**1.8451**	**0**	**(2)**	**92**	**8**	**K.LVLYSMISTLMGLSHHR.V**
9466	**660.7132**	**1979.1177**	**1980.0251**	**-0.9074**	**0**	**7**	**28**	**3**	**R.AAIAFFIGAISGVSMNQGAR.R** 9456
9526	**663.8055**	**1988.3947**	**1985.9894**	**2.4053**	**2**	**5**	**39**	**4**	**K.FTWMLRISGGDGFTSRR.G**
9553	**664.6265**	**1990.8577**	**1990.8916**	**-0.0338**	**1**	**4**	**50**	**7**	**R.GGVQMSPDTFTGRGGSHER.D**
9570	664.9255	1991.7547	1989.0176	2.7371	0	14	5.3	2	K.LVLYSMISTLMGLSHHR.V 9542 9544 9550 9562 9564 9569
9663	1002.4336	2002.8527	2001.9843	0.8684	2	(0)	1.3e+02	9	K.FTWMLRISGGDGFTSRR.G
9704	670.6539	2008.9397	2005.9759	2.9639	1	2	91	6	R.HLFSPESPATRGDPGPWR.R
9763	1008.7861	2015.5577	2016.1116	-0.5539	1	2	75	6	R.AVFSERGILGGITVQSNLR.D
9873	**676.7525**	**2027.2357**	**2028.0851**	**-0.8494**	**0**	**3**	**62**	**10**	**R.QILSGSQSLQQLSTVNTPK.Y**
9906	**678.2299**	**2031.6677**	**2031.1081**	**0.5596**	**2**	**3**	**68**	**7**	**K.NQSIAALCMITVKAARLR.Q**
10023	**681.5502**	**2041.6287**	**2040.0610**	**1.5677**	**1**	**2**	**74**	**7**	**K.MVSFPKCSPIMIQFLVK.E**
10415	696.2425	2085.7057	2087.1958	-1.4901	2	9	18	5	R.IILRKNQSIAALCMITVK.A
10554	702.6782	2105.0127	2102.0143	2.9984	0	5	45	4	K.TLFMLPDGGGSAFSYASLPR.L
10561	1054.1901	2106.3657	2105.0398	1.3259	2	4	51	1	R.RMPKVGIVWAADTVMDER.D 10560
10700	**710.0429**	**2127.1067**	**2126.1095**	**0.9972**	**1**	**7**	**23**	**1**	**R.CTTLSAFLGRIFLHFTSR.R**
10762	713.4415	2137.3027	2137.0415	0.2612	1	2	69	3	R.RVSTFDLHDPMFYSPIGR.L
10808	**715.0839**	**2142.2297**	**2140.0873**	**2.1425**	**1**	**0**	**1.2e+02**	**1**	**R.LSSHSSPRSVESQVTTSVPR.S**
10923	**719.5572**	**2155.6497**	**2155.0307**	**0.6190**	**2**	**5**	**39**	**1**	**R.DQRIAQRPDKHGWDYDR.G**
11062	**725.8882**	**2174.6427**	**2176.1899**	**-1.5471**	**2**	**2**	**79**	**7**	**R.YAQRPALSCSVILTTRGRK.C**
11079	726.8822	2177.6247	2175.1284	2.4963	1	1	95	4	R.SHQTEGNGPSIRLPVDVELK.A
11284	**736.2125**	**2205.6157**	**2205.0605**	**0.5552**	**2**	**1**	**1e+02**	**2**	**R.CSKQGSMSWQLPAVRAMPR.E**
11292	1104.2556	2206.4967	2204.1154	2.3813	2	5	43	2	R.RTGETRPCKSSPATMGIVTR.Q 11280
11640	753.8102	2258.4087	2256.2213	2.1874	0	2	72	7	R.VVEETTKPLGATLVVETDISR.K
11665	754.8075	2261.4007	2260.1667	1.2340	2	0	1.2e+02	9	K.NVAEVQRAMTDNGIKCTLLK.L
12029	771.2805	2310.8197	2312.1994	-1.3797	2	11	10	2	R.SCKPCKFATGPLHRGASIVAR.L 12028 12035 12062
12099	**773.8119**	**2318.4137**	**2316.0555**	**2.3582**	**0**	**1**	**97**	**6**	**K.TYDMMNVSVNAIGDGTAFPWK.G**
12213	**780.1909**	**2337.5507**	**2338.1259**	**-0.5751**	**0**	**1**	**94**	**3**	**K.LAPSTTPESMVMIDSFIAGMPK.A**
12220	**780.7332**	**2339.1777**	**2338.2605**	**0.9173**	**2**	**6**	**28**	**1**	**K.VPESARPVALVDAERGKSVGSSK.C**
12257	782.6335	2344.8787	2344.1555	0.7232	2	4	50	2	R.MPKVGIVWAADTVMDERDAPK.M
12378	790.7629	2369.2667	2370.2179	-0.9512	0	1	88	4	R.VLINNFSAAGGNTALIVEDAPER.H 12414
12397	791.1742	2370.5007	2371.2035	-0.7028	0	4	55	3	R.HSPPFMLFTVISEPPTIWTR.V 12420
12660	803.8829	2408.6267	2408.1473	0.4794	0	2	72	5	K.VLMMMQHDTIPPHCGIKPGSK.I
12857	**812.5345**	**2434.5817**	**2432.1907**	**2.3911**	**2**	**4**	**56**	**6**	**R.RLDVSYPVPSIEYDQHCAKR.A**
12900	**814.4739**	**2440.3997**	**2438.2138**	**2.1859**	**2**	**4**	**51**	**6**	**R.YQGTFIARRVSEAAHVHHGMR.I**
12981	818.7969	2453.3687	2454.3053	-0.9366	2	3	61	2	K.GPQLLRTTLTMEWPPKAAATTR.S
13085	**823.4275**	**2467.2607**	**2466.2939**	**0.9668**	**2**	**2**	**79**	**10**	**K.VARLSSHSSPRSVESQVTTSVPR.S**
13295	**832.2429**	**2493.7067**	**2491.1777**	**2.5291**	**0**	**5**	**35**	**1**	**K.APHMPLTWSSMAFAWATSAAGLR.R**
13391	**836.4682**	**2506.3827**	**2506.2427**	**0.1400**	**1**	**1**	**90**	**1**	**R.YELGHSFHFSLKSTPSRPTMGK.R**

13500	841.3169	2520.9287	2522.3519	-1.4232	1	3	53	10	R.LWGPFLQLAHRPRHHQSLSSR.K
13664	847.8485	2540.5237	2540.0188	0.5049	0	4	47	1	R.DPENMNCTHGAMIESFCNEIR.R 13667 13670
13699	850.6325	2548.8757	2549.2692	-0.3934	1	3	59	9	K.LAPSTTPESMVMIDSFIAGMPKAR.R
13850	858.2382	2571.6927	2571.1225	0.5702	1	(1)	93	3	K.EAPQMDPAQRMALMSTYEAMER.A
13859	858.6312	2572.8717	2572.2236	0.6481	2	2	74	2	R.WMDYCVLKRQGSTSISKPECK.R 13863 13873
13991	869.5172	2605.5297	2603.1124	2.4173	1	7	21	1	K.EAPQMDPAQRMALMSTYEAMER.A
14114	876.4499	2626.3277	2625.4027	0.9250	2	2	66	6	R.KLLGATELTAAQYTPWRETHALR.L
14141	878.8705	2633.5897	2631.2838	2.3059	1	2	75	1	K.APHMPLTWSSMAFAWATSAAGLRR.N
14160	880.3369	2637.9887	2636.3823	1.6064	0	1	1e+02	5	K.GWPTTLGIQRPTNSHGFTSPTLIR.S
14319	888.0205	2661.0397	2660.3592	0.6805	2	0	1e+02	8	R.QVKVWEGSLEDVSLLSECIRGTR.A
14489	896.1462	2685.4167	2683.2695	2.1472	0	1	87	8	R.TPNLLAGYVEALGLSMYDPMEPMR.I
14557	901.1605	2700.4597	2700.3582	0.1016	0	4	42	1	R.IPDIGLDCDSIGTIGLDLFNHFLR.G
14698	909.2912	2724.8517	2722.5091	2.3426	2	1	80	3	K.MTLGDKISTLPTLAPNKAIWPSLQK.I
14808	919.7319	2756.1737	2755.3534	0.8203	1	1	87	8	K.LPAMHNRSTSLSLFEPCTGGPGTGLR.S
14986	935.7805	2804.3197	2803.2827	1.0371	1	0	1e+02	10	R.MALMSTYEAMERAGLVPDTTPSTQR.D
15063	944.1089	2829.3047	2829.4353	-0.1306	2	1	92	7	R.MHMNSILDFHIPFSVVRCLLRGR.R 15044 15060
15261	968.7559	2903.2457	2900.6191	2.6266	1	2	63	8	R.QLVSQSSLVLEAVMANLVLLLTMTRR.G
15535	1014.2785	3039.8137	3038.4682	1.3456	1	0	97	3	R.AQSSSPWPHWQPPRPSASPRAPPAMSGR.L
15663	1027.5592	3079.6557	3078.6470	1.0087	2	5	33	1	R.RCLISAVYLRGAPLSMSAAVVVISADGFR.K
15709	1033.2145	3096.6217	3094.6420	1.9798	2	(4)	38	1	R.RCLISAVYLRGAPLSMSAAVVVISADGFR.K
15830	1056.3179	3165.9317	3164.5713	1.3604	1	2	59	7	R.NWPVPVTSLERTRPSVAEAAGMVTFYDR.J
15967	1082.8969	3245.6687	3247.6329	-1.9642	1	2	64	10	K.GSIDYIVCGMSALEQNQNIAVDPILRLSR.G
15989	1086.8752	3257.6037	3259.5399	-1.9362	2	2	64	4	K.VYEVEFRVNPFSMGGCLPSIGGCPIMRR.J
16063	1097.0789	3288.2147	3289.8043	-1.5896	2	1	72	2	R.SSVPLPVGMLHPVRSLFLSCLRSIPPLSSK.S
16085	1099.1872	3294.5397	3292.6307	1.9090	1	1	79	4	R.GWMSAIVTYIPAAAHARAVANPMPDAPPVMR.A
16236	1690.5311	3379.0477	3380.7481	-1.7004	1	1	85	3	K.MVGLTAAMMPTTGTTAMAVTWNQFRPIVKIK.F
16386	1157.8399	3470.4977	3470.6210	-0.1233	2	1	67	9	K.GMHFMIQKRTEFGPDGWDTIMPGASFDIVR.A

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244. gi|220698533|gb|EED54873.1| **Mass:** 33288 **Score:** 108 **Queries matched:** 15 **emPAI:** 0.33
mitochondrial 2-oxodicarboxylate carrier protein, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1363	551.4171	1100.8197	1100.6302	0.1896	2	6	51	8	R.KIVKNEGASR.L
2050	614.8086	1227.6027	1225.6740	1.9287	0	8	23	8	R.GISAPILMEAPK.R
4637	761.9776	1521.9407	1521.7439	0.1969	0	45	0.0048	1	K.YNWAWPAVGTVMK.E 4645
4782	513.3729	1537.0967	1537.7388	-0.6420	0	(2)	94	10	K.YNWAWPAVGTVMK.E
7476	884.3411	1766.6677	1765.7440	0.9237	0	66	3.9e-05	1	R.AAGEEFYTGMFDCLR.K
7678	595.2572	1782.7497	1781.7389	1.0108	0	(12)	9.9	1	R.AAGEEFYTGMFDCLR.K
8016	908.2136	1814.4127	1814.0236	0.3891	2	3	69	6	R.LYRGISAPILMEAPKR.A 8025
11659	1131.4671	2260.9197	2259.1899	1.7298	0	46	0.0031	1	K.IVQTEGPLALYNGLESTLWR.H 11668
15226	961.3582	2881.0527	2882.5663	-1.5136	2	4	40	1	K.VLRLGPGGGILLVVFTGVMDFFRTMR.G

15427	**996.5949**	**2986.7627**	**2984.5601**	**2.2026**	**1**	**1**	**71**	**4**	**K.TQQTRNDLIAGTIGGTAGTILNTPMDVVK.S**
15889	**1066.9435**	**3197.8087**	**3197.6008**	**0.2079**	**2**	**2**	**63**	**9**	**K.VAGQTPKYNWAWPAVGTVMKEEGFGALYK.G** 15887

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245. gi\|220693029\|gb\|EED49375.1\| **Mass:** 18072 **Score:** 107 **Queries matched:** 11 **emPAI:** 0.41

peptidyl-prolyl cis-trans isomerase/cyclophilin, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5580	**805.7461**	**1609.4777**	**1607.8130**	**1.6647**	**0**	**71**	**1.2e-05**	**1**	**R.VIPQFMLQGGDFTR.G** 5550 5593
5779	**812.9011**	**1623.7877**	**1623.8079**	**-0.0202**	**0**	**(39)**	**0.018**	**1**	**R.VIPQFMLQGGDFTR.G** 5751 5753 5770 5772 5783 5796 5800

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246. gi\|220693751\|gb\|EED50096.1\| **Mass:** 14616 **Score:** 107 **Queries matched:** 12 **emPAI:** 0.87

60S ribosomal protein L35 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
96	715.5640	714.5567	714.4249	0.1318	2	10	20	2	R.DLRRR.L 94
600	**464.0471**	**926.0797**	**925.4770**	**0.6027**	**0**	**29**	**0.17**	**1**	**R.EIHFPQR.K** 601
1441	**558.1746**	**1114.3347**	**1113.6546**	**0.6801**	**0**	**27**	**0.33**	**1**	**K.YLPLDLRPK.L** 1432 1442
5640	**807.7181**	**1613.4217**	**1612.8784**	**0.5433**	**1**	**71**	**1.2e-05**	**1**	**K.QLEELKQELSQLR.V** 5641 5648 5650 5652

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247. gi\|220699141\|gb\|EED55480.1\| **Mass:** 67948 **Score:** 107 **Queries matched:** 26 **emPAI:** 0.10

intermembrane space AAA protease IAP-1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
79	694.5290	693.5217	694.3650	-0.8433	0	16	3.8	8	R.FSSLGGK.L
85	**704.1170**	**703.1097**	**702.3912**	**0.7186**	**1**	**15**	**7.6**	**6**	**K.GEKLEK.L**
436	438.9421	875.8697	875.4647	0.4050	1	20	1.9	5	R.GRMDILR.H
536	456.0091	910.0037	909.4048	0.5989	0	24	0.58	2	K.IMMGAEAR.S 532 534 537
1077	**524.4236**	**1046.8327**	**1044.5927**	**2.2400**	**1**	**16**	**4.2**	**1**	**R.ATNILTEKR.H** 1073
1160	532.6081	1063.2017	1064.5250	-1.3233	1	9	23	6	R.NERDAAYVK.Q
1479	561.3846	1120.7547	1120.5369	0.2179	1	11	14	6	K.DKIMMGAEAR.S
1611	570.5791	1139.1437	1136.5318	2.6119	1	(8)	25	8	K.DKIMMGAEAR.S
1672	577.2411	1152.4677	1152.5267	-0.0590	1	(4)	53	9	K.DKIMMGAEAR.S
1685	**1156.1390**	**1155.1317**	**1152.5379**	**2.5938**	**1**	**0**	**1.5e+02**	**7**	**K.IMMGAEARSR.V**
1883	**599.5496**	**1197.0847**	**1195.5954**	**1.4893**	**1**	**10**	**14**	**6**	**R.MDILRHHMK.D** 1892
3286	**456.4409**	**1366.3007**	**1363.6700**	**2.6307**	**2**	**12**	**9.8**	**2**	**K.DKIMMGAEARSR.V**
3584	699.9946	1397.9747	1395.6598	2.3149	2	(3)	84	5	K.DKIMMGAEARSR.V
3789	**713.7521**	**1425.4897**	**1424.7129**	**0.7768**	**2**	**3**	**83**	**3**	**R.GRMDILRHHMK.D**
3952	722.2236	1442.4327	1440.8300	1.6028	2	2	91	9	K.LEKLESRASAPLK.L
6196	829.2936	1656.5727	1655.9134	0.6593	0	48	0.0023	1	K.APAIIFIDELDAIGAK.R 6204
8718	**630.6962**	**1889.0667**	**1889.0040**	**0.0627**	**2**	**2**	**94**	**5**	**R.LVEEARMRATNILTEK.R**
12204	**1168.9056**	**2335.7967**	**2334.1604**	**1.6363**	**0**	**55**	**0.00041**	**1**	**R.GTPGFSGADLENLVNQAAIFASR.N** 12197
15539	1014.5835	3040.7287	3038.4484	2.2803	1	3	49	4	R.AVAGEAGVPFFYMSGSEFDEVYVGVGAKR.V

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248. gi|220701789|gb|EED58127.1| **Mass:** 37153 **Score:** 105 **Queries matched:** 6 **emPAI:** 0.19

eukaryotic translation initiation factor 3 subunit EifCf, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
854	497.1876	992.3607	993.4549	-1.0942	0	23	0.83	2	R.TQMELSNR.L 860
4133	732.2791	1462.5437	1461.7463	0.7974	0	66	4.1e-05	1	R.AANIFTDIEALER.A 4131
5721	811.1211	1620.2277	1618.8355	1.3922	0	30	0.14	1	R.AADSAAFIPVPYEIR.Y
13573	843.4089	2527.2047	2528.1377	-0.9330	0	3	67	4	R.TTFAVGHTETTDQVEVDMEYQK.Q

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249. gi|220699805|gb|EED56144.1| **Mass:** 100280 **Score:** 105 **Queries matched:** 12 **emPAI:** 0.07

protein transport protein Sec24, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
121	733.1260	732.1187	731.4541	0.6646	1	10	24	6	K.KVLGTSK.E
1410	555.1711	1108.3277	1107.5448	0.7829	0	7	29	5	R.ENIETFLDK.L
3295	684.6351	1367.2557	1366.6340	0.6218	0	52	0.00095	1	R.SSDLCAFPAFPR.D 3294
3595	700.5941	1399.1737	1398.6027	0.5710	0	4	62	8	R.MSTFYGNFFNR.S
7077	863.4196	1724.8247	1724.9349	-0.1102	0	70	1.5e-05	1	R.DAVPQLIVDVFGLPDK.S 7080
9027	641.7172	1922.1297	1921.0098	1.1199	0	3	67	1	R.LGFIAVDSSLHYFSIPR.D 9032
11857	763.5942	2287.7607	2284.9987	2.7620	0	5	43	2	K.LQEMFQNTQNNGCAMGSALR.A
12200	779.5872	2335.7397	2334.2597	1.4801	2	1	99	7	R.RTRLGFIAVDSSLHYFSIPR.D
12383	1185.7411	2369.4677	2367.1965	2.2713	2	1	1e+02	2	K.QNLPDLDNDMNQRVRAVIEK.S

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250. gi|220696548|gb|EED52890.1| **Mass:** 34216 **Score:** 105 **Queries matched:** 20 **emPAI:** 0.59

prohibitin, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
949	509.1311	1016.2477	1015.5549	0.6928	0	20	1.9	1	R.SAELIGDAIK.K
1224	537.8101	1073.6057	1073.5869	0.0188	0	47	0.0038	1	R.VDALPQIYR.T 1229
1487	561.6826	1121.3507	1118.5978	2.7529	2	9	22	7	R.MVRDSLARR.A 1484
1918	603.3541	1204.6937	1203.5884	1.1053	0	51	0.0013	1	K.EIYSEGTHIR.I
1944	606.2431	1210.4717	1209.7333	0.7385	0	48	0.0023	1	R.VLPSIVNEVLK.S 1957
2256	629.2806	1256.5467	1255.5735	0.9733	0	27	0.3	1	R.GGFGFGGFPSGGGR.G 2260
2656	650.5111	1299.0077	1297.6990	1.3087	0	13	7.8	1	R.QIAQILQENGGK.N 2655
3211	454.2475	1359.7207	1358.7769	0.9438	2	8	29	7	R.SAELIGDAIKKSK.S
4746	767.5471	1533.0797	1531.7889	1.2908	2	2	1.1e+02	6	R.ENVARMVRDSLAR.R
5486	801.9776	1601.9407	1599.8661	2.0747	0	28	0.27	1	R.IPWIETPVIYDVR.A 5460 5499
7888	901.8696	1801.7247	1800.9482	0.7765	1	1	1.2e+02	2	K.QVAQQEAQRAAFLVDK.A
10151	686.0202	2055.0387	2052.1520	2.8867	1	1	98	4	R.IPWIETPVIYDVRAKPR.N
13485	840.7919	2519.3537	2520.3099	-0.9561	2	2	70	10	R.LQVILQNRGSRGGFGFGGFPSGGGR.G

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251. gi|220689446|gb|EED45797.1| **Mass:** 24312 **Score:** 104 **Queries matched:** 11 **emPAI:** 0.29

nitroreductase family protein, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
870	**499.1226**	**996.2307**	**995.4746**	**0.7561**	**0**	**7**	**26**	**7**	**-.MGSAQVEFK.N** 869
1904	601.4066	1200.7987	1199.5935	1.2053	0	9	20	6	K.EAFENHTKPK.L
2681	**651.9546**	**1301.8947**	**1301.7191**	**0.1757**	**0**	**24**	**0.69**	**1**	**K.NASTNTLLELVK.A** 2676 2688
6526	**561.3089**	**1680.9047**	**1680.8988**	**0.0060**	**2**	**2**	**83**	**9**	**K.EFAPLENRFKVFGK.S**
12438	792.6672	2374.9797	2375.2808	-0.3011	2	0	1.1e+02	4	M.GSAQVEFKNASTNTLLELVKAR.R
13543	841.9519	2522.8337	2522.3162	0.5175	2	3	55	7	-.MGSAQVEFKNASTNTLLELVKAR.R
16123	1106.2262	3315.6567	3314.6266	1.0301	0	74	3.5e-06	1	K.AESPISDDAIQSIVETSVLHVPSSFNTQTSR.V 16127

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252. gi|220696653|gb|EED52995.1| **Mass:** 33376 **Score:** 103 **Queries matched:** 19 **emPAI:** 0.33

60S ribosomal protein L19 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
810	**493.3681**	**984.7217**	**984.5968**	**0.1250**	**0**	**52**	**0.001**	**1**	**K.LVSDGLIIR.K** 808 809 812
1244	539.9841	1077.9537	1077.5376	0.4161	1	23	0.95	1	R.VLKEEMDAK.R
1433	**557.5846**	**1113.1547**	**1112.6917**	**0.4630**	**1**	**55**	**0.00048**	**1**	**R.KLVSDGLIIR.K** 1436
1656	**575.2446**	**1148.4747**	**1146.5678**	**1.9069**	**0**	**18**	**3.1**	**1**	**R.MPSQVLWMR.R** 1658
1801	590.4196	1178.8247	1178.5576	0.2671	0	(10)	17	4	R.MPSQVLWMR.R
2110	619.6246	1237.2347	1237.6489	-0.4141	1	5	46	9	R.YADIKMVNLR.T
2821	660.1596	1318.3047	1318.6638	-0.3591	1	(1)	1.4e+02	9	R.MPSQVLWMRR.M
2970	668.2846	1334.5547	1334.6587	-0.1040	1	13	7.6	3	R.MPSQVLWMRR.M
3932	**480.9892**	**1439.9457**	**1438.7357**	**1.2100**	**0**	**44**	**0.006**	**1**	**K.HLYHELYHLSK.G**
5404	798.7051	1595.3957	1594.8501	0.5456	2	6	40	7	R.YADIKMVNLRTQK.R 5397
6479	**560.1749**	**1677.5027**	**1674.8446**	**2.6581**	**2**	**4**	**58**	**8**	**K.EARMPSQVLWMRR.M**
9017	641.1762	1920.5067	1921.0931	-0.5864	1	3	71	7	K.LVSDGLIIRKPVTMHSR.V
13111	**824.2329**	**2469.6767**	**2469.3393**	**0.3374**	**2**	**3**	**60**	**3**	**K.VSTQPAYLQTPHFWILTRRR.V**

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253. gi|220693956|gb|EED50301.1| **Mass:** 73401 **Score:** 102 **Queries matched:** 23 **emPAI:** 0.04

AIF-like mitochondrial oxidoreductase (Nfrl), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
293	**415.4061**	**828.7977**	**829.4545**	**-0.6568**	**0**	**17**	**3.6**	**1**	**K.ALISDPSK.I**
552	**914.0720**	**913.0647**	**913.5233**	**-0.4585**	**0**	**7**	**36**	**1**	**R.IIQGNLEK.A** 558
1605	570.1531	1138.2917	1138.6029	-0.3112	1	7	31	9	-.MHVPLSRGAR.N 1601
1987	1217.3360	1216.3287	1216.5936	-0.2648	0	4	70	4	K.DNDVTIVGQEK.A
4851	**772.5806**	**1543.1467**	**1543.9086**	**-0.7619**	**2**	**0**	**1.5e+02**	**6**	**R.IIQGNLEKAGVKFK.L**
4862	773.0296	1544.0447	1543.8246	0.2201	2	1	1.3e+02	10	R.TVATKSGKTYPYTK.L
7111	**577.2412**	**1728.7017**	**1729.9727**	**-1.2710**	**0**	**2**	**82**	**6**	**K.LVIVGGGSGTFGVVEAIR.E**
7962	905.7866	1809.5587	1808.7986	0.7602	1	9	18	3	K.EMDKVESEVEGIEDGK.V 7963

8084	911.1716	1820.3287	1817.9134	2.4153	0	2	83	6	K.VLVVNYEGQFHAMSPK.C
8208	918.8616	1835.7087	1833.9039	1.8048	0	(1)	1.1e+02	7	K.GDTVVAVATMGMDPIMVK.C
8476	622.3155	1863.9247	1865.8937	-1.9690	0	2	95	7	K.GDTVVAVATMGMDPIMVK.C
9001	960.2111	1918.4077	1917.0360	1.3717	0	61	0.00011	1	R.TLPVEGFNDLGNIFLLR.F 8996 9008
9054	643.0349	1926.0827	1923.9989	2.0838	1	4	56	5	K.CTHYGAPLKLGVVAPEGR.I
9375	985.0011	1967.9877	1968.0237	-0.0360	2	10	15	2	K.MAQEYKLKDISSLADIK.E
9493	992.2211	1982.4277	1981.7499	0.6778	0	3	76	5	R.NSTTCSCSCCAHPTSPR.R
11726	759.2262	2274.6567	2276.2562	-1.5995	2	4	46	2	K.NKKIVVVGSSFIGMEVGNALAK.D
13574	843.4129	2527.2167	2526.3363	0.8804	2	1	89	3	K.NMPSKSQIESGVDVLKVGLPEGVK.I
14168	880.7905	2639.3497	2640.3177	-0.9680	2	0	1.1e+02	5	K.DNDVTIVGQEKAPMERVLGEEVGR.I

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254. gi|220699065|gb|EED55404.1| **Mass:** 24557 **Score:** 101 **Queries matched:** 8 **emPAI:** 0.14

50S ribosomal protein L24 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1918	603.3541	1204.6937	1203.6400	1.0537	0	21	1.4	3	K.ELGVFGWQLR.W
2017	1222.6630	1221.6557	1221.6241	0.0316	0	0	1.5e+02	9	K.EITKPTYNEK.Q
4467	501.8579	1502.5517	1503.7868	-1.2350	1	4	60	4	K.VMQTPKIQEQFR.Q
8149	914.6886	1827.3627	1825.9250	1.4377	0	71	1e-05	1	R.LGLPEPPSFEEWVAQK.E 8137
9646	1001.2456	2000.4767	2002.0596	-1.5828	2	1	1.1e+02	9	R.KSGGLDNYLLDDRPGRVK.E
10832	715.9919	2144.9537	2143.0732	1.8805	1	1	1e+02	6	K.QSNSGLYGGVMIQFGNKISK.G
13966	866.2909	2595.8507	2596.3020	-0.4513	2	0	1.2e+02	5	K.AQAEDLTNIKEITKPTYNEKQY.-

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255. gi|220695578|gb|EED51921.1| **Mass:** 73009 **Score:** 101 **Queries matched:** 15 **emPAI:** 0.09

aminopeptidase P, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3777	713.4416	1424.8687	1424.7987	0.0700	0	74	5.8e-06	1	K.VVGVDPALITASGAR.S 3775 3795 3808 3809
4832	771.7556	1541.4967	1540.8348	0.6619	0	28	0.21	1	R.NLIEPSLLSDAELK.W
5401	532.6612	1594.9617	1594.6801	0.2817	0	4	55	7	K.THHFFENDEYTR.S
6227	554.1692	1659.4857	1656.7824	2.7033	1	8	25	5	K.NDVELAGMRACHIR.D 6223
7497	885.2546	1768.4947	1767.9301	0.5646	1	3	72	2	R.IENVIMAREVQTTHK.F
9076	965.7201	1929.4257	1930.0007	-0.5750	2	2	88	6	K.KSTLDEVDAADKLEQIR.S
9883	1014.9136	2027.8127	2026.0848	1.7280	0	34	0.052	1	K.NGSTLVGVQQNLVDLVWGK.D
12034	771.4205	2311.2397	2310.1532	1.0866	1	18	2.1	1	R.DGAALTEYFAWLENELVNKK.S 12050
16380	1156.4262	3466.2567	3466.7368	-0.4801	2	0	76	5	R.EFISGFSGSAGTAIVSLSKAALSTDGRYFNQASK.Q

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256. gi|220693985|gb|EED50330.1| **Mass:** 17736 **Score:** 101 **Queries matched:** 7 **emPAI:** 0.19

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1680	578.2781	1154.5417	1154.4781	0.0636	0	6	36	6	R.DPHGDWWDK.Q 1678 1684

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      2128    620.6981  1239.3817  1238.7095   0.6722    2      9        17    4    K.ELGGPNAVKARK.S 2119
     15743   1039.5429  3115.6067  3114.4683   1.1384    0     67   2.1e-05    1    R.NFGEPVHEENEILGVFSPEQYTHVTSR.K 15745
```

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257.   gi|220694594|gb|EED50938.1|      Mass: 53680     Score: 101     Queries matched: 17    emPAI: 0.20
       NADH-ubiquinone oxidoreductase 49 kDa subunit, putative [Aspergillus flavus NRRL3357]
      Query   Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect Rank   Peptide
        231   400.5331    799.0517   798.4712    0.5806    1      8        29    8    R.LAGSAPKR.L
       1250  1080.5840   1079.5767  1079.5862   -0.0095    1      4        62    6    R.GTEKLIEYK.T
       1279   543.3551   1084.6957  1082.5906    2.1051    1      6        48    8    K.LSPPPRAAMK.E
       1447  1116.5590   1115.5517  1113.6043    1.9474    0     13       9.6    2    R.ADPHVGLLHR.G 1449
       2268   629.8371   1257.6597  1256.7313    0.9284    2      3        85   10    R.SRSIATTLPRR.Q
       3637   702.7536   1403.4927  1403.6544   -0.1616    0     10        17    1    K.TYMQALPYFDR.L
       3906   480.1112   1437.3117  1435.6588    1.6529    1      6        36    5    K.YIRTMFGEMTR.I
       4591   760.2301   1518.4457  1516.8137    1.6320    0     33     0.084    1    R.LIPTDPTFTSLANK.E 4594
       7322   876.4496   1750.8847  1748.8621    2.0226    0     15       4.5    1    K.GYAVPPGETYSAIEAPK.G 7323
       8160   610.7699   1829.2877  1827.9341    1.3536    0     36     0.039    1    K.ENMEALIHHFLLFSK.G 8161
       8984   639.7815   1916.3227  1913.8942    2.4286    0     10        13    1    K.GEMGVFLVSDGSERPYR.C
       9658   668.3265   2001.9577  2000.0129    1.9448    0     52   0.00078    1    R.HYTVNFGPQHPAAHGVLR.L 9650
```

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258.   gi|220696680|gb|EED53022.1|      Mass: 57267     Score: 100     Queries matched: 14    emPAI: 0.06
       cystathionine beta-synthase, putative [Aspergillus flavus NRRL3357]
      Query   Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect Rank   Peptide
        561   914.7820    913.7747   913.5484    0.2263    0     10        16    3    K.TIITLPEK.M
       3343   458.1262   1371.3567  1372.6333   -1.2766    0      5        53    5    K.SPVSDVMFNFSK.I
       5856   816.3906   1630.7667  1629.8620    0.9047    2      0   1.4e+02   10    R.IALRMIEEAERSGR.I
       8305   924.7101   1847.4057  1847.9815   -0.5758    1      8        24    2    R.KFVEITMDTPLGVLNR.F
       8638   629.5095   1885.5067  1884.8853    0.6214    0     71   1.1e-05    1    R.TPNEAAYDSPESHIGVAK.R 8645
       9404   658.1575   1971.4507  1970.1485    1.3022    2      1   1.2e+02   10    K.TIITLPEKMSAEKVAVLK.A
      12061  1158.2201   2314.4257  2312.2587    2.1670    0      2        81    1    R.LIAEEGLLVGGSSGSAISALAQAAK.D
      12680   805.1609   2412.4607  2411.2081    1.2527    2      4        46   10    R.TPNEAAYDSPESHIGVAKRLEK.E
      13117   824.4585   2470.3537  2468.3598    1.9939    1      2        80    3    R.RLIAEEGLLVGGSSGSAISALAQAAK.D
      13543   841.9519   2522.8337  2520.4163    2.4174    0      9        15    2    R.IKPGDTLIEPTSGNTGIGLALVGAVK.G 13492 13506
      14609   903.7092   2708.1057  2706.3139    1.7918    1      1        98    5    R.LKPITTVQSNTPCETAIEMMRDR.G
```

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259.   gi|220688465|gb|EED44818.1|      Mass: 23039     Score: 99      Queries matched: 14    emPAI: 0.15
       xanthine-guanine phosphoribosyl transferase Xpt1, putative [Aspergillus flavus NRRL3357]
      Query   Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect Rank   Peptide
       2401   637.1831   1272.3517  1270.6629    1.6888    1      9        23    7    K.DVEQAQKQLGR.E 2393
       2633   433.0455   1296.1147  1293.5693    2.5454    0      6        38   10    K.GVLPADMMESGR.Y
```

3633	702.6781	1403.3417	1400.7147	2.6270	0	4	64	4	K.NILIVDEVDDTR.T
5935	546.7549	1637.2427	1636.7913	0.4515	2	1	1.2e+02	5	K.SKKGVLPADMMESGR.Y
9117	968.3436	1934.6727	1933.9819	0.6908	0	2	87	1	R.TQWLDLSSLEMANLIGK.N
11443	1114.3841	2226.7537	2225.1692	1.5846	0	59	0.00014	1	R.AGEPNIPIQAIGLSLYEDLGR.G 11437
11583	1126.3406	2250.6667	2248.1699	2.4968	2	2	90	5	R.TTLEYAVRELQKDVEQAQK.Q 11586
12122	775.4849	2323.4327	2324.0572	-0.6245	0	6	37	4	R.YHAAVTTDDVWICYPWEAK.D 12127
15162	953.7299	2858.1677	2856.5497	1.6180	2	11	8.9	1	R.SFLKRAGEPNIPIQAIGLSLYEDLGR.G 15163

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260. gi|220700344|gb|EED56682.1| **Mass:** 153300 **Score:** 99 **Queries matched:** 30 **emPAI:** 0.04

DNA mismatch repair protein Msh3 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
790	980.3830	979.3757	979.5702	-0.1945	1	3	70	6	R.KLTNLYTK.G
2031	613.4951	1224.9757	1223.5670	1.4087	0	13	8.2	2	K.FASSPATEGETK.E
2414	637.7276	1273.4407	1271.5928	1.8479	1	10	17	4	K.INMHAAKNDDK.Y
2776	438.9419	1313.8037	1314.7871	-0.9833	2	24	0.71	2	R.IKTDLEKSLIR.V
2869	663.6141	1325.2137	1324.6598	0.5539	0	6	39	1	K.YVLCQYNIPR.S
3403	689.2721	1376.5297	1374.6813	1.8484	0	(5)	57	10	-.MPLSSQPSSSNLK.R
3522	696.4721	1390.9297	1391.7144	-0.7847	1	1	1.3e+02	6	K.LEGVDDTSKLSTK.I
3531	464.9512	1391.8317	1390.6762	1.1555	0	14	6.6	1	-.MPLSSQPSSSNLK.R
3538	697.3056	1392.5967	1391.7694	0.8273	2	0	1.4e+02	8	K.KKIATVMDELTK.V
3795	713.8796	1425.7447	1423.7493	1.9954	1	2	86	5	R.SAKLGMLDAVFTR.M
4062	485.5882	1453.7427	1453.7889	-0.0461	0	4	63	6	R.NAQNPLVELITSR.I
6433	837.9236	1673.8327	1674.8723	-1.0395	2	1	1.1e+02	6	-.MPLSSQPSSSNLKRK.Q
6741	566.3609	1696.0607	1696.9220	-0.8613	1	8	25	2	K.SRNAQNPLVELITSR.I
7288	873.9531	1745.8917	1744.9036	0.9881	0	84	6.1e-07	1	R.NVVTSFTALTEAFFAK.L 7296
7349	878.3766	1754.7387	1754.8125	-0.0737	1	8	22	5	K.FRFDEHPSEAHLDR.F 7365
9382	657.2539	1968.7397	1966.1072	2.6326	2	15	4.2	1	K.SRNAQNPLVELITSRIR.G 9380
9656	668.2045	2001.5917	2001.0425	0.5492	2	4	55	2	K.VGVVRQMETAALKAAGDNR.N
10745	712.5535	2134.6387	2133.0385	1.6002	2	5	43	1	R.QMETAALKAAGDNRNAPFGR.K 10735
12137	776.1942	2325.5607	2323.2940	2.2667	0	23	0.63	1	K.NLPIALIFLPAADIPTFVGEGR.V
13287	831.6855	2492.0347	2489.2697	2.7651	1	9	17	1	R.GTSTHDGVAIAQAVLDYMIRSIR.S 13288
14316	887.8535	2660.5387	2660.1514	0.3873	2	8	17	1	K.NDDKYEFFRESEETDEITEHK.L 14296
14785	916.8972	2747.6697	2746.2093	1.4604	0	1	84	10	R.NTAPEAVPEEVGEGDEDDEPSPPPAAK.G 14783
15783	1046.7159	3137.1257	3134.7492	2.3765	1	0	86	4	K.NLPIALIFLPAADIPTFVGEGRVDLGITGR.D

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261. gi|220697500|gb|EED53841.1| **Mass:** 72158 **Score:** 98 **Queries matched:** 18 **emPAI:** 0.09

ATP dependent RNA helicase (Dbp1), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
194	780.7870	779.7797	781.3355	-1.5558	0	3	71	2	R.EGSGYGGR.G

210	786.5970	785.5897	785.5011	0.0887	0	5	57	6	R.ISLVNIK.Y
877	999.5510	998.5437	998.6236	-0.0799	1	7	33	6	R.GRISLVNIK.Y 878
1187	534.7106	1067.4067	1066.5229	0.8838	1	2	90	9	R.ERALEMFR.S
1660	575.6406	1149.2667	1148.6012	0.6655	0	8	25	10	K.YSIPIVMNGR.D
2008	611.1711	1220.3277	1219.5840	0.7437	2	9	25	2	R.GRGANATRDMR.R
3004	670.1771	1338.3397	1338.6680	-0.3283	0	39	0.021	1	R.AGNTGIATAFFNR.G 2999
3835	716.1791	1430.3437	1429.8293	0.5145	1	7	30	7	R.KAYPTSLILAPTR.E
6530	561.3849	1681.1327	1680.8253	0.3074	1	13	8.4	1	K.RMADSLSDFLLNQR.F
12369	790.1639	2367.4697	2368.1337	-0.6640	1	1	91	9	K.YSIPIVMNGRDLMACAQTGSGK.T
13147	825.6692	2473.9857	2475.1778	-1.1921	1	1	98	10	K.EAHQEVPSFLESIAREGSGYGGR.G
13556	842.4692	2524.3857	2522.3380	2.0477	1	1	97	4	R.DLIDLLKEAHQEVPSFLESIAR.E
14936	929.9089	2786.7047	2787.2915	-0.5868	1	4	40	1	-.MADSLKMGSLSLNESQHAPAPNSSSGR.A
15247	965.9239	2894.7497	2893.4247	1.3251	0	53	0.00046	1	R.GLDIPNVTHVINYDLPTDIDDYVHR.I 15242
15406	992.8909	2975.6507	2975.3693	0.2815	1	0	1e+02	7	R.QRQTGANMDGAPAAAPPAPGPSGPGNSWGSR.G

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262. gi\|220700881\|gb\|EED57219.1\| **Mass:** 39353 **Score:** 98 **Queries matched:** 9 **emPAI:** 0.17

casein kinase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3583	699.8771	1397.7397	1397.6715	0.0683	0	57	0.00033	1	R.FVSDEAIDFLDK.L 3579
7620	593.7605	1778.2597	1779.9407	-1.6810	1	5	46	10	R.FVSDEAIDFLDKLLR.Y
8281	923.4396	1844.8647	1845.9010	-1.0362	1	5	41	9	R.KEPFFHGNSNSDQLVK.I
9315	981.3756	1960.7367	1960.1469	0.5898	0	57	0.00027	1	K.ILQNLAGGPNVVALLDVVR.D 9311 9318 9337
13395	836.5535	2506.6387	2505.3915	1.2472	1	1	1e+02	5	K.ILQNLAGGPNVVALLDVVRDSQSK.T

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263. gi\|220697523\|gb\|EED53864.1\| **Mass:** 22794 **Score:** 98 **Queries matched:** 6 **emPAI:** 0.15

proteasome component Pup3, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4767	768.6681	1535.3217	1534.7814	0.5404	0	10	15	1	R.LGMQALTVSNNFPK.I
8396	928.7056	1855.3967	1855.8267	-0.4300	0	(5)	48	6	-.MSSPFDINGGACVAMVGK.D 8380
8545	625.2199	1872.6377	1871.8216	0.8161	0	7	28	4	-.MSSPFDINGGACVAMVGK.D
9429	988.4616	1974.9087	1975.0374	-0.1287	0	98	2.3e-08	1	R.NIAPQTLANLVSSSLYER.R 9447

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264. gi\|220699291\|gb\|EED55630.1\| **Mass:** 22797 **Score:** 98 **Queries matched:** 8 **emPAI:** 0.51

40S ribosomal protein S8e [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
27	650.4840	649.4767	649.3547	0.1220	1	20	1.6	2	K.RAFEK.G 28
2214	625.8826	1249.7507	1249.6415	0.1093	2	4	58	2	K.KQAERFAESGK.V
5797	813.7386	1625.4627	1624.7481	0.7146	0	84	5.7e-07	1	R.LESGNFSWGSEGISR.K 5816
6925	855.7396	1709.4647	1708.9260	0.5387	0	34	0.053	1	R.VIVVAYHPSNNELVR.T 6927 6930

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265.  gi|220700470|gb|EED56808.1|     Mass: 16863    Score: 98     Queries matched: 7   emPAI: 0.73
      40S ribosomal protein S13 [Aspergillus flavus NRRL3357]
     Query  Observed    Mr(expt)    Mr(calc)    Delta Miss Score  Expect Rank  Peptide
       326  422.6636    843.3127    842.5225   0.7902   0     26     0.47    1   R.LILIESR.I 325
      8614  941.5621   1881.1097   1880.9883   0.1214   0     56  0.00036    1   K.SSGLAPELPEDLYHLIK.K 8619 8622 8626 8627

266.  gi|220690774|gb|EED47123.1|     Mass: 38099    Score: 97     Queries matched: 7   emPAI: 0.18
      thioredoxin reductase Trr1/Trr2, putative [Aspergillus flavus NRRL3357]
     Query   Observed    Mr(expt)    Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      3144   677.3286   1352.6427   1351.6983   0.9444   0     73    7e-06    1   R.FGTEVITETISR.V 3154
      6695   846.8921   1691.7697   1691.9617  -0.1920   2      3       72    3   K.AMANRLLSHPKVTVR.F
      8772   632.8565   1895.5477   1895.0629   0.4849   0      1  1.1e+02   10   K.VVIIGSGPAAHTAAIYLSR.A
     15272   971.8412   2912.5017   2912.5365  -0.0347   1      2       61    5   K.VTVRFNTVATQVLGDEKPMGLMTHLR.V 15274
     15484  1007.6459   3019.9157   3017.4618   2.4539   0     55  0.00038    1   K.NTVTGEEETVDANGLFYAVGHDPATALVK.G

267.  gi|220691607|gb|EED47955.1|     Mass: 128918   Score: 97     Queries matched: 27   emPAI: 0.03
      ubiquitin C-terminal hydrolase, putative [Aspergillus flavus NRRL3357]
     Query   Observed    Mr(expt)    Mr(calc)    Delta Miss Score  Expect Rank  Peptide
       501   902.6180    901.6107    901.5709   0.0398   2      9       25    3   R.LSKRTGIK.G 500
      1722  1164.7460   1163.7387   1162.5329   1.2059   1      3       76    6   K.MTYDQFSKK.V
      2081   617.7111   1233.4077   1232.6587   0.7490   0      6       47    2   R.FAPVMASTGKPK.Q
      2430   638.6911   1275.3677   1274.6329   0.7348   2      3       81    9   R.KMTYDQFSKK.V
      3079   674.4926   1346.9707   1345.7089   1.2618   0      6       38    2   R.DGTISDLLSGLQK.K
      3590   700.3761   1398.7377   1398.7905  -0.0527   1     10       15    6   K.SRLDDVLLPIMK.E 3588 3602 3614
      4213   737.7591   1473.5037   1473.8039  -0.3001   1      0  1.5e+02    3   R.DGTISDLLSGLQKK.A
      4563   758.9946   1515.9747   1515.7690   0.2057   1      3       81   10   K.RSMNAYMLVYIR.K
      4613   760.9801   1519.9457   1521.6075  -1.6618   0     12       11    3   R.MPEEEVNMGEGER.T
      4621   761.2551   1520.4957   1521.6075  -1.1118   0    (2)    1e+02    3   R.MPEEEVNMGEGER.T
      5394   798.1886   1594.3627   1594.8355  -0.4728   0      1  1.1e+02    8   K.IAGINEFVTLYAER.M
      7460   883.4866   1764.9587   1764.9597  -0.0009   1      3       78    5   R.FAPVMASTGKPKQFIK.R 7469
      8183   917.0996   1832.1847   1830.8094   1.3753   1      0  1.4e+02    1   K.DPDMSVEEAYSRFGTK.G
      8198   918.2686   1834.5227   1832.0349   2.4878   0      2       85    7   K.GVIFESFPPVLHLHLK.R
      9904   678.1889   2031.5447   2029.9349   1.6098   2      1       94    5   R.FEYDINRDAMMKINDR.H
     11282   736.1689   2205.4847   2203.1677   2.3170   1      3       65    2   R.QYYDYLLNRISVTFAPIK.A 11281
     12451   793.3385   2376.9937   2375.2532   1.7405   2      1       90    9   R.FWVMVNRQNKTTRPDQVIK.D
     12761   808.1442   2421.4107   2423.3478  -1.9371   1      3       66    1   R.DLNRPHGVPFKFVLKPGEVFK.E
     12988   819.2505   2454.7297   2452.1540   2.5757   1      1       96    1   K.TTRPDQVIKDPDMSVEEAYSR.F
     14600   903.2049   2706.5927   2704.4119   2.1808   1      1       83    3   K.VGEHLNVESTHLRFAPVMASTGKPK.Q
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15236	**963.9729**	**2888.8967**	**2887.3611**	**1.5356**	**0**	**97**	**2e-08**	**1**	**R.YLEDDDILSDIVGDSDDLLGLDHVNK.N**

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268. gi\|220693628\|gb\|EED49973.1\| **Mass:** 34193 **Score:** 97 **Queries matched:** 3 **emPAI:** 0.10

COPII-coated vesicle protein SurF4/Erv29, putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
6092	**825.5286**	**1649.0427**	**1647.8984**	**1.1443**	**0**	**11**	**11**	**1**	**R.IITQWSDQLLYLR.E**
12498	**795.5879**	**2383.7417**	**2381.2631**	**2.4786**	**0**	**62**	**7.6e-05**	**1**	**K.IEDWLDTLADPVKPYLPAIGR.F** 12484

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269. gi\|220693132\|gb\|EED49478.1\| **Mass:** 27297 **Score:** 97 **Queries matched:** 10 **emPAI:** 0.12

Hsp90 binding co-chaperone (Sba1), putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
136	744.0140	743.0067	742.4701	0.5366	0	10	22	2	R.LQLLTR.Y
1397	554.5946	1107.1747	1108.5950	-1.4203	1	2	1.1e+02	5	R.SLNYMQKII.-
2350	633.9521	1265.8897	1264.6961	1.1936	2	8	22	10	R.RSLNYMQKII.- 2351
2488	**641.0111**	**1280.0077**	**1281.6611**	**-1.6534**	**2**	**1**	**1.2e+02**	**10**	**K.SRRSLNYMQK.I**
3128	**676.5871**	**1351.1597**	**1349.6827**	**1.4770**	**0**	**64**	**5.6e-05**	**1**	**K.ITPTNVTFAGDSK.K** 3106
6739	**566.2832**	**1695.8277**	**1692.9271**	**2.9006**	**2**	**7**	**28**	**2**	**K.VNHSDREVELVLRK.K**
11913	766.7665	2297.2777	2296.1223	1.1555	1	3	65	1	K.GVRYEVSLDLYAEIDPENSK.V
14530	898.6052	2692.7937	2692.2616	0.5321	1	0	1e+02	8	R.YEVSLDLYAEIDPENSKVNHSDR.E

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270. gi\|220688475\|gb\|EED44828.1\| **Mass:** 56256 **Score:** 97 **Queries matched:** 18 **emPAI:** 0.12

mitochondrial outer membrane protein (Sam50), putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
239	**803.7220**	**802.7147**	**802.4297**	**0.2850**	**2**	**9**	**30**	**4**	**R.KGEEGRK.G**
498	**451.3111**	**900.6077**	**899.5341**	**1.0736**	**1**	**18**	**2.8**	**2**	**R.IHAIYRK.A** 499
1144	**530.4606**	**1058.9067**	**1059.5713**	**-0.6646**	**0**	**28**	**0.34**	**1**	**R.FLVGGPTDVR.G**
2262	**629.6876**	**1257.3607**	**1256.6196**	**0.7411**	**1**	**7**	**36**	**10**	**K.IRWMSQSGHR.H**
2293	**631.2506**	**1260.4867**	**1259.6874**	**0.7994**	**0**	**34**	**0.067**	**1**	**R.IFNPLLSSNQK.R**
2693	**652.2886**	**1302.5627**	**1301.6768**	**0.8859**	**0**	**3**	**90**	**10**	**K.AFNELAGWGPLK.G**
4003	**724.6456**	**1447.2767**	**1446.8235**	**0.4533**	**0**	**7**	**28**	**4**	**R.FELNFSLPLVLR.K** 4011
6765	**850.2071**	**1698.3997**	**1697.8665**	**0.5332**	**0**	**64**	**6e-05**	**1**	**R.FDIFQQPVSVYLDK.S** 6783
8459	621.4819	1861.4237	1862.0050	-0.5813	1	6	31	2	R.GFLERIFNPLLSSNQK.R
9045	642.7072	1925.0997	1924.9907	0.1090	2	10	13	3	K.AWASHEEALKGGWSKIR.W
10187	1030.3321	2058.6497	2056.9742	1.6755	0	12	7.8	2	R.SAYQATFETPILSDPDFR.L 10192
10658	**708.4279**	**2122.2617**	**2121.0684**	**1.1934**	**1**	**3**	**60**	**3**	**K.AFNELAGWGPLKGDVSFWK.S**
12122	775.4849	2323.4327	2325.1964	-1.7637	1	2	74	8	R.LEIGGIASSTQKAWASHEEALK.G 12143

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271. gi\|220692288\|gb\|EED48635.1\| **Mass:** 40460 **Score:** 96 **Queries matched:** 12 **emPAI:** 0.17

NADH-ubiquinone oxidoreductase 304 kDa subunit precursor [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1113	527.5831	1053.1517	1053.5059	-0.3542	1	11	12	2	-.MASARSLMR.L
2757	**656.7231**	**1311.4317**	**1310.6507**	**0.7811**	**0**	**48**	**0.0027**	**1**	**K.DFPLTGYTELR.Y**
4613	760.9801	1519.9457	1520.7082	-0.7625	0	23	0.84	1	R.IMTDYGFDGHPLR.K
4715	**765.8756**	**1529.7367**	**1527.8661**	**1.8707**	**0**	**78**	**2.5e-06**	**1**	**R.IVIEPLELTQAFR.N** 4721
4786	**769.7071**	**1537.3997**	**1536.7031**	**0.6966**	**0**	**(14)**	**5.5**	**1**	**R.IMTDYGFDGHPLR.K**
6244	554.5945	1660.7617	1661.8995	-1.1378	2	5	45	10	R.SLMRLGTGRSLASAAR.S
7849	**600.0382**	**1797.0927**	**1795.9073**	**1.1854**	**1**	**3**	**65**	**4**	**R.SSRMCRPFSTTPLLK.E**
12319	786.3452	2356.0137	2354.1431	1.8707	0	1	97	6	K.YHTAAEFTQISDITAVDFPTK.D
14804	**918.8619**	**2753.5637**	**2753.3297**	**0.2340**	**1**	**4**	**43**	**5**	**K.YHTAAEFTQISDITAVDFPTKDQR.F** 14798
15838	**1057.3292**	**3168.9657**	**3167.6291**	**1.3366**	**2**	**6**	**25**	**1**	**R.IRVKTYADEATPVPSVTGLFEGALWYER.E**

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272. gi|220690385|gb|EED46735.1| **Mass:** 50863 **Score:** 96 **Queries matched:** 15 **emPAI:** 0.29

dihydrolipoamide succinyltransferase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
67	687.5450	686.5377	686.3963	0.1415	0	14	8.1	6	K.AIADLGK.K
314	421.0041	839.9937	839.5229	0.4708	0	20	1.3	1	K.GLVTPVVR.N
938	508.3311	1014.6477	1014.4957	0.1520	0	36	0.047	1	K.LGFMSAFSR.A
1556	**566.6856**	**1131.3567**	**1132.6856**	**-1.3289**	**1**	**7**	**40**	**6**	**R.EAVTFLVKVK.E**
2839	660.8641	1319.7137	1318.6438	1.0699	0	(37)	0.032	1	R.NAETMDLVGIEK.A
2974	668.6181	1335.2217	1334.6388	0.5830	0	69	2e-05	1	R.NAETMDLVGIEK.A 2992
3703	**472.4942**	**1414.4607**	**1415.7231**	**-1.2624**	**1**	**7**	**32**	**4**	**K.TGVKLGFMSAFSR.A**
9684	**669.4072**	**2005.1997**	**2003.0245**	**2.1752**	**1**	**22**	**0.9**	**1**	**R.NAETMDLVGIEKAIADLGK.K** 9662 9671 9676
9872	**1014.5836**	**2027.1527**	**2027.0422**	**0.1105**	**1**	**1**	**1.1e+02**	**2**	**K.LELGGAPETKTEEATEKPK.E**
10777	**713.7522**	**2138.2347**	**2140.1562**	**-1.9215**	**1**	**3**	**63**	**6**	**K.GLVTPVVRNAETMDLVGIEK.A**
13948	**864.7379**	**2591.1917**	**2591.3352**	**-0.1435**	**1**	**0**	**1.2e+02**	**6**	**K.IEIRPMMYLALTYDHRLLDGR.E**

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273. gi|220699042|gb|EED55381.1| **Mass:** 51095 **Score:** 96 **Queries matched:** 17 **emPAI:** 0.06

homocitrate synthase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1395	554.2501	1106.4857	1105.6495	0.8362	1	8	27	3	R.FKIIESTLR.E
1611	570.5791	1139.1437	1139.5355	-0.3918	0	11	11	4	R.MMVADPAYVK.G
1978	**608.4066**	**1214.7987**	**1214.6441**	**0.1546**	**0**	**6**	**45**	**9**	**R.NGITPLGGLMAR.M**
5694	540.2372	1617.6897	1615.8102	1.8795	2	0	1.4e+02	9	R.MMVADPAYVKGKYK.L
5699	810.2906	1618.5667	1617.8582	0.7085	2	1	1.1e+02	8	R.LDCEAICKLGLKAK.I
5936	819.6591	1637.3037	1636.8560	0.4478	0	96	4e-08	1	R.SDLVDLLSIYSAVDK.V 5918 5956
10244	**688.7435**	**2063.2087**	**2061.1470**	**2.0618**	**2**	**2**	**80**	**10**	**K.NTAIEVIEYVKSKGIEIR.F** 10242
10747	1068.3386	2134.6627	2135.1111	-0.4483	0	3	69	2	R.VAVETGVDGVDVVIGTSSYLR.E 10743

11558	749.1529	2244.4367	2244.1711	0.2656	2	1	1.1e+02	6	K.DMTYIKNTAIEVIEYVKSK.G
13144	1237.8821	2473.7497	2472.1115	1.6382	0	2	78	2	K.ALDDFGVDYIELTSPCASEQSR.L
13517	841.6595	2521.9567	2521.2855	0.6712	2	13	5.6	2	R.NGITPLGGLMARMMVADPAYVKGK.Y
13529	841.7582	2522.2527	2521.2855	0.9672	2	(3)	60	5	R.NGITPLGGLMARMMVADPAYVKGK.Y
14997	937.4642	2809.3707	2810.4199	-1.0492	1	1	86	2	R.VAVETGVDGVDVVIGTSSYLREHSHGK.D

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274. gi|220699676|gb|EED56015.1| **Mass:** 45077 **Score:** 95 **Queries matched:** 10 **emPAI:** 0.15
cAMP-dependent protein kinase regulatory subunit PkaR [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
611	465.8936	929.7727	928.5229	1.2498	0	2	1.4e+02	7	K.IADALDAIK.F 612
1264	541.6911	1081.3677	1079.5433	1.8244	0	5	43	7	R.ILMDSAFQR.R
3847	716.4616	1430.9087	1430.7041	0.2046	0	2	1e+02	3	R.AEYEQIQPKPAAS.-
6909	855.1691	1708.3237	1707.8104	0.5133	0	43	0.0069	1	R.GDYFGELALLDDQPR.A
10347	693.5249	2077.5527	2078.0255	-0.4728	0	0	1.2e+02	6	K.AGTIGPGGSFGELALMYNAPR.A
12703	805.7775	2414.3107	2413.2239	1.0868	0	53	0.00055	1	R.MYEAFLEEVPLLSSLKPYER.S 12698
13918	862.7052	2585.0937	2585.3199	-0.2262	1	3	61	9	R.RMYEAFLEEVPLLSSLKPYER.S 13922

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275. gi|220697931|gb|EED54271.1| **Mass:** 115238 **Score:** 95 **Queries matched:** 28 **emPAI:** 0.09
poly(A)+ RNA transport protein (UbaA), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
206	392.9781	783.9417	784.4807	-0.5389	0	10	14	9	K.NIALAGVK.S 201 202
2634	649.1036	1296.1927	1295.5993	0.5934	0	4	64	6	K.QGEIDESLYSR.Q 2635
2804	659.2966	1316.5787	1316.6183	-0.0396	0	6	42	5	K.DQLAIADFCHK.N
3159	678.4221	1354.8297	1353.6486	1.1811	0	(3)	78	9	K.IYVTDMDQIEK.S
3344	686.7266	1371.4387	1369.6435	1.7952	0	13	9.6	2	K.IYVTDMDQIEK.S
4474	1503.8550	1502.8477	1501.7850	1.0627	0	13	9.2	2	K.VVDNMIIPEFTPK.S 4454 4472 4473 4486
4528	755.6056	1509.1967	1507.7558	1.4409	0	24	0.59	1	K.FVDYQPLEEQLK.K
4597	760.4991	1518.9837	1517.7562	1.2276	2	0	1.4e+02	7	R.TYVDRRCVFFR.K
5572	537.2839	1608.8297	1605.8515	2.9783	1	3	74	6	K.SLAGFRLNPVEFEK.D
10043	682.0835	2043.2287	2041.0745	2.1542	2	8	18	3	K.TSSGQPFWSGPKRAPTPLK.F
10075	682.9585	2045.8537	2045.9753	-0.1215	1	3	71	2	K.ISNDLASNQEDKVELDEK.L
10675	709.1545	2124.4417	2123.0681	1.3737	2	7	28	3	K.GKIYVTDMDQIEKSNLNR.Q
14307	887.5982	2659.7727	2658.3979	1.3749	1	4	46	3	K.GLEISMVSSGVSLLYASFYPPSKVK.D 14296 14322
14847	923.7175	2768.1307	2766.6041	1.5266	2	3	57	9	R.MGTSNVLVVGLKGLGVEIAKNIALAGVK.S
15085	945.1589	2832.4547	2830.3340	2.1208	2	2	66	5	K.NWAMMGLGTGPKGKIYVTDMDQIEK.S
16025	1094.2612	3279.7617	3278.6823	1.0794	0	20	1	1	K.SLTLYDPAPVAISDLSSQFFLQSQDVGKPR.A 16024
16260	1131.5105	3391.5097	3389.5437	1.9661	0	72	5.4e-06	1	R.VGQDTEHIFNEEFWEGLDGVTNALDNVDAR.T 16262

276. gi|209156402|pdb|2ZKA|A **Mass:** 34370 **Score:** 94 **Queries matched:** 14 **emPAI:** 0.32
Chain A, Urate Oxidase Complexed With 8-Azaxanthine Under 1.0 Mpa Oxygen Pressure

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
273	410.5556	819.0967	816.4453	2.6514	1	4	73	10	-.DSAVKAAR.Y
648	**474.7731**	**947.5317**	**946.4906**	**1.0412**	**0**	**17**	**4.1**	**2**	**K.MAEQILAR.Q**
1044	**520.6721**	**1039.3297**	**1037.4930**	**1.8367**	**0**	**4**	**61**	**9**	**K.FDATWATAR.E**
1100	**526.3086**	**1050.6027**	**1048.5302**	**2.0726**	**0**	**12**	**9.6**	**3**	**K.NFSGLQEVR.S**
1288	**1086.6920**	**1085.6847**	**1085.5717**	**0.1130**	**0**	**42**	**0.012**	**1**	**R.NVQVDVVEGK.G**
3045	672.1581	1342.3017	1341.6466	0.6551	0	48	0.0027	1	K.STNSQFWGFLR.D 3036
4214	737.7876	1473.5607	1473.7041	-0.1434	0	10	16	3	K.HYFEIDLSWHK.G 4227
5060	**782.1716**	**1562.3287**	**1561.7777**	**0.5511**	**0**	**1**	**1.3e+02**	**3**	**R.ILSTDVDATWQWK.N**
5305	**794.1446**	**1586.2747**	**1585.8001**	**0.4746**	**1**	**1**	**1.2e+02**	**2**	**R.SHVPKFDATWATAR.E**
6316	**556.2842**	**1665.8307**	**1664.8093**	**1.0214**	**0**	**4**	**53**	**5**	**R.MDIDGKPHPHSFIR.D**
12126	**775.5875**	**2323.7407**	**2323.2212**	**0.5195**	**0**	**28**	**0.23**	**1**	**K.QNPVTPPELFGSILGTHFIEK.Y** 12133

Proteins matching the same set of peptides:
gi|209156403|pdb|2ZKB|A **Mass:** 34370 **Score:** 94 **Queries matched:** 14
Chain A, Urate Oxidase Complexed With 8-Azaxanthine Under 2.5 Mpa Oxygen Pressure
gi|209156470|pdb|3CKS|A **Mass:** 34370 **Score:** 94 **Queries matched:** 14
Chain A, Urate Oxidase Complexed With 8-Azaxanthine Under 4.0 Mpa Oxygen Pressure
gi|209156471|pdb|3CKU|A **Mass:** 34370 **Score:** 94 **Queries matched:** 14
Chain A, Urate Oxidase From Aspergillus Flavus Complexed With Its Inhibitor 8-Azaxanthin And Chloride

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277. gi|46370500|gb|AAS90034.1| **Mass:** 43446 **Score:** 94 **Queries matched:** 12 **emPAI:** 0.16
OmtB [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
649	474.9836	947.9527	947.5440	0.4087	0	45	0.0053	1	R.TQAAFGLIK.E
843	495.6116	989.2087	988.5706	0.6382	0	59	0.00023	1	K.VGIDLGIFR.S 842
4777	769.3351	1536.6557	1534.7814	1.8743	0	14	5.7	1	K.VLMVDIGGGFGQQSK.A 4744 4770 4784
5794	813.6756	1625.3367	1624.8568	0.4799	1	3	70	8	-.MTGLDMEIIFAKIK.E
7588	**592.6812**	**1775.0217**	**1776.0033**	**-0.9816**	**2**	**3**	**73**	**7**	**R.SLKKSDTPITLAEFVK.K**
8760	632.3142	1893.9207	1890.9986	2.9221	1	2	77	9	K.VLMVDIGGGFGQQSKALR.A
10446	697.8545	2090.5417	2090.1306	0.4111	2	6	32	6	K.VLMVDIGGGFGQQSKALRAK.F
11743	759.4955	2275.4647	2273.1435	2.3212	2	2	81	7	-.MTGLDMEIIFAKIKEEYAR.T

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278. gi|220693637|gb|EED49982.1| **Mass:** 21016 **Score:** 93 **Queries matched:** 14 **emPAI:** 0.56
ADP-ribosylation factor, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
129	738.5340	737.5267	737.4323	0.0944	0	9	15	7	K.TTILYK.L 128
378	858.6040	857.5967	857.4719	0.1248	1	19	2.5	4	R.DRIVEAR.E 372

5524	**803.3441**	**1604.6737**	**1605.7787**	**-1.1050**	**0**	**0**	**1.5e+02**	**4**	**K.NIQFTVWDVGGQDK.I**
5876	817.2341	1632.4537	1630.8898	1.5639	2	9	18	8	K.KEMRILMVGLDAAGK.T
6087	825.2571	1648.4997	1646.8847	1.6150	2	(3)	77	8	K.KEMRILMVGLDAAGK.T
6277	555.2745	1662.8017	1662.8797	-0.0779	2	(7)	31	6	K.KEMRILMVGLDAAGK.T
10548	702.4549	2104.3427	2103.1034	1.2393	1	47	0.0027	1	R.MLNEDELRDALLLVFANK.Q 10551
10647	707.6702	2119.9887	2119.0983	0.8904	1	(39)	0.016	1	R.MLNEDELRDALLLVFANK.Q 10645
12770	**808.6012**	**2422.7817**	**2423.1618**	**-0.3801**	**1**	**12**	**6.9**	**1**	**R.HYFQNTQGIIFVVDSNDRDR.I**
13450	**838.5842**	**2512.7307**	**2510.2799**	**2.4509**	**0**	**45**	**0.0037**	**1**	**K.QDLPNAMSPAEITQQLGLQSLTR.R**

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279. gi|6714971|gb|AAF26223.1|AF159789_1 **Mass:** 43304 **Score:** 92 **Queries matched:** 19 **emPAI:** 0.16

O-methyltransferase B [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
649	474.9836	947.9527	947.5440	0.4087	0	45	0.0053	1	R.TQAAFGLIK.E
1882	599.5156	1197.0167	1196.7241	0.2926	1	8	24	6	K.EQAILVAVAKR.T
2033	613.6811	1225.3477	1224.6060	0.7417	0	23	0.7	2	M.TGLDMETIFAK.I
4777	769.3351	1536.6557	1534.7814	1.8743	0	14	5.7	1	K.VLMVDIGGGFGQQSK.A 4744 4770 4784
8760	632.3142	1893.9207	1890.9986	2.9221	1	2	77	9	K.VLMVDIGGGFGQQSKALR.A
9813	675.0902	2022.2487	2020.9175	1.3312	0	54	0.00056	1	K.AFGSDLTMFEWMPQHPK.H 9804 9815
10446	697.8545	2090.5417	2090.1306	0.4111	2	6	32	6	K.VLMVDIGGGFGQQSKALRAK.F
11190	**731.6762**	**2192.0067**	**2190.1143**	**1.8924**	**1**	**2**	**83**	**6**	**K.FPAPDKVLMVDIGGGFGQQSK.A**
11668	754.8792	2261.6157	2263.0864	-1.4707	2	2	78	2	-.MTGLDMETIFAKIKDEYAR.T 11665
13685	**849.3169**	**2544.9287**	**2546.3315**	**-1.4028**	**2**	**7**	**23**	**1**	**K.FPAPDKVLMVDIGGGFGQQSKALR.A** 13683
14467	895.1245	2682.3517	2683.2687	-0.9170	1	6	27	1	R.AEWDDLMEQAGLEIIQSKVYDSK.E
15011	938.8859	2813.6357	2814.2604	-0.6247	1	2	70	2	K.DCVFQKAFGSDLTMFEWMPQHPK.H

Proteins matching the same set of peptides:

gi|220694813|gb|EED51157.1| **Mass:** 43304 **Score:** 92 **Queries matched:** 19

aflO/ omtB/ dmtA/ O-methyltransferase B [Aspergillus flavus NRRL3357]

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280. gi|220699574|gb|EED55913.1| **Mass:** 139048 **Score:** 91 **Queries matched:** 34 **emPAI:** 0.07

eukaryotic translation initiation factor subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2074	**617.2476**	**1232.4807**	**1231.6044**	**0.8763**	**0**	**39**	**0.022**	**2**	**R.SSLAEEALEAGR.I** 2067
2081	617.7111	1233.4077	1231.6772	1.7306	2	2	1e+02	10	R.AAKAVETASKEK.S
2266	629.7576	1257.5007	1256.7493	0.7515	0	54	0.00072	1	R.IVGQSIVPGIFK.Q 2264
2769	657.5946	1313.1747	1313.6808	-0.5061	2	4	63	10	K.ESRMHVIRMR.E
3188	679.8726	1357.7307	1356.7613	0.9695	1	2	98	8	K.VTPTTLRAEIEK.H
3566	698.7346	1395.4547	1394.7591	0.6956	2	5	45	8	R.YLGKLAQMSKEK.G 3564
3689	**707.5736**	**1413.1327**	**1410.7540**	**2.3787**	**2**	**(5)**	**48**	**2**	**R.YLGKLAQMSKEK.G** 3682 3688
3702	**708.2001**	**1414.3857**	**1414.7052**	**-0.3195**	**1**	**2**	**1.1e+02**	**7**	**K.VPATNGASQEEGKK.K**

5717	810.8731	1619.7317	1616.8297	2.9020	0	6	38	1	R.INDFVELSEVPDLK.A 5708
5743	541.5559	1621.6457	1619.8089	1.8368	2	3	69	5	R.HKMSQYVKAEVER.R
6634	563.3452	1687.0137	1687.9120	-0.8982	1	7	29	6	K.TALVYIKHAMDLWK.I
6755	566.7992	1697.3757	1697.9749	-0.5992	0	10	14	4	R.LDALTLLLVQEMIAR.A 6758 6766
6778	850.6916	1699.3687	1698.8618	0.5070	0	2	1e+02	4	K.DVVATHPDFVPVFEK.L
8803	633.9932	1898.9577	1897.8918	1.0659	1	8	24	5	K.QREPGEHQIDYGGVEGK.D 8802
8935	638.7509	1913.2307	1910.9697	2.2610	1	2	80	3	K.SQLPAKVPATNGASQEEGK.K 8928
9645	667.8239	2000.4497	1998.1295	2.3202	1	5	42	9	K.GARLDALTLLLVQEMIAR.A
9749	672.3232	2013.9477	2011.0334	2.9143	2	1	1.1e+02	7	R.HDLEGSVETKGLLGTDGRK.Y
11149	730.6855	2189.0347	2190.0950	-1.0603	1	1	1.1e+02	10	R.SSLAEEALEAGRISLMQNQK.Q
12263	783.1652	2346.4737	2344.3300	2.1437	2	7	23	3	K.GARLDALTLLLVQEMIARAFK.H 12260
13139	825.2739	2472.7997	2470.4047	2.3951	0	15	3.7	1	R.AASPEKPAVSIVPDDIVNIVPLVK.D
14905	927.7855	2780.3347	2777.3993	2.9355	0	4	44	2	K.IIYGPNHPDSITTMNNAAVMLQHLK.Q
15477	1005.9342	3014.7807	3014.6739	0.1069	2	0	95	10	R.LDALTLLLVQEMIARAFKHIANSYLR.N
16357	1151.8262	3452.4567	3449.6959	2.7608	1	1	75	7	R.SKVMPELIQDLHDGDVGFPMDGQSLSQLLHK.R

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281. gi|220696542|gb|EED52884.1| **Mass:** 30502 **Score:** 90 **Queries matched:** 13 **emPAI:** 0.23
NADH-ubiquinone dehydrogenase 24 kDa subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
323	843.6510	842.6437	842.5113	0.1324	0	11	14	9	R.LIDEILK.R
2510	642.6346	1283.2547	1282.7067	0.5480	0	56	0.00043	1	K.AAVMPLLDLGQR.Q 2504
2754	656.6116	1311.2087	1309.6813	1.5275	0	6	35	2	K.TVQIPAPGPMSGR.N
3362	458.6185	1372.8337	1374.6060	-1.7723	0	2	1.1e+02	8	K.NPVWDPETMMR.K
3820	477.3662	1429.0767	1426.7966	2.2801	1	17	3	1	K.KAAVMPLLDLGQR.Q
5187	526.5882	1576.7427	1577.8501	-1.1073	2	11	12	1	-.MASKFFPAVPRVGR.Q
6670	845.9886	1689.9627	1690.8097	-0.8470	0	3	71	1	R.QHGFTSISVMNEVAR.L
8343	618.0112	1851.0117	1851.0057	0.0061	2	(5)	43	7	K.FFPAVPRVGRQFFQR.A 8344 8352
11566	749.7335	2246.1787	2245.0876	1.0912	0	38	0.022	1	R.NKPTNNPSIPFTFNEQNQR.L
14248	885.4742	2653.4007	2655.2535	-1.8528	1	2	71	5	R.LLEMPPMRVYEVATFYTMYNR.E

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282. gi|220692216|gb|EED48563.1| **Mass:** 25174 **Score:** 90 **Queries matched:** 5 **emPAI:** 0.13
60S acidic ribosomal protein P1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
6079	824.7671	1647.5197	1645.8716	1.6482	0	59	0.0002	1	K.VQEVEPIWTSIFAK.A 6078
12370	790.1669	2367.4787	2364.9881	2.4906	0	2	86	3	R.FACMMGSMTGTGTDDAMIPAIR.L
14709	909.7349	2726.1827	2727.2983	-1.1155	0	0	1.1e+02	10	-.MSTAELACSYAALILADDGIEVTADK.L
15905	1070.7539	3209.2397	3210.4236	-1.1839	2	3	53	1	R.TKTSGGTGRFACMMGSMTGTGTDDAMIPAIR.L

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283. gi|220701302|gb|EED57640.1| **Mass:** 61175 **Score:** 89 **Queries matched:** 17 **emPAI:** 0.05

glutathione oxidoreductase Glr1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
431	**874.6110**	**873.6037**	**873.4920**	**0.1118**	**0**	**10**	**21**	**1**	**K.TLIVESGR.S**
2046	614.5906	1227.1667	1227.6935	-0.5268	2	9	20	4	K.EVQLVRDGKGK.D
2952	667.5176	1333.0207	1333.6119	-0.5912	0	9	21	6	R.SGGTCVNVGCVPK.K
4537	756.7096	1511.4047	1511.7112	-0.3065	1	(8)	22	3	K.FDPMIQKTMTER.Y 4540
4696	764.7591	1527.5037	1527.7061	-0.2024	1	10	17	4	K.FDPMIQKTMTER.Y 4704 4712
5693	**809.7286**	**1617.4427**	**1616.8410**	**0.6017**	**0**	**24**	**0.59**	**1**	**R.APEVEDLHLDVPGVK.L**
6606	**843.7651**	**1685.5157**	**1685.8638**	**-0.3480**	**2**	**1**	**1.1e+02**	**1**	**R.SYSRSFPVQAFKNR.L**
6624	**563.1709**	**1686.4907**	**1687.7803**	**-1.2896**	**0**	**2**	**89**	**5**	**K.FTAMYYDVVPPEEK.K**
11185	**1096.9526**	**2191.8907**	**2189.0933**	**2.7974**	**1**	**3**	**75**	**3**	**K.TLIVESGRSGGTCVNVGCVPK.K** 11173
11991	**769.8235**	**2306.4487**	**2308.2977**	**-1.8490**	**0**	**7**	**23**	**1**	**K.VVGLHILGLGVGEMLQGFGVAVK.M**
14071	872.6255	2614.8547	2615.3628	-0.5081	1	0	1e+02	6	K.LLKLISNDGSEMEVNEILWAIGR.A
15299	**976.8859**	**2927.6357**	**2926.4713**	**1.1645**	**0**	**58**	**0.00016**	**1**	**K.LSYDNIPTVVFSHPEVGTVGLTEPEAR.E** 15300

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284. gi|220699939|gb|EED56278.1| **Mass:** 14588 **Score:** 89 **Queries matched:** 5 **emPAI:** 0.23

cytochrome b5, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2505	642.4211	1282.8277	1282.7496	0.0781	0	57	0.00031	1	R.EILDGLLVGNLK.R 2513
4668	**509.0752**	**1524.2037**	**1522.7052**	**1.4985**	**0**	**12**	**9.2**	**1**	**K.EFTFQEVSGHNTK.K** 4658
10605	**705.2675**	**2112.7807**	**2111.9582**	**0.8225**	**1**	**2**	**74**	**9**	**-.MSENKEFTFQEVSGHNTK.K**

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285. gi|220697662|gb|EED54003.1| **Mass:** 45468 **Score:** 88 **Queries matched:** 9 **emPAI:** 0.07

branched-chain amino acid aminotransferase, cytosolic [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4741	**767.2471**	**1532.4797**	**1532.7253**	**-0.2455**	**1**	**6**	**43**	**2**	**K.IRMSEVAEAADEGR.L** 4749
6466	839.0966	1676.1787	1675.8828	0.2960	2	3	75	9	R.LFRPDKNMERLNK.S
6809	851.6676	1701.3207	1702.7587	-1.4380	0	0	1.5e+02	9	K.NWIEGIQYGDEDHK.W
7676	**892.3161**	**1782.6177**	**1782.9727**	**-0.3550**	**0**	**24**	**0.52**	**1**	**K.ELVTAPLDGTILEGVTR.D**
8058	909.7796	1817.5447	1816.9935	0.5513	2	4	62	10	K.TSSPKELTPAKDLVFGK.T
8256	615.1499	1842.4277	1842.0462	0.3815	2	6	39	8	R.LAGIDPSKLTVTKTSSPK.E
10270	**1033.8806**	**2065.7467**	**2065.1671**	**0.5797**	**0**	**88**	**2.1e-07**	**1**	**R.IALPTVDGEALTQLVGELVK.L** 10273

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286. gi|46370637|gb|AAS90104.1| **Mass:** 47130 **Score:** 87 **Queries matched:** 11 **emPAI:** 0.22

OmtA [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3764	**475.3542**	**1423.0407**	**1420.6405**	**2.4002**	**0**	**13**	**7.6**	**2**	**K.EWNSLNTMVDGR.L**
5076	783.5086	1565.0027	1562.7253	2.2774	0	7	28	1	K.GLFDYYSTVDEVR.G

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       7334   877.2966  1752.5787  1752.8101  -0.2314   1     1  1.2e+02   7    R.STKEWNSLNTMVDGR.L
       9615   999.1591  1996.3037  1995.9762   0.3275   1     2       85   6    R.ERTPSSTEHAQAWEIVR.T
      10289   690.5172  2068.5297  2066.9585   1.5712   0    41    0.011   1    R.FIFEEVAPDQYAHTDASK.M 10286
      10520  1051.0501  2100.0857  2100.0595   0.0262   0    36    0.032   1    R.ILLDEMIMPDLLAQDSQR.F
      10814   715.2352  2142.6837  2140.0657   2.6181   1     2       79   1    R.FMNQIDMTVVLTLNGKER.S
      11043   725.0985  2172.2737  2171.1051   1.1686   0    51  0.00098   1    K.GKPPSWNVPSPFSLAFDPTK.G 11051
      12437   792.6655  2374.9747  2375.1824  -0.2077   1     2       79   6    K.SRILLDEMIMPDLLAQDSQR.F
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287.  gi|46370555|gb|AAS90087.1|     Mass: 47027     Score: 87     Queries matched: 11    emPAI: 0.23
      OmtA [Aspergillus flavus]
     Query   Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect Rank   Peptide
       3889   719.1501  1436.2857  1435.6766   0.6092   0     3       78   6    K.EWNSLITMVDGR.L
       5076   783.5086  1565.0027  1562.7253   2.2774   0     7       28   1    K.GLFDYYSTVDEVR.G
       9615   999.1591  1996.3037  1995.9762   0.3275   1     2       85   6    R.ERTPSSTEHAQAWEIVR.T
      10289   690.5172  2068.5297  2066.9585   1.5712   0    41    0.011   1    R.FIFEEVAPDQYAHTDASK.M 10286
      10520  1051.0501  2100.0857  2100.0595   0.0262   0    36    0.032   1    R.ILLDEMIMPDLLAQDSQR.F
      10814   715.2352  2142.6837  2140.0657   2.6181   1     2       79   1    R.FMNQIDMTVVLTLNGKER.S
      11043   725.0985  2172.2737  2171.1051   1.1686   0    51  0.00098   1    K.GKPPSWNVPSPFSLAFDPTK.G 11051
      12437   792.6655  2374.9747  2375.1824  -0.2077   1     2       79   6    K.SRILLDEMIMPDLLAQDSQR.F
      12881   813.2212  2436.6417  2436.2505   0.3912   2     2       83   9    R.FMNQIDMTVVLTLNGKERSPK.E
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288.  gi|413844|gb|AAA32698.1|     Mass: 47089     Score: 87     Queries matched: 10    emPAI: 0.23
      O-methyltransferase [Aspergillus flavus]
     Query   Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect Rank   Peptide
       5076   783.5086  1565.0027  1562.7253   2.2774   0     7       28   1    K.GLFDYYSTVDEVR.G
       7823   599.3252  1794.9537  1792.8778   2.0760   1     5       46   3    R.STKEWNSLITMVDNR.L
       7985   906.8531  1811.6917  1808.8727   2.8190   1   (0)  1.3e+02   7    R.STKEWNSLITMVDNR.L
      10289   690.5172  2068.5297  2066.9585   1.5712   0    41    0.011   1    R.FIFEEVAPDQYAHTDASK.M 10286
      10520  1051.0501  2100.0857  2100.0595   0.0262   0    36    0.032   1    R.ILLDEMIMPDLLAQDSQR.F
      10814   715.2352  2142.6837  2140.0657   2.6181   1     2       79   1    R.FMNQIDMTVVLTLNGKER.S
      11043   725.0985  2172.2737  2171.1051   1.1686   0    51  0.00098   1    K.GKPPSWNVPSPFSLAFDPTK.G 11051
      12437   792.6655  2374.9747  2375.1824  -0.2077   1     2       79   6    K.SRILLDEMIMPDLLAQDSQR.F

      Proteins matching the same set of peptides:
      gi|2498701|sp|P55790.1|OMTA_ASPFL     Mass: 47089     Score: 87     Queries matched: 10
      RecName: Full=Sterigmatocystin 8-O-methyltransferase; Flags: Precursor
      gi|220694812|gb|EED51156.1|     Mass: 47089     Score: 87     Queries matched: 10
      aflP/ omtA/ omt-1/ O-methyltransferase A [Aspergillus flavus NRRL3357]
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289. gi|220700882|gb|EED57220.1| **Mass:** 119864 **Score:** 86 **Queries matched:** 26 **emPAI:** 0.06
valyl-tRNA synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
186	**773.9730**	**772.9657**	**773.4647**	**-0.4989**	**2**	**14**	**8.9**	**2**	**K.KEKIEK.E**
277	822.9160	821.9087	821.4283	0.4804	0	1	1.4e+02	6	K.ENGLYVK.W
531	455.4256	908.8367	909.4378	-0.6011	0	12	10	8	K.NGGIFAGMK.R 529
578	**459.6906**	**917.3667**	**916.5131**	**0.8537**	**0**	**9**	**29**	**3**	**K.LTGQVPFR.E**
882	500.7736	999.5327	998.4781	1.0546	0	13	8.3	2	R.NQNADAAAPK.V 883
918	**505.0436**	**1008.0727**	**1009.4618**	**-1.3890**	**0**	**4**	**58**	**1**	**R.VGGSFDWSR.E**
1011	517.7266	1033.4387	1033.5477	-0.1090	2	11	15	9	R.EMEEKKLK.D
1163	**532.6611**	**1063.3077**	**1062.5709**	**0.7368**	**2**	**8**	**30**	**8**	**R.EFEKLRLE.-**
1370	**551.7526**	**1101.4907**	**1100.5462**	**0.9446**	**0**	**23**	**0.93**	**2**	**K.EINEALEQR.E**
1457	**559.6151**	**1117.2157**	**1115.5876**	**1.6281**	**1**	**0**	**1.8e+02**	**7**	**K.FAKHPFVDR.L**
2406	1273.6240	1272.6167	1271.6332	0.9835	1	0	1.7e+02	10	R.FCNKIYQATK.Y
2546	**644.4871**	**1286.9597**	**1284.6925**	**2.2672**	**0**	**21**	**1.4**	**1**	**K.GDIVIKPESAEK.S**
3008	670.4551	1338.8957	1338.6456	0.2501	0	29	0.17	1	R.DLFKPEFGSDGK.V
5731	541.2385	1620.6937	1619.8281	0.8657	2	3	71	8	K.NALRRVGGSFDWSR.E
7788	896.6576	1791.3007	1789.9210	1.3797	1	0	1.3e+02	6	K.TKGDIIIQTYDATSHK.T
8807	**634.1969**	**1899.5687**	**1897.0316**	**2.5372**	**2**	**0**	**1.3e+02**	**1**	**R.LPRRPNDNTISIMKAR.Y**
9278	978.6446	1955.2747	1953.9571	1.3176	0	1	1.1e+02	7	K.AEFNDVEAETAYELILK.T
9741	**672.0649**	**2013.1727**	**2015.0588**	**-1.8861**	**2**	**4**	**56**	**4**	**R.ESLSERWILHKFNSAAK.E**
10507	**1050.3876**	**2098.7607**	**2098.0041**	**0.7566**	**0**	**82**	**9.6e-07**	**1**	**R.EAFTMDPNLSAAVTETFVR.L**
11351	738.6195	2212.8367	2211.1106	1.7261	2	4	56	3	R.RPNDNTISIMKARYPEYK.A 11329
13637	**846.2689**	**2535.7847**	**2534.3050**	**1.4797**	**0**	**20**	**1.3**	**1**	**K.SLGNVIDPIDVMEGIQLQTLHDK.L** 13641
15253	967.4352	2899.2837	2896.4674	2.8163	1	3	57	9	K.MSKSLGNVIDPIDVMEGIQLQTLHDK.L

290. gi|220694687|gb|EED51031.1| **Mass:** 60098 **Score:** 83 **Queries matched:** 28 **emPAI:** 0.17
GMP synthase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
441	878.6630	877.6557	878.4168	-0.7610	0	10	19	7	R.MTEGQGLK.L 439
968	511.5406	1021.0667	1018.5229	2.5438	1	8	27	4	K.RMTEGQGLK.L 971
1148	**530.6766**	**1059.3387**	**1058.5621**	**0.7766**	**0**	**21**	**1.7**	**3**	**K.THHNVGGLPK.R** 1145
1478	**374.5692**	**1120.6857**	**1119.6288**	**1.0570**	**1**	**8**	**27**	**8**	**R.EYGLAQLKAK.K**
1992	609.5841	1217.1537	1217.6227	-0.4689	0	18	3.2	2	K.ADHIFISMIR.E
2163	**623.5971**	**1245.1797**	**1244.6513**	**0.5284**	**0**	**53**	**0.00092**	**1**	**K.IGQAFAALDPSR.A** 2164
2801	659.2111	1316.4077	1315.6377	0.7701	0	4	63	8	R.QLGIAHEMVMR.H
5191	789.4496	1576.8847	1574.8199	2.0648	1	1	1.1e+02	4	R.VSTRIVNEVSGVCR.V
9460	**660.6265**	**1978.8577**	**1977.9982**	**0.8595**	**1**	**2**	**84**	**8**	**K.ADHIFISMIREAGLYDK.I**
9785	**1010.3276**	**2018.6407**	**2018.0255**	**0.6152**	**1**	**11**	**11**	**1**	**K.IGQAFAALDPSRAVGVMGDK.R** 9775
11324	**738.0472**	**2211.1197**	**2210.2271**	**0.8926**	**1**	**18**	**2.2**	**1**	**R.KLVGPTGQVLGAVSGGVDSTVAAK.L** 11327 11337 11338 1134

11525	747.2189	2238.6347	2240.1154	-1.4807	2	1	1.2e+02	5	K.DEVRDLGRQLGIAHEMVMR.H
13944	**864.5205**	**2590.5397**	**2588.2257**	**2.3140**	**0**	**(33)**	**0.065**	**1**	**R.AVETTDFMTAIAYPFEHEFLTR.V** 13935
13996	**869.6775**	**2606.0107**	**2604.2206**	**1.7901**	**0**	**41**	**0.0084**	**1**	**R.AVETTDFMTAIAYPFEHEFLTR.V** 13988

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291. gi|220692642|gb|EED48988.1| **Mass:** 79847 **Score:** 83 **Queries matched:** 16 **emPAI:** 0.13

mycelial catalase Cat1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
345	**848.5660**	**847.5587**	**845.4355**	**2.1232**	**0**	**4**	**83**	**7**	**K.NAGIQTSR.D**
598	463.9856	925.9567	925.5022	0.4546	1	6	37	4	R.TFKFLDR.F
2557	645.2321	1288.4497	1286.7122	1.7375	0	3	92	5	K.IVPEEYVPITK.L
2722	654.6611	1307.3077	1306.6921	0.6156	0	69	2e-05	1	R.GPTLLEDFIFR.Q
3757	474.7729	1421.2967	1421.7878	-0.4911	2	9	22	7	K.TTDVGTFGQKLKK.L
4197	**491.3629**	**1471.0667**	**1469.8507**	**1.2160**	**2**	**9**	**21**	**5**	**K.LVKFHWKSLQGK.A**
4203	**736.9381**	**1471.8617**	**1472.8351**	**-0.9734**	**0**	**3**	**81**	**5**	**R.FGKPVGAVGSAATALK.N**
5289	**529.3735**	**1585.0987**	**1584.9127**	**0.1860**	**1**	**5**	**50**	**1**	**K.IVPEEYVPITKLGK.M**
5520	**803.2166**	**1604.4187**	**1603.7631**	**0.6556**	**0**	**25**	**0.51**	**1**	**R.AVSPSFEDVWSQPR.L** 5545
5993	**822.5946**	**1643.1747**	**1640.8536**	**2.3211**	**1**	**1**	**1.1e+02**	**9**	**R.SLRHVDGFGIHTFR.F**
9319	**654.6609**	**1960.9607**	**1960.0894**	**0.8713**	**2**	**31**	**0.1**	**1**	**R.GPTLLEDFIFRQKIQR.F**
10366	694.1942	2079.5607	2078.0102	1.5505	1	1	1.1e+02	7	K.SLQGKASMVWEEAQQVSGK.N
12347	**787.6492**	**2359.9257**	**2361.1423**	**-1.2166**	**0**	**0**	**1.2e+02**	**7**	**R.DGAGQMFIPLNPNAYSPNTLNK.G**
15004	**937.8055**	**2810.3947**	**2807.4422**	**2.9526**	**2**	**3**	**56**	**1**	**M.RALSLASVIGIASAACPYMTGELERR.D**
16278	**1136.7689**	**3407.2847**	**3404.5799**	**2.7048**	**1**	**2**	**58**	**1**	**R.YPEWELGVQIMDEEDQLKFGFDLFDPTK.I**

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292. gi|220694061|gb|EED50405.1| **Mass:** 72458 **Score:** 82 **Queries matched:** 10 **emPAI:** 0.09

oxidoreductase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1347	**549.1856**	**1096.3567**	**1097.5287**	**-1.1720**	**1**	**8**	**25**	**1**	**K.LRDAMYSAR.F**
1715	**388.3559**	**1162.0457**	**1160.5309**	**1.5148**	**0**	**15**	**5**	**2**	**R.ESLGGSGQPDSK.R**
2810	659.6476	1317.2807	1316.6320	0.6487	1	6	42	5	R.ESLGGSGQPDSKR.R
4250	738.6541	1475.2937	1472.7332	2.5606	2	0	1.5e+02	7	R.ESLGGSGQPDSKRR.A
5233	**527.8055**	**1580.3947**	**1579.9198**	**0.4749**	**0**	**9**	**19**	**3**	**K.HGVIHPLIEPSLLR.A**
5240	791.5671	1581.1197	1579.7631	1.3567	1	43	0.0073	1	R.FRDGLFEPSEQQK.Y
8250	**614.8005**	**1841.3797**	**1842.9588**	**-1.5791**	**2**	**2**	**96**	**3**	**R.FREYLSSVTGSGKLSGR.K**
8929	**638.3585**	**1912.0537**	**1912.8551**	**-0.8014**	**1**	**3**	**63**	**8**	**R.RGQDYTLASGYDGEEPR.L**
11423	1112.8391	2223.6637	2224.0582	-0.3945	2	0	1.2e+02	9	R.DAMYSARFREYLSSVTGSGK.L
12800	**1214.2596**	**2426.5047**	**2425.8524**	**0.6523**	**0**	**67**	**2.3e-05**	**1**	**K.EADEEEEEEDDEEGENGESEK.K**

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293. gi|220689997|gb|EED46347.1| **Mass:** 94438 **Score:** 82 **Queries matched:** 37 **emPAI:** 0.19

plasma membrane H+-ATPase Pma1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
900	**501.8581**	**1001.7017**	**1000.5553**	**1.1464**	**0**	**40**	**0.021**	**1**	**K.QAADVVASLK.G**
1379	1104.6170	1103.6097	1102.6056	1.0041	0	(14)	7.8	2	K.MLTGDALAIAK.E
1467	**560.4941**	**1118.9737**	**1118.6005**	**0.3732**	**0**	**40**	**0.016**	**1**	**K.MLTGDALAIAK.E**
1699	**580.6041**	**1159.1937**	**1157.5676**	**1.6261**	**0**	**47**	**0.0035**	**1**	**R.DGQEQEILAR.E** 1690
1840	**595.1676**	**1188.3207**	**1186.6016**	**1.7191**	**0**	**6**	**46**	**4**	**K.IENMLSHLSK.L**
2603	**647.7346**	**1293.4547**	**1292.6547**	**0.8000**	**0**	**(2)**	**97**	**5**	**K.YQVVEMLQQR.G**
2632	**648.8791**	**1295.7437**	**1296.6417**	**-0.8980**	**1**	**6**	**39**	**4**	**K.ETCKMLALSTK.V**
2739	655.5511	1309.0877	1308.6496	0.4381	0	11	12	2	K.YQVVEMLQQR.G 2738
2957	667.5881	1333.1617	1332.7877	0.3740	2	4	68	7	K.RGKAYGIVVATAK.Q
3067	**673.7396**	**1345.4647**	**1345.6303**	**-0.1655**	**0**	**30**	**0.18**	**1**	**K.ADGFAEVFPEHK.Y** 3076
3375	**688.2311**	**1374.4477**	**1371.7510**	**2.6967**	**1**	**3**	**94**	**1**	**R.EILARNWITEK.Y**
5291	793.6671	1585.3197	1585.8134	-0.4936	1	8	26	4	K.ADTKIENMLSHLSK.L 5290
5445	**534.2315**	**1599.6727**	**1598.8892**	**0.7835**	**2**	**6**	**39**	**3**	**K.AREILARNWITEK.Y**
5456	**801.1911**	**1600.3677**	**1601.8083**	**-1.4405**	**1**	**(2)**	**87**	**3**	**K.ADTKIENMLSHLSK.L** 5503
5593	806.2066	1610.3987	1609.9403	0.4584	1	27	0.29	2	K.NLDPIDKVTILTLR.R 5580 5597
5917	546.4632	1636.3677	1636.8164	-0.4487	1	4	56	6	K.MLTGDALAIAKETCK.M 5922
7918	903.3506	1804.6867	1804.7219	-0.0352	1	3	77	2	K.YMADTCYYTTGCKR.G
7922	903.4666	1804.9187	1803.9288	0.9899	0	28	0.22	1	K.LTAIESLAGVDILCSDK.T 7914 7919 7921 7929
8037	909.2841	1816.5537	1816.9353	-0.3815	2	1	1e+02	4	R.SKADTKIENMLSHLSK.L
12599	**800.8872**	**2399.6397**	**2397.2317**	**2.4080**	**2**	**11**	**8.9**	**2**	**K.MLTGDALAIAKETCKMLALSTK.V** 12580
13108	**824.1965**	**2469.5677**	**2470.2638**	**-0.6961**	**1**	**0**	**1.2e+02**	**8**	**K.IENMLSHLSKLAIEHEVDAHGK.S**
14390	1336.4381	2670.8617	2671.2291	-0.3674	2	1	91	8	R.YVCAKGAPKAILNMSECSEEEAAK.F 14386
15867	**1064.3359**	**3189.9857**	**3187.6603**	**2.3255**	**0**	**1**	**72**	**3**	**K.AVMDNIGTSLLVLVMFWILAAWIGGFYR.H**

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294. gi|220694335|gb|EED50679.1| **Mass:** 62329 **Score:** 82 **Queries matched:** 5 **emPAI:** 0.05

MFS monosaccharide transporter, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
786	**490.2151**	**978.4157**	**977.4786**	**0.9371**	**0**	**16**	**4**	**4**	**-.MGVSNLMAR.L**
857	497.6781	993.3417	993.4736	-0.1318	0	(11)	14	4	-.MGVSNLMAR.L
4549	**505.4149**	**1513.2227**	**1511.6782**	**1.5445**	**2**	**6**	**41**	**5**	**R.CIAQEMKDMKDK.L**
4619	**761.2071**	**1520.3997**	**1519.7783**	**0.6214**	**0**	**82**	**9.7e-07**	**1**	**K.AAGQAGIFEVFTGPR.M**
14892	**926.8299**	**2777.4677**	**2776.5997**	**0.8680**	**1**	**0**	**99**	**7**	**R.NGLIVGLLSIGTMIGALVAAPIADRIGR.K**

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295. gi|220689217|gb|EED45568.1| **Mass:** 34079 **Score:** 82 **Queries matched:** 5 **emPAI:** 0.10

opsin, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3289	**684.3381**	**1366.6617**	**1366.7861**	**-0.1243**	**0**	**2**	**1e+02**	**2**	**R.FFGTVSGVSLLIK.A**

3792	713.8201	1425.6257	1424.8755	0.7502	0	62	9.6e-05	1	K.ALFPVAIAAGALALK.I 3785 3797
13036	822.1625	2463.4657	2463.4327	0.0330	0	0	1.2e+02	3	R.TLWVVVVLMAISAIVFYILASR.A

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296. gi|220693342|gb|EED49687.1| **Mass:** 62379 **Score:** 82 **Queries matched:** 14 **emPAI:** 0.05

phosphoglucomutase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3504	695.4651	1388.9157	1390.7205	-1.8047	0	3	84	1	R.SAPSNLPPVAPEGR.A
4560	506.0672	1515.1797	1515.7504	-0.5707	0	14	6.4	4	K.GSIMVTGSHIPFDR.N
6159	827.7316	1653.4487	1653.8434	-0.3947	1	4	53	7	K.KDEQPINNNVQVTR.E 6189
6572	842.2546	1682.4947	1680.8795	1.6153	0	3	79	3	R.ADAIASQGVAEPNGLLR.S
6796	851.3116	1700.6087	1699.9079	0.7008	0	67	3e-05	1	R.DAVLPLLCALFAAGNR.G 6813
9002	960.2301	1918.4457	1916.0190	2.4268	1	1	1e+02	1	K.TKIGSPYVIAGMQHSLSK.G
10319	692.1415	2073.4027	2072.0949	1.3078	2	4	57	2	K.IGSPYVIAGMQHSLSKGRR.R
12370	790.1669	2367.4787	2368.1369	-0.6581	0	3	60	1	R.EELLSQPYAESLFNQQGMLR.S
13340	834.2442	2499.7107	2500.2672	-0.5564	0	5	41	2	K.DEGMHPINLGAIPTPALTYYALK.H 13344
13550	842.3065	2523.8977	2521.2747	2.6230	2	5	36	2	K.GSIMVTGSHIPFDRNGYKLNTSK.G
15038	943.7929	2828.3567	2827.4464	0.9103	1	0	1e+02	5	R.IYAVADTQERADAIASQGVAEPNGLLR.S

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297. gi|220699827|gb|EED56166.1| **Mass:** 53418 **Score:** 81 **Queries matched:** 17 **emPAI:** 0.13

catalase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
974	513.0636	1024.1127	1023.5237	0.5891	1	13	8.1	2	K.LTKEDGSFK.Y 975
1040	520.5406	1039.0667	1040.4749	-1.4082	0	9	20	3	R.MFAYPDAAR.Y
1106	527.0481	1052.0817	1052.5978	-0.5161	0	7	34	5	R.TIANLSGHIK.N
2305	631.6761	1261.3377	1260.6350	0.7027	0	44	0.0075	1	K.IAGEDPDYLIR.D 2302
3417	460.1969	1377.5687	1375.6343	1.9344	1	10	15	4	R.MFAYPDAARYR.L
3512	695.7081	1389.4017	1388.6547	0.7470	1	6	39	4	K.YRWNIFDMTK.V
3590	700.3761	1398.7377	1398.7765	-0.0388	2	(12)	9.1	3	R.QIGKLTMNRNPK.N 3602 3614
4003	724.6456	1447.2767	1446.6951	0.5817	0	51	0.0014	1	R.VSTVGPEAGSADTTR.D
7091	864.2296	1726.4447	1725.9315	0.5133	2	6	32	3	K.VWSHKDYPLRQIGK.L
11060	725.8275	2174.4607	2172.9600	1.5007	0	0	1.2e+02	9	R.FDDNYGGDPNYVGSSLQPTK.F
11530	747.5405	2239.5997	2240.0671	-0.4673	1	5	38	5	K.IAGEDPDYLIRDMFEAIEK.G
11917	1149.8231	2297.6317	2295.0518	2.5799	0	4	53	1	K.GDYPVWNVYVQVMDPADAEK.Y
15965	1082.3855	3244.1347	3243.5315	0.6032	2	5	29	2	K.NMTAEESLKIAGEDPDYLIRDMFEAIEK.G

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298. gi|220690790|gb|EED47139.1| **Mass:** 42488 **Score:** 81 **Queries matched:** 12 **emPAI:** 0.08

glutamine synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
366	856.9270	855.9197	854.5086	1.4111	1	4	60	5	R.GGSIRIPR.Q

632	470.2471	938.4797	938.4280	0.0517	0	16	3.5	2	K.YMNLDQR.G
897	501.7006	1001.3867	1001.4930	-0.1063	0	17	3.4	3	R.DIVEAHYR.A 895
4960	**776.9306**	**1551.8467**	**1553.7243**	**-1.8776**	**0**	**0**	**1.3e+02**	**10**	**M.SESTTISNTENLMK.Y**
5135	**786.3451**	**1570.6757**	**1569.7192**	**0.9565**	**0**	**(0)**	**1.5e+02**	**4**	**M.SESTTISNTENLMK.Y**
7550	**887.1366**	**1772.2587**	**1771.7988**	**0.4599**	**0**	**55**	**0.00042**	**1**	**K.GGFPGAQGPYYCGVGTGK.V** 7574
8383	619.0132	1854.0177	1854.8973	-0.8796	0	4	54	8	K.GEWNGAGLHSNVSTVATR.A
10984	**722.7529**	**2165.2367**	**2166.0640**	**-0.8273**	**2**	**4**	**47**	**1**	**R.GRVQAEYVWIDSVGGCRSK.T**
11542	**748.2292**	**2241.6657**	**2241.0563**	**0.6095**	**1**	**3**	**61**	**9**	**K.FEARHVEHIAVYGEGNEER.L**
13288	831.7119	2492.1137	2490.1366	1.9771	1	1	88	8	M.SESTTISNTENLMKYMNLDQR.G

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299. gi|220698453|gb|EED54793.1| **Mass:** 63341 **Score:** 80 **Queries matched:** 11 **emPAI:** 0.05
nucleolar protein nop5 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
830	494.4811	986.9477	986.5648	0.3829	0	7	36	10	R.LASLLDEVK.D
2760	656.9186	1311.8227	1311.7333	0.0895	0	9	20	1	K.LAGMEGKPLKPR.G
2862	**662.6866**	**1323.3587**	**1323.7510**	**-0.3923**	**0**	**4**	**59**	**3**	**R.LIAHAGSLTNLSK.S**
4342	744.2966	1486.5787	1486.8242	-0.2455	2	8	23	2	R.LASLLDEVKDEKK.V 4356
5174	525.5425	1573.6057	1574.8528	-1.2471	2	5	45	6	K.AALGTEARFNLERK.L
7965	604.4855	1810.4347	1807.8588	2.5759	2	8	24	4	R.KYNADADAVDEPSSAKK.Q
8916	**956.1331**	**1910.2517**	**1909.0455**	**1.2062**	**0**	**80**	**1.3e-06**	**1**	**R.MNAIAPNLTALVGELVGAR.L** 8904
10415	696.2425	2085.7057	2086.1384	-0.4327	1	9	17	3	-.MTLFILTETSAGYALLKAK.D
11291	1104.2441	2206.4737	2205.0913	1.3824	2	1	1.2e+02	7	R.KLERGEIEFDAEGNPSSISK.K

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300. gi|220701606|gb|EED57944.1| **Mass:** 37465 **Score:** 80 **Queries matched:** 6 **emPAI:** 0.09
eukaryotic translation initiation factor 3 subunit 2i, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4022	**484.0702**	**1449.1887**	**1447.6667**	**1.5221**	**0**	**7**	**30**	**7**	**K.IVCAWWSANGER.L**
6259	**831.7701**	**1661.5257**	**1660.8672**	**0.6585**	**0**	**80**	**1.5e-06**	**1**	**K.TYVADTPLNSAAITPK.K**
8979	**639.6739**	**1915.9997**	**1917.0320**	**-1.0322**	**2**	**1**	**1e+02**	**10**	**K.RVEFTPDGSRLLAVTEK.R**
11725	**759.2239**	**2274.6497**	**2274.0204**	**0.6293**	**0**	**2**	**74**	**7**	**R.VHHFDKPYFDFMYEVER.E**
15408	**993.2565**	**2976.7477**	**2975.3897**	**1.3580**	**0**	**8**	**16**	**1**	**K.TGEQLENVQAHEFDNLISDIQFSADR.T** 15410

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301. gi|220696664|gb|EED53006.1| **Mass:** 58654 **Score:** 80 **Queries matched:** 10 **emPAI:** 0.06
cytosolic hydroxymethyltransferase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
628	937.8920	936.8847	937.4505	-0.5658	0	0	1.4e+02	10	K.QAQSTEFK.T
4654	762.6321	1523.2497	1522.8191	0.4307	2	5	49	7	K.SLRGPRGAMIFYR.K
6549	**841.7656**	**1681.5167**	**1680.8094**	**0.7073**	**0**	**8**	**24**	**1**	**R.LDESTGLIDYDALEK.Q**
8068	**607.1489**	**1818.4247**	**1819.8781**	**-1.4534**	**0**	**3**	**80**	**6**	**R.QEVEDWVGTFSLPWK.D**

8901	637.2899	1908.8477	1908.0469	0.8009	1	1	1.1e+02	9	K.LIIAGTSAYSRLIDYPR.M
11737	759.3292	2274.9657	2274.1216	0.8442	0	4	49	2	R.LMGLDLPHGGHLSHGYQTPTK.K
12628	**802.1775**	**2403.5107**	**2402.2165**	**1.2942**	**1**	**2**	**71**	**3**	**R.LMGLDLPHGGHLSHGYQTPTKK.I** 12608
16393	**1159.3032**	**3474.8877**	**3474.7531**	**0.1346**	**0**	**71**	**6.1e-06**	**1**	**R.LNPEEWGVNVQPLSGSPANLYAISALLNTHDR.L** 16392

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302. gi\|220691646\|gb\|EED47994.1\| **Mass:** 113354 **Score:** 80 **Queries matched:** 27 **emPAI:** 0.12

plasma membrane H(+)ATPase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
171	**763.4390**	**762.4317**	**762.2919**	**0.1398**	**0**	**9**	**24**	**4**	**K.EEEEVE.-** 170
900	501.8581	1001.7017	1000.5553	1.1464	0	40	0.021	1	K.QAADVVASLK.G
1379	1104.6170	1103.6097	1102.6056	1.0041	0	(14)	7.8	2	K.MLTGDALAIAK.E
1467	560.4941	1118.9737	1118.6005	0.3732	0	40	0.016	1	K.MLTGDALAIAK.E
1661	575.6806	1149.3467	1148.5978	0.7489	1	17	3.3	2	K.FKWLDDLGR.E 1660
1699	580.6041	1159.1937	1157.5676	1.6261	0	47	0.0035	1	R.DGQEQEILAR.E 1690
1916	603.2901	1204.5657	1203.6282	0.9376	0	2	1.1e+02	4	R.IVTIASCDGIR.Y
2628	648.7461	1295.4777	1294.6340	0.8438	0	6	36	5	K.YQVVQMLQDR.G
3067	673.7396	1345.4647	1345.6303	-0.1655	0	30	0.18	1	K.ADGFAEVFPEHK.Y 3076
3650	704.0981	1406.1817	1405.7354	0.4463	2	7	34	2	K.FKWLDDLGREK.R
4335	**496.2102**	**1485.6087**	**1485.7973**	**-0.1886**	**1**	**8**	**23**	**3**	**K.GAPKAVLQLTNCSK.Q**
5917	546.4632	1636.3677	1636.8164	-0.4487	1	4	56	6	K.MLTGDALAIAKETCK.M 5922
6996	**859.0436**	**1716.0727**	**1713.9010**	**2.1718**	**1**	**2**	**83**	**3**	**R.TTVVRDGQEQEILAR.E** 6989
9301	**653.9272**	**1958.7597**	**1956.9649**	**1.7949**	**2**	**2**	**94**	**3**	**K.ETCKMLALGTKVYNSDK.L**
9622	666.6602	1996.9587	1994.9882	1.9705	1	2	86	5	R.VAQAPGSQGRLSTSEGHASR.R
9665	668.6535	2002.9387	2000.0704	2.8683	2	4	49	2	K.AQEFAHRGFRSLGVAVQK.E
9756	672.6525	2014.9357	2013.0136	1.9222	2	2	88	3	K.RIVTIASCDGIRYTCTK.G
12359	**789.4205**	**2365.2397**	**2363.2898**	**1.9499**	**0**	**1**	**96**	**6**	**K.IWFISCLLGLLLAMGTWVVR.G**
15309	**1467.5201**	**2933.0257**	**2931.4511**	**1.5747**	**1**	**0**	**1e+02**	**1**	**R.SLGVAVQKEGEEWTLLGMLPMFDPPR.E**
15909	1071.2992	3210.8757	3208.5205	2.3552	2	0	87	8	M.AEQGGASNDVERVAQAPGSQGRLSTSEGHASR.R
16016	**1092.5282**	**3274.5627**	**3271.7048**	**2.8579**	**1**	**1**	**76**	**2**	**R.DGQEQEILARELVPGDVIIIGDGQVVPADAR.I**

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303. gi\|220691457\|gb\|EED47805.1\| **Mass:** 53959 **Score:** 79 **Queries matched:** 12 **emPAI:** 0.06

fatty acid desaturase family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1607	1139.7120	1138.7047	1137.4981	1.2067	0	1	1.3e+02	10	K.MPMLMDSTGR.R
2873	663.8056	1325.5967	1325.5890	0.0077	1	19	2.1	2	K.MPMLMDSTGRR.I
2876	664.1221	1326.2297	1325.5890	0.6407	1	(12)	10	4	K.MPMLMDSTGRR.I 2883
4337	**496.2862**	**1485.8367**	**1483.7783**	**2.0584**	**1**	**8**	**25**	**5**	**K.EHPGGKAFISSAVGK.D**
7710	**893.1951**	**1784.3757**	**1783.0244**	**1.3513**	**0**	**70**	**1.5e-05**	**1**	**R.ALVTIGGVIHDITSFIK.E** 7700
10702	**1064.6656**	**2127.3167**	**2126.1960**	**1.1207**	**1**	**6**	**35**	**1**	**K.ATLPLRIYLAAAGAGAGQGSIR.W**

11118	729.1789	2184.5147	2185.1348	-0.6200	2	1	96	10	R.IVRAGDQVTRMVQPVPMVSA.-
12883	813.2992	2436.8757	2435.2002	1.6755	1	1	89	4	M.ALDAKSPTVATLNDGTTDYVPMR.K
13896	**861.4855**	**2581.4347**	**2582.2356**	**-0.8009**	**1**	**3**	**57**	**3**	**-.MALDAKSPTVATLNDGTTDYVPMR.K**
14621	**904.5289**	**2710.5647**	**2710.3306**	**0.2341**	**2**	**2**	**65**	**2**	**-.MALDAKSPTVATLNDGTTDYVPMRK.K**

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304. gi|220701658|gb|EED57996.1| **Mass:** 49696 **Score:** 79 **Queries matched:** 18 **emPAI:** 0.14
eukaryotic translation initiation factor 4, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
26	650.4130	649.4057	648.3456	1.0601	1	5	60	8	R.GGRFGR.K
1276	**543.0841**	**1084.1537**	**1083.6652**	**0.4885**	**0**	**67**	**3.2e-05**	**1**	**R.VLIATDLLAR.G**
1691	579.9471	1157.8797	1157.6656	0.2142	1	26	0.47	3	K.KQELTLEGIK.Q 1689
3408	**689.4101**	**1376.8057**	**1375.7096**	**1.0961**	**0**	**3**	**84**	**5**	**K.GVAINFVTADDVR.M**
3981	723.6671	1445.3197	1444.8038	0.5159	2	11	13	1	R.KVDWLTDKLTAR.D
5022	**520.5405**	**1558.5997**	**1557.8838**	**0.7159**	**1**	**11**	**13**	**1**	**R.SGSSRVLIATDLLAR.G**
8000	**907.3266**	**1812.6387**	**1809.8866**	**2.7521**	**1**	**0**	**1.4e+02**	**1**	**K.GVAINFVTADDVRMMR.E**
9541	**996.0236**	**1990.0327**	**1990.0959**	**-0.0632**	**2**	**2**	**89**	**4**	**K.EFRSGSSRVLIATDLLAR.G**
10618	**1058.3581**	**2114.7017**	**2113.1168**	**1.5850**	**0**	**11**	**11**	**1**	**R.GIDVQQVSLVINYDLPANR.E**
11894	**1148.4486**	**2294.8827**	**2295.0372**	**-0.1545**	**1**	**(1)**	**1.1e+02**	**1**	**K.LTARDFTVSAMHGDMEQSQR.D**
12032	**771.3519**	**2311.0337**	**2311.0321**	**0.0016**	**1**	**1**	**1e+02**	**8**	**K.LTARDFTVSAMHGDMEQSQR.D**
12180	**778.0212**	**2331.0417**	**2332.1958**	**-1.1541**	**1**	**2**	**85**	**2**	**K.ALGEGPEVVVGTPGRVHDMIQR.R**
12529	797.1885	2388.5437	2389.2437	-0.7000	2	2	85	9	K.HPHLYTSRCGLRSQLPIAVQG.-
13482	**840.6809**	**2519.0207**	**2516.2944**	**2.7263**	**2**	**5**	**40**	**5**	**R.VLKTDHLKQFILDEADEMLSR.G**
14411	**1338.3441**	**2674.6737**	**2672.3367**	**2.3370**	**0**	**46**	**0.0031**	**1**	**K.LDTLSDLYETVTITQAVIFCNTR.R**
15850	**1060.3039**	**3177.8897**	**3178.7714**	**-0.8817**	**1**	**1**	**70**	**10**	**R.VLIATDLLARGIDVQQVSLVINYDLPANR.E** 15854

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305. gi|220699434|gb|EED55773.1| **Mass:** 79179 **Score:** 77 **Queries matched:** 22 **emPAI:** 0.04
trehalose synthase (Ccg-9), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
259	408.4841	814.9537	813.4709	1.4829	0	10	19	6	K.GTPVIATR.A 257
1002	**516.5986**	**1031.1827**	**1029.5791**	**1.6036**	**2**	**8**	**27**	**3**	**R.SSLRQQRR.L** 991
1189	534.8451	1067.6757	1067.5975	0.0782	0	10	15	5	R.AGGIPLQVADK.Q
1489	561.7016	1121.3887	1120.5183	0.8705	0	12	11	1	-.MADDSNAILR.R 1483
2937	**666.2666**	**1330.5187**	**1329.7140**	**0.8047**	**0**	**10**	**19**	**6**	**R.EDDTLTIAIAIR.D**
3241	681.8566	1361.6987	1360.7537	0.9451	1	13	8.5	5	K.FIGLAMPERIAK.Q 3233
3337	**686.3906**	**1370.7667**	**1369.5746**	**1.1921**	**0**	**7**	**32**	**1**	**R.AGAGQEYTSDESR.L**
3861	**717.2366**	**1432.4587**	**1429.7314**	**2.7274**	**1**	**12**	**11**	**1**	**K.AVQHYATDLKER.K**
4184	**735.2441**	**1468.4737**	**1467.8297**	**0.6441**	**0**	**77**	**2.7e-06**	**1**	**R.LGPSDQLLNALLSK.A**
4930	776.0496	1550.0847	1547.8195	2.2652	0	5	47	3	K.VALQLSTQEGFEVK.V
5310	794.6816	1587.3487	1588.7991	-1.4504	2	(0)	1.5e+02	3	K.IRGIDEQAESMGRK.C

5548	804.3496	1606.6847	1604.7940	1.8907	2	2	1.1e+02	1	K.IRGIDEQAESMGRK.C
6322	834.1741	1666.3337	1667.8672	-1.5334	1	4	65	1	K.FTFGIPDSTTWKIR.G
7181	580.6912	1739.0517	1737.8872	1.1645	0	3	72	8	K.IAFFSATPQGGGVALMR.H
8235	614.1859	1839.5357	1839.9115	-0.3758	0	6	33	10	R.SDLIDKPGTPQAEAWGR.L
9675	669.1059	2004.2957	2005.0341	-0.7383	1	2	89	9	R.VTKNNHNILQGVASPEER.L
15976	1084.2895	3249.8467	3249.4958	0.3509	1	3	44	1	K.DDQSLCSVLEKFVIDQLQEWSDAHMEK.F
16201	1119.3655	3355.0747	3352.5281	2.5466	2	1	69	4	K.VGYMPASTDWLDGLNKNMREWDIAYYGR.V

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306. gi|220699831|gb|EED56170.1| **Mass:** 127414 **Score:** 77 **Queries matched:** 29 **emPAI:** 0.05

leucyl-tRNA synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
540	911.6840	910.6767	910.4252	0.2515	1	6	37	6	K.VGKMGEMK.K
788	490.4151	978.8157	978.4957	0.3200	0	15	4.5	1	K.VEFMAGVAR.M 794
1563	567.1771	1132.3397	1130.6005	1.7392	0	10	19	5	R.ILPMEGVSASK.G 1560
2718	654.5606	1307.1067	1305.6499	1.4568	0	6	45	4	K.IFNNEMNGLVR.E
4334	743.8061	1485.5977	1485.7423	-0.1446	0	9	20	1	M.AAAAASAAALDPSNGTK.N 4336
4494	753.7601	1505.5057	1502.7987	2.7070	2	10	16	6	K.SGISKEALQQMRR.E 4454 4487 4495 4497
5396	532.6082	1594.8027	1591.8417	2.9610	1	1	1.1e+02	7	R.ATSSSITSAEAQLAKK.A
5687	809.5336	1617.0527	1614.8002	2.2526	1	0	1.4e+02	6	K.SGLYDLVSARDTYR.E
7499	590.5339	1768.5797	1769.8878	-1.3081	2	8	26	2	K.MGEMKKAMPFVQTLK.R
8333	617.6792	1850.0157	1849.9608	0.0550	2	3	62	5	K.GEGVGPQEYTAMKLKVK.E
8700	630.2025	1887.5857	1886.9203	0.6654	1	13	6.6	1	R.EFEYWYPLDVRVSGK.D 8696
10438	697.5245	2089.5517	2089.0473	0.5044	1	5	38	2	-.MAAAAASAAALDPSNGTKNTLK.L 10447
11202	731.8362	2192.4867	2194.1270	-1.6402	1	2	92	6	K.YIDLVREAFDGLNLSINDK.E
11558	749.1529	2244.4367	2242.1230	2.3137	2	2	72	4	K.STGNFLTLKDSVDKFGADATR.I 11553
11722	1138.2406	2274.4667	2273.0311	1.4357	0	63	6e-05	1	K.SLYESGDAFPFADPMGEVVSR.S
11751	760.2302	2277.6687	2275.1428	2.5259	2	3	57	10	R.MDGKRALFPLGFHCTGMPIK.A
12600	800.9495	2399.8267	2401.1260	-1.2993	1	1	1e+02	3	R.KSLYESGDAFPFADPMGEVVSR.S
14961	931.8119	2792.4137	2793.2751	-0.8614	2	3	59	4	R.RQMVTTDANPYYDAFVRWQMNR.L
16307	1142.4669	3424.3787	3422.7470	1.6317	0	37	0.018	1	K.SQDQLPLVAEAPGSAYVGTLVNAPLSFHTEGVR.I

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307. gi|220696823|gb|EED53164.1| **Mass:** 68387 **Score:** 76 **Queries matched:** 16 **emPAI:** 0.15

actin-binding protein, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
357	426.9941	851.9737	851.4501	0.5236	0	24	0.57	1	R.IATTGFSR.M
2399	424.8899	1271.6477	1270.5724	1.0753	0	5	54	7	R.GVNMHENEVAR.A
2709	653.8121	1305.6097	1302.6568	2.9529	0	6	41	4	R.VSANAWDSNLVK.V
5865	816.7076	1631.4007	1629.7972	1.6036	0	2	96	9	R.QERPAHEVQGHSGAK.N
7244	871.6016	1741.1887	1740.9159	0.2729	1	6	41	4	R.VSANAWDSNLVKVNPK.Y 7231

7667	594.8149	1781.4227	1782.9013	-1.4786	1	8	23	8	R.TVESASPVKTSAWHQR.E 7664
7950	**904.7371**	**1807.4597**	**1805.9564**	**1.5034**	**0**	**60**	**0.00014**	**1**	**K.TVGDTYIEPISFIVPR.R**
9181	**648.7155**	**1943.1247**	**1943.0014**	**0.1234**	**1**	**2**	**78**	**2**	**R.VVWLGEHDRIATTGFSR.M**
12385	790.8889	2369.6447	2370.1411	-0.4964	1	5	37	2	R.EESKSQTASKPSTPVPAQNNDR.S
13423	**837.6845**	**2510.0317**	**2509.2019**	**0.8298**	**2**	**5**	**39**	**1**	**R.KEQCYDNLRVSANAWDSNLVK.V**
14869	**925.1962**	**2772.5667**	**2771.4640**	**1.1027**	**1**	**0**	**1e+02**	**3**	**K.LTHMVGPLLNEVHEQKQQIESLTK.T**
15860	1063.3369	3186.9887	3185.6027	1.3860	2	0	83	3	K.LTLNVGDMVYSQSWSANGSLLVTTSRDKK.L
15914	**1071.7959**	**3212.3657**	**3210.5332**	**1.8325**	**1**	**33**	**0.042**	**1**	**R.RAETFQDDIYPPTVGLTPAMSPSEWFAGK.E** 15911

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308. gi|220696271|gb|EED52613.1| **Mass:** 13124 **Score:** 76 **Queries matched:** 10 **emPAI:** 0.26

40S ribosomal protein S10a [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
71	690.4360	689.4287	689.4072	0.0215	0	16	5.7	5	R.ITLTSR.K
186	773.9730	772.9657	773.4647	-0.4990	1	22	1.2	1	R.KVASLEK.V
271	818.5800	817.5727	817.4658	0.1070	0	28	0.32	1	K.TLQISTR.K
1513	**564.5751**	**1127.1357**	**1127.5070**	**-0.3712**	**1**	**20**	**1.5**	**1**	**K.TWDKYEMR.I**
2766	**657.2536**	**1312.4927**	**1311.7650**	**0.7278**	**0**	**66**	**4e-05**	**1**	**R.LIDLLAPTETVK.Q** 2764
4172	734.7001	1467.3857	1467.8661	-0.4803	1	2	97	9	K.RLIDLLAPTETVK.Q
7078	**863.4696**	**1724.9247**	**1723.8239**	**1.1008**	**1**	**10**	**13**	**1**	**-.MSFQKPEKDFGEGPK.V** 7062
8808	950.8081	1899.6017	1897.8628	1.7389	2	2	84	6	K.TPNGEGSKTWDKYEMR.I

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309. gi|220696529|gb|EED52871.1| **Mass:** 8114 **Score:** 76 **Queries matched:** 3 **emPAI:** 1.06

Mitochondrial ATP synthase epsilon chain domain-containing protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3851	716.6331	1431.2517	1430.7412	0.5105	2	10	16	4	R.LAAERRGQMDLR.F
5794	813.6756	1625.3367	1623.7852	1.5515	0	77	2.9e-06	1	R.SLGEANQEAAVAHAEK.- 5784

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310. gi|220701312|gb|EED57650.1| **Mass:** 7717 **Score:** 76 **Queries matched:** 10 **emPAI:** 0.45

Ribosomal protein S28e [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1629	571.6441	1141.2737	1139.7503	1.5235	2	23	0.79	2	K.LVKVTRVLGR.T 1608 1612 1628
1682	578.3381	1154.6617	1154.7023	-0.0406	2	7	34	7	M.DSAKAPVKLVK.V
1901	**401.0609**	**1200.1607**	**1200.7051**	**-0.5444**	**2**	**12**	**10**	**7**	**K.VTRVLGRTGSR.G**
4132	**732.2561**	**1462.4977**	**1460.7181**	**1.7796**	**0**	**68**	**2.6e-05**	**1**	**R.VDDILCLLESER.E** 4120
12007	770.6239	2308.8497	2308.1594	0.6903	2	6	31	5	R.GGVTQVRVEFMDDQSRSIIR.N 11999

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311. gi|220701329|gb|EED57667.1| **Mass:** 38755 **Score:** 75 **Queries matched:** 7 **emPAI:** 0.18

3-isopropylmalate dehydrogenase Leu2A [Aspergillus flavus NRRL3357]

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       Query   Observed    Mr(expt)    Mr(calc)     Delta Miss Score  Expect Rank  Peptide
        2621   648.6471   1295.2797   1294.7245    0.5552   0     57  0.0003    1  K.NADAVLLGAIGGPK.W 2631
        5146   786.7236   1571.4327   1570.8315    0.6013   0     44  0.0059    1  R.AIEQAVSNVIESGVR.T 5126 5170
       11796   761.5639   2281.6697   2282.2171   -0.5474   2      0  1.2e+02   5  R.GVNFNIIRELTGGIYFGERK.E
       15590  1019.4132   3055.2177   3056.7247   -1.5070   2      2      66    2  K.NADAVLLGAIGGPKWGTGAVRPEQGILKLR.K

312.   gi|215478516|gb|ACJ67040.1|     Mass: 13662     Score: 74     Queries matched: 10    emPAI: 0.56
       O-methyltransferase [Aspergillus flavus]
       Query  Observed    Mr(expt)    Mr(calc)     Delta Miss Score  Expect Rank  Peptide
        2285  630.7351   1259.4557   1259.6721   -0.2164   0      7      34   10  -.VTATGVSEDLLR.R 2279 2291
        4044  726.7251   1451.4357   1451.6966   -0.2609   0      9      20    7  R.FDLGMGGTEATKPL.- 4031
        5076  783.5086   1565.0027   1562.7253    2.2774   0      7      28    1  K.GLFDYYSTVDEVR.G
       10289  690.5172   2068.5297   2066.9585    1.5712   0     41   0.011    1  R.FIFEEVAPDQYAHTDASK.M 10286
       11043  725.0985   2172.2737   2171.1051    1.1686   0     51 0.00098    1  K.GKPPSWNVPSPFSLAFDPTK.G 11051

       Proteins matching the same set of peptides:
       gi|215478518|gb|ACJ67041.1|     Mass: 13662     Score: 74     Queries matched: 10
       O-methyltransferase [Aspergillus flavus]

313.   gi|74273764|gb|ABA01534.1|     Mass: 13793     Score: 74     Queries matched: 9    emPAI: 0.56
       O-methyltransferase [Aspergillus flavus]
       Query   Observed    Mr(expt)    Mr(calc)     Delta Miss Score  Expect Rank  Peptide
        1277  1085.4380   1084.4307   1083.4543    0.9764   0      2   1e+02   10  R.FDLGMGGTEAA.- 1278
        5076   783.5086   1565.0027   1562.7253    2.2774   0      7      28    1  K.GLFDYYSTVDEVR.G
        7397   880.8521   1759.6897   1758.9363    0.7534   0      2   1e+02   10  -.SLDTIVAATGVSEDLLR.R
        8963   639.3409   1915.0007   1915.0374   -0.0367   1      3      74    1  -.SLDTIVAATGVSEDLLRR.I
       10289   690.5172   2068.5297   2066.9585    1.5712   0     41   0.011    1  R.FIFEEVAPDQYAHTDASK.M 10286
       11043   725.0985   2172.2737   2171.1051    1.1686   0     51 0.00098    1  K.GKPPSWNVPSPFSLAFDPTK.G 11051

314.   gi|8308126|gb|AAF74483.1|AF261846_1     Mass: 9573     Score: 74     Queries matched: 5    emPAI: 0.86
       O-methyltransferase [Aspergillus flavus]
       Query  Observed    Mr(expt)    Mr(calc)    Delta Miss Score  Expect Rank  Peptide
         385  431.1001    860.1857    859.5504   0.6353   2     15     6.4    6  -.FRRILR.G
       10289  690.5172   2068.5297   2066.9585   1.5712   0     41   0.011    1  R.FIFEEVAPDQYAHTDASK.M 10286
       11043  725.0985   2172.2737   2171.1051   1.1686   0     51 0.00098    1  K.GKPPSWNVPSPFSLAFDPTK.G 11051

       Proteins matching the same set of peptides:
       gi|8308136|gb|AAF74488.1|AF261851_1     Mass: 9573     Score: 74     Queries matched: 5
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O-methyltransferase [Aspergillus flavus]

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315. gi|74273707|gb|ABA01506.1| **Mass:** 13859 **Score:** 74 **Queries matched:** 8 **emPAI:** 0.55

O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1570	**567.4776**	**1132.9407**	**1133.4812**	**-0.5404**	**0**	**2**	**1.2e+02**	**7**	**R.FDLGMGGTEAH.-**
5076	783.5086	1565.0027	1562.7253	2.2774	0	7	28	1	K.GLFDYYSTVDEVR.G
7397	880.8521	1759.6897	1758.9363	0.7534	0	2	1e+02	10	-.SLDTIVAATGVSEDLLR.R
8963	639.3409	1915.0007	1915.0374	-0.0367	1	3	74	1	-.SLDTIVAATGVSEDLLRR.I
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M 10286
11043	725.0985	2172.2737	2171.1051	1.1686	0	51	0.00098	1	K.GKPPSWNVPSPFSLAFDPTK.G 11051

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316. gi|74273732|gb|ABA01518.1| **Mass:** 14035 **Score:** 74 **Queries matched:** 8 **emPAI:** 0.55

O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4402	748.1041	1494.1937	1494.7137	-0.5200	1	1	1.2e+02	2	R.RFDLGMGGTEATKP.-
5076	783.5086	1565.0027	1562.7253	2.2774	0	7	28	1	K.GLFDYYSTVDEVR.G
7397	880.8521	1759.6897	1758.9363	0.7534	0	2	1e+02	10	-.SLDTIVAATGVSEDLLR.R
8963	639.3409	1915.0007	1915.0374	-0.0367	1	3	74	1	-.SLDTIVAATGVSEDLLRR.I
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M 10286
11043	725.0985	2172.2737	2171.1051	1.1686	0	51	0.00098	1	K.GKPPSWNVPSPFSLAFDPTK.G 11051

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317. gi|114384135|gb|ABI73969.1| **Mass:** 11812 **Score:** 74 **Queries matched:** 5 **emPAI:** 0.67

O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M 10286
11043	725.0985	2172.2737	2171.1051	1.1686	0	51	0.00098	1	K.GKPPSWNVPSPFSLAFDPTK.G 11051
12195	**779.2862**	**2334.8367**	**2333.3001**	**1.5366**	**2**	**3**	**61**	**1**	**-.HSIPMVAATGVSEDLLRRILR.G**

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318. gi|8308140|gb|AAF74490.1|AF261853_1 **Mass:** 9540 **Score:** 74 **Queries matched:** 8 **emPAI:** 0.86

O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M 10286
11043	725.0985	2172.2737	2171.1051	1.1686	0	51	0.00098	1	K.GKPPSWNVPSPFSLAFDPTK.G 11051
11456	743.8942	2228.6607	2228.1378	0.5229	0	1	1.1e+02	5	K.GKPPSWNRPSPFSLAFDPTK.G
12184	**778.1952**	**2331.5637**	**2329.1743**	**2.3894**	**1**	**4**	**46**	**2**	**K.GKPPSWNSPSPFSLAFDPTKGL.-** 12167
12325	**786.7235**	**2357.1487**	**2357.1692**	**-0.0205**	**1**	**1**	**1e+02**	**10**	**K.GKPPSWNDPSPFSLAFDPTKGL.-**

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319. gi|2815742|gb|AAC01647.1| **Mass:** 9231 **Score:** 74 **Queries matched:** 5 **emPAI:** 0.90

O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M 10286
11043	725.0985	2172.2737	2171.1051	1.1686	0	51	0.00098	1	K.GKPPSWNVPSPFSLAFDPTK.G 11051
16189	**1117.7632**	**3350.2677**	**3347.6067**	**2.6610**	**1**	**2**	**55**	**2**	**R.VTGIHALVGFSCDEAMRSAAYFSNFLQQTK.G**

Proteins matching the same set of peptides:

gi|2815762|gb|AAC01657.1| **Mass:** 9231 **Score:** 74 **Queries matched:** 5

O-methyltransferase [Aspergillus flavus]

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320. gi|15193503|gb|AAF74494.2|AF261857_1 **Mass:** 9412 **Score:** 74 **Queries matched:** 5 **emPAI:** 0.87

O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M 10286
10685	709.3819	2125.1237	2127.0789	-1.9552	0	2	78	2	K.GKPPSWNVPSPFSLAFDPGK.G
11043	725.0985	2172.2737	2171.1051	1.1686	0	51	0.00098	1	K.GKPPSWNVPSPFSLAFDPTK.G 11051

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321. gi|220699478|gb|EED55817.1| **Mass:** 41060 **Score:** 74 **Queries matched:** 13 **emPAI:** 0.08

saccharopine dehydrogenase Lys1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
544	456.5946	911.1747	910.5964	0.5783	0	16	3.5	2	K.ILVIGALGR.C 545
1434	557.6711	1113.3277	1112.5026	0.8251	0	27	0.36	1	R.IFDDEEFAK.I
1966	**607.2381**	**1212.4617**	**1212.6350**	**-0.1733**	**0**	**11**	**11**	**10**	**K.DVGIPESDIIR.W**
2553	**430.1452**	**1287.4137**	**1288.7027**	**-1.2890**	**1**	**7**	**30**	**9**	**K.DAPKDAYVLGLK.E** 2551
7479	884.6261	1767.2377	1766.9203	0.3175	1	14	5.3	3	K.IGAPLVEEGSWAKDAPK.D 7486
9226	**650.8025**	**1949.3857**	**1947.0062**	**2.3796**	**1**	**10**	**14**	**3**	**R.GGGTLLDLEFLTDEVGRR.V**
9806	**1011.9201**	**2021.8257**	**2020.0550**	**1.7707**	**0**	**54**	**0.00047**	**1**	**R.ESSEMFSQALLPSLLQLK.N** 9795
12882	**813.2665**	**2436.7777**	**2434.2889**	**2.4888**	**2**	**10**	**12**	**2**	**R.ESSEMFSQALLPSLLQLKNRK.D** 12873

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322. gi|220690500|gb|EED46849.1| **Mass:** 42759 **Score:** 74 **Queries matched:** 16 **emPAI:** 0.16

acyl-CoA dehydrogenase family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1288	1086.6920	1085.6847	1085.5249	0.1598	0	4	80	8	R.CSIYLVMGK.S
2129	620.6991	1239.3837	1238.6983	0.6854	0	42	0.01	1	R.VPVSNIVLGEGR.G 2127
2356	**423.0459**	**1266.1157**	**1267.6925**	**-1.5767**	**0**	**6**	**34**	**6**	**K.QQWLAPLLDGK.I** 2357
3231	**681.6271**	**1361.2397**	**1360.6962**	**0.5436**	**0**	**0**	**1.5e+02**	**4**	**R.QQGLWNMFLPK.N**
3774	**713.3186**	**1424.6227**	**1423.8399**	**0.7829**	**0**	**43**	**0.0073**	**1**	**K.VLVPQTALTVIDR.A**
3897	719.3581	1436.7017	1433.7561	2.9456	1	10	16	4	R.IHHAMRTIGAAEK.A

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         4810    770.9481  1539.8817  1538.8457    1.0361   0    11        11    1   K.SLSSHGVILEWLAK.S 4796
        10206   1031.2446  2060.4747  2058.0534    2.4213   1     5        46    2   K.YGNEAQKQQWLAPLLDGK.I
        11575    750.4735  2248.3987  2246.0215    2.3772   0     5        38   10   R.MLSVYGYDDAPHGHGHISFK.D
        12285    784.0412  2349.1017  2347.1325    1.9692   1     1        92    2   K.SKLASEATNNAAPDTGNMEVLAK.Y
        12620    801.7685  2402.2837  2402.3004   -0.0167   2     2        76    8   R.IHHAMRTIGAAEKAIEWLIAR.I
        13405    836.9339  2507.7797  2509.3765   -1.5968   2     2        79    3   K.DVRVPVSNIVLGEGRGFEIIQGR.L
        14453    894.1232  2679.3477  2678.3333    1.0144   1     3        54    9   R.SAFLMTEPEVASSDATNIQLNIRR.E

323.   gi|220690752|gb|EED47101.1|     Mass: 27493    Score: 71     Queries matched: 8    emPAI: 0.12
       class II aldolase/adducin domain protein [Aspergillus flavus NRRL3357]
      Query   Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect Rank   Peptide
         4835    771.8131  1541.6117  1541.8024   -0.1907   2     2     1e+02    5   R.GKGKGMLGFFDTLR.I
        10056   1023.2266  2044.4387  2046.0860   -1.6472   0     7        24    3   K.ELMKPENIFVLQFPTPK.Y 10063 10072 10094
        10633   1060.1936  2118.3727  2118.0732    0.2995   0    71   9.7e-06    1   R.IPIIENTAFEEDLTGSLEK.A 10632
        16010   1090.9755  3269.9047  3271.6322   -1.7275   1     1        70    3   K.GMLGFFDTLRIPIIENTAFEEDLTGSLEK.A

324.   gi|220695921|gb|EED52263.1|     Mass: 32977    Score: 71     Queries matched: 14    emPAI: 0.21
       NADH-cytochrome B5 reductase, putative [Aspergillus flavus NRRL3357]
      Query  Observed    Mr(expt)   Mr(calc)     Delta Miss Score   Expect Rank  Peptide
         1716   582.6291  1163.2437  1162.5659    0.6779   0    50    0.0015    1  R.FEYVYTVSR.L 1717
         2697   652.7286  1303.4427  1302.7408    0.7019   2    29      0.21    2  K.RGILDRLGFEK.G 2685 2698
         4367   497.6335  1489.8787  1490.7994   -0.9207   2     6        44   10  K.RLVFEFPDKNAR.S
         5498   802.3496  1602.6847  1601.8777    0.8070   0    26      0.36    1  K.LVFGVNSEQDLLLR.E 5457 5487 5488 5502 5510
         8251   614.8089  1841.4047  1843.0567   -1.6520   1     4        58   10  K.IKLVFGVNSEQDLLLR.E
        10835   716.0252  2145.0537  2146.1647   -1.1110   2     1   1.1e+02    5  K.FGFTTLRVQSVKAVNHNTK.R

325.   gi|220692391|gb|EED48738.1|     Mass: 77184    Score: 71     Queries matched: 9    emPAI: 0.04
       NADH-ubiquinone oxidoreductase 64 kDa subunit, putative [Aspergillus flavus NRRL3357]
      Query   Observed    Mr(expt)   Mr(calc)     Delta Miss Score Expect Rank  Peptide
         1374    552.1451  1102.2757  1102.5560   -0.2802   1     3   1e+02    8  K.SSFRNAFFK.T
         3631    702.6071  1403.1997  1400.7299    2.4698   2     4      70    3  R.TIAWEKGKDPEK.L 3628
         7501    590.6262  1768.8567  1765.9435    2.9132   2     6      38    6  R.DHVDVLTNSRVKEVR.D
         8450    930.8016  1859.5887  1859.0047    0.5840   1     4      57   10  -.MSTVLLRSRPDQTALR.R
         9217    650.4802  1948.4187  1947.9976    0.4212   1     9      16    1  R.DDKVVFTQMEDGKPVLK.E
        12263    783.1652  2346.4737  2348.0624   -1.5887   0     5      38    4  K.NQVLENMELACLPTTSDEER.K
        16124   1106.3775  3316.1107  3313.6765    2.4342   0    49  0.0011    1  R.LIGAPLGDVYAIGDCSTVQNNVADHIVSFLR.T 16120

326.   gi|220689379|gb|EED45730.1|     Mass: 26068    Score: 71     Queries matched: 11    emPAI: 0.27
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```
     ubiquinol-cytochrome c reductase iron-sulfur subunit precursor [Aspergillus flavus NRRL3357]
    Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
     1963  607.1486  1212.2827  1211.6761   0.6066   0    70  1.6e-05   1   K.VEIGLASIPEGK.N
     2225  418.1959  1251.5657  1251.6493  -0.0835   0    11       11   4   -.MSLSSASSTLLR.A
     2364  634.7366  1267.4587  1267.6442  -0.1855   0   (3)       68   3   -.MSLSSASSTLLR.A
     7644  890.8326  1779.6507  1779.0506   0.6002   1     5       43   2   K.VEIGLASIPEGKNVIIK.W
    10064  682.7379  2045.1917  2045.9654  -0.7737   0     2       84   9   R.TQDEINEANSIEWQTLR.D 10080
    13494  841.1462  2520.4167  2520.2900   0.1267   2     1       83   3   -.MSLSSASSTLLRACARQQLPTSR.A
    13844 1286.2921  2570.5697  2570.3268   0.2429   1    34     0.05   1   R.KGPAPLNLEVPQYSFPDESTLVIG.- 13845 13855 13860
```

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327.  gi|220695252|gb|EED51595.1|    Mass: 49674    Score: 71    Queries matched: 14    emPAI: 0.07
      GTP cyclohydrolase II, putative [Aspergillus flavus NRRL3357]
    Query Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      685 480.4011   958.7877   956.5291   2.2587   0     4       75   4   K.LAEIGEAVR.D
     1888 599.7531  1197.4917  1198.7033  -1.2116   2     2  1.1e+02   3   R.KEGRALGEVIK.Y
     2714 654.2921  1306.5697  1307.7925  -1.2228   1     2  1.1e+02   9   R.GPVVVSRSGPLLK.R
     3024 671.2081  1340.4017  1339.6329   0.7688   0     7       31   5   R.QYTMEELAEVK.G
     3034 671.7101  1341.4057  1340.6250   0.7807   1     4       64  10   K.IDRMLSMSNMK.H
     4460 752.0026  1501.9907  1500.7098   1.2809   2     0  1.6e+02   5   K.KIDRMLSMSNMK.H
     5224 790.8886  1579.7627  1577.8889   1.8738   1     1  1.3e+02   7   K.HDAIVQSGIKILER.V
     5788 813.3336  1624.6527  1623.8369   0.8158   1     0  1.4e+02   8   R.EAQNGGSGVVIYFRK.E
     6391 836.5536  1671.0927  1669.8828   1.2099   0    71  1.2e-05   1   K.VAVEPVWYLPGVADR.F
     8152 610.1735  1827.4987  1827.9050  -0.4063   2     3       66  10   K.YFTRTENIAGVRDMR.F 8146
    11126 729.6655  2185.9747  2183.1384   2.8364   1     4       48   3   R.DMRFQALMPDILHWLGIK.K
    12444 792.8735  2375.5987  2373.1967   2.4021   2     3       54   4   K.IDRMLSMSNMKHDAIVQSGIK.I
    13614 844.8349  2531.4827  2532.2862  -0.8035   2     0    1e+02   6   R.MLSMSNMKHDAIVQSGIKILER.V
```

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328.  gi|220688981|gb|EED45333.1|    Mass: 89255    Score: 71    Queries matched: 19    emPAI: 0.04
      U5 snRNP component Snu114, putative [Aspergillus flavus NRRL3357]
    Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
      107  720.8230   719.8157   719.3636   0.4521   0     3       97   4   K.MLDGLR.K
      737  485.5646   969.1147   968.5403   0.5744   0    60  0.00017   1   R.GGGQIIPTAR.R 732 734 735
     1296  544.7286  1087.4427  1088.5655  -1.1227   0     1  1.6e+02   5   K.FLEPELWR.G
     1543  565.9231  1129.8317  1129.6529   0.1788   1   (5)       55  10   K.MDRLILELK.I
     1651  574.1791  1146.3437  1145.6478   0.6959   1     8       29   9   K.MDRLILELK.I 1648
     4044  726.7251  1451.4357  1451.7198  -0.2840   0    13      7.9   1   R.LWGDIFFNPTSR.K
     4393  747.5546  1493.0947  1491.7933   1.3014   0     3       74   9   R.LTDVSLADQVIYR.G
     7630  593.9559  1778.8457  1777.9251   0.9207   0     7       32   8   R.GLIPVIDSFGFETDLR.I
     9557  664.6769  1991.0087  1992.1367  -1.1280   1     2       88  10   R.TLASVGIHLKPSQLKSDAK.E
```

11288	736.2815	2205.8227	2207.1984	-1.3756	2	1	1.1e+02	7	K.VAVEPVNPSELPKMLDGLRK.V
12444	792.8735	2375.5987	2374.1573	1.4414	1	1	99	9	K.NKITMIAEPLDDGIAEDIESGK.V
12925	**815.4549**	**2443.3427**	**2442.3231**	**1.0197**	**1**	**6**	**30**	**1**	**R.LTDVSLADQVIYRGGGQIIPTAR.R** 12909 12927
15521	**1013.2752**	**3036.8037**	**3038.5569**	**-1.7532**	**2**	**1**	**74**	**8**	**R.HMTESVFKVAVEPVNPSELPKMLDGLR.K**

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329. gi|220701581|gb|EED57919.1| **Mass:** 31235 **Score:** 70 **Queries matched:** 5 **emPAI:** 0.22

proteasome regulatory particle subunit (RpnL), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3303	457.0392	1368.0957	1365.7364	2.3593	0	10	14	3	R.TLVSELHNALNR.K 3295
9232	**975.9801**	**1949.9457**	**1949.0258**	**0.9199**	**0**	**71**	**1e-05**	**1**	**R.VPSEDFGLFSNVLVGTIR.S**
11160	**731.1192**	**2190.3357**	**2191.1821**	**-0.8464**	**2**	**3**	**67**	**9**	**M.ANGADLRTLVSELHNALNRK.Q**
12777	**808.7585**	**2423.2537**	**2421.3842**	**1.8695**	**0**	**18**	**1.9**	**1**	**R.TLLLQNALIPTSSTSPELIALAR.E**

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330. gi|220689713|gb|EED46063.1| **Mass:** 81215 **Score:** 70 **Queries matched:** 30 **emPAI:** 0.04

dynamin family GTPase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
228	793.4880	792.4807	792.3800	0.1008	0	15	5.3	4	K.MAEGTLR.G 229
1796	393.6009	1177.7807	1179.5778	-1.7971	2	9	23	5	K.RMGESRTTAR.A
1913	**602.8286**	**1203.6427**	**1203.5852**	**0.0575**	**1**	**(5)**	**53**	**7**	**K.CPMRIVSADR.F**
2007	611.0676	1220.1207	1219.5802	0.5406	1	7	39	3	K.CPMRIVSADR.F 2010 2015
4323	**495.6115**	**1483.8127**	**1483.6799**	**0.1328**	**0**	**8**	**22**	**10**	**R.FIDNVAMQVMER.H** 4322 4333
6505	560.9172	1679.7297	1678.8335	0.8962	1	6	40	5	K.KELTSEVMEEIIDK.A 6520
6754	566.6855	1697.0347	1698.9417	-1.9070	0	3	78	10	K.EIPHIITEITQHLR.E
7475	**589.8865**	**1766.6377**	**1766.8734**	**-0.2356**	**1**	**28**	**0.22**	**1**	**R.GQHQDIPSTDAKAMLR.Y** 7501
7557	**591.8915**	**1772.6527**	**1770.8546**	**1.7982**	**1**	**4**	**64**	**4**	**K.DTMCTRFPIQISFR.Q**
8173	916.7461	1831.4777	1831.0163	0.4614	2	2	97	8	K.STKQLTLSDATLRIER.S
9125	646.2249	1935.6527	1937.0370	-1.3843	2	0	1.3e+02	7	R.SLPGSVHPDVEEKLFRK.L
12782	**808.9542**	**2423.8407**	**2422.1522**	**1.6886**	**2**	**0**	**1.1e+02**	**6**	**R.TTARAQRYYVLQFCNEMQK.M**
13167	826.3685	2476.0837	2476.3545	-0.2708	2	3	62	4	K.IMVTDCYNILLKIAIPNSKVR.L 13173
13377	**835.9322**	**2504.7747**	**2504.2217**	**0.5530**	**0**	**55**	**0.00041**	**1**	**R.NPSLLSFTSMTDEILLGHSSNNK.A** 13375 13396
13784	853.8102	2558.4087	2557.2377	1.1710	2	1	1e+02	7	K.MAEGTLRGQHQDIPSTDAKAMLR.Y
14129	877.7735	2630.2987	2627.2957	3.0030	2	3	59	3	R.FIDNVAMQVMERHVLGPKCPMR.I
15013	**938.9609**	**2813.8607**	**2812.3510**	**1.5097**	**2**	**8**	**17**	**1**	**K.KELTSEVMEEIIDKATECIFGDQK.S**
16380	1156.4262	3466.2567	3464.7373	1.5194	2	3	39	3	R.LDGYYDIALWRFIDNVAMQVMERHVLGPK.C 16377 16382

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331. gi|220695044|gb|EED51387.1| **Mass:** 16084 **Score:** 70 **Queries matched:** 2 **emPAI:** 0.21

NADH-ubiquinone oxidoreductase subunit B17.2, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2075	**617.3591**	**1232.7037**	**1231.5986**	**1.1052**	**0**	**53**	**0.0008**	**1**	**K.YSAWDPVAAPR.N** 2074

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332. gi|220697363|gb|EED53704.1| **Mass:** 34947 **Score:** 69 **Queries matched:** 5 **emPAI:** 0.09

possible apospory-associated protein c [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1162	532.6421	1063.2697	1064.5098	-1.2401	1	10	19	2	K.SSSESLGKDR.S
2277	**630.3346**	**1258.6547**	**1257.5336**	**1.1211**	**0**	**2**	**1.3e+02**	**3**	**K.GMADFGPGEAYK.N**
4043	**484.7652**	**1451.2737**	**1449.7100**	**1.5638**	**1**	**5**	**44**	**8**	**K.ETDRVYQSLDPK.V**
10057	682.5445	2044.6117	2044.1205	0.4913	0	69	1.7e-05	1	K.VPIIVSSASDDKPIFSITR.E
12292	**784.3982**	**2350.1727**	**2349.2764**	**0.8963**	**1**	**5**	**37**	**2**	**M.DRSNKPSAIGVGASVPQPTISLR.D**

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333. gi|220692698|gb|EED49044.1| **Mass:** 17830 **Score:** 69 **Queries matched:** 8 **emPAI:** 0.19

60S ribosomal protein L24a [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
695	481.4921	960.9697	959.5287	1.4410	1	11	18	6	K.KGISEEVAK.K
784	**490.0271**	**978.0397**	**978.5134**	**-0.4737**	**0**	**52**	**0.0011**	**1**	**K.SESLFLQR.K** 789
1283	**543.6396**	**1085.2647**	**1084.6492**	**0.6155**	**0**	**13**	**9**	**2**	**R.AIVGASLDVIK.E** 1282
2603	647.7346	1293.4547	1292.7605	0.6943	2	2	1.1e+02	7	K.IYPGKGKLYVR.G
4441	**751.2181**	**1500.4217**	**1499.8168**	**0.6049**	**2**	**2**	**1.1e+02**	**8**	**K.NAAAGKGTAQRIQSK.Q**
4666	**509.0462**	**1524.1167**	**1525.8940**	**-1.7773**	**2**	**9**	**18**	**2**	**R.AIVGASLDVIKERR.N**

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334. gi|220688938|gb|EED45290.1| **Mass:** 43100 **Score:** 68 **Queries matched:** 7 **emPAI:** 0.08

cystathionine gamma-lyase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1859	596.4076	1190.8007	1190.5932	0.2076	0	8	29	2	R.EAAGVFDDLVR.M
4512	**754.7276**	**1507.4407**	**1505.6892**	**1.7515**	**1**	**2**	**87**	**5**	**-.MTNSTNGAPAQDKR.F**
5337	530.6565	1588.9477	1589.7798	-0.8321	1	1	1.3e+02	9	K.DQREAAGVFDDLVR.M
5370	531.6992	1592.0757	1592.7300	-0.6543	1	5	44	3	K.QHRQGMGGGMLSFR.I 5391
9141	646.7195	1937.1367	1937.0806	0.0561	2	1	1.2e+02	7	K.TLHLRAREATTNATAIAK.A
15257	**968.3439**	**2902.0097**	**2899.4460**	**2.5638**	**0**	**68**	**1.6e-05**	**1**	**K.VFTLAESLGGVESLCEVPASMTHAGIPK.D**

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335. gi|220698606|gb|EED54946.1| **Mass:** 51334 **Score:** 67 **Queries matched:** 20 **emPAI:** 0.13

30S ribosomal subunit S4, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
359	428.6501	855.2857	855.3909	-0.1051	0	5	49	8	R.AMFASSAR.Q
460	**443.1111**	**884.2077**	**884.5192**	**-0.3114**	**2**	**11**	**12**	**9**	**K.KDNKRPK.R** 458
843	495.6116	989.2087	988.5818	0.6269	1	42	0.013	2	R.RLDVAIFR.A 842
1889	**599.7531**	**1197.4917**	**1195.5907**	**1.9010**	**1**	**2**	**96**	**7**	**R.VMYATGAPKDK.H**
2075	617.3591	1232.7037	1232.6150	0.0888	1	3	82	5	R.GAGVEGTKDFPR.L

2312	632.2156	1262.4167	1261.5786	0.8381	1	7	36	2	K.EAESEEQGQKK.E
3066	673.6541	1345.2937	1343.6681	1.6256	2	10	17	8	K.KENDDPRETLK.V
3204	680.5581	1359.1017	1360.6470	-1.5452	1	7	37	1	K.KSAEAQEAEAEAK.E 3201
3997	724.3491	1446.6837	1445.8276	0.8562	1	1	1.3e+02	2	K.VLLAQAKTIMAGSK.D
5474	534.6929	1601.0567	1601.7984	-0.7417	2	3	80	4	R.VMYATGAPKDKHER.R
6123	826.6856	1651.3567	1650.8440	0.5128	0	43	0.0078	1	R.LTPFTQMTFAPLER.R 6146
8998	640.4189	1918.2347	1917.0968	1.1379	2	0	1.3e+02	5	R.ETLKVLLAQAKTIMAGSK.D
9267	652.1742	1953.5007	1952.0380	1.4627	2	7	28	9	K.LRQSWSKYNLFNLQR.L
10695	1064.2431	2126.4717	2125.1327	1.3390	2	3	66	1	R.QARQFVVHGAVTVNGKQMR.Y
13395	836.5535	2506.6387	2507.2267	-0.5880	1	0	1.2e+02	8	K.QMRYPGYLLNPGDLFQVDPER.V
13598	844.4025	2530.1857	2531.3179	-1.1322	2	2	72	1	R.AMFASSARQARQFVVHGAVTVNGK.Q

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336. gi|220690532|gb|EED46881.1| **Mass:** 36386 **Score:** 67 **Queries matched:** 5 **emPAI:** 0.09

aldo/keto reductase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1246	540.2371	1078.4597	1077.5706	0.8891	0	10	19	1	R.IEGLEYLNK.I
1412	555.2746	1108.5347	1107.5924	0.9423	1	8	24	8	K.REDLFVTTK.V
5250	791.8931	1581.7717	1581.7562	0.0155	0	51	0.0012	1	R.YDDVLWSLEDSLK.N 5257
10974	722.3702	2164.0887	2164.1892	-0.1005	2	3	68	5	K.HQPKLGPDGKYIILEDLTK.N

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337. gi|220696592|gb|EED52934.1| **Mass:** 237325 **Score:** 67 **Queries matched:** 45 **emPAI:** 0.03

acetyl-CoA carboxylase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
59	684.5530	683.5457	682.4490	1.0967	1	9	14	5	R.KLGIPR.I 58
669	479.6541	957.2937	956.5767	0.7170	1	4	69	10	K.QLQKTIAR.F
793	980.6790	979.6717	979.5273	0.1444	1	4	56	3	R.RVTFICGK.N 790
1259	1081.5370	1080.5297	1080.6655	-0.1358	1	7	33	3	R.HKITTIIGAK.D 1257
1378	1104.3450	1103.3377	1101.6216	1.7161	0	1	1.4e+02	7	R.LSQMELILR.S
1915	603.1361	1204.2577	1203.6459	0.6119	1	5	62	4	K.LTELESRSAAK.V
2848	441.4799	1321.4177	1318.7622	2.6555	1	4	61	5	R.YFVRAVVRPGR.L
3441	691.8831	1381.7517	1381.7929	-0.0412	0	34	0.061	1	R.ALADGGLLVLLDGR.S 3446
3549	697.8746	1393.7347	1392.6885	1.0462	0	5	47	2	K.GIVTVEDEVYNR.G
3604	700.8906	1399.7667	1399.8009	-0.0342	1	0	1.5e+02	3	K.KILFIGPPASAMR.S
3787	713.7196	1425.4247	1424.8173	0.6074	1	1	1.2e+02	5	K.HMVIALKELSIR.G
3926	480.5212	1438.5417	1438.7126	-0.1709	0	11	13	1	R.GFDNQVIMGTTLK.E 3929
3945	721.8566	1441.6987	1442.7841	-1.0854	2	2	98	9	R.NTRDEDAILKLR.D
4003	724.6456	1447.2767	1445.6535	1.6232	0	13	7.1	2	K.AHQASEAGVEEYR.K
4992	778.7946	1555.5747	1554.8082	0.7665	0	57	0.00033	1	K.TVFPVDFIYEGLR.Y
5106	523.6045	1567.7917	1566.8154	0.9763	0	1	1.2e+02	9	R.HSEPALAFQLELGR.L

5371	531.7249	1592.1527	1590.8076	1.3452	0	8	26	6	R.AIQFTVMATPEDLR.A
5954	**820.7036**	**1639.3927**	**1638.9239**	**0.4688**	**1**	**5**	**46**	**9**	**R.ARLGGIPMGVIAVETR.S** 5955
6805	567.9982	1700.9727	1701.8760	-0.9033	0	8	21	9	R.ILCTDPTTGVPYPLR.V
7362	586.4289	1756.2647	1755.8791	0.3856	1	4	62	5	R.NIHVYEAIGKGPESDK.A
7574	887.8536	1773.6927	1771.9655	1.7273	1	4	58	7	K.ILFIGPPASAMRSLGDK.I
7880	601.4505	1801.3297	1799.9629	1.3669	0	6	39	5	R.SLEDSSLNVAQLLIGNK.D 7885
8293	924.2841	1846.5537	1845.9982	0.5555	1	2	92	4	R.LSQMELILRSSVVESR.Y
8353	**618.2485**	**1851.7237**	**1851.9149**	**-0.1911**	**1**	**2**	**83**	**10**	**K.QLDTMARLDATYGELR.R**
8625	**628.7912**	**1883.3517**	**1884.0403**	**-0.6886**	**2**	**1**	**1e+02**	**3**	**K.HMVIALKELSIRGDFR.T**
9303	**654.1135**	**1959.3187**	**1961.0366**	**-1.7178**	**0**	**(0)**	**1.3e+02**	**5**	**K.MYMPLIAQEDGIVQLIK.Q**
9602	998.4836	1994.9527	1993.0264	1.9263	0	3	76	3	K.MYMPLIAQEDGIVQLIK.Q 9596
9662	668.6179	2002.8317	2000.9915	1.8402	2	9	18	2	K.AHQASEAGVEEYRKGLEK.G
9787	**673.9985**	**2018.9737**	**2018.0619**	**0.9118**	**2**	**3**	**63**	**3**	**K.EIGFPVMIKASEGGGGKGIR.K**
10012	681.1569	2040.4487	2039.1051	1.3436	2	6	36	7	K.ELSIRGDFRTTVEYLIK.L
11469	744.5109	2230.5107	2231.1837	-0.6730	1	4	57	3	R.KGVLLPVQYLEDAEEYLPR.A
11566	749.7335	2246.1787	2244.1824	1.9964	0	9	18	2	K.IIEEAPVTIAKPTTFQAMER.A
12559	798.1889	2391.5447	2389.1590	2.3857	0	3	66	7	K.GIQYHSSGEPPLLSWDFTLDK.L
12563	798.6969	2393.0687	2394.2002	-1.1314	1	10	11	1	R.AIQFTVMATPEDLRANADYIR.M
12604	**801.1912**	**2400.5517**	**2399.2068**	**1.3450**	**0**	**2**	**72**	**5**	**R.DVEDLDDTQIVSQINGILADVK.D**
13809	**855.4479**	**2563.3217**	**2564.3573**	**-1.0356**	**1**	**1**	**90**	**4**	**K.LGSMHLRPVSTPYPTKEWLQPK.R**
14710	909.7625	2726.2657	2726.2858	-0.0200	1	0	1e+02	6	K.GIVTVEDEVYNRGCTFSPEEGLQK.A

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338. gi|220692623|gb|EED48969.1| **Mass:** 40060 **Score:** 67 **Queries matched:** 14 **emPAI:** 0.08

mitochondrial phosphate carrier protein, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
352	851.4700	850.4627	850.4297	0.0330	0	15	5	2	R.GSFSGIGAR.L
862	498.0806	994.1467	993.4596	0.6871	0	50	0.0015	1	K.FGGYEFFK.Q 865
1372	551.9041	1101.7937	1101.5852	0.2085	0	13	9.4	3	K.AMGAVGGVEIAK.- 1371 1373
2201	**625.2381**	**1248.4617**	**1245.6751**	**2.7866**	**1**	**1**	**1.4e+02**	**8**	**K.KAMGAVGGVEIAK.-**
3770	**475.6019**	**1423.7837**	**1422.6925**	**1.0912**	**0**	**18**	**2.4**	**1**	**-.MQADLASAGSGLFR.D** 3764
7059	862.7186	1723.4227	1722.8941	0.5286	0	33	0.068	2	R.LVSEPTFASGLVSGFGR.I 7043 7068 7074
14211	**883.2635**	**2646.7687**	**2648.3204**	**-1.5517**	**1**	**4**	**40**	**2**	**R.FAFAGAVCCSVTHGGLTPVDVVKTR.I**

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339. gi|220696165|gb|EED52507.1| **Mass:** 53065 **Score:** 67 **Queries matched:** 9 **emPAI:** 0.13

Fasciclin domain family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3458	**693.2926**	**1384.5707**	**1383.7187**	**0.8520**	**0**	**65**	**4.9e-05**	**1**	**K.INAFLFSPYGQK.Y**
6160	827.8281	1653.6417	1651.9158	1.7259	1	1	1.2e+02	4	K.GFTHLDLPTLLGGRR.L
12058	**1157.8871**	**2313.7597**	**2315.1685**	**-1.4088**	**0**	**28**	**0.22**	**1**	**R.TLYSDVIYTEEGEIRPFGVK.G**

12245	781.7845	2342.3317	2340.3555	1.9762	2	0	1.3e+02	10	K.TIYELITESKYTTILAKLIK.E
14052	871.4142	2611.2207	2609.4653	1.7554	2	3	53	3	R.VAVADALGRDGNVHIVDQVLVPPKK.V 14057
14674	908.1832	2721.5277	2723.4382	-1.9104	2	2	75	6	K.FSTFDLAILKTNLTIPENTGKDTGK.G 14708
15390	990.6752	2969.0037	2969.2338	-0.2301	0	3	53	1	R.LAAWVEDDQDDYDEGMELWAHAFDL.-

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340. gi|220694386|gb|EED50730.1| **Mass:** 34275 **Score:** 66 **Queries matched:** 10 **emPAI:** 0.10

mitochondrial phosphate transporter Pic2, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2495	641.7091	1281.4037	1280.6765	0.7272	0	66	3.6e-05	1	K.IVAQEGFGGLYK.G
4743	767.4426	1532.8707	1531.7558	1.1149	0	14	7.1	4	K.FATFEETVNAIYK.T
6081	824.8126	1647.6107	1647.7174	-0.1066	0	(0)	1.5e+02	1	K.YLYGDQMFPNMNR.T
6549	841.7656	1681.5167	1679.7072	1.8095	0	7	27	2	K.YLYGDQMFPNMNR.T
8096	608.4069	1822.1987	1823.9022	-1.7035	1	2	91	6	K.VRMQTTLPPYAQTMR.E
9285	652.9975	1955.9707	1953.0182	2.9525	1	3	65	2	K.GLYPLWARQIPYTMTK.F
10791	1071.2151	2140.4157	2140.0081	0.4076	1	5	39	1	R.MQTTLPPYAQTMREGWSK.I
12142	776.2859	2325.8357	2323.2324	2.6033	2	3	72	8	R.QVDPKIYTSNISAWRSIFAK.E
12690	805.4039	2413.1897	2411.1726	2.0171	2	4	49	4	K.VRMQTTLPPYAQTMREGWSK.I
15756	1041.2595	3120.7567	3118.6413	2.1155	2	0	95	4	R.QIPYTMTKFATFEETVNAIYKTLGKPK.E

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341. gi|220695459|gb|EED51802.1| **Mass:** 71403 **Score:** 66 **Queries matched:** 18 **emPAI:** 0.05

glutaminyl-tRNA synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1196	535.4421	1068.8697	1067.4923	1.3774	0	1	1.3e+02	7	R.ESYEWLNK.T
1503	563.2691	1124.5237	1123.5662	0.9575	0	10	15	1	K.YEPQTAFLR.M
2654	650.3991	1298.7837	1298.6691	0.1146	2	12	9.4	6	K.LQRGGEDGKSPR.F 2659
3926	480.5212	1438.5417	1436.6493	1.8924	0	6	35	6	K.SAEPTLDPDAMFK.Q 3929
4996	779.1486	1556.2827	1555.7664	0.5163	1	1	1.3e+02	10	R.EYGRLNVSGTVMSK.R
6459	838.8081	1675.6017	1675.8471	-0.2453	0	16	3.7	1	R.FPPEPNGYLHLGHAK.A 6468
10305	691.2709	2070.7907	2069.1058	1.6850	2	0	1.2e+02	10	K.DAPKPKAYIQWVPEGSRK.V
10483	1048.5181	2095.0217	2093.0993	1.9224	1	2	83	2	K.AIAINFGFARYHGGVTMLR.F
11059	725.7979	2174.3717	2172.2089	2.1628	2	6	30	8	R.RYLETSVPRLMLVLDPVR.V
11808	1142.3981	2282.7817	2281.2206	1.5611	0	66	3e-05	1	R.VVIQDLGDLDGQELVLPFSPK.Q
12289	784.2842	2349.8307	2348.3005	1.5302	1	3	69	9	K.DFFRLSPGQTVGLLQVPHPIK.A
12298	784.6862	2351.0367	2349.1522	1.8845	2	2	77	2	K.LKMTSTVYIDQSDFREVSSK.D
12663	804.1729	2409.4967	2407.1776	2.3191	1	8	20	2	R.MRQELLTSGNPQMWDIVAYR.I 12647
12793	809.5335	2425.5787	2423.0699	2.5088	1	4	50	1	R.YHGGVTMLRFDDTNPDAEEEK.Y

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342. gi|220698176|gb|EED54516.1| **Mass:** 172254 **Score:** 66 **Queries matched:** 46 **emPAI:** 0.04

pentafunctional polypeptide (AroM), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
69	688.5100	687.5027	687.3551	0.1476	0	8	40	9	K.EAELAR.H
263	**816.5720**	**815.5647**	**815.4752**	**0.0895**	**1**	**16**	**5**	**4**	**K.LEGKELK.E**
545	456.6136	911.2127	911.5916	-0.3789	1	6	34	6	K.GVAVARIVK.C 550
585	921.4650	920.4577	920.4637	-0.0060	1	8	28	10	K.AMKDELAK.F
654	475.6021	949.1897	946.5157	2.6740	0	14	7.5	5	K.GLSLMGEIK.Q
1319	546.5991	1091.1837	1090.6056	0.5781	1	12	10	3	R.KGLSLMGEIK.Q 1320
1852	595.7601	1189.5057	1190.6264	-1.1206	1	5	50	7	K.NKGNVMLIMR.D
1877	**599.3161**	**1196.6177**	**1196.7968**	**-0.1791**	**2**	**8**	**24**	**7**	**K.KKIVLLSAIGR.T**
1911	602.7651	1203.5157	1202.6693	0.8465	1	6	41	3	K.GLSLMGEIKQK.K 1908
2010	611.2821	1220.5497	1218.6642	1.8855	1	(6)	42	5	K.GLSLMGEIKQK.K
2013	611.6301	1221.2457	1221.6064	-0.3606	0	5	48	9	K.QVMDFLNIDK.T
2158	623.1881	1244.3617	1243.6521	0.7097	0	4	69	3	K.DASALVIGGGGTAR.A
2370	635.0111	1268.0077	1267.7037	0.3040	0	11	13	2	K.NLIGAIWQPTR.I 2368
2627	**432.8292**	**1295.4657**	**1292.6798**	**2.7859**	**0**	**5**	**49**	**6**	**K.CIAAYGLPTSLK.D**
3079	674.4926	1346.9707	1346.7591	0.2116	2	3	85	4	R.KGLSLMGEIKQK.K
3135	676.8951	1351.7757	1351.7249	0.0509	1	17	3.3	2	K.KFAVFGTPVSGSR.S
4112	**731.1191**	**1460.2237**	**1459.7154**	**0.5083**	**1**	**4**	**63**	**4**	**R.AQEADADVVKTGEK.A**
4415	**748.8761**	**1495.7377**	**1493.8024**	**1.9353**	**1**	**3**	**70**	**2**	**R.ATASVFIIGMRGAGK.T**
4637	761.9776	1521.9407	1522.7524	-0.8117	0	1	1.2e+02	6	R.FAVEVLGPMGCTVK.Q
4891	**773.7731**	**1545.5317**	**1543.8471**	**1.6846**	**1**	**1**	**1.4e+02**	**2**	**K.GSLPLKVAASGGFAGGR.I**
5133	**524.4679**	**1570.3817**	**1571.7791**	**-1.3973**	**1**	**10**	**17**	**1**	**K.ELKEEESSPLAGAGR.A**
6113	**826.2801**	**1650.5457**	**1647.8468**	**2.6989**	**1**	**1**	**1.3e+02**	**5**	**R.LETANVEDVKDFIR.S**
6405	837.0396	1672.0647	1671.9420	0.1227	2	2	83	1	R.KGSLPLKVAASGGFAGGR.I
7574	887.8536	1773.6927	1771.9502	1.7425	1	4	65	10	K.VCVGSDAVELRVDLLK.D 7543
8042	909.3371	1816.6597	1814.9679	1.6918	1	3	67	7	R.KPGQRWFEGIEDILK.A
8680	629.7755	1886.3047	1885.0170	1.2878	2	2	84	7	R.ILASARHKAYVVSADER.E
9982	1019.7181	2037.4217	2034.9080	2.5137	1	3	71	3	K.GELSWANMSWMKYYNR.A
10738	**712.0539**	**2133.1397**	**2134.0582**	**-0.9185**	**0**	**0**	**1.2e+02**	**3**	**R.LGAATFSWEEEGEVLVVNGK.G**
11423	1112.8391	2223.6637	2222.1232	1.5405	0	1	98	7	R.SPVLHNTLFSQAGLPHEYGR.L 11424
11666	**754.8239**	**2261.4497**	**2260.1344**	**1.3153**	**1**	**5**	**39**	**3**	**K.LTAGKHCSVDQLLFNMALDK.K**
11891	**765.8759**	**2294.6057**	**2292.2266**	**2.3791**	**1**	**3**	**60**	**1**	**K.ILGQESIIADFGLWRNYVAK.D**
12328	**786.7865**	**2357.3377**	**2358.2583**	**-0.9206**	**1**	**7**	**27**	**1**	**K.HSFFVSLTLPDLRTAGDILEK.V** 12321
13231	829.1845	2484.5317	2486.3533	-1.8216	2	0	1.1e+02	6	K.KHSFFVSLTLPDLRTAGDILEK.V
13569	**843.2185**	**2526.6337**	**2527.2993**	**-0.6655**	**0**	**3**	**67**	**4**	**R.DTVVIALGGGVIGDLTGFVASTYMR.G**
14239	**884.9572**	**2651.8497**	**2650.2973**	**1.5524**	**0**	**52**	**0.00074**	**1**	**K.TAAISSEEEFTALEDNAEAILTAVR.S**
15452	**999.3449**	**2995.0127**	**2993.4692**	**1.5435**	**1**	**41**	**0.0087**	**1**	**R.VDLLKDPASDSDIPSVDYVAEQMAFLR.S**
15889	1066.9435	3197.8087	3198.5777	-0.7689	2	2	52	2	K.QVMDFLNIDKTRPAYVEDMMGVWLRR.K
16312	**1142.8019**	**3425.3837**	**3423.7353**	**1.6484**	**1**	**1**	**68**	**6**	**K.TIPTVAIGTIPADKPIDPVMRETLCHMFER.A** 16316

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343. gi|220701102|gb|EED57440.1| **Mass:** 40943 **Score:** 66 **Queries matched:** 13 **emPAI:** 0.08
Phe-inhibited DAHP synthase AroG [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
835	495.1251	988.2357	987.4807	0.7550	0	18	3	3	K.LSAQGMEPR.L 833 838
3133	676.7001	1351.3857	1350.7184	0.6674	0	54	0.0006	1	R.ELASGLSFPVGFK.N 3111
4101	730.5006	1458.9867	1456.6794	2.3073	0	5	55	6	R.QEASAVVHGTDTDK.R
4972	518.5735	1552.6987	1551.8330	0.8657	2	20	1.5	1	K.EKYKDELLIVMR.A 4975
13007	820.7039	2459.0897	2459.1829	-0.0932	1	6	27	6	M.SFFIENPNVGDTNHLEDSRIR.G
13212	828.4615	2482.3627	2481.2322	1.1305	0	7	25	1	R.GYNPLTPPNLLQHEIAMTETSR.Q 13222
13929	863.2415	2586.7027	2588.2073	-1.5046	0	8	18	1	R.LLVVVGPCSIHDPEMALEYCDR.L
15469	1003.6915	3008.0527	3005.4660	2.5867	0	10	9.7	1	K.GMPIASEMLDTISPQFLADCLSVGAVGAR.T

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344. gi|220700807|gb|EED57145.1| **Mass:** 54855 **Score:** 66 **Queries matched:** 18 **emPAI:** 0.06
protein phosphatase PP2A regulatory B subunit, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
103	717.4400	716.4327	717.3194	-0.8867	0	11	20	8	R.FSHDGR.Y
908	502.6171	1003.2197	1001.5366	1.6831	2	8	29	7	K.GANGKKGNTR.A
1199	535.6416	1069.2687	1069.5954	-0.3267	1	9	18	8	K.KVGVPTPMNK.G
1901	401.0609	1200.1607	1201.6554	-1.4946	1	13	8.2	5	K.SLEIEEKINK.I
2065	615.7411	1229.4677	1228.6346	0.8331	2	7	37	4	R.AGSPGGPGSRMKK.E
2549	644.6191	1287.2237	1284.7224	2.5013	2	6	42	4	K.AKKVGVPTPMNK.G 2526
2622	648.6486	1295.2827	1294.5677	0.7150	0	5	51	3	K.ETDADQIDFNK.K 2624
4536	504.7979	1511.3717	1512.8082	-1.4365	2	7	26	4	K.KVGVPTPMNKGANGK.K 4542
5316	794.7901	1587.5657	1585.7988	1.7669	0	66	4.2e-05	1	R.SFFSEIISSISDVR.F
6765	850.2071	1698.3997	1697.7930	0.6067	2	4	54	8	R.MKKETDADQIDFNK.K
10622	706.1682	2115.4827	2113.9747	1.5080	1	1	1.2e+02	7	K.FTHMEMLISLNRCFGDK.G 10614
13136	825.2125	2472.6157	2470.2937	2.3220	2	2	81	7	K.DPSMLKLPRMTHHDTVVAAVPR.R
13251	829.9812	2486.9217	2486.2886	0.6331	2	(0)	1.1e+02	6	K.DPSMLKLPRMTHHDTVVAAVPR.R
13269	830.7009	2489.0807	2486.2886	2.7921	2	(1)	1e+02	4	K.DPSMLKLPRMTHHDTVVAAVPR.R

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345. gi|220699111|gb|EED55450.1| **Mass:** 23790 **Score:** 65 **Queries matched:** 2 **emPAI:** 0.14
hypothetical protein AFLA_027220 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
6726	848.0761	1694.1377	1693.8927	0.2451	0	65	4.5e-05	1	R.VPIDASETFLQLYAK.V
12861	812.7009	2435.0807	2432.2183	2.8624	0	8	20	3	R.LTGDEDIAIGTTSAEDGRPFVLR.V

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346. gi|220689935|gb|EED46285.1| **Mass:** 8589 **Score:** 65 **Queries matched:** 1 **emPAI:** 0.41
NADH-ubiquinone oxidoreductase 9.5 kDa subunit, putative [Aspergillus flavus NRRL3357]

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

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     11765 1140.4156 2278.8167 2278.1634  0.6533  0    65 4.2e-05   1   R.AFGDVDPEPIPLTYPIPQGPR.V

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347.  gi|220701509|gb|EED57847.1|    Mass: 28319    Score: 64    Queries matched: 10   emPAI: 0.25
      eukaryotic translation initiation factor 3 subunit EifCk, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score Expect Rank  Peptide
       541   456.3911   910.7677   909.4379   1.3299   0     7     29    9  R.VGVEMFGR.V
      2507   428.6502  1282.9287  1281.6136   1.3152   1    12    9.4    5  K.SERVGVEMFGR.V
      3814   715.2351  1428.4557  1427.7119   0.7439   0    42   0.01    1  R.TFDCYANLALLK.L 3803
      4132   732.2561  1462.4977  1460.7219   1.7758   2    16      4    2  K.ENEVRSEVKSER.V
      7067   575.6809  1724.0207  1724.8516  -0.8308   2     7     25    4  R.SEVKSERVGVEMFGR.V
      8798   633.7699  1898.2877  1899.9472  -1.6595   0     1 1e+02    7  K.CETRPANIDAILSGLDR.Y
     12057   772.2602  2313.7587  2312.2528   1.5059   0    34  0.045    1  K.LYQFNPHLLQAETVTNILAK.A 12023
     13407  1254.9266  2507.8387  2505.1118   2.7269   0    31  0.087    1  R.YNPETTTIFQDYVVQQCEDR.T

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348.  gi|220690835|gb|EED47184.1|    Mass: 59030    Score: 64    Queries matched: 12   emPAI: 0.11
      aldehyde dehydrogenase, putative [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
       588  461.6341   921.2537   920.4902   0.7635   1    11      14    3  K.FMNPKIR.K
      1102  526.5926  1051.1707  1050.5233   0.6474   0    10      16    1  K.AEDIDLTFK.F 1103
      2618  648.5826  1295.1507  1294.6261   0.5246   1     0 1.5e+02   10  K.GKILMGGTMDEK.E
      4367  497.6335  1489.8787  1490.8205  -0.9418   1    15     4.9    1  R.YILTLGGGSAKAGAGR.A
      5226  527.5972  1579.7697  1579.7698  -0.0001   2     5      49    8  K.GKILMGGTMDEKER.F
      8019  908.2731  1814.5317  1812.0873   2.4444   0     2      88    6  R.AVVVAAVAYLVLQVLER.R 8013
      9355  655.9339  1964.7797  1963.9599   0.8198   0    59 0.00017    1  K.DHEQEIADASALDLGKPR.F
     10407  695.4652  2083.3737  2083.9952  -0.6215   2     3      70    2  K.SMLDNTKGKILMGGTMDEK.E
     11893  765.9392  2294.7957  2294.3362   0.4595   0    21       1    1  K.AAAPHLTPVVLELGGINPAIITK.S 11909

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349.  gi|220689366|gb|EED45717.1|    Mass: 25691    Score: 64    Queries matched: 4   emPAI: 0.13
      UDP-glucose 4-epimerase [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank  Peptide
       567  915.9530   914.9457   914.5549   0.3908   1     4      74    4  R.RIELISGK.K
      3552  698.0856  1394.1567  1393.7453   0.4115   0     3      79    2  R.QEPPAELLEQLK.K
      7023  860.8326  1719.6507  1719.8791  -0.2284   0    64 6.3e-05    1  K.VVVADNLYNSSAEALR.R
     13013  820.7999  2459.3777  2459.2557   0.1220   1     4      49    2  K.SHDGTAIRDYIHILDLADGHLK.A

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350.  gi|220696697|gb|EED53039.1|    Mass: 53916    Score: 63    Queries matched: 21   emPAI: 0.06
      actin-bundling protein Sac6, putative [Aspergillus flavus NRRL3357]
     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score Expect Rank  Peptide
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1245	540.1241	1078.2337	1077.6546	0.5791	0	18	3	2	R.LPPEQILLR.W 1240
1440	558.1316	1114.2487	1112.4622	1.7866	0	2	1e+02	8	R.SDEEAYSNAK.L
2375	**635.6021**	**1269.1897**	**1267.6884**	**1.5013**	**0**	**9**	**21**	**4**	**R.GPLQTQDLLQR.A**
2707	653.6971	1305.3797	1304.6156	0.7641	2	4	68	8	R.WANDMSRRGGR.T
3063	673.3176	1344.6207	1343.7449	0.8758	0	63	8e-05	1	K.FLTPTSLVAGNPK.L 3053 3054
5469	**534.6385**	**1600.8937**	**1599.7246**	**1.1691**	**0**	**4**	**62**	**6**	**R.HVNRPPTSGGEMMR.F**
5536	**536.3252**	**1605.9537**	**1603.7698**	**2.1839**	**1**	**5**	**47**	**5**	**R.MGKHEITDLEMIR.W**
8165	611.0679	1830.1817	1831.9131	-1.7314	2	3	78	9	R.WFNYHLRNARWNR.Q
10487	**699.6505**	**2095.9297**	**2094.1527**	**1.7771**	**1**	**5**	**44**	**6**	**R.LPPEQILLRWFNYHLR.N**
10606	**705.3589**	**2113.0547**	**2112.1150**	**0.9397**	**1**	**3**	**65**	**10**	**K.LGATIWLVPEDICQVRSR.L**
11843	**1143.7746**	**2285.5347**	**2284.1773**	**1.3574**	**1**	**8**	**19**	**1**	**R.SFKDQSIGSGIFLLDVLNGMK.S**
12292	784.3982	2350.1727	2350.2856	-0.1129	2	5	41	3	K.LINDSVPDTIDERVLNKPGKK.I
13993	**869.6112**	**2605.8117**	**2606.2958**	**-0.4841**	**1**	**2**	**74**	**4**	**K.IIPGSVNWRHVNRPPTSGGEMMR.F**
14960	**931.6992**	**2792.0757**	**2793.4555**	**-1.3798**	**2**	**4**	**40**	**6**	**R.GPLQTQDLLQRAEQVLANADKLGCR.K** 14961
15263	**968.8679**	**2903.5817**	**2903.4481**	**0.1337**	**2**	**1**	**89**	**6**	**K.DITNTLSSLAQRMGKHEITDLEMIR.W**
15472	**1005.2115**	**3012.6127**	**3011.5967**	**1.0160**	**2**	**3**	**57**	**2**	**K.IDIKLHPELYRLLEEDETLEQFLR.L** 15475

351. gi|220689881|gb|EED46231.1| **Mass:** 107446 **Score:** 61 **Queries matched:** 14 **emPAI:** 0.06
conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
661	477.3661	952.7177	951.5865	1.1312	0	9	17	5	K.LLLGAVNPR.D
1360	551.1806	1100.3467	1101.5567	-1.2100	0	0	1.7e+02	6	R.VLGWSANNNK.T
5138	**524.6342**	**1570.8807**	**1570.8175**	**0.0632**	**1**	**3**	**72**	**9**	**R.QNVSRSAAADNGLLR.A**
9762	**672.7769**	**2015.3087**	**2014.0517**	**1.2570**	**0**	**48**	**0.0022**	**1**	**R.ITQSEMTVVSSVSHAILGR.W** 9767
9913	678.6622	2032.9647	2030.0466	2.9181	0	(8)	22	2	R.ITQSEMTVVSSVSHAILGR.W
11166	**1096.5806**	**2191.1467**	**2191.2252**	**-0.0785**	**1**	**2**	**82**	**5**	**R.SVLYKYLNPNLILATAVGDK.S** 11185
11258	1100.9981	2199.9817	2199.1059	0.8758	0	3	65	4	R.ILTSFVTDEVSNLDSFGISR.Q
11416	**741.9639**	**2222.8697**	**2223.1081**	**-0.2384**	**2**	**2**	**86**	**3**	**R.RRMNWNINISIMTWLPF.-** 11415
13156	**826.0002**	**2474.9787**	**2475.3705**	**-0.3918**	**1**	**0**	**1.1e+02**	**7**	**-.MRLQATLLLLASCVPSALAIYR.D**
15456	**1000.1375**	**2997.3907**	**2996.5026**	**0.8881**	**1**	**4**	**38**	**1**	**K.DANVYFTRITQSEMTVVSSVSHAILGR.W** 15457

352. gi|220693660|gb|EED50005.1| **Mass:** 17860 **Score:** 61 **Queries matched:** 3 **emPAI:** 0.19
conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
1256	541.2201	1080.4257	1079.6451	0.7806	1	6	36	7	R.LNAHGVLKTK.D
3332	**686.3221**	**1370.6297**	**1368.7361**	**1.8936**	**0**	**61**	**0.00013**	**1**	**R.VNIDAPLAVGSASR.S**
4791	**513.5515**	**1537.6327**	**1536.7936**	**0.8391**	**0**	**29**	**0.16**	**1**	**R.FNIESGKPVVEYR.V**

353. gi|220693774|gb|EED50119.1| **Mass:** 68768 **Score:** 61 **Queries matched:** 8 **emPAI:** 0.05
RNase L inhibitor of the ABC superfamily, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2550	644.6316	1287.2487	1287.7485	-0.4998	2	3	78	5	R.VIKRFIMHTK.K
9055	**964.1236**	**1926.2327**	**1925.9339**	**0.2988**	**0**	**61**	**0.00012**	**1**	**R.AQMDNMEHILDVLELR.Q**
10647	707.6702	2119.9887	2121.0897	-1.1010	2	1	95	8	K.IAFISERLCIGCGICPKK.C
14163	880.5125	2638.5157	2640.2350	-1.7193	2	3	58	4	R.DPNSYRPRINKYQSQMDQEQK.L 14167 14172
14301	887.2652	2658.7737	2658.2748	0.4990	2	8	16	4	R.LAEAGDEFLVNRDRAFTYPSMEK.T
15453	**999.7092**	**2996.1057**	**2993.4555**	**2.6502**	**1**	**3**	**46**	**3**	**R.FAIGLVCVQKADVYMFDEPSSYLDVK.Q**

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354. gi|220698304|gb|EED54644.1| **Mass:** 44331 **Score:** 61 **Queries matched:** 11 **emPAI:** 0.07
60S ribosomal protein L3 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2769	657.5946	1313.1747	1311.7187	1.4561	0	8	28	3	K.YLLPSPPVEAAR.E
3306	**685.2311**	**1368.4477**	**1366.7034**	**1.7444**	**0**	**17**	**2.8**	**1**	**K.GWYLYSPLNVR.V** 3304
7383	880.3676	1758.7207	1757.8849	0.8358	0	61	0.00012	1	R.HLNISDLFNFSQPAR.D
11838	**762.6949**	**2285.0627**	**2286.1790**	**-1.1163**	**2**	**6**	**28**	**1**	**R.LCARENFEPPVAKIISETGR.K**
12063	**772.5809**	**2314.7207**	**2315.1618**	**-0.4411**	**0**	**1**	**1e+02**	**7**	**R.VLPGTDVNAGPVTGTERPNEHR.K** 12079
12161	776.9305	2327.7697	2328.1460	-0.3763	0	4	57	6	K.EWGVEMAAVPGGEVDPGLLQFK.R
13667	848.0552	2541.1437	2541.3739	-0.2301	1	1	1e+02	10	R.LPLTVIFAAMYAYVGPKSLAAMAK.E
15506	1011.7335	3032.1787	3032.4987	-0.3200	1	4	39	1	K.SLAAMAKEWGVEMAAVPGGEVDPGLLQFK.R 15507

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355. gi|220700181|gb|EED56520.1| **Mass:** 31757 **Score:** 59 **Queries matched:** 7 **emPAI:** 0.22
proteasome subunit alpha type 3, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
679	479.9816	957.9487	958.4971	-0.5484	0	11	14	10	K.QLLEEAEK.A
1418	555.7696	1109.5247	1109.6193	-0.0946	0	22	1.1	1	K.GPIPVSALSNR.L
2761	**657.0796**	**1312.1447**	**1310.6255**	**1.5192**	**1**	**6**	**38**	**4**	**R.DEAASWRSVYK.G**
3389	**688.6636**	**1375.3127**	**1375.7572**	**-0.4445**	**0**	**58**	**0.00027**	**1**	**R.HVGIVSAGLVPDGR.H**
12330	**1179.8726**	**2357.7307**	**2355.2580**	**2.4727**	**2**	**1**	**1e+02**	**7**	**K.AVENGGTAIGIRCKDGVVLAVEK.I**
12874	**812.9009**	**2435.6807**	**2435.1063**	**0.5744**	**1**	**7**	**26**	**1**	**K.DKDFELEMSWISSLDGPTHGR.H**
13574	843.4129	2527.2167	2527.3493	-0.1326	2	1	1.1e+02	4	K.AELEKLDLSSGNLSLVDAVKEAAR.I

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356. gi|220698578|gb|EED54918.1| **Mass:** 41800 **Score:** 59 **Queries matched:** 7 **emPAI:** 0.16
aminotransferase, class V, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1758	**1171.9220**	**1170.9147**	**1170.6608**	**0.2539**	**1**	**3**	**91**	**3**	**R.KDIDNAIAALK.E**
6346	557.3169	1668.9287	1667.9471	0.9816	2	8	24	2	K.RGVIFAAGLHKEAATK.Y
6387	**836.4761**	**1670.9377**	**1668.8691**	**2.0686**	**0**	**44**	**0.0061**	**1**	**K.AIGCPPGLSILMTSPR.A**

7584	592.5899	1774.7477	1772.8978	1.8499	1	1	1.2e+02	9	K.DIDNAIAALKEAMAEAK.Q
8941	638.9302	1913.7687	1912.9894	0.7793	0	42	0.0086	1	K.APIGERPSFEEIEQALK.E 8977
16211	1121.5942	3361.7607	3360.6085	1.1522	0	16	2.5	1	K.GENALVLHTGYFADSFATCLQTYGANATQLK.A

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357. gi|220697943|gb|EED54283.1| **Mass:** 52045 **Score:** 58 **Queries matched:** 6 **emPAI:** 0.06
aldehyde dehydrogenase family protein, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
611	465.8936	929.7727	928.5593	1.2134	1	2	1.3e+02	3	R.ALDILEKK.K 612
1062	523.4381	1044.8617	1045.5629	-0.7011	1	12	12	7	K.NSGRGVTLSR.F
1697	580.5296	1159.0447	1158.6033	0.4414	0	58	0.00027	1	R.IPEVAQEAFR.S
5568	537.2475	1608.7207	1607.8631	0.8576	1	3	77	5	R.AKDTIQAHVADAIQK.G
10988	722.7919	2165.3537	2166.1433	-0.7896	2	0	1.2e+02	10	R.IPEVAQEAFRSFSRSTTLK.Q

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358. gi|220697660|gb|EED54001.1| **Mass:** 40101 **Score:** 58 **Queries matched:** 12 **emPAI:** 0.08
casein kinase II beta subunit CKB1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1642	382.5445	1144.6117	1143.6335	0.9782	2	15	5.9	10	R.TGPRMKWLR.M
6528	841.5241	1681.0337	1678.8712	2.1625	0	1	1.2e+02	3	R.YITSRPGIQQMLEK.Y 6523
9262	652.0962	1953.2667	1953.8713	-0.6046	0	1	1.1e+02	3	K.LFCPSCQDLYTPPNSR.F
11619	752.5055	2254.4947	2252.0565	2.4382	1	7	26	1	R.MKPTDVEELNEMARYEAAR.R
12450	793.2362	2376.6867	2376.0135	0.6732	0	0	1.2e+02	9	R.EADNDGDTEMGAAPAGGAQNSAIAK.R
12605	801.2369	2400.6887	2399.2696	1.4191	0	47	0.0024	1	R.VASDLSVIESSAELLYGLIHQR.Y 12599
13635	846.0322	2535.0747	2532.1146	2.9601	1	5	41	3	R.EADNDGDTEMGAAPAGGAQNSAIAKR.K
14316	887.8535	2660.5387	2660.2096	0.3291	2	3	55	9	R.EADNDGDTEMGAAPAGGAQNSAIAKRK.K 14296
15290	975.7279	2924.1617	2925.3659	-1.2042	2	2	60	2	K.YEMQHFGVCPRVYCNGCKVLPVGR.S

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359. gi|220699758|gb|EED56097.1| **Mass:** 14061 **Score:** 58 **Queries matched:** 22 **emPAI:** 1.38
60S ribosomal protein L31e [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
573	917.5710	916.5637	916.4978	0.0659	0	33	0.1	1	R.SAIADVVSR.E 570 572 574 581
635	472.0851	942.1557	942.5399	-0.3842	1	7	32	5	K.RLHGVSFK.K
728	968.4610	967.4537	967.4645	-0.0107	0	8	24	7	-.MSTTVQTGK.K 715
1193	535.2906	1068.5667	1068.5088	0.0580	0	22	0.85	1	K.GLHTAVVDEE.- 1195
1235	1077.3320	1076.3247	1075.4781	0.8466	1	5	55	3	R.NDEENAKEK.L
1423	556.9916	1111.9687	1110.5492	1.4196	1	6	45	5	K.AFTERAMGTK.D
2535	1286.9950	1285.9877	1285.6740	0.3137	0	(18)	2.7	1	K.LYSMVYAVNVK.E 2540
2683	652.0961	1302.1777	1301.6689	0.5088	0	46	0.0041	1	K.LYSMVYAVNVK.E 2672 2685 2691
2921	665.6021	1329.1897	1328.7524	0.4373	2	4	74	2	K.KQRSAIADVVSR.E
6030	823.3216	1644.6287	1643.8665	0.7623	2	6	43	1	R.AMGTKDVRIDPALNK.K 6019 6035

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360. gi|220699360|gb|EED55699.1| **Mass:** 90472 **Score:** 57 **Queries matched:** 12 **emPAI:** 0.11

proliferating cell nuclear antigen (PCNA) [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
409	867.5030	866.4957	866.4385	0.0572	0	8	23	5	R.LSEYDIK.L
601	464.0951	926.1757	925.4294	0.7464	0	11	10	8	K.AEGFSPYR.C
1445	**1116.4290**	**1115.4217**	**1115.5683**	**-0.1466**	**1**	**4**	**64**	**5**	**R.LEDQAQTRR.C**
1635	**572.6161**	**1143.2177**	**1140.6615**	**2.5563**	**1**	**7**	**37**	**5**	**R.AKQAAALLEAR.L**
3176	**679.2686**	**1356.5227**	**1354.8184**	**1.7043**	**0**	**32**	**0.094**	**1**	**R.NIALGINLVSLTK.V**
3769	475.5265	1423.5577	1421.7263	1.8315	1	6	34	4	R.ATEDQYSLRALR.T
5353	795.9661	1589.9177	1587.8355	2.0822	0	10	17	2	R.DLNALSESVVIEATK.E 5314 5315
13574	843.4129	2527.2167	2525.3312	1.8855	0	45	0.004	1	K.VSLCLSQEVPLLVEYGLGSGHLR.F
15609	**1020.8192**	**3059.4357**	**3058.4196**	**1.0161**	**0**	**1**	**87**	**9**	**M.ESLVYENSPLADYLQGEGEHDPSWPVK.E**
16154	**1112.7745**	**3335.3017**	**3333.5533**	**1.7484**	**0**	**23**	**0.46**	**1**	**K.LMDIDQEHLAIPETEYAATVEMPSAEFQR.I**

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361. gi|220690750|gb|EED47099.1| **Mass:** 64173 **Score:** 57 **Queries matched:** 21 **emPAI:** 0.05

methylmalonate-semialdehyde dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
233	800.5750	799.5677	799.4552	0.1125	0	17	3.6	4	R.VQANLGAK.N 232
2157	**623.1776**	**1244.3407**	**1243.6772**	**0.6636**	**1**	**2**	**1.2e+02**	**3**	**K.RIEDLIASAEK.E**
2658	**650.5326**	**1299.0507**	**1298.6904**	**0.3603**	**0**	**57**	**0.00035**	**1**	**R.DPGAAMILAELAK.E**
2773	657.6781	1313.3417	1314.6853	-1.3436	0	(8)	27	5	R.DPGAAMILAELAK.E
3499	**463.8619**	**1388.5637**	**1387.7823**	**0.7814**	**1**	**6**	**45**	**8**	**K.ILLDGRGYKPEK.Y**
4209	**737.3736**	**1472.7327**	**1472.7722**	**-0.0395**	**1**	**4**	**66**	**2**	**R.IEDLIASAEKEGAK.I** 4202
4388	747.2191	1492.4237	1490.7816	1.6421	1	1	1.1e+02	5	K.AFPAWRAMSVIAR.Q
4675	763.4206	1524.8267	1524.8486	-0.0219	1	10	14	2	R.QQIMFKFVSLIR.A
4751	**767.7986**	**1533.5827**	**1530.7018**	**2.8810**	**0**	**5**	**50**	**5**	**R.SLMTASMSSSSALAR.R**
6163	**552.4255**	**1654.2547**	**1651.8682**	**2.3865**	**0**	**4**	**54**	**3**	**K.EAGFPAGVVNIVHGSAK.T**
7574	887.8536	1773.6927	1771.9217	1.7711	1	4	54	6	R.ANWDRLAASITLEQGK.T
9309	**654.3642**	**1960.0707**	**1957.9592**	**2.1115**	**1**	**1**	**1.2e+02**	**7**	**R.VPQSTDEELRAAVESAEK.A**
9665	668.6535	2002.9387	2000.9619	1.9768	1	2	85	7	R.SATSRSLMTASMSSSSALAR.R
9784	**673.8219**	**2018.4437**	**2016.9568**	**1.4869**	**1**	**(1)**	**1.1e+02**	**5**	**R.SATSRSLMTASMSSSSALAR.R**
11707	**757.6485**	**2269.9237**	**2269.2439**	**0.6798**	**2**	**1**	**1.1e+02**	**10**	**R.AMSVIARQQIMFKFVSLIR.A**
12171	**777.4405**	**2329.2997**	**2331.2546**	**-1.9549**	**2**	**1**	**91**	**3**	**R.LAASITLEQGKTFADARGDVLR.G**
12801	**810.0785**	**2427.2137**	**2427.2281**	**-0.0144**	**1**	**2**	**72**	**1**	**K.ALNVNGGFEEGADLGPVISPESKK.R**
14125	**877.3015**	**2628.8827**	**2626.3602**	**2.5225**	**2**	**4**	**49**	**2**	**R.AKALNVNGGFEEGADLGPVISPESKK.R**
15754	1040.9625	3119.8657	3119.5479	0.3179	1	0	93	9	R.GLQVAETACGITTQLTGEVLEVAKDMETR.S

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362. gi|220692901|gb|EED49247.1| **Mass:** 40176 **Score:** 55 **Queries matched:** 9 **emPAI:** 0.17
disulfide isomerase (TigA), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
641	**945.9070**	**944.8997**	**945.4403**	**-0.5406**	**0**	**31**	**0.17**	**1**	**K.VDAEAENAK.A**
2079	617.6791	1233.3437	1234.7074	-1.3637	1	0	1.7e+02	9	K.KFGIQGFPTLK.W
3806	714.8081	1427.6017	1426.6616	0.9401	0	42	0.01	1	R.SEEAFVEFVNEK.A 3800 3804 3810
9171	**648.2782**	**1941.8127**	**1942.8652**	**-1.0525**	**2**	**3**	**69**	**2**	**R.QFLSQEKADMDMKDEL.-**
12608	801.2705	2400.7897	2398.1210	2.6687	1	5	35	2	K.QEPSEVEMLTDSSFKTTIGGDK.D 12591

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363. gi|220698099|gb|EED54439.1| **Mass:** 30185 **Score:** 55 **Queries matched:** 7 **emPAI:** 0.11
26S proteasome regulatory subunit S5A [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
78	**691.9480**	**690.9407**	**690.3184**	**0.6223**	**1**	**7**	**44**	**3**	**K.KEDGDK.M**
8068	607.1489	1818.4247	1816.8746	1.5501	1	9	20	2	K.MRVHPQSAVGLMSMGGK.G
10230	**688.4409**	**2062.3007**	**2063.0423**	**-0.7415**	**0**	**6**	**37**	**1**	**K.INVSIDVIAFGDLESDQTK.K**
11140	**730.3592**	**2188.0557**	**2187.1324**	**0.9233**	**0**	**43**	**0.0061**	**1**	**K.GPEVLSTFTSDFGAILAGLHR.T** 11135
13099	**823.7369**	**2468.1887**	**2466.2676**	**1.9211**	**2**	**2**	**77**	**2**	**K.MKKINVSIDVIAFGDLESDQTK.K** 13093

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364. gi|220696140|gb|EED52482.1| **Mass:** 116943 **Score:** 55 **Queries matched:** 23 **emPAI:** 0.09
glycine dehydrogenase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3	**603.4080**	**602.4007**	**602.3024**	**0.0984**	**0**	**13**	**12**	**6**	**K.AELDR.F**
425	**437.5196**	**873.0247**	**873.4920**	**-0.4672**	**1**	**5**	**60**	**5**	**R.KQIDVSGK.T**
1653	1148.1930	1147.1857	1146.5768	0.6089	0	19	2.2	2	K.TSNLDLEDLK.A
1696	**580.3856**	**1158.7567**	**1157.6808**	**1.0759**	**0**	**35**	**0.06**	**1**	**K.LAALGYNVPIK.T**
3506	**463.9869**	**1388.9387**	**1389.7980**	**-0.8592**	**0**	**4**	**66**	**7**	**K.ITLLNANYILSR.L**
3706	708.4281	1414.8417	1412.6895	2.1522	0	1	1.4e+02	6	R.QEIAEVESGAQPR.E
5712	810.7801	1619.5457	1619.7692	-0.2235	0	33	0.074	1	K.APGEFGADIAFGNAQR.F 5727
6269	555.0185	1662.0337	1661.8712	0.1626	2	11	13	6	R.CAHEFILDVRKFK.E
6281	**555.3255**	**1662.9547**	**1662.8114**	**0.1433**	**0**	**8**	**24**	**3**	**R.DLLSNEWNRPYTR.E**
9424	**988.2856**	**1974.5567**	**1974.0020**	**0.5548**	**0**	**36**	**0.033**	**1**	**K.EMLATLDPPVASLDEFVK.Q**
9493	992.2211	1982.4277	1982.0877	0.3400	0	7	26	2	K.TYIGTGYYGTIVPPVILR.N 9494
9624	999.7091	1997.4037	1996.9975	0.4062	0	1	1.1e+02	4	K.AYVVSHLCHPQTIAVMR.S
10131	**685.2312**	**2052.6717**	**2053.0440**	**-0.3722**	**1**	**3**	**64**	**4**	**R.QEIAEVESGAQPREGNVLK.M** 10122 10130
13232	**829.2645**	**2484.7717**	**2482.2243**	**2.5474**	**1**	**1**	**1e+02**	**2**	**K.RNICLIPVSAHGTNPASAAMAGMK.V**
14347	889.8975	2666.6707	2667.3254	-0.6547	1	2	77	8	K.HKDELAAVMITYPSTFGVYEPGVK.E
15066	944.1335	2829.3787	2827.4174	1.9613	2	2	75	2	K.TNLYRDNVGGGLGETDMLKLLDVYR.K
15258	**968.6005**	**2902.7797**	**2902.4503**	**0.3294**	**2**	**0**	**98**	**9**	**R.YIRHLESKDLSLAHSMIPLGSCTMK.L**
15372	**988.2855**	**2961.8347**	**2963.4950**	**-1.6603**	**1**	**13**	**5.7**	**1**	**R.HIGPSPDAAKEMLATLDPPVASLDEFVK.Q**
15571	**1018.4399**	**3052.2977**	**3053.4772**	**-1.1795**	**0**	**15**	**3.3**	**1**	**K.ATSNICTAQALLANMSAMYAVYHGPTGLK.S**

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365. gi|220700026|gb|EED56365.1| **Mass:** 67076 **Score:** 54 **Queries matched:** 9 **emPAI:** 0.05
phosphoenolpyruvate carboxykinase AcuF [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
992	515.6901	1029.3657	1028.5978	0.7679	2	9	24	3	R.SPSDKRIVK.E
2099	618.8401	1235.6657	1235.6258	0.0399	1	4	63	10	R.ERAVDYLNTR.N
5568	537.2475	1608.7207	1608.8017	-0.0810	1	2	98	9	R.VVCARAYHALFMR.N
6488	840.1981	1678.3817	1677.8726	0.5091	0	54	0.00055	1	R.FGSVLENVVFDPISR.V
10732	711.3279	2130.9617	2129.0442	1.9175	2	2	88	7	R.NRIYVIDGFAGWDERYR.I 10736
10882	717.2365	2148.6877	2149.1062	-0.4185	1	2	75	4	R.NMVATSVNRTALHPGGVQPGK.G
13651	**846.8229**	**2537.4467**	**2537.3139**	**0.1328**	**1**	**0**	**1.1e+02**	**4**	**K.ISQHKANAWLLNTGWVGAGATTGGK.R**
15904	**1070.1725**	**3207.4957**	**3208.6262**	**-1.1305**	**2**	**0**	**93**	**9**	**K.EMVILGTEYAGEMKKGVFTVLFYEMPVK.H**

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366. gi|220697448|gb|EED53789.1| **Mass:** 20499 **Score:** 54 **Queries matched:** 9 **emPAI:** 0.16
mitochondrial hypoxia responsive domain protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
6157	552.1452	1653.4137	1654.8209	-1.4072	2	3	73	8	R.QRHAAMEAAAAEAGKK.T
7584	592.5899	1774.7477	1773.7960	0.9517	2	6	34	1	R.SMKAGDSVEMNRMFR.A 7573
7777	896.2206	1790.4267	1789.7909	0.6358	2	(6)	37	7	R.SMKAGDSVEMNRMFR.A
8507	**935.1996**	**1868.3847**	**1866.9183**	**1.4664**	**2**	**1**	**1.1e+02**	**4**	**K.TAPHDAARSAIERSEEK.S**
9087	**644.4872**	**1930.4397**	**1930.0371**	**0.4026**	**2**	**5**	**48**	**6**	**R.SAIERSEEKSIGVLDAVK.E**
11681	**756.2429**	**2265.7067**	**2264.1874**	**1.5193**	**1**	**38**	**0.02**	**1**	**R.LKEEPLIPLGCAATSYALYR.A** 11682
14389	891.2629	2670.7667	2669.1803	1.5864	0	2	72	5	-.MSSDPVPSSFEGNPQFEEETSLQK.F

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367. gi|220692210|gb|EED48557.1| **Mass:** 16780 **Score:** 54 **Queries matched:** 7 **emPAI:** 0.20
40S ribosomal protein S26 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
701	482.3616	962.7087	962.5522	0.1565	2	7	35	4	R.RNRAPPPR.I
915	503.9706	1005.9267	1005.4913	0.4354	0	12	10	1	R.NMVESAAIR.D
2226	**627.1851**	**1252.3557**	**1250.5318**	**1.8239**	**1**	**2**	**97**	**6**	**R.CSNCARCVPK.D**
5818	**814.7261**	**1627.4377**	**1626.7777**	**0.6600**	**0**	**52**	**0.00095**	**1**	**R.DISDASVFTDYAVPK.M** 5831
13904	**861.8019**	**2582.3837**	**2580.2905**	**2.0932**	**2**	**3**	**64**	**7**	**M.TGLAQPHHESPGASRQPNPTSQRK.A**
14081	**873.3319**	**2616.9737**	**2614.2585**	**2.7153**	**1**	**1**	**95**	**4**	**R.NMVESAAIRDISDASVFTDYAVPK.M**

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368. gi|220701562|gb|EED57900.1| **Mass:** 34827 **Score:** 54 **Queries matched:** 4 **emPAI:** 0.10
regulatory protein SUAPRGA1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
14	635.4920	634.4847	634.3472	0.1375	0	5	59	5	-.MLSLR.T

10662	**708.6729**	**2122.9967**	**2120.0273**	**2.9694**	**1**	**9**	**14**	**1**	**K.QSQAEGDFELAAKLEDELK.H**
13902	**861.7275**	**2582.1607**	**2581.2336**	**0.9271**	**0**	**39**	**0.015**	**1**	**R.QSLYAGPPFENLDEDLQTFLER.Y** 13899

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369. gi\|220699124\|gb\|EED55463.1\| **Mass:** 49720 **Score:** 54 **Queries matched:** 9 **emPAI:** 0.07

saccharopine dehydrogenase Lys9, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
8042	909.3371	1816.6597	1815.8648	0.7950	1	7	27	2	R.DMVMLQHKFEIEHK.D 8041
9176	648.5825	1942.7257	1940.8318	1.8939	0	2	81	3	R.TSTMCEYGVIGGYSAMAK.T 9173
9813	675.0902	2022.2487	2022.8961	-0.6474	1	3	60	8	K.MQYGPEERDMVMLQHK.F
9867	676.5959	2026.7657	2024.0877	2.6780	2	2	81	6	K.TIVRGTLRYQGFPEMIK.V
12149	1164.3561	2326.6977	2327.0232	-0.3255	1	0	1.2e+02	5	K.ETRTSTMCEYGVIGGYSAMAK.T
12989	**819.3265**	**2454.9577**	**2453.3934**	**1.5644**	**0**	**48**	**0.0019**	**1**	**K.ALEQVDLAISLIPYTFHALVIK.S** 12991

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370. gi\|220699549\|gb\|EED55888.1\| **Mass:** 109134 **Score:** 53 **Queries matched:** 19 **emPAI:** 0.03

SNARE-dependent exocytosis protein (Sro7), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
83	702.3110	701.3037	700.3868	0.9170	0	8	35	8	K.QNLAQK.Y
280	826.5550	825.5477	825.3361	0.2117	0	14	6	3	K.MQEQMK.L
499	451.3476	900.6807	901.4882	-0.8075	1	15	6.9	4	R.SSFLRHR.S 498
630	938.6990	937.6917	937.4361	0.2556	1	7	29	8	K.KMQEQMK.L
1364	**1101.9310**	**1100.9237**	**1100.5686**	**0.3551**	**2**	**3**	**87**	**10**	**K.LEDQERRR.L**
4426	**749.7906**	**1497.5667**	**1497.7787**	**-0.2120**	**0**	**5**	**50**	**4**	**K.GNGDDSGLLIAGGKPK.A**
5212	527.2382	1578.6927	1579.6970	-1.0043	1	2	95	7	K.MQEQMKLEDQER.R
5412	799.1471	1596.2797	1595.6919	0.5878	1	(0)	1.4e+02	3	K.MQEQMKLEDQER.R
5443	534.2212	1599.6417	1599.8667	-0.2250	2	5	44	7	-.MAHFLRGKQAGIQK.D
7151	579.8092	1736.4057	1734.7085	1.6972	1	7	27	7	K.EMGCKEINYMADMK.R
7915	**602.5242**	**1804.5507**	**1805.9498**	**-1.3991**	**1**	**5**	**43**	**5**	**R.FCPVIALSFSPRDIGK.I** 7943
8983	959.1546	1916.2947	1914.9548	1.3399	1	5	41	5	R.FEDRNVITTAHADGTIR.L 8982
9368	**984.6486**	**1967.2827**	**1965.9320**	**1.3507**	**0**	**53**	**0.00063**	**1**	**K.DLSDGLSPDLFALDDFAR.Y**
11720	**759.0389**	**2274.0947**	**2271.2012**	**2.8935**	**0**	**5**	**44**	**1**	**K.HSQVGFVAAGFEGGSLVIIDLR.G**
13382	**836.1155**	**2505.3247**	**2507.1929**	**-1.8681**	**0**	**1**	**84**	**2**	**R.LWDVGHDDEIENGDVIQVDLAR.A**
13856	858.5289	2572.5647	2574.4381	-1.8734	0	0	1.1e+02	8	K.VISIIPINAETGDLALATPNAVGGLR.N

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371. gi\|220695582\|gb\|EED51925.1\| **Mass:** 33191 **Score:** 53 **Queries matched:** 16 **emPAI:** 0.21

pyridoxine biosynthesis protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2291	631.1161	1260.2177	1259.6761	0.5416	0	35	0.055	1	R.ELEVPYELLR.E 2288
3091	450.3429	1348.0067	1347.7292	0.2775	2	1	1.3e+02	10	R.RISEGAAMIRTK.G
3848	**716.5616**	**1431.1087**	**1430.7513**	**0.3574**	**0**	**42**	**0.01**	**1**	**K.EIMEAVTIPVMAK.A** 3841

4180	**1469.1470**	**1468.1397**	**1468.8038**	**-0.6641**	**1**	**7**	**27**	**1**	**K.AIVQAVTHYKDPK.V**
4557	758.4056	1514.7967	1516.7555	-1.9588	0	4	65	3	R.IAEEAGAAAVMALER.V
5710	**810.6466**	**1619.2787**	**1616.8046**	**2.4742**	**0**	**11**	**11**	**1**	**R.AILQSSPDYEPELR.A**
6671	846.0321	1690.0497	1689.8793	0.1704	1	1	1.1e+02	10	K.EIMEAVTIPVMAKAR.I 6655
7023	860.8326	1719.6507	1718.8345	0.8163	1	3	79	9	K.APFVCGCRNLGEALR.R
8277	**615.6542**	**1843.9407**	**1843.9428**	**-0.0021**	**1**	**2**	**79**	**9**	**R.ARAILQSSPDYEPELR.A**
12315	**785.7579**	**2354.2517**	**2352.1449**	**2.1069**	**1**	**1**	**98**	**4**	**R.MSDPSMIKEIMEAVTIPVMAK.A**
13889	**861.0735**	**2580.1987**	**2579.2831**	**0.9156**	**2**	**8**	**18**	**3**	**R.MSDPSMIKEIMEAVTIPVMAKAR.I** 13888
13964	**866.2682**	**2595.7827**	**2595.2780**	**0.5047**	**2**	**(1)**	**91**	**1**	**R.MSDPSMIKEIMEAVTIPVMAKAR.I**

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372. gi\|220699084\|gb\|EED55423.1\| **Mass:** 43958 **Score:** 53 **Queries matched:** 27 **emPAI:** 0.08

3-ketoacyl-coA thiolase peroxisomal A precursor [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
367	**428.9971**	**855.9797**	**855.5542**	**0.4256**	**1**	**4**	**66**	**10**	**R.LGQKIIGK.Y**
1657	**575.3101**	**1148.6057**	**1149.6506**	**-1.0449**	**2**	**5**	**58**	**2**	**R.SALTKGGKGGFK.D** 1659
1835	**1188.5650**	**1187.5577**	**1187.6510**	**-0.0933**	**1**	**1**	**1.3e+02**	**8**	**K.TITVKADDGIR.D** 1837
2716	**654.3976**	**1306.7807**	**1306.6261**	**0.1546**	**0**	**21**	**1.2**	**1**	**K.VPMGVLSENMAK.D**
3456	**693.1961**	**1384.3777**	**1384.6623**	**-0.2846**	**0**	**9**	**20**	**1**	**R.AVQDAFAASSYQK.A**
5721	811.1211	1620.2277	1619.8559	0.3718	0	8	23	8	K.AGLFNEEIYPLQVK.W
6994	858.9536	1715.8927	1717.8846	-1.9919	2	4	53	9	K.SGEEKTITVKADDGIR.D
6999	**859.2356**	**1716.4567**	**1717.8887**	**-1.4319**	**2**	**1**	**1.2e+02**	**10**	**K.WTDPKSGEEKTITVK.A**
7744	894.7326	1787.4507	1786.9247	0.5260	0	47	0.0033	1	R.QCSSGLQAIVDIANAIK.S 7742
8172	916.5801	1831.1457	1831.0091	0.1366	1	3	79	4	K.DTAAADILAGIFKGVIEK.S 8158 8159
9414	**658.6942**	**1973.0607**	**1974.9979**	**-1.9372**	**2**	**2**	**96**	**9**	**K.VPMGVLSENMAKDRGISR.A**
10712	**710.5982**	**2128.7727**	**2129.9731**	**-1.2003**	**0**	**2**	**75**	**2**	**K.IGVTSMCVGTGMGMAAVWVR.E**
10844	**716.1839**	**2145.5297**	**2146.0589**	**-0.5292**	**1**	**3**	**59**	**3**	**-.MSSAQQRLTQVASHFTPGGK.K** 10827 10833 10839 10856 108
11458	1115.4701	2228.9257	2226.0782	2.8475	1	1	1e+02	2	K.KIGVTSMCVGTGMGMAAVWVR.E
11663	**754.7275**	**2261.1607**	**2259.0157**	**2.1451**	**1**	**0**	**1.2e+02**	**6**	**K.IGVTSMCVGTGMGMAAVWVRE.-**
12378	790.7629	2369.2667	2371.1157	-1.8490	2	5	35	2	K.KIGVTSMCVGTGMGMAAVWVRE.-
13860	858.6879	2573.0417	2570.2478	2.7940	2	1	92	6	R.TDKKIGVTSMCVGTGMGMAAVWVR.E

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373. gi\|220694197\|gb\|EED50541.1\| **Mass:** 20389 **Score:** 53 **Queries matched:** 2 **emPAI:** 0.16

cytochrome c subunit Vb, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
8485	**622.7622**	**1865.2647**	**1863.8971**	**1.3676**	**0**	**47**	**0.0028**	**1**	**K.MQGIDIFDMRPLDASR.K** 8491

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374. gi\|220694193\|gb\|EED50537.1\| **Mass:** 13528 **Score:** 53 **Queries matched:** 4 **emPAI:** 0.57

ribosomal protein L34 protein, putative [Aspergillus flavus NRRL3357]

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

777	489.5991	977.1837	976.5229	0.6608	0	41	0.015	1	R.AFLIEEQK.I 776
1230	538.3631	1074.7117	1074.6662	0.0455	0	32	0.12	1	K.LPGVPALRPR.E
1394	**554.2311**	**1106.4477**	**1106.5720**	**-0.1243**	**0**	**11**	**13**	**5**	**R.EYSQISRPK.K**

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375. gi|220691333|gb|EED47681.1| **Mass:** 145847 **Score:** 53 **Queries matched:** 20 **emPAI:** 0.05

phospholipase D (PLD), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
263	816.5720	815.5647	815.5116	0.0531	1	18	3.5	1	K.ELLSKVK.G 261
1211	**536.5761**	**1071.1377**	**1070.5833**	**0.5545**	**1**	**4**	**72**	**1**	**R.QVPGAKTASGR.W**
1966	607.2381	1212.4617	1211.6047	0.8570	0	12	8.9	7	R.LSSFGHPSQPR.G 1964
3674	**705.8286**	**1409.6427**	**1409.7627**	**-0.1199**	**0**	**9**	**20**	**1**	**R.INVSGPLVQAEQR.S**
4227	738.2371	1474.4597	1473.6567	0.8030	0	12	11	2	R.IAFMGGLDMCFGR.W 4214 4217 4222 4231
4514	**503.4985**	**1507.4737**	**1505.6465**	**1.8272**	**0**	**(2)**	**1e+02**	**9**	**R.IAFMGGLDMCFGR.W**
4776	**513.1795**	**1536.5167**	**1536.7321**	**-0.2154**	**1**	**8**	**22**	**1**	**R.FGSFAPDRQGNDVK.W**
5349	530.7885	1589.3437	1587.8515	1.4922	2	3	71	9	R.LDRMLQSAAQRGVK.V 5314
9121	**646.1249**	**1935.3527**	**1934.0010**	**1.3517**	**0**	**37**	**0.026**	**1**	**R.LVADPLADTLHNLWNSR.A** 9136
9978	1019.4761	2036.9377	2034.0417	2.8960	0	36	0.032	1	K.GTLVEMPLMFLIEEDVAK.S 9967
12010	770.7095	2309.1067	2308.1383	0.9685	1	2	87	4	R.MGWSDISVSLHGHVVEDLRR.H

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376. gi|220693980|gb|EED50325.1| **Mass:** 23266 **Score:** 53 **Queries matched:** 7 **emPAI:** 0.31

adenine phosphoribosyltransferase 1 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
642	**473.5626**	**945.1107**	**944.5444**	**0.5664**	**0**	**37**	**0.038**	**1**	**R.LGASFVPVR.K**
1635	572.6161	1143.2177	1142.6812	0.5366	0	44	0.007	1	R.GFLIGPSLALR.L
10634	**707.1485**	**2118.4237**	**2116.0988**	**2.3249**	**0**	**0**	**1.3e+02**	**2**	**K.MGGELMSFLFILELEFLK.G**
11757	1140.1081	2278.2017	2276.1836	2.0181	1	3	60	2	K.KMGGELMSFLFILELEFLK.G 11760 11762
16280	**1136.9722**	**3407.8947**	**3406.7965**	**1.0982**	**0**	**3**	**41**	**2**	**R.QFPDFPSPGILFEDILPIFANPTLHEALLR.S**

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377. gi|220692310|gb|EED48657.1| **Mass:** 28516 **Score:** 53 **Queries matched:** 10 **emPAI:** 0.12

proteasome component Pre9, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2860	**662.5846**	**1323.1547**	**1321.6734**	**1.4814**	**1**	**4**	**56**	**1**	**K.EACAMAVKVLSK.T**
4689	**509.8109**	**1526.4107**	**1527.7318**	**-1.3210**	**1**	**5**	**43**	**4**	**R.YDSRTTIFSPEGR.L**
6458	838.8021	1675.5897	1675.8992	-0.3095	2	4	55	3	K.KVTSKLLEQDTSAEK.L
9405	658.1592	1971.4557	1968.9682	2.4875	2	(0)	1.3e+02	8	K.EACAMAVKVLSKTMDSTK.L
9506	**662.5845**	**1984.7317**	**1984.9632**	**-0.2314**	**2**	**2**	**91**	**6**	**K.EACAMAVKVLSKTMDSTK.L**
9633	**667.4069**	**1999.1987**	**2000.9581**	**-1.7593**	**2**	**(1)**	**1.1e+02**	**3**	**K.EACAMAVKVLSKTMDSTK.L**
10434	**697.3055**	**2088.8947**	**2087.0456**	**1.8491**	**2**	**1**	**1.1e+02**	**8**	**K.TMDSTKLSSEKIEFATVGK.T**
12843	**811.8292**	**2432.4657**	**2430.3158**	**2.1499**	**0**	**53**	**0.00061**	**1**	**R.LYQVEYALEAISHAGTALGILAK.D** 12829 12837

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378. gi|220701423|gb|EED57761.1| **Mass:** 107781 **Score:** 53 **Queries matched:** 21 **emPAI:** 0.03

Hsp70 family chaperone Lhs1/Orp150, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
62	**685.4680**	**684.4607**	**684.3806**	**0.0801**	**0**	**8**	**23**	**5**	**K.EQAPLK.E** 63
234	401.0606	800.1067	801.4708	-1.3641	1	19	2.6	4	K.TELGRVK.A
1556	566.6856	1131.3567	1131.6400	-0.2833	1	11	15	3	K.GAALSPSFRVK.D
2027	613.0426	1224.0707	1223.6299	0.4409	0	9	19	4	R.FYGGDALALAAR.Y
2692	652.2681	1302.5217	1302.6820	-0.1603	0	11	15	2	K.LFTPTSQVGPEK.Q
3080	674.6756	1347.3367	1347.6969	-0.3601	2	9	22	4	K.TMARLWKDAEK.V 3104
3281	**683.8791**	**1365.7437**	**1364.6718**	**1.0719**	**2**	**0**	**1.4e+02**	**6**	**K.MGAAAAKSGKDQSK.K**
3676	706.1306	1410.2467	1410.6449	-0.3982	0	2	95	5	K.ESFGCSPANITTK.F 3670
3746	710.7916	1419.5687	1418.7630	0.8057	2	3	76	6	R.VKARLAAFDASDR.D
5648	539.1325	1614.3757	1615.8967	-1.5210	2	5	49	8	K.NAKTVLDLMEKQVK.Q
6251	554.7192	1661.1357	1660.9109	0.2248	0	3	73	5	K.DIFLVEELLAMQLK.Q
6383	**836.4151**	**1670.8157**	**1669.8279**	**0.9878**	**2**	**3**	**79**	**1**	**R.TMNRIYEKMGAAAAK.S**
10513	**1050.7201**	**2099.4257**	**2100.1943**	**-0.7686**	**2**	**2**	**80**	**1**	**R.FTSSPLGIPALSKTELGRVK.A**
11063	726.0342	2175.0807	2175.3354	-0.2547	2	21	1	2	K.AVLVKPGIPLEIVLTKDSKR.K 11074
13585	843.9092	2528.7057	2530.2949	-1.5892	1	1	86	2	K.TLGGDSLNDLVVGDMIANLVQDKK.L
14850	**924.2839**	**2769.8297**	**2771.4739**	**-1.6442**	**2**	**2**	**76**	**4**	**K.TLGGDSLNDLVVGDMIANLVQDKKLK.D**
15540	**1014.6622**	**3040.9647**	**3038.6513**	**2.3135**	**0**	**53**	**0.00056**	**1**	**R.VGQPLEQALAAAGLQLNDIDSVILHGGAIR.T**

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379. gi|220696618|gb|EED52960.1| **Mass:** 19331 **Score:** 52 **Queries matched:** 4 **emPAI:** 0.17

glutathione S-transferase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5165	525.3512	1573.0317	1570.8177	2.2140	0	11	13	3	K.NPALFMLLDPTAPR.E
7433	882.5811	1763.1477	1761.9566	1.1911	0	2	93	3	K.YPQLATALGAVWFVAR.S
12509	**796.0645**	**2385.1717**	**2383.2899**	**1.8818**	**0**	**44**	**0.0053**	**1**	**R.AHANFLENAPQTILYTLVAGLK.Y** 12514

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380. gi|220691712|gb|EED48060.1| **Mass:** 47020 **Score:** 52 **Queries matched:** 9 **emPAI:** 0.15

homocysteine synthase CysD [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2065	615.7411	1229.4677	1229.6615	-0.1938	0	16	4	2	K.LISNLANVGDSK.T
2584	646.6121	1291.2097	1291.6482	-0.4385	0	(3)	85	10	R.IMNPTVDVFEK.R
2712	**654.1136**	**1306.2127**	**1307.6431**	**-1.4304**	**0**	**3**	**81**	**2**	**R.IMNPTVDVFEK.R**
7148	**579.5505**	**1735.6297**	**1733.8413**	**1.7884**	**0**	**39**	**0.016**	**1**	**R.FPQFVEPSEGYHGLK.F** 7147
7800	897.3716	1792.7287	1791.9492	0.7795	1	7	31	4	R.AERHASNALALANWLR.T
8306	**616.8312**	**1847.4717**	**1844.8905**	**2.5813**	**0**	**32**	**0.088**	**1**	**K.FVQGDKPEDIGAAIDDR.T**
12716	**806.4842**	**2416.4307**	**2414.2052**	**2.2255**	**2**	**1**	**98**	**3**	**K.EFGNIYSRIMNPTVDVFEKR.I**

15023	940.0735	2817.1987	2816.4571	0.7416	2	1	94	7	R.LFGLKEFGNIYSRIMNPTVDVFEK.R

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381. gi|220693972|gb|EED50317.1| **Mass:** 46080 **Score:** 52 **Queries matched:** 10 **emPAI:** 0.15
mRNA binding post-transcriptional regulator (Csx1), putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
1895	**600.2921**	**1198.5697**	**1196.5761**	**1.9936**	**0**	**28**	**0.23**	**1**	**K.GCGFVQFVQR.H**
2024	612.6681	1223.3217	1222.5686	0.7531	0	14	5.7	3	K.IMTDPISGMSR.G 2023
4645	762.3271	1522.6397	1521.7504	0.8893	0	52	0.00083	1	R.SFFQGFGEITYVK.I 4637
4676	763.4736	1524.9327	1524.7276	0.2051	1	2	1e+02	8	K.SAKIMTDPISGMSR.G
5685	**809.4706**	**1616.9267**	**1617.8627**	**-0.9360**	**1**	**1**	**1.3e+02**	**2**	**R.LFKLNWATGGGLADR.S**
10847	716.2075	2145.6007	2144.0064	1.5943	2	5	43	7	R.FPSCKSAKIMTDPISGMSR.G 10811 10815

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382. gi|220698373|gb|EED54713.1| **Mass:** 92024 **Score:** 51 **Queries matched:** 22 **emPAI:** 0.07
phosphoketolase, putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
128	738.4240	737.4167	735.4167	2.0001	0	18	1.8	2	K.LAEIYK.A 129
1473	561.0271	1120.0397	1119.6651	0.3746	2	4	64	9	K.LAEIYKAGKK.V
1622	**1141.9260**	**1140.9187**	**1140.6404**	**0.2784**	**0**	**1**	**1.4e+02**	**4**	**R.RPLQLPDFR.D**
2837	**660.7221**	**1319.4297**	**1318.7721**	**0.6576**	**2**	**1**	**1.3e+02**	**3**	**K.EPLKVEHLKAR.L**
2942	666.5516	1331.0887	1330.6881	0.4006	0	5	53	9	K.GNIDTPFELAVR.N 2940
3011	**670.6896**	**1339.3647**	**1338.6602**	**0.7045**	**1**	**0**	**1.4e+02**	**1**	**R.DVVKENMTTFR.V**
5967	547.7352	1640.1837	1639.7230	0.4607	0	3	75	4	R.ASMYLCLGMLYMR.D
6424	837.7606	1673.5067	1673.7944	-0.2876	1	2	84	3	R.LINEKDHPHGMPDR.Q
8620	**628.3579**	**1882.0517**	**1880.0243**	**2.0274**	**2**	**1**	**98**	**5**	**R.WPMIVLRSPKGWSAPR.E**
8634	**629.2519**	**1884.7337**	**1883.0265**	**1.7072**	**0**	**16**	**3.1**	**1**	**R.SHQIPITDVLTNPAHLK.L**
8650	**943.8646**	**1885.7147**	**1886.7952**	**-1.0805**	**0**	**5**	**42**	**1**	**-.MAPSSESDDNISAYGATR.S**
12083	**773.4325**	**2317.2757**	**2316.0539**	**1.2218**	**1**	**2**	**80**	**2**	**-.MAPSSESDDNISAYGATRSTIK.G**
12703	805.7775	2414.3107	2415.1410	-0.8303	2	2	77	7	R.DYALKDIDPGVSVRGSMTNMSK.F 12698
12794	**809.5335**	**2425.5787**	**2423.2856**	**2.2932**	**1**	**3**	**59**	**4**	**R.MSANPVGNGGILRRPLQLPDFR.D** 12788
13837	**857.1519**	**2568.4337**	**2567.1503**	**1.2834**	**2**	**4**	**45**	**3**	**R.KMDAYFRASMYLCLGMLYMR.D**
14751	913.9399	2738.7977	2737.3105	1.4873	0	52	0.0007	1	R.HGILNSYEPFIHVIDSMVNQHCK.W
15181	**956.1332**	**2865.3777**	**2865.5130**	**-0.1353**	**2**	**4**	**40**	**1**	**K.LVEELKALAPSGNSRMSANPVGNGGILR.R**
15816	1053.4612	3157.3617	3157.6290	-0.2673	1	1	74	2	R.QWKAVFTDDKPIIFNFHSYPWLIHR.L

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383. gi|220698336|gb|EED54676.1| **Mass:** 17557 **Score:** 51 **Queries matched:** 4 **emPAI:** 0.19
peroxiredoxin, putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
12856	**812.4892**	**2434.4457**	**2433.2363**	**1.2095**	**1**	**4**	**53**	**1**	**K.EKGVQVVAVVASNDPFVMSAWGK.A** 12849
16032	**1095.3399**	**3282.9977**	**3281.7271**	**1.2706**	**0**	**46**	**0.0027**	**1**	**K.VVLFSVPGAFTPTCSVNHVPGYIQNLPQLK.E** 16031

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384.  gi|220701739|gb|EED58077.1|    Mass: 18594    Score: 51     Queries matched: 12   emPAI: 0.65
      40S ribosomal protein S11 [Aspergillus flavus NRRL3357]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score Expect Rank  Peptide
         2  601.4700   600.4627   600.3959  0.0668   0    13     9.9    2   R.TIVIR.R 1
        21  648.5450   647.5377   647.3755  0.1622   0    13      11    6   R.FNVLR.V
      1086  524.8136  1047.6127  1047.5389  0.0738   0    32    0.13    1   R.EYLHYVPK.Y 1084 1097
      1742  585.0601  1168.1057  1166.5576  1.5481   0    21     1.2    1   K.CPFTGMVSIR.G
      1816  592.6776  1183.3407  1181.6305  1.7102   0    37    0.03    1   K.NLAAHVSPAFR.V 1818
      2126  620.6356  1239.2567  1237.6554  1.6013   1    36   0.036    1   K.TAIEGTYIDKK.C
      5000  779.3946  1556.7747  1554.9028  1.8719   2     3      77    4   R.VVSTKMHRTIVIR.R
      9134  646.4979  1936.4717  1936.0135  0.4582   2     2      85    8   K.CPFTGMVSIRGRILTGR.V
```

```
385.  gi|220691683|gb|EED48031.1|    Mass: 55679    Score: 51     Queries matched: 15   emPAI: 0.06
      vacuolar aspartyl aminopeptidase Lap4, putative [Aspergillus flavus NRRL3357]
     Query    Observed   Mr(expt)   Mr(calc)     Delta Miss Score Expect Rank  Peptide
        86    704.5610   703.5537   701.4072    2.1465   0    20      2.5    1   R.SVLDLR.D
      1301    545.0776  1088.1407  1086.6509    1.4898   2     7       40    9   M.TKRSVLDLR.D 1302
      1736    584.5091  1167.0037  1165.5397    1.4640   0     7       29    4   R.SGGTIGPMTSSR.I
      1944    606.2431  1210.4717  1209.7234    0.7484   1     8       21   10   K.LVKLDWPIAR.I
      2000    610.1736  1218.3327  1217.6914    0.6413   2     9       24    8   -.MTKRSVLDLR.D
      5905    818.6521  1635.2897  1635.8766   -0.5869   0   (3)       73    4   R.AIDVGIPQLSMHSIR.A
      6148    827.3156  1652.6167  1651.8716    0.7452   0     3       66    5   R.AIDVGIPQLSMHSIR.A 6160
      6940    856.5921  1711.1697  1710.7957    0.3740   0    51   0.0012    1   K.MVGMFDDEEIGSLLR.Q
      7411    587.9055  1760.6947  1757.9272    2.7675   1     3       67    4   R.DLSIGGRVLVQDSNTGK.V
     10485    699.4549  2095.3427  2093.1238    2.2190   1     2       79    6   R.IGMRAIDVGIPQLSMHSIR.A
     14720    910.5139  2728.5197  2729.4442   -0.9245   1     1       91    1   K.LDWPIARIPTLAPHFGAPSQGPFNK.E
     14928    929.3735  2785.0987  2783.5004    1.5984   2     0   1e+02    8   R.DYKSGNGMAIVAGHIDALTAKLKPVSK.L
     16140   1109.0042  3323.9907  3321.5428    2.4479   2     1       69    9   K.MVGMFDDEEIGSLLRQGARSNFMSSVIER.I
```

```
386.  gi|3845477|dbj|BAA34135.1|    Mass: 15942    Score: 51     Queries matched: 1   emPAI: 0.21
      cytochrome b [Aspergillus flavus]
     Query  Observed   Mr(expt)   Mr(calc)    Delta Miss Score Expect Rank  Peptide
      2146  622.3326  1242.6507  1241.6849  0.9659   0    51  0.0014    1   R.LPFAPYFIFK.D


      Proteins matching the same set of peptides:
      gi|3845479|dbj|BAA34136.1|    Mass: 15942    Score: 51     Queries matched: 1
      cytochrome b [Aspergillus flavus]
```

gi|3845481|dbj|BAA34137.1| **Mass:** 15942 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|3845483|dbj|BAA34138.1| **Mass:** 15942 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|3845485|dbj|BAA34139.1| **Mass:** 15942 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|3845487|dbj|BAA34140.1| **Mass:** 15942 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|3845529|dbj|BAA34161.1| **Mass:** 15942 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|6009463|dbj|BAA34141.2| **Mass:** 16396 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|6009465|dbj|BAA34159.2| **Mass:** 16396 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|6009466|dbj|BAA34160.2| **Mass:** 16396 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|6014790|sp|P56629.1|CYB_ASPFL **Mass:** 16298 **Score:** 51 **Queries matched:** 1
RecName: Full=Cytochrome b; AltName: Full=Ubiquinol-cytochrome-c reductase complex cytochrome b subunit; AltName: Full=Cyt
gi|19909791|dbj|BAB87090.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]
gi|19909793|dbj|BAB87091.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]
gi|19909795|dbj|BAB87092.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]
gi|19909801|dbj|BAB87095.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]
gi|19909803|dbj|BAB87096.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]
gi|19909805|dbj|BAB87097.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]
gi|19909807|dbj|BAB87098.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|19909809|dbj|BAB87099.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|19909821|dbj|BAB87105.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|19909823|dbj|BAB87106.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus var. columnaris]
gi|19909825|dbj|BAB87107.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus var. columnaris]

gi|19909827|dbj|BAB87108.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus var. columnaris]

gi|19909829|dbj|BAB87109.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus var. columnaris]

gi|19909831|dbj|BAB87110.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]

gi|167735735|dbj|BAG07148.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735737|dbj|BAG07149.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735739|dbj|BAG07150.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735741|dbj|BAG07151.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735743|dbj|BAG07152.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735745|dbj|BAG07153.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735747|dbj|BAG07154.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735749|dbj|BAG07155.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735751|dbj|BAG07156.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735753|dbj|BAG07157.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735755|dbj|BAG07158.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735757|dbj|BAG07159.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus parasiticus]

gi|167735775|dbj|BAG07168.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]

gi|167735777|dbj|BAG07169.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]

gi|167735779|dbj|BAG07170.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]

gi|167735781|dbj|BAG07171.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]

gi|167735783|dbj|BAG07172.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]

gi|167735785|dbj|BAG07173.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|167735787|dbj|BAG07174.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|167735789|dbj|BAG07175.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|167735791|dbj|BAG07176.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]
gi|167735793|dbj|BAG07177.1| **Mass:** 14988 **Score:** 51 **Queries matched:** 1
cytochrome b [Aspergillus flavus]

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387. gi|220692549|gb|EED48895.1| **Mass:** 42449 **Score:** 50 **Queries matched:** 5 **emPAI:** 0.08
tyrosyl-tRNA synthetase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
736	485.4406	968.8667	968.4121	0.4547	0	5	49	10	K.MSSSVEDSK.I
1044	520.6721	1039.3297	1039.5662	-0.2365	0	50	0.0015	1	K.APLELVENR.A 1040 1049
12334	**787.2489**	**2358.7247**	**2358.1413**	**0.5834**	**1**	**0**	**1.2e+02**	**5**	**K.SPEYVMDVYRLSSLISEGDAK.K**

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388. gi|220699128|gb|EED55467.1| **Mass:** 18751 **Score:** 49 **Queries matched:** 2 **emPAI:** 0.18
ubiquinol-cytochrome c reductase complex 17 kd protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
13404	836.9332	2507.7777	2506.0352	1.7426	0	42	0.0076	1	K.EDCVEEFFHLAHCASECAAPK.L 13387

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389. gi|220701045|gb|EED57383.1| **Mass:** 65678 **Score:** 49 **Queries matched:** 24 **emPAI:** 0.05
TPR domain protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1320	546.6386	1091.2627	1090.5805	0.6823	1	12	10	2	K.LKTAMDAVAR.M 1319 1323
1904	601.4066	1200.7987	1199.6398	1.1590	0	12	9.7	2	R.LDTSQAPEVIK.K
2438	639.1011	1276.1877	1274.6176	1.5701	0	9	23	2	R.MEASVPEEVLR.M
4937	**776.1906**	**1550.3667**	**1549.7480**	**0.6187**	**1**	**4**	**62**	**4**	**R.MEASVPEEVLRMK.S** 4942
5587	537.6095	1609.8067	1608.9060	0.9008	1	2	1.1e+02	8	R.ADLGLDNTLIRPRR.H
6213	**830.1561**	**1658.2977**	**1656.8869**	**1.4109**	**1**	**6**	**42**	**2**	**R.LGKTEQAAMIEPTLR.L**
10147	**1028.4556**	**2054.8967**	**2051.9631**	**2.9336**	**1**	**4**	**57**	**3**	**R.MKSPPMADWLENFMTVR.V** 10112 10145
10263	**689.3492**	**2065.0257**	**2064.0575**	**0.9683**	**2**	**1**	**1e+02**	**2**	**R.FDPQDLAVCLKRAFAASR.R**
10550	**702.5459**	**2104.6157**	**2106.0085**	**-1.3928**	**1**	**0**	**1.2e+02**	**8**	**K.TAMDAVARMEASVPEEVLR.M**
10930	719.7572	2156.2497	2158.1494	-1.8997	1	2	75	2	K.AESVYRADLGLDNTLIRPR.R
11491	**745.6935**	**2234.0587**	**2232.1902**	**1.8685**	**0**	**49**	**0.0016**	**1**	**K.ELSVHALPWEQALADALTLR.Y**
12300	**784.8455**	**2351.5147**	**2349.1490**	**2.3657**	**2**	**2**	**82**	**3**	**K.TAMDAVARMEASVPEEVLRMK.S**
12652	803.3442	2407.0107	2406.2001	0.8106	1	5	40	2	R.HAYAALMLEQGQIEKAESVYR.A 12648

13066	823.1302	2466.3687	2465.3563	1.0124	1	6	35	1	K.TEQAAMIEPTLRLALAVADVPIK.A 13050 13062
14879	925.7732	2774.2977	2773.3689	0.9289	2	2	65	1	R.MKSPPMADWLENFMTVRVHVMVR.F 14886

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390. gi\|220694187\|gb\|EED50531.1\| **Mass:** 23440 **Score:** 49 **Queries matched:** 8 **emPAI:** 0.14

secretory pathway protein Ssp120, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
239	803.7220	802.7147	801.4708	1.2439	1	7	41	7	R.LISEGKR.L
3062	673.2041	1344.3937	1342.7278	1.6659	1	4	63	9	R.MQIVEKNIPQK.F
4712	765.7876	1529.5607	1530.8075	-1.2468	1	2	94	10	R.LEQLERMQIVEK.N
6984	858.6241	1715.2337	1714.9804	0.2534	2	1	1e+02	8	R.MQIVEKNIPQKFLK.R
7192	580.9549	1739.8427	1740.7438	-0.9011	0	2	84	10	K.TYGLDDESNAGVSEER.K
7358	878.8766	1755.7387	1754.8628	0.8759	0	49	0.0018	1	R.EVFGLFDPGNTGFVTR.D 7348
13750	852.2502	2553.7287	2552.1204	1.6083	1	4	47	2	K.YHGDDAKEEDLTHPEDIEHFR.R

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391. gi\|220689992\|gb\|EED46342.1\| **Mass:** 46230 **Score:** 48 **Queries matched:** 16 **emPAI:** 0.15

ran GTPase activating protein 1 (RNA1 protein) [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
894	501.5586	1001.1027	1001.5505	-0.4478	0	24	0.74	1	R.QEGISSLLR.E
1466	560.4696	1118.9247	1119.5131	-0.5884	0	9	22	5	R.AYEVHAAGMR.S
1660	575.6406	1149.2667	1148.5972	0.6695	1	13	8.4	4	R.SVKMTQNGIR.Q
1770	588.0461	1174.0777	1172.5925	1.4853	0	11	14	1	K.EVDELAEALGK.T
3121	1351.7030	1350.6957	1349.6827	1.0130	0	18	2.2	1	R.LQYNDITAEGVK.Q
3445	692.1416	1382.2687	1380.6456	1.6231	0	6	39	3	R.LGGNTFGVTACER.L
4083	729.3076	1456.6007	1456.7998	-0.1990	1	24	0.58	2	R.QEGISSLLREGLR.H 4084 4103
5508	535.4422	1603.3047	1601.9756	1.3291	0	25	0.49	1	R.LIEEIPIALTHLLK.A 5507
8052	606.7395	1817.1967	1817.9418	-0.7450	1	4	58	8	K.MTQNGIRQEGISSLLR.E
10901	718.5989	2152.7747	2152.1528	0.6219	0	34	0.046	1	K.ALLEIPTLHTVNLSDNAFGK.R 10912
12832	811.2989	2430.8747	2431.1947	-0.3200	2	1	84	10	K.EVPQLESIVCGRNRLENGSMK.A
12880	813.1729	2436.4967	2437.1543	-0.6576	2	2	70	7	R.RIELNGNKFMEEDDNVTELR.E

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392. gi\|8308146\|gb\|AAF74493.1\|AF261856_1 **Mass:** 9498 **Score:** 47 **Queries matched:** 5 **emPAI:** 0.36

O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
10289	690.5172	2068.5297	2066.9585	1.5712	0	41	0.011	1	R.FIFEEVAPDQYAHTDASK.M 10286
12165	777.2165	2328.6277	2327.1586	1.4691	0	2	80	10	K.GKPPSWNVPSPFSLAFDPTNGL.-
12169	777.3342	2328.9807	2328.1427	0.8381	0	7	27	1	K.GKPPSWNVPSPFSLAFDPTDGL.- 12176

Proteins matching the same set of peptides:

gi|8308150|gb|AAF74495.1|AF261858_1 **Mass:** 9498 **Score:** 47 **Queries matched:** 5
O-methyltransferase [Aspergillus flavus]

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393. gi|220697698|gb|EED54038.1| **Mass:** 58603 **Score:** 47 **Queries matched:** 21 **emPAI:** 0.12
hypothetical protein AFLA_012900 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
473	444.5156	887.0167	887.4712	-0.4545	0	8	37	4	K.NGIVEGATK.D 469
1392	554.1691	1106.3237	1104.5597	1.7640	0	8	25	6	K.EMIAAGTQLR.L
2562	645.5886	1289.1627	1289.6761	-0.5134	1	6	46	3	K.GKEMIAAGTQLR.L 2574 2586
2632	648.8791	1295.7437	1295.6907	0.0530	0	17	3.4	1	R.LPLTDLVNHMK.G
2773	657.6781	1313.3417	1312.7755	0.5662	0	53	0.00074	1	R.IPGVLTTWISVK.G
3078	674.3671	1346.7197	1347.6419	-0.9222	0	7	35	2	K.DYTIQLDPGNGR.G 3080
3421	690.1651	1378.3157	1376.7234	1.5923	0	31	0.13	1	R.LIVSLFNCAGQR.I 3414
8805	634.0499	1899.1277	1896.9581	2.1696	0	5	42	4	K.NLAAPIETGITEHFADAK.E 8784
12107	774.6892	2321.0457	2320.1547	0.8910	1	2	87	4	R.IESNGGTTFVPDSKNGIVEGATK.D
13408	836.9709	2507.8907	2506.2533	1.6374	2	2	71	1	-.MERLPLTDLVNHMKGHQTTNR.W
14217	883.4865	2647.4377	2648.3890	-0.9513	2	1	97	2	K.GKEMIAAGTQLRLIVSLFNCAGQR.I 14223
15471	1004.9949	3011.9627	3013.5154	-1.5526	1	1	75	10	K.ASSASVIISSHTMANCFFIPSLLRNFK.N 15474
16409	1165.7999	3494.3777	3494.8926	-0.5149	2	3	42	2	K.LLEPVAFNFSITPPDNDRRIPGVLTTWISVK.G

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394. gi|220691608|gb|EED47956.1| **Mass:** 23872 **Score:** 47 **Queries matched:** 3 **emPAI:** 0.14
endosomal cargo receptor (Erp3), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
113	723.4480	722.4407	722.3711	0.0696	0	17	2.7	9	R.NFSTVR.S
2975	668.6536	1335.2927	1334.5714	0.7214	0	47	0.0031	1	K.ACFYNYVDQR.N
3987	723.8581	1445.7017	1444.7998	0.9020	1	1	1.2e+02	2	K.LSAQLSTISRNQK.Y

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395. gi|220690403|gb|EED46752.1| **Mass:** 46343 **Score:** 47 **Queries matched:** 15 **emPAI:** 0.15
nucleosome assembly protein Nap1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2511	642.6796	1283.3447	1282.6128	0.7319	0	(8)	26	1	R.MEYLDRPGFR.L
2656	650.5111	1299.0077	1298.6077	0.4000	0	8	25	2	R.MEYLDRPGFR.L
3393	688.7266	1375.4387	1374.7143	0.7244	0	39	0.024	1	R.SSGYIESLPAPVR.R 3417
3421	690.1651	1378.3157	1377.8092	0.5065	2	4	64	10	R.VAGLKGIQKEHAK.L
4481	502.1382	1503.3927	1502.7729	0.6198	2	9	21	2	K.IDWKDDKDLTVR.V 4479
7070	863.2111	1724.4077	1722.8651	1.5426	0	30	0.13	1	K.VSSTAGIPEFWLSAMK.N 7073
7196	871.0721	1740.1297	1738.8600	1.2697	0	(8)	26	2	K.VSSTAGIPEFWLSAMK.N
9387	657.5512	1969.6317	1969.9705	-0.3388	1	4	57	2	R.RATIVNGAAEPTDGEVDAGK.G
9667	668.7089	2003.1047	2000.8388	2.2659	0	3	76	6	K.EENGYGGDFIYDHAEGTK.I
10545	702.2469	2103.7187	2103.0266	0.6921	1	19	1.9	1	K.NQISLAEMVTERDEEALR.H

10775	**713.7199**	**2138.1377**	**2137.8771**	**0.2606**	**1**	**6**	**32**	**2**	**R.KSDGDVDDDSDEEDGTSKPK.K**
11902	**766.2862**	**2295.8367**	**2297.1903**	**-1.3535**	**2**	**3**	**63**	**2**	**K.EHAKLEAQFQEEVLELEKK.Y**

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396. gi\|220690768\|gb\|EED47117.1\| **Mass:** 66062 **Score:** 46 **Queries matched:** 33 **emPAI:** 0.05

histidyl-tRNA synthetase, mitochondrial precursor [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1116	527.8051	1053.5957	1053.5277	0.0680	1	11	10	6	K.GFTGMLKER.M 1128
1372	551.9041	1101.7937	1101.5666	0.2272	0	9	23	8	K.DEALLANASAK.A
2138	621.7116	1241.4087	1240.5394	0.8693	0	8	23	10	K.EMGLEDGHPEK.E
2672	651.6126	1301.2107	1300.7099	0.5009	2	11	15	2	R.LEREKSAEALR.S 2668
2736	655.4586	1308.9027	1309.7394	-0.8367	1	4	57	6	R.IFTTIADVFKR.H 2741
3221	454.5569	1360.6487	1357.7176	2.9311	2	10	17	8	K.LDKMPWADVRK.E
3389	688.6636	1375.3127	1373.7125	1.6002	2	(2)	1e+02	7	K.LDKMPWADVRK.E
3465	462.7452	1385.2137	1382.8245	2.3892	0	7	30	5	R.ALTATAAVRPTALK.N
3979	**482.7515**	**1445.2327**	**1446.7112**	**-1.4784**	**1**	**11**	**13**	**1**	**R.WLAMNPDVRSMK.R**
4294	**741.1851**	**1480.3557**	**1478.7010**	**1.6547**	**1**	**(1)**	**1.2e+02**	**4**	**R.WLAMNPDVRSMK.R**
4537	756.7096	1511.4047	1511.7733	-0.3685	0	4	63	8	R.HGGTALDTPVFELR.E
4794	769.8886	1537.7627	1535.7225	2.0403	0	4	60	6	R.MNVCQTLWNAGVK.A
5795	**542.7999**	**1625.3777**	**1622.9580**	**2.4197**	**2**	**3**	**76**	**5**	**R.SARRAIADPVVVTLR.R**
6289	**832.7711**	**1663.5277**	**1661.8413**	**1.6864**	**0**	**5**	**46**	**1**	**K.IVTEVFEELGWQGR.Y**
8085	607.8189	1820.4347	1820.8662	-0.4314	1	5	45	3	K.ERMNVCQTLWNAGVK.A
8598	**627.1965**	**1878.5677**	**1878.9146**	**-0.3468**	**0**	**1**	**1.1e+02**	**6**	**K.LIYDLQDQGGEICSLR.Y**
9886	**677.0765**	**2028.2077**	**2027.1150**	**1.0927**	**1**	**43**	**0.0069**	**1**	**R.DLLETLLKDEALLANASAK.A** 9890
11230	732.7339	2195.1797	2194.0439	1.1358	1	0	1.2e+02	10	R.SSEVDAFVMAFGGKGFTGMLK.E
12177	777.6382	2329.8927	2327.1177	2.7750	0	1	92	8	K.AGLEDMGLLMDYLEAFGVLDR.I 12150
13576	**843.6939**	**2528.0597**	**2525.2914**	**2.7683**	**2**	**1**	**92**	**3**	**K.DWSGSDALLRDRIFTTIADVFK.R**
13663	**847.8069**	**2540.3987**	**2541.2508**	**-0.8521**	**2**	**2**	**83**	**2**	**R.YDLTVPFARWLAMNPDVRSMK.R**
13760	**852.6399**	**2554.8977**	**2555.2447**	**-0.3470**	**2**	**3**	**61**	**8**	**K.GFTGMLKERMNVCQTLWNAGVK.A** 13771
14539	**899.2945**	**2694.8617**	**2695.4545**	**-0.5927**	**2**	**4**	**48**	**4**	**K.AAEQGGVPFAVILGEDELAEGKVRIK.E** 14538
14799	918.5162	2752.5267	2750.3698	2.1569	1	1	87	5	R.SNDPTLGVGSVAAGGRYDNLVGMFLPK.A
14902	**927.6592**	**2779.9557**	**2777.3793**	**2.5764**	**1**	**0**	**1e+02**	**3**	**K.EMGLEDGHPEKEGVLVDLASLPAEVK.A**
16123	1106.2262	3315.6567	3314.8099	0.8468	1	1	70	6	R.ALTATAAVRPTALKNIISTSSIHDPTIPHYR.H

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397. gi\|220692215\|gb\|EED48562.1\| **Mass:** 50812 **Score:** 46 **Queries matched:** 11 **emPAI:** 0.06

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
785	490.1251	978.2357	977.4600	0.7757	0	9	20	2	K.LNSIDNMR.V 787
1445	1116.4290	1115.4217	1114.6094	0.8123	2	4	64	5	R.KLDRIDEAR.V
1541	**565.8191**	**1129.6237**	**1127.5247**	**2.0990**	**0**	**2**	**1.3e+02**	**3**	**R.ETDLFGYQR.K** 1542

3391	**688.6986**	**1375.3827**	**1376.6718**	**-1.2891**	**1**	**2**	**1e+02**	**4**	**K.LNSIDNMRVDGK.F**
3790	476.1852	1425.5337	1423.9238	1.6099	2	5	46	8	R.LLRTRDALLLIK.Q
5967	547.7352	1640.1837	1639.8318	0.3519	2	1	1.2e+02	9	R.ETDLFGYQRKLDR.I
13954	**864.9849**	**2591.9327**	**2590.4330**	**1.4997**	**0**	**46**	**0.0028**	**1**	**K.LQSGLAQLSPELVSTHETLVSILR.S**
14208	**883.0562**	**2646.1467**	**2645.2829**	**0.8638**	**2**	**3**	**57**	**1**	**R.CLLEVKESGGVANSRELYPYSMK.L** 14203

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398. gi|220699636|gb|EED55975.1| **Mass:** 25091 **Score:** 46 **Queries matched:** 12 **emPAI:** 0.13

phosphoglycolate phosphatase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1438	557.8341	1113.6537	1113.6506	0.0031	1	22	1	3	K.GVAAVKTALER.N 1437
2537	429.7132	1286.1177	1284.7302	1.3875	0	10	18	5	K.AHHVPIAIVSNK.G 2551
2590	**646.8021**	**1291.5897**	**1290.6932**	**0.8965**	**0**	**7**	**31**	**2**	**R.LIASGAGLADTFR.A** 2597
3720	709.1546	1416.2947	1415.7660	0.5287	0	46	0.0042	1	K.AFPGAQELLTELK.A
11931	**1150.8066**	**2299.5987**	**2297.2015**	**2.3972**	**1**	**2**	**79**	**1**	**R.NGLAGYVPEELIIGDKTPGAQR.K** 11915 11926
12474	**794.7462**	**2381.2167**	**2380.3703**	**0.8465**	**2**	**1**	**85**	**3**	**K.AHHVPIAIVSNKGVAAVKTALER.N**
15722	1035.3975	3103.1707	3100.6306	2.5401	1	1	81	8	R.FGINVVADEGVLVVGDTVADIQFARNIGGR.V

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399. gi|220697818|gb|EED54158.1| **Mass:** 12041 **Score:** 46 **Queries matched:** 2 **emPAI:** 0.29

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
9473	**660.9302**	**1979.7687**	**1977.9068**	**1.8619**	**0**	**45**	**0.0038**	**1**	**R.GGENFTETAHEIELEFR.D** 9455

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400. gi|220701324|gb|EED57662.1| **Mass:** 46400 **Score:** 46 **Queries matched:** 2 **emPAI:** 0.07

fatty acid hydroxylase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2724	436.8105	1307.4097	1304.7313	2.6784	2	8	25	6	R.VYRQLRLSDR.V
7428	**882.4406**	**1762.8667**	**1761.8937**	**0.9730**	**0**	**46**	**0.004**	**1**	**K.GGESAPLFGNFLEPLSK.T**

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401. gi|220699278|gb|EED55617.1| **Score:** 45 **Queries matched:** 10

tartrate dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
842	495.5941	989.1737	988.5488	0.6250	1	40	0.018	3	R.VGIERIMR.F 843
1028	519.6511	1037.2877	1037.4522	-0.1644	0	6	44	3	K.QLMDCVEK.V
3279	**456.1765**	**1365.5077**	**1363.7493**	**1.7584**	**1**	**8**	**26**	**8**	**K.LLTVVTKSNSMR.N**
4379	498.0805	1491.2197	1491.8443	-0.6246	2	1	1.1e+02	10	R.KLLTVVTKSNSMR.N
8324	**617.3719**	**1849.0937**	**1850.9937**	**-1.9000**	**2**	**2**	**83**	**10**	**R.IMRFAFEVAQSRPRK.L**
9853	**676.3122**	**2025.9147**	**2024.0902**	**1.8245**	**2**	**2**	**83**	**7**	**R.VSDLTSSARSLESRILYK.M**
10902	**718.6545**	**2152.9417**	**2154.0126**	**-1.0709**	**1**	**1**	**98**	**7**	**K.DFPDVTWDKMLVDAMTVR.M**

12023	771.1449	2310.4127	2308.2435	2.1692	2	3	68	3	-.MLSFIHVMKIKDTNIIYSR.C
16342	**1149.2565**	**3444.7477**	**3445.6892**	**-0.9414**	**1**	**1**	**74**	**6**	**K.QLMDCVEKVCAAGILTPDLGGTSNTQGVVDAVK.K**

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402. gi|220694833|gb|EED51177.1| **Mass:** 38700 **Score:** 45 **Queries matched:** 10 **emPAI:** 0.09
aflU / cypA / P450 monooxygenase [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
763	488.5926	975.1707	976.4866	-1.3158	0	12	12	8	R.DLGFTAPEK.G 765
2983	669.1056	1336.1967	1335.7584	0.4383	0	45	0.0048	2	R.TITITFMLAGLR.S 2991 2996 3001
5620	**538.2385**	**1611.6937**	**1608.9021**	**2.7916**	**1**	**9**	**19**	**1**	**K.TRTITITFMLAGLR.S** 5594
10378	**1041.3416**	**2080.6687**	**2081.1489**	**-0.4802**	**2**	**(3)**	**60**	**1**	**K.CISKTRTITITFMLAGLR.S**
10500	**1049.9406**	**2097.8667**	**2097.1438**	**0.7229**	**2**	**5**	**43**	**2**	**K.CISKTRTITITFMLAGLR.S**

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403. gi|220694637|gb|EED50981.1| **Mass:** 11365 **Score:** 45 **Queries matched:** 10 **emPAI:** 0.30
histone H4, putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
2057	**615.3571**	**1228.6997**	**1227.5805**	**1.1192**	**0**	**9**	**24**	**1**	**R.ISAMIYEETR.G**
2870	**663.7216**	**1325.4287**	**1324.7463**	**0.6824**	**0**	**42**	**0.0098**	**1**	**R.DNIQGITKPAIR.R** 2872 2880
5359	796.2846	1590.5547	1591.9297	-1.3750	2	1	1.2e+02	6	K.RKTVTSLDVVYALK.R
6910	**855.1756**	**1708.3367**	**1707.0155**	**1.3212**	**1**	**5**	**51**	**4**	**K.ILRDNIQGITKPAIR.R** 6887 6911
7661	891.5046	1780.9947	1780.9505	0.0442	2	0	1.2e+02	4	K.RISAMIYEETRGVLK.S 7654

Proteins matching the same set of peptides:
gi|220698170|gb|EED54510.1| **Mass:** 11349 **Score:** 45 **Queries matched:** 10
histone H4.1 [Aspergillus flavus NRRL3357]

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404. gi|220698104|gb|EED54444.1| **Mass:** 99516 **Score:** 45 **Queries matched:** 16 **emPAI:** 0.03
acetylglutamate kinase, putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
858	994.5830	993.5757	992.5291	1.0467	1	4	66	10	R.YVEGLKER.D 859
1996	609.9801	1217.9457	1215.6207	2.3250	1	1	1.3e+02	10	R.EGLDARATVER.Y
3068	**673.7461**	**1345.4777**	**1344.7613**	**0.7164**	**0**	**5**	**51**	**10**	**R.STVVQLLSNIGSK.R**
3210	**680.8361**	**1359.6577**	**1359.7915**	**-0.1337**	**2**	**5**	**47**	**4**	**K.KDFPKLVWTVK.E**
3960	722.6921	1443.3697	1441.8477	1.5220	2	8	22	6	R.TAVRRASTSKPLR.A 3966
4355	**744.9141**	**1487.8137**	**1486.7488**	**1.0649**	**2**	**0**	**1.5e+02**	**8**	**R.DREGLDARATVER.Y**
7051	862.3606	1722.7067	1720.8784	1.8283	0	47	0.0028	1	K.SGWLTNVADNVFASIK.K 7038
7509	**885.7916**	**1769.5687**	**1769.8625**	**-0.2937**	**0**	**1**	**1.2e+02**	**6**	**R.FDSTWTYGLPELVSR.S**
8913	**637.7349**	**1910.1827**	**1909.9785**	**0.2042**	**1**	**4**	**49**	**8**	**K.IVYLAEKGGLFNGDTGEK.I** 8914
10153	**686.0789**	**2055.2147**	**2054.1021**	**1.1126**	**1**	**5**	**44**	**4**	**R.ASTSKPLRAFSAPHAISSAR.L**
12213	780.1909	2337.5507	2336.2165	1.3342	2	1	1.1e+02	6	K.SGWLTNVADNVFASIKKDFPK.L

14715	**909.9859**	**2726.9357**	**2726.2680**	**0.6677**	**0**	**2**	**66**	**5**	**K.GAATQCLQNMNLALGYGEYQGIPLE.-**

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405. gi|220700658|gb|EED56996.1| **Mass:** 15438 **Score:** 44 **Queries matched:** 7 **emPAI:** 0.22
cytokinesis EF-hand protein Cdc4, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1905	601.4506	1200.8867	1200.6714	0.2153	0	44	0.007	1	K.VSLESLGDLLR.A
5733	**811.5536**	**1621.0927**	**1619.7831**	**1.3096**	**1**	**1**	**1.2e+02**	**8**	**M.ASTNYKEAFSLFDK.R**
7469	883.7726	1765.5307	1766.8185	-1.2878	1	3	64	5	-.MASTNYKEAFSLFDK.R
10732	711.3279	2130.9617	2130.0569	0.9049	1	5	46	5	R.GFQVFDKDMTGFIGVGQLR.Y 10713 10721 10724

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406. gi|220697389|gb|EED53730.1| **Mass:** 54245 **Score:** 44 **Queries matched:** 11 **emPAI:** 0.06
aldehyde dehydrogenase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
486	**897.4690**	**896.4617**	**895.4624**	**0.9993**	**1**	**16**	**3.1**	**2**	**K.DIERAHR.V**
1420	**556.0711**	**1110.1277**	**1108.5877**	**1.5400**	**0**	**44**	**0.0065**	**1**	**K.VAFTGSTLTGR.E** 1422
2775	**438.9265**	**1313.7577**	**1314.7408**	**-0.9831**	**1**	**11**	**13**	**5**	**R.VPFGGIKQSGIGR.E**
3782	**713.6481**	**1425.2817**	**1423.8221**	**1.4596**	**1**	**2**	**89**	**10**	**K.LLPPTDRGALMLK.L**
6870	**569.4369**	**1705.2887**	**1706.9501**	**-1.6614**	**1**	**5**	**46**	**3**	**R.GALMLKLADLIEQHR.E**
10453	**698.2325**	**2091.6757**	**2091.0596**	**0.6161**	**1**	**1**	**1.1e+02**	**10**	**K.QSGIGRELGEAGLEAYSQVK.A**
12693	**805.5509**	**2413.6307**	**2412.2648**	**1.3659**	**1**	**3**	**67**	**3**	**R.ELGEAGLEAYSQVKAIHVNLGSK.L**
13869	**859.1725**	**2574.4957**	**2572.3384**	**2.1573**	**1**	**3**	**60**	**3**	**K.NITLETGGKSPLVVFGDADIEQAAK.W**
15498	**1009.7075**	**3026.1007**	**3024.4651**	**1.6356**	**1**	**3**	**51**	**2**	**R.VASEIEAGMVWINSSNDSDFRVPFGGIK.Q**
16093	1100.5492	3298.6257	3295.8287	2.7970	0	6	22	1	K.LGPALACGNTIVMKPAEQTPLSILYLATLIK.E

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407. gi|89212054|gb|ABD63389.1| **Mass:** 10162 **Score:** 44 **Queries matched:** 3 **emPAI:** 0.34
O-methyltransferase B [Aspergillus parasiticus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1185	534.6666	1067.3187	1066.6386	0.6801	0	39	0.02	1	K.EQAILVAVPK.R 1186
14467	895.1245	2682.3517	2683.2687	-0.9170	1	6	27	1	R.AEWDDLMEQAGLEIIQSKVYDSK.E

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408. gi|220701646|gb|EED57984.1| **Mass:** 31064 **Score:** 43 **Queries matched:** 5 **emPAI:** 0.11
pyruvate dehydrogenase complex component Pdx1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5218	790.7716	1579.5287	1580.8410	-1.3122	1	10	16	2	K.GIPDSEVSKIPASGPK.G 5231
8254	921.9626	1841.9107	1841.0411	0.8696	0	43	0.0065	1	K.IQETLGVNVPLATFLAR.A 8267
11291	1104.2441	2206.4737	2205.1066	1.3671	0	29	0.16	1	K.GDVLAYLGSIPADYPATQQAR.F

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409. gi|220690307|gb|EED46657.1| **Mass:** 128071 **Score:** 43 **Queries matched:** 25 **emPAI:** 0.05

cytoskeleton assembly control protein Sla2, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
892	501.3986	1000.7827	1001.5658	-0.7831	0	7	40	9	R.GGIGYGPLIR.E
1008	517.4991	1032.9837	1031.5135	1.4703	0	6	42	10	K.ATSIEESAPK.R
1210	536.5266	1071.0387	1070.4855	0.5532	0	10	16	8	K.SSAAFWAGMK.V
2891	**664.4941**	**1326.9737**	**1326.7255**	**0.2482**	**1**	**4**	**72**	**9**	**K.AADAIDAAAARLAK.L**
3220	**454.5189**	**1360.5347**	**1358.6976**	**1.8371**	**1**	**6**	**42**	**10**	**K.NLELADMIRER.D** 3210
4089	**729.6656**	**1457.3167**	**1457.7586**	**-0.4419**	**2**	**1**	**1.3e+02**	**2**	**K.AASAQEAIERREK.L**
5324	**795.2286**	**1588.4427**	**1586.8528**	**1.5899**	**2**	**6**	**40**	**1**	**K.KNNRWTEGLISAAK.A**
5570	805.4036	1608.7927	1608.7565	0.0362	1	9	18	4	K.YNREMADLEEALR.N 5584
5753	812.3366	1622.6587	1622.7531	-0.0944	0	4	64	10	K.SGMEQALMELEELK.M
6180	828.8126	1655.6107	1652.9097	2.7010	1	1	1.1e+02	10	R.QEHLDLLQTTKSLK.L
6382	**836.4076**	**1670.8007**	**1669.8999**	**0.9008**	**0**	**16**	**4**	**1**	**K.INDIIDSVLQTGVQR.V**
6647	844.8351	1687.6557	1688.9131	-1.2573	2	1	1.1e+02	7	R.ELKTKNLELADMIR.E
6767	**567.1769**	**1698.5087**	**1698.8689**	**-0.3602**	**1**	**6**	**38**	**8**	**R.GLQSFRLEGLEADHK.T** 6760
6953	**856.9166**	**1711.8187**	**1711.8199**	**-0.0012**	**0**	**9**	**18**	**2**	**R.AMHTTTGDAEALEPLR.G**
8346	**618.1022**	**1851.2847**	**1850.8944**	**0.3903**	**2**	**4**	**51**	**6**	**K.YNREMADLEEALRNK.N** 8348
11316	**737.7875**	**2210.3407**	**2209.2113**	**1.1294**	**2**	**1**	**1.1e+02**	**8**	**K.AVGAACRALVRQVQEIIAER.N** 11333
11826	**762.3272**	**2283.9597**	**2282.1978**	**1.7619**	**2**	**2**	**77**	**6**	**R.ALVRQVQEIIAERNQDGSEK.V**
14765	**914.4429**	**2740.3067**	**2738.4562**	**1.8505**	**1**	**2**	**66**	**1**	**R.NSPEQLIVASNDVAASTAQLVAASRVK.A**
15536	**1014.3139**	**3039.9197**	**3038.4370**	**1.4828**	**0**	**44**	**0.0042**	**1**	**K.ASASATEFSTAFNNFIADGPNSTHAEIIR.T**
15740	**1039.2892**	**3114.8457**	**3114.4339**	**0.4118**	**0**	**1**	**80**	**5**	**K.TINDPNEGYETISDLMTLQDQIDAFQK.L**

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410. gi|220690854|gb|EED47203.1| **Mass:** 48650 **Score:** 43 **Queries matched:** 13 **emPAI:** 0.22

MAP kinase MpkA [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
980	**513.5516**	**1025.0887**	**1022.4855**	**2.6032**	**0**	**8**	**25**	**3**	**R.MLAFDPSSR.I**
2427	638.3586	1274.7027	1274.6731	0.0296	1	7	33	7	R.IGSPRAQEYVR.N 2446
4747	**767.5886**	**1533.1627**	**1532.8688**	**0.2939**	**2**	**1**	**1.4e+02**	**9**	**R.EIKLLQHFRGHR.N**
5536	536.3252	1605.9537	1607.8130	-1.8592	1	6	41	4	R.AQEYVRNLPFMPK.I
6207	**829.7526**	**1657.4907**	**1655.8519**	**1.6389**	**0**	**42**	**0.0097**	**1**	**R.LFPSANPDALDLLDR.M** 6180 6208
9978	1019.4761	2036.9377	2034.9873	1.9504	1	0	1.2e+02	4	R.WYRAPEIMLSFQSYTK.A
13539	**841.9062**	**2522.6967**	**2522.2628**	**0.4339**	**0**	**20**	**1.1**	**1**	**R.SGQPLTDAHFQSFIYQILCGLK.Y** 13550
14219	883.6535	2647.9387	2647.3639	0.5748	1	2	68	2	K.ELGQGAYGIVCAATNIQTGEGVAIKK.V
14666	**907.3265**	**2718.9577**	**2717.3297**	**1.6281**	**0**	**19**	**1.3**	**1**	**R.DYVDQLNQILHYLGTPNEETLSR.I**

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411. gi|220701288|gb|EED57626.1| **Mass:** 20817 **Score:** 42 **Queries matched:** 13 **emPAI:** 0.16

mitochondrial F1F0-ATP synthase g subunit, putative [Aspergillus flavus NRRL3357]

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

653	475.5266	949.0387	948.4512	0.5875	0	5	50	9	K.AGEAASSAASK.A
1849	**595.6131**	**1189.2117**	**1187.6445**	**1.5673**	**1**	**4**	**72**	**10**	**-.MPATASRAVLR.Q**
2941	**666.5396**	**1331.0647**	**1330.6629**	**0.4018**	**0**	**42**	**0.01**	**1**	**K.NANFVSPGDIAAR.V**
5323	**530.4609**	**1588.3607**	**1585.8325**	**2.5283**	**1**	**10**	**15**	**2**	**K.NANFVSPGDIAARVR.N**
8816	**634.3379**	**1899.9917**	**1901.0595**	**-1.0678**	**2**	**1**	**1.1e+02**	**8**	**M.PATASRAVLRQSQFLTR.R**
9055	964.1236	1926.2327	1927.0123	-0.7796	0	7	30	4	R.VTSTAGPALSNAAQGVGSALR.K 9083
9084	**644.2812**	**1929.8217**	**1928.9958**	**0.8260**	**0**	**5**	**44**	**1**	**K.VIAFVDSMIPPTLYYGK.V** 9086
13290	**831.8555**	**2492.5447**	**2492.3349**	**0.2098**	**0**	**1**	**1e+02**	**7**	**K.ELALAGVTLAEVIGFFTVGEMIGR.M**
13923	**862.7425**	**2585.2057**	**2584.3723**	**0.8334**	**2**	**2**	**75**	**4**	**K.VGGRTGKVIAFVDSMIPPTLYYGK.V**
14173	880.8819	2639.6237	2639.4284	0.1953	1	3	58	6	K.VIAFVDSMIPPTLYYGKVGLELAK.L 14171

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412. gi\|220692411\|gb\|EED48758.1\| **Mass:** 69473 **Score:** 42 **Queries matched:** 19 **emPAI:** 0.05

cytoplasmic asparaginyl-tRNA synthetase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1564	**567.2286**	**1132.4427**	**1131.5884**	**0.8543**	**1**	**4**	**64**	**6**	**R.AAGDKEAITTR.V** 1562
2202	625.2786	1248.5427	1249.6778	-1.1351	2	4	63	5	K.KATNLYEQRK.K
3730	709.6186	1417.2227	1417.7354	-0.5127	0	4	69	10	R.ELHADFFTIIGR.A 3733
4689	509.8109	1526.4107	1526.8239	-0.4132	1	10	14	1	R.HLVLRGETASAVMK.V
7161	869.6546	1737.2947	1736.0560	1.2388	2	1	1.2e+02	2	K.KIIIKEDTSLPKPVR.I
10182	687.1332	2058.3777	2056.0881	2.2896	0	3	69	4	R.YVNVSIQTQLLYLFDIQ.- 10173
10850	716.2495	2145.7267	2147.0603	-1.3335	0	5	44	2	R.VTESVDVLMPGVGEIVGGSMR.M 10853 10886
12103	**774.3475**	**2320.0207**	**2319.1563**	**0.8644**	**1**	**3**	**65**	**8**	**R.RVTESVDVLMPGVGEIVGGSMR.M**
12326	**786.7389**	**2357.1947**	**2355.2661**	**1.9287**	**1**	**36**	**0.029**	**1**	**R.KMTDIINQPIFLTHFPAEIK.A** 12323
12426	792.3479	2374.0217	2371.2610	2.7608	1	(2)	76	5	R.KMTDIINQPIFLTHFPAEIK.A
14574	901.8699	2702.5877	2704.2352	-1.6474	1	3	60	1	M.TTIYIDEDVGRDDSTATGTESAPYK.T
14797	**918.2689**	**2751.7847**	**2750.3441**	**1.4406**	**1**	**4**	**41**	**5**	**K.AYDIMTLTLGTSMSIHGEMRAVPPK.Q**
16155	**1112.8392**	**3335.4957**	**3332.7149**	**2.7808**	**2**	**3**	**39**	**4**	**R.LRSQKDVVFITLTDGYGYLQCILTGDMVK.A**

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413. gi\|220688822\|gb\|EED45174.1\| **Mass:** 866113 **Score:** 42 **Queries matched:** 118 **emPAI:** 0.00

nonribosomal peptide synthase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
31	656.3770	655.3697	655.4381	-0.0683	0	22	0.64	1	R.LLAALR.Q 32
127	737.5570	736.5497	737.4072	-0.8575	0	3	80	4	K.SYITVR.Y
306	**832.6880**	**831.6807**	**832.3974**	**-0.7166**	**1**	**3**	**1.1e+02**	**9**	**R.MGPNSRR.Q**
331	**423.0331**	**844.0517**	**842.4069**	**1.6448**	**0**	**9**	**24**	**2**	**K.GVMVEHR.N**
360	428.7006	855.3867	855.4926	-0.1059	0	11	11	10	R.LQQALQR.L
406	**865.7240**	**864.7167**	**863.4687**	**1.2480**	**0**	**2**	**1.1e+02**	**5**	**R.NLLAFMR.H**
450	441.7731	881.5317	880.5746	0.9571	0	6	30	10	R.VVLVPVQK.L 449
480	894.6300	893.6227	893.4607	0.1621	0	4	56	2	K.ALSDVYAR.H

489	898.6200	897.6127	898.4508	-0.8381	0	13	8.2	8	K.TQHSALDK.V 487
526	454.6286	907.2427	904.4614	2.7813	1	6	43	7	R.TASDKLDR.K
879	500.5621	999.1097	998.5873	0.5225	0	14	6.2	6	K.VQVTAAAIAR.A 877 880
916	**504.0046**	**1005.9947**	**1007.5447**	**-1.5500**	**1**	**5**	**59**	**8**	**K.GLRHCLPR.D**
989	515.4361	1028.8577	1028.5727	0.2850	2	7	38	9	R.RDDQVKIR.G 987
1114	527.5971	1053.1797	1052.5363	0.6434	0	(8)	24	5	R.IVHAADGSGAR.L 1109 1117
1120	528.1866	1054.3587	1053.7022	0.6565	1	4	58	8	R.AIRLLSLLR.K
1494	562.4756	1122.9367	1122.6033	0.3334	1	6	41	8	R.EQKSYITVR.Y
1505	**1125.6280**	**1124.6207**	**1124.7393**	**-0.1186**	**1**	**9**	**19**	**6**	**R.AISLLALLRR.N**
1532	565.3721	1128.7297	1127.6775	1.0522	2	6	50	9	R.ITGLDIRRGK.V
1946	606.3316	1210.6487	1210.8125	-0.1638	2	5	45	9	R.LLSLLRKAGLK.L
2042	614.1741	1226.3337	1225.7255	0.6082	2	42	0.0098	2	R.ADGQIKLRGLR.V
2569	645.8406	1289.6667	1288.5717	1.0950	1	5	55	4	K.VKDHTEMEER.V
3146	**452.1029**	**1353.2867**	**1354.8258**	**-1.5391**	**0**	**(5)**	**44**	**5**	**R.GVDMVIAILAILK.A**
3175	679.1996	1356.3847	1355.6834	0.7014	0	5	50	5	R.SFLSDPHIVGER.M 3174
3270	683.1791	1364.3437	1362.6337	1.7101	0	(7)	32	9	R.AMLGDGEAETLEK.L 3256 3272 3275
3324	686.0786	1370.1427	1370.8207	-0.6780	0	6	39	1	R.GVDMVIAILAILK.A 3360 3367
3365	687.6706	1373.3267	1371.5951	1.7316	0	2	1.1e+02	8	K.MLASMPYWADR.T 3342
3434	**691.1161**	**1380.2177**	**1378.6286**	**1.5891**	**0**	**8**	**25**	**2**	**R.AMLGDGEAETLEK.L** 3424
3481	**694.4091**	**1386.8037**	**1388.7048**	**-1.9011**	**0**	**2**	**1.1e+02**	**6**	**R.SHPDSIAIVHEGK.E**
3735	709.7236	1417.4327	1418.7877	-1.3550	0	4	65	9	K.GLDMIVTMLAVLK.A
3889	719.1501	1436.2857	1434.7826	1.5031	0	(3)	85	8	K.GLDMIVTMLAVLK.A
3940	721.5381	1441.0617	1440.7937	0.2681	0	4	61	5	K.GVVGELVVTGDGLAR.G
4061	**485.5645**	**1453.6717**	**1452.8300**	**0.8417**	**1**	**12**	**11**	**1**	**R.LLDKPLPRTASDK.L** 4055
4265	**739.4721**	**1476.9297**	**1475.8282**	**1.1015**	**0**	**3**	**84**	**8**	**R.HPLQIGIAQCLVK.R**
4615	761.0221	1520.0297	1518.8518	1.1779	0	4	58	5	K.DQQVLGPVLAPQVR.N
5225	**790.8886**	**1579.7627**	**1579.8511**	**-0.0884**	**1**	**2**	**86**	**1**	**R.IPFSTYVRFVHSK.L**
5302	**794.0536**	**1586.0927**	**1583.7548**	**2.3379**	**1**	**1**	**1.1e+02**	**1**	**R.SICRTLDMFSAGAR.D**
5525	**803.3636**	**1604.7127**	**1603.7856**	**0.9272**	**0**	**4**	**59**	**10**	**R.DGENVQVVHPFAHR.Q**
5555	804.6766	1607.3387	1604.9436	2.3951	1	(3)	82	2	R.LLRLALGMTISVFR.N 5558
6138	551.7049	1652.0927	1651.8392	0.2535	0	7	32	2	K.SEIMPLVFNYQGVR.H
6391	836.5536	1671.0927	1669.8464	1.2463	0	13	7.1	2	K.AGAAFVPLEPGYPPER.L
6644	**844.7841**	**1687.5537**	**1686.7962**	**0.7576**	**0**	**8**	**23**	**2**	**R.SSNDPQHNFSVSQLK.S** 6631 6648
7050	862.3331	1722.6517	1723.7909	-1.1392	0	1	1.1e+02	9	R.VTSLLCNPDYGNPMK.Q
7083	**576.1865**	**1725.5377**	**1724.8846**	**0.6531**	**0**	**2**	**94**	**8**	**R.LPDNGIQGWETIVQR.V**
7362	586.4289	1756.2647	1753.8958	2.3689	1	4	58	4	K.TQEITQRLPESPAER.L
7855	**600.4769**	**1798.4087**	**1795.8080**	**2.6007**	**1**	**6**	**38**	**6**	**R.MREENGQDVEMTVVK.S**
7887	**901.8646**	**1801.7147**	**1800.9217**	**0.7930**	**1**	**0**	**1.3e+02**	**4**	**R.IIKQEPVATESESSAGR.V**
8117	**609.2715**	**1824.7927**	**1821.8832**	**2.9095**	**1**	**1**	**1.1e+02**	**3**	**R.SFLSDPHIVGERMYR.S**
8123	**609.5259**	**1825.5557**	**1824.9595**	**0.5962**	**1**	**9**	**16**	**3**	**K.NEGRFVHVVIGQDTVR.A** 8130
8173	916.7461	1831.4777	1830.9060	0.5717	2	1	1.1e+02	10	R.GAFDAIFHRMGPNSRR.Q

8213	**613.1825**	**1836.5257**	**1834.7978**	**1.7279**	**0**	**6**	**35**	**2**	**R.VECSHGEIFEPAMTGR.V**	8202
8543	**625.1762**	**1872.5067**	**1872.9442**	**-0.4375**	**1**	**4**	**52**	**2**	**R.QEARSHPDSIAIVHEGK.E**	
8739	**631.6139**	**1891.8197**	**1891.9688**	**-0.1491**	**0**	**1**	**1.1e+02**	**8**	**R.SIGWFTAIIPMILDCR.C**	
8753	**632.1665**	**1893.4777**	**1891.9799**	**1.4978**	**1**	**5**	**40**	**4**	**K.GNMHNLAGARGVTPAAISR.A**	
8763	**632.5625**	**1894.6657**	**1892.9891**	**1.6767**	**2**	**4**	**48**	**2**	**R.LTQDKMIVRQSFAQGR.L**	
8877	636.2072	1905.5997	1904.0078	1.5920	1	10	14	3	R.FVPIEVMPLTTSGKVDR.R	
8929	638.3585	1912.0537	1910.0122	2.0415	2	2	83	9	K.TQHSALDKVKYHNTLR.D	
9317	**654.6449**	**1960.9127**	**1960.9775**	**-0.0648**	**1**	**2**	**87**	**9**	**R.AMLGDGEAETLEKLQAASK.Q**	
9445	989.6771	1977.3397	1977.0320	0.3078	0	6	31	2	K.SAYFATITVHLGDSLNLR.T	
10130	685.1322	2052.3747	2050.0769	2.2978	1	1	96	10	R.LLEMTGKGSPFSTVIVDTR.C	
10190	687.2395	2058.6967	2060.1089	-1.4121	2	6	34	6	R.FVPIEVMPLTTSGKVDRR.Q	
10223	**688.2309**	**2061.6707**	**2058.9615**	**2.7092**	**1**	**8**	**19**	**1**	**K.VHGDGMIEWVGRMDSQVK.L**	10218
10240	**688.6722**	**2062.9947**	**2062.1112**	**0.8835**	**1**	**5**	**46**	**3**	**R.LHLKIHHALYDEAFLSR.I**	
10493	**1049.3686**	**2096.7227**	**2095.0810**	**1.6417**	**1**	**3**	**63**	**6**	**R.RNNFQLNLTDLGSFSTIR.S**	
10497	**700.1855**	**2097.5347**	**2099.0899**	**-1.5552**	**0**	**3**	**67**	**3**	**K.TVSTPATPNAALPSYPSLQGK.A**	
10952	**721.0995**	**2160.2767**	**2159.0429**	**1.2338**	**1**	**1**	**1.1e+02**	**7**	**R.YRSIACNEVVPQVPEDQR.I**	
11453	743.7645	2228.2717	2227.2185	1.0532	2	6	31	4	R.ANITPNVAFSRLGGDSIRAIR.L	
11857	763.5942	2287.7607	2286.2664	1.4944	1	1	1e+02	6	R.NDLPFILEILPPKEGVFFAK.I	11856
11973	**769.1149**	**2304.3227**	**2303.1501**	**1.1726**	**1**	**3**	**58**	**3**	**R.DLLTPMTLGDVARAMSPSSTPK.K**	11974 11978
12125	**1162.8326**	**2323.6507**	**2322.1968**	**1.4539**	**0**	**1**	**1e+02**	**6**	**R.ETTQNPLVQTVFAVHPQTQGK.E**	
12142	776.2859	2325.8357	2323.2610	2.5747	0	2	88	10	R.SALGFGHIPVSLILTDVPTVCK.A	
12148	776.5552	2326.6437	2325.0067	1.6370	0	1	95	6	K.VDDTMPTETSSITHAFDDTAR.N	
12456	793.6842	2378.0307	2375.1519	2.8788	1	2	68	4	R.TTFEHRDGENVQVVHPFAHR.Q	
13145	**825.6602**	**2473.9587**	**2475.2679**	**-1.3092**	**1**	**2**	**76**	**2**	**K.TMKTVSTPATPNAALPSYPSLQGK.A**	
13171	826.6635	2476.9687	2476.1872	0.7815	1	1	1e+02	8	R.QEGMNCSLRDLLTPMTLGDVAR.A	
13230	**829.1572**	**2484.4497**	**2486.2046**	**-1.7549**	**2**	**5**	**37**	**1**	**R.DIAKVHGDGMIEWVGRMDSQVK.L**	
13243	**829.7079**	**2486.1017**	**2487.1774**	**-1.0757**	**1**	**7**	**23**	**2**	**K.DPVPPSLCKTFLQEEVEPSCR.N**	13258 13264
13374	**835.8759**	**2504.6057**	**2503.2972**	**1.3085**	**0**	**1**	**95**	**1**	**K.EEQSTPFDLQVHPGWRPLVLR.Q**	
13628	845.7562	2534.2467	2535.3492	-1.1025	2	1	96	7	R.SLIWKGNMHNLAGARGVTPAAISR.A	13644
13808	855.3872	2563.1397	2564.3383	-1.1985	1	9	14	2	R.LPSYMVPSRFVPIEVMPLTTSGK.V	
13830	856.7945	2567.3617	2566.3114	1.0503	2	17	2.4	2	R.WSTANARKSEIMPLVFNYQGVR.H	
14014	**870.8829**	**2609.6267**	**2607.2526**	**2.3741**	**1**	**2**	**77**	**1**	**K.IAVQYELSQFMTYGELDRESTK.L**	
14231	**884.6262**	**2650.8567**	**2651.4072**	**-0.5504**	**2**	**4**	**43**	**4**	**R.IPFSTYVRFVHSKLGTAPSTSTAGK.F**	
15548	**1014.9309**	**3041.7707**	**3042.6134**	**-0.8427**	**2**	**1**	**92**	**2**	**R.DQKDQPLVPICFDKSVDMVVAIVAVLK.A**	
15799	**1049.7552**	**3146.2437**	**3143.6359**	**2.6079**	**1**	**0**	**92**	**8**	**K.GLDMIVTMLAVLKAGAAYIPLDISHSEQR.L**	
15824	**1055.4969**	**3163.4687**	**3164.6466**	**-1.1779**	**2**	**3**	**47**	**1**	**K.KSTEDATDIDAHTGPVALGPIAGRYAGIQLK.Y**	
15939	**1074.8202**	**3221.4387**	**3218.4696**	**2.9692**	**1**	**3**	**45**	**1**	**K.GVMVNHANLVSFMRSATNETYMSWTANR.L**	
16241	1127.6335	3379.8787	3381.7564	-1.8777	1	4	38	2	R.MPVAAYTFDVSMADLLISLAIGARVALVDSEK.M	16246
16333	**1148.1605**	**3441.4597**	**3438.6303**	**2.8294**	**0**	**1**	**64**	**1**	**K.WSQPVDSRPSDSYPCIHDLITGWAAQVPEK.V**	

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414. gi|45477402|gb|AAS66025.1| **Mass:** 56033 **Score:** 42 **Queries matched:** 13 **emPAI:** 0.06

hypothetical protein [Aspergillus parasiticus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
121	733.1260	732.1187	731.4177	0.7010	1	11	17	3	R.QTEKVK.Q
3675	471.0512	1410.1317	1407.7068	2.4249	0	5	47	9	R.SDLITYAALGCPK.L
4030	1450.6890	1449.6817	1449.7616	-0.0799	1	5	51	6	K.LYPDRITGYQPK.Q 4031
5563	805.2696	1608.5247	1605.8297	2.6950	1	2	99	8	-.MGSHAPAVAGKPDPKK.G
6989	858.7501	1715.4857	1716.8617	-1.3760	2	1	1.1e+02	3	R.MSDPNWVRQTEKVK.Q
7732	893.8816	1785.7487	1782.9312	2.8176	1	3	78	1	R.GQHSQVSAIMLRWVR.W
11118	729.1789	2184.5147	2184.1109	0.4038	1	2	78	5	R.KTAEILQASAYICGAAQHPR.K
12042	771.6852	2312.0337	2311.2001	0.8336	2	2	83	4	K.VKQMSAQGRGQHSQVSAIMLR.W
12571	799.1472	2394.4197	2393.2015	1.2182	0	44	0.0054	1	K.ELIPHLSYFQVEPTEHDLAR.K 12572
12956	817.2935	2448.8587	2447.3020	1.5567	1	9	15	3	R.LDPVVATAVGPEDGNNRIADALLK.R 12952

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415. gi|220697554|gb|EED53895.1| **Mass:** 43388 **Score:** 42 **Queries matched:** 14 **emPAI:** 0.08

diphosphomevalonate decarboxylase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1886	599.6486	1197.2827	1196.5496	0.7331	0	10	16	1	-.MAAPSDSTVFR.A 1879
2643	649.7981	1297.5817	1296.6172	0.9645	0	27	0.3	1	R.DFPAFAEITMR.D 2652
3564	698.6566	1395.2987	1394.7188	0.5800	1	5	50	4	R.SLRTLTTASCSAK.Y
6402	**836.9341**	**1671.8537**	**1670.8587**	**0.9950**	**1**	**3**	**72**	**7**	**R.SLRQELEAADSSLPR.L** 6391
9983	**1019.7236**	**2037.4327**	**2035.9891**	**1.4436**	**0**	**30**	**0.14**	**1**	**K.AILGASSEGWDGPFYEPLK.S** 9939
12430	1188.2586	2374.5027	2372.2659	2.2368	1	1	93	3	R.DATLNLPTNSSLSVTLSQRSLR.T 12433
12866	**812.7409**	**2435.2007**	**2433.2652**	**1.9355**	**0**	**42**	**0.0086**	**1**	**R.IVSENNFPTAAGLASSAAGFAALVR.A**
13317	**833.2532**	**2496.7377**	**2495.2301**	**1.5077**	**1**	**1**	**86**	**4**	**R.MAAIETAIQNRDFPAFAEITMR.D**
14398	**891.5105**	**2671.5097**	**2670.1868**	**1.3230**	**0**	**2**	**65**	**6**	**R.AGTLADGSDSLAEEVAPESHWPEMR.A**

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416. gi|220699123|gb|EED55462.1| **Mass:** 37045 **Score:** 42 **Queries matched:** 16 **emPAI:** 0.19

Aha1 domain family [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3593	467.3049	1398.8927	1400.7161	-1.8233	1	10	14	2	R.GAPRQFEGAQVGGK.F
5050	**781.6581**	**1561.3017**	**1560.7460**	**0.5557**	**0**	**32**	**0.11**	**1**	**K.FAIFDGNVTGEYTK.L** 5058
5752	541.8365	1622.4877	1621.8312	0.6566	0	3	79	8	K.VAVNTTTVIASDEFR.T 5761
7731	**893.8351**	**1785.6557**	**1784.8217**	**0.8340**	**0**	**32**	**0.09**	**1**	**R.TTAEELYNTFTDPQR.I**
10225	1031.9156	2061.8167	2061.0524	0.7643	2	11	9.4	2	K.ISNLLSMDGDVDVSQRKGK.V 10231 10234 10241
10589	**1056.3421**	**2110.6697**	**2109.1721**	**1.4976**	**2**	**1**	**1.1e+02**	**2**	**K.VITLFDVKVQLEYEGKTK.D** 10577 10582 10585 10587 10592

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417. gi|220689776|gb|EED46126.1| **Mass:** 67150 **Score:** 41 **Queries matched:** 13 **emPAI:** 0.05

Glycosyl hydrolases family 32 superfamily [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
378	858.6040	857.5967	857.4971	0.0997	0	18	2.9	5	K.TLGIDIAR.E 372
2152	622.7311	1243.4477	1243.6884	-0.2407	1	2	99	10	K.TLGIDIARETR.E
2940	666.4426	1330.8707	1329.6888	1.1819	0	41	0.013	2	K.TISNVVDNELAR.E 2942
4566	759.1931	1516.3717	1514.7670	1.6047	1	12	11	2	R.FALSTWARSWYK.N 4567
9222	650.6139	1948.8197	1950.0534	-1.2337	1	5	49	4	R.ELHIKTISNVVDNELAR.E 9216
10187	1030.3321	2058.6497	2057.0939	1.5558	2	(1)	98	6	K.TLGIDIARETREALMSGPK.I
10314	**691.6772**	**2072.0097**	**2073.0888**	**-1.0791**	**2**	**5**	**46**	**4**	**K.TLGIDIARETREALMSGPK.I**
11339	**738.3545**	**2212.0417**	**2213.0139**	**-0.9722**	**0**	**3**	**66**	**7**	**K.EMSLESWEYLGLWWQEK.V**
15419	**995.2149**	**2982.6227**	**2982.5087**	**0.1140**	**1**	**1**	**84**	**1**	**R.DLNPNGSQFITPGGKNDPVAVFDGSVIPK.G**

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418. gi|220699286|gb|EED55625.1| **Mass:** 40405 **Score:** 41 **Queries matched:** 11 **emPAI:** 0.08

30S ribosomal protein S7, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1106	527.0481	1052.0817	1053.5203	-1.4386	0	8	26	2	R.SQAELHGQGK.S
1307	545.6311	1089.2477	1088.5614	0.6863	1	9	24	2	K.WIIDGSDKR.R
4279	**493.8639**	**1478.5697**	**1475.8130**	**2.7568**	**2**	**11**	**13**	**3**	**K.LLMTDGKLSRAQK.D**
6467	**839.1076**	**1676.2007**	**1674.9781**	**1.2226**	**0**	**41**	**0.011**	**1**	**K.GIAGGGASVQIPVPLALR.Q** 6445
6678	564.5975	1690.7707	1691.8519	-1.0812	1	14	5.8	3	K.FDPVETLPKTENFR.T 6689
7124	**578.0392**	**1731.0957**	**1728.9271**	**2.1686**	**1**	**5**	**44**	**3**	**K.FAQRVANELVAVAEGR.S**
10605	705.2675	2112.7807	2114.1571	-1.3764	2	5	37	3	-.MPPRLNLFNARTAVPVFR.Q
12602	**801.1712**	**2400.4917**	**2402.2626**	**-1.7708**	**1**	**1**	**92**	**4**	**R.QTSINVSRPSIATTINSNRSTR.H**
15704	**1032.7035**	**3095.0887**	**3096.5033**	**-1.4146**	**2**	**0**	**89**	**7**	**K.CDGTPASPELEQGTPISEILQRDKEAQK.H**

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419. gi|220696411|gb|EED52753.1| **Mass:** 129737 **Score:** 41 **Queries matched:** 15 **emPAI:** 0.03

carbamoyl-phosphate synthase, large subunit [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
967	511.4011	1020.7877	1021.5080	-0.7203	0	9	21	9	K.EVEYEVVR.D
1014	518.0751	1034.1357	1033.5597	0.5760	0	3	96	10	K.SFGITPWVK.K
1325	547.1576	1092.3007	1090.6022	1.6985	0	8	31	8	K.EIGSLFGIQK.E
1724	**583.1751**	**1164.3357**	**1161.6546**	**2.6811**	**1**	**1**	**1.3e+02**	**6**	**R.KSFGITPWVK.K**
1832	**594.6091**	**1187.2037**	**1184.5673**	**2.6364**	**0**	**9**	**23**	**1**	**K.ADQEGAQPELK.V** 1831
1866	**597.3821**	**1192.7497**	**1191.6724**	**1.0773**	**2**	**2**	**95**	**6**	**R.GTFNLAKTRGK.T**
2851	661.8026	1321.5907	1321.7282	-0.1374	0	4	66	7	K.IVEYLQPLGYK.F
3230	681.6201	1361.2257	1360.7238	0.5019	0	1	1.3e+02	8	K.ESVSVQVIEFPK.K
4410	**748.6746**	**1495.3347**	**1492.8137**	**2.5210**	**0**	**4**	**64**	**6**	**R.VPEPGEGILLGGDIK.N**
5114	**785.3901**	**1568.7657**	**1566.7752**	**1.9905**	**0**	**41**	**0.012**	**1**	**R.NAVDFGVPLFMETK.T**
6243	**554.5125**	**1660.5157**	**1658.9355**	**1.5802**	**0**	**8**	**27**	**2**	**K.IGLGHTLPELPNAVTK.T**
6647	844.8351	1687.6557	1688.8006	-1.1448	0	1	1.2e+02	8	K.FENLDEVLQNPTDR.R
7864	**900.8486**	**1799.6827**	**1798.8989**	**0.7838**	**0**	**15**	**4.8**	**1**	**K.TTTANFEPSLDYIVTK.I**

9844	676.1889	2025.5447	2024.0724	1.4723	2	2	85	9	K.ALVGRDVPEPVDLMTEKR.D

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420. gi\|220696354\|gb\|EED52696.1\| **Mass:** 43567 **Score:** 41 **Queries matched:** 11 **emPAI:** 0.08
mannitol-1-phosphate dehydrogenase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1471	560.9171	1119.8197	1119.5785	0.2412	1	4	63	4	R.ARFANSAIDR.I
1833	**594.6511**	**1187.2877**	**1187.6299**	**-0.3421**	**0**	**6**	**49**	**3**	**R.FIGPASQLAER.G**
4460	752.0026	1501.9907	1503.8158	-1.8250	0	3	80	2	R.IVPNQPPNSGLNVR.I
4921	775.4846	1548.9547	1548.8195	0.1353	2	6	38	3	-.MGKKAIQFGGGNIGR.G 4907
5495	802.2696	1602.5247	1600.8685	1.6562	2	1	1.2e+02	10	R.KERFIGPASQLAER.G
6483	839.8551	1677.6957	1676.7642	0.9315	0	2	90	3	R.FQNVPGDEESSELAR.I
6709	**847.2866**	**1692.5587**	**1691.7850**	**0.7738**	**0**	**41**	**0.012**	**1**	**K.ENSAEDATSQLTGLEK.D**
6753	566.6849	1697.0327	1698.8974	-1.8647	2	6	34	7	R.GKKMIAEALEDPEIR.E
6998	859.2126	1716.4107	1714.8923	1.5184	2	(2)	96	9	R.GKKMIAEALEDPEIR.E
16262	1131.7849	3392.3327	3390.6878	1.6450	2	2	57	7	R.GQKFDALLGAIEMALRFQNVPGDEESSELAR.I

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421. gi\|8308154\|gb\|AAF74497.1\|AF261860_1 **Score:** 41 **Queries matched:** 6
O-methyltransferase [Aspergillus flavus]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3161	**678.6131**	**1355.2117**	**1354.7979**	**0.4138**	**2**	**10**	**16**	**2**	**-.LIRILRGCAQR.F**
3355	**687.1441**	**1372.2737**	**1370.7565**	**1.5173**	**2**	**2**	**1.1e+02**	**7**	**-.LERILRGCAQR.F**
10289	690.5172	2068.5297	2065.9745	2.5552	0	6	33	4	R.FIFEEVAPNQYAHTDASK.M 10286
11043	725.0985	2172.2737	2171.0688	1.2050	0	39	0.016	5	K.GNPPTWNVPSPFSLAFDPTK.G 11051

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422. gi\|220699888\|gb\|EED56227.1\| **Mass:** 76431 **Score:** 41 **Queries matched:** 9 **emPAI:** 0.04
GTP binding protein, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
89	707.5200	706.5127	707.3272	-0.8145	0	41	0.013	1	K.MDLASR.A
1416	555.6031	1109.1917	1106.5754	2.6164	1	1	1.2e+02	9	K.MDLASRASLK.Q
1977	608.2726	1214.5307	1213.7394	0.7913	1	11	15	7	K.QNLTKVLSALK.L
6434	837.9396	1673.8647	1674.9086	-1.0439	2	12	10	3	K.MDLASRASLKQNLTK.V 6456
10662	708.6729	2122.9967	2121.1946	1.8021	2	5	39	8	R.LAFVSDLPGSVRYLKSTLR.G
11764	**760.6082**	**2278.8027**	**2280.2365**	**-1.4338**	**1**	**6**	**35**	**1**	**R.TISPSKALPPPALPTNIFDSSK.E**
13042	822.5949	2464.7627	2465.2550	-0.4923	0	1	96	8	K.ENHGDELVIGPLLDNALPEHGVK.V
13301	**832.4589**	**2494.3547**	**2494.3292**	**0.0255**	**0**	**0**	**1.1e+02**	**1**	**K.RPAILPVQSGSSEASLDLHHVGPK.D**

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423. gi\|220697813\|gb\|EED54153.1\| **Mass:** 29814 **Score:** 41 **Queries matched:** 8 **emPAI:** 0.11
pyrroline-5-carboxylate reductase [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5365	**796.6541**	**1591.2937**	**1591.7876**	**-0.4938**	**1**	**4**	**59**	**6**	**K.MLVESSDSPSQLRK.N**
6448	**559.3345**	**1674.9817**	**1674.8611**	**0.1207**	**0**	**6**	**35**	**3**	**K.MAALGVQTTTANVEAAK.D**
8811	950.8856	1899.7567	1898.9275	0.8292	1	14	4.9	2	K.QNIWVSEPWDVNREK.M 8809
9006	**640.6805**	**1919.0197**	**1918.0346**	**0.9851**	**0**	**2**	**87**	**5**	**K.LAFIGGGNMASAIIGGLVNK.G**
9670	**1002.7956**	**2003.5767**	**2003.0423**	**0.5345**	**1**	**41**	**0.012**	**1**	**K.DVTSEEKELVNAVLGSVSK.A**
12967	**818.0709**	**2451.1907**	**2451.4101**	**-0.2194**	**0**	**3**	**62**	**6**	**R.TTLPVVVSIAAGITLDSLVQWLR.T**
14500	**896.7079**	**2687.1017**	**2687.4316**	**-0.3299**	**1**	**1**	**77**	**3**	**M.PSLQESKLAFIGGGNMASAIIGGLVNK.G**

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424. gi|220700182|gb|EED56521.1| **Mass:** 21709 **Score:** 40 **Queries matched:** 2 **emPAI:** 0.15

DMRL synthase family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2818	**660.1416**	**1318.2687**	**1317.6313**	**0.6374**	**0**	**40**	**0.015**	**1**	**K.GPGATPSFDGSGLR.I**
11230	732.7339	2195.1797	2194.9776	0.2022	0	1	1e+02	5	K.GETMHFEYIADAVSHGLMR.V

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425. gi|220697521|gb|EED53862.1| **Mass:** 11971 **Score:** 40 **Queries matched:** 15 **emPAI:** 0.66

60S ribosomal protein L36 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
26	650.4130	649.4057	649.3548	0.0510	0	14	6.4	1	R.LGTFGR.G
158	378.6831	755.3517	755.4905	-0.1388	0	29	0.16	4	R.IIELLR.N 157 159 161
464	886.7790	885.7717	885.5284	0.2434	0	24	0.75	1	R.SGIVVGLNK.G
549	**457.0391**	**912.0637**	**911.5916**	**0.4721**	**1**	**37**	**0.027**	**1**	**R.RIIELLR.N**
1524	565.1146	1128.2147	1127.6299	0.5849	1	8	30	9	K.TTPLNTPKTR.V
1558	**566.7991**	**1131.5837**	**1131.5924**	**-0.0087**	**0**	**34**	**0.078**	**1**	**R.EVVGLAPYER.R** 1559
2357	423.0795	1266.2167	1263.6796	2.5371	2	11	13	2	K.GQSSRRTAFVR.D 2356
3307	**685.2321**	**1368.4497**	**1369.7677**	**-1.3180**	**1**	**2**	**84**	**4**	**M.AQERSGIVVGLNK.G**
5336	**530.6525**	**1588.9357**	**1586.8416**	**2.0941**	**1**	**5**	**49**	**5**	**R.DIAREVVGLAPYER.R**
5352	**795.8921**	**1589.7697**	**1587.8151**	**1.9546**	**2**	**5**	**52**	**2**	**K.VEDMQRVIAESRR.V**

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426. gi|220692396|gb|EED48743.1| **Mass:** 11176 **Score:** 40 **Queries matched:** 4 **emPAI:** 0.31

mitochondrial F1F0 ATP synthase subunit F (Atp17), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
592	925.5830	924.5757	924.5644	0.0113	0	16	3.6	1	R.GLSTLIPPK.I
3438	**691.6771**	**1381.3397**	**1380.7725**	**0.5672**	**0**	**40**	**0.015**	**1**	**R.GSAPEVKPTGLIGR.Y**
8268	**615.4535**	**1843.3387**	**1842.9370**	**0.4017**	**2**	**3**	**79**	**3**	**K.IASPNAIGAAKDAARMDR.V**
12184	778.1952	2331.5637	2331.3274	0.2363	2	1	91	8	R.GLSTLIPPKIASPNAIGAAKDAAR.M

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427. gi|220698230|gb|EED54570.1| **Mass:** 32404 **Score:** 40 **Queries matched:** 16 **emPAI:** 0.10

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
764	**488.6456**	**975.2767**	**975.5284**	**-0.2517**	**1**	**2**	**1.2e+02**	**1**	**R.GLTRAVGMR.G** 768
2693	652.2886	1302.5627	1299.7333	2.8294	0	(3)	90	9	R.GGLSMLGLNGLLR.R
2776	438.9419	1313.8037	1315.7282	-1.9245	0	40	0.019	1	R.GGLSMLGLNGLLR.R 2777
8012	605.7592	1814.2557	1814.0019	0.2539	1	8	22	5	R.AVGMRGGLSMLGLNGLLR.R 8016 8034
9644	**667.7232**	**2000.1477**	**2002.0928**	**-1.9451**	**2**	**3**	**65**	**3**	**R.AVGMRGGLSMLGLNGLLRR.I**
11379	**739.6959**	**2216.0657**	**2216.8635**	**-0.7978**	**0**	**(5)**	**35**	**2**	**K.MGSYEAMYGDMASYSVHMR.G**
11388	740.2889	2217.8447	2216.8635	0.9812	0	8	20	2	K.MGSYEAMYGDMASYSVHMR.G 11389
15817	**1054.1039**	**3159.2897**	**3158.3864**	**0.9033**	**2**	**(0)**	**90**	**3**	**K.MGSYEAMYGDMASYSVHMRGLTRAVGMR.G**
15819	1054.3972	3160.1697	3158.3864	1.7833	2	1	77	5	K.MGSYEAMYGDMASYSVHMRGLTRAVGMR.G
16032	1095.3399	3282.9977	3282.4817	0.5160	1	10	11	2	R.VNDALIGAIAKMGSYEAMYGDMASYSVHMR.G 16031

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428. gi\|220694974\|gb\|EED51317.1\| **Mass:** 108549 **Score:** 40 **Queries matched:** 19 **emPAI:** 0.03

chromosome segregation protein Cse1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
394	864.4300	863.4227	864.4705	-1.0478	0	10	17	4	K.YDILVSR.A 400
2488	641.0111	1280.0077	1280.6223	-0.6146	0	4	62	5	K.GWGFTCEALLK.L
2825	660.4796	1318.9447	1317.6565	1.2882	0	3	77	2	R.WDTLVDDLVSR.L
3640	703.1851	1404.3557	1403.7813	0.5745	1	5	49	3	K.YLYTFRSIITK.E 3642
6153	552.0962	1653.2667	1654.7629	-1.4962	1	2	96	10	K.VQENEFLMKCAMR.V
7456	589.2249	1764.6527	1761.9486	2.7042	2	2	85	7	R.LQNSKTENLTGRFVR.F
7689	**892.6626**	**1783.3107**	**1783.9469**	**-0.6361**	**1**	**3**	**80**	**2**	**R.WDTLVDDLVSRLQPK.N**
9632	**667.2505**	**1998.7297**	**1999.0044**	**-0.2747**	**0**	**2**	**79**	**6**	**-.MADNLGAVAQLLEASLDPR.Q**
11962	**768.6212**	**2302.8417**	**2302.1157**	**0.7260**	**0**	**3**	**69**	**8**	**K.FGNPFLALFEGLDSYLEENK.T**
12348	**787.7045**	**2360.0917**	**2358.1227**	**1.9690**	**1**	**4**	**44**	**2**	**R.NYTDEDGNYKLQLDEVTTIK.Q**
12368	790.1205	2367.3397	2369.2009	-1.8611	1	2	78	5	-.MADNLGAVAQLLEASLDPRQNK.Q 12377
12820	**810.7802**	**2429.3187**	**2429.3655**	**-0.0468**	**2**	**0**	**1.1e+02**	**3**	**R.LQPKNPAVNNGVLQVAHSIFKR.W**
13458	838.8202	2513.4387	2514.2238	-0.7851	2	1	99	3	K.RNYTDEDGNYKLQLDEVTTIK.Q
13470	839.6719	2515.9937	2515.2132	0.7805	0	1	84	9	K.VVLHYTEGHLAQYTSDPASNWK.A
13629	**845.8142**	**2534.4207**	**2532.3548**	**2.0660**	**0**	**37**	**0.023**	**1**	**K.EGVVPHTDSVLQNLINITEVISR.N** 13621

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429. gi\|220691400\|gb\|EED47748.1\| **Mass:** 29314 **Score:** 40 **Queries matched:** 11 **emPAI:** 0.24

proteasome component Pre6, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
627	468.7291	935.4437	933.5032	1.9405	0	3	87	5	K.YIAGVQQR.Y
767	976.6210	975.6137	975.5172	0.0966	1	6	44	7	R.GTCAVGVKGK.D
1639	572.7536	1143.4927	1143.6499	-0.1572	0	42	0.012	1	K.SLLEVVQTGAK.N
1907	1203.2690	1202.2617	1202.6329	-0.3712	1	5	55	2	K.GKDVVVLGCEK.R

4131	732.2171	1462.4197	1462.8103	-0.3906	1	5	52	6	K.TARTSTTTAAILTR.G
5734	**811.5616**	**1621.1087**	**1619.8658**	**1.2429**	**0**	**20**	**1.3**	**1**	**R.LTVEDPVTIEYITK.Y** 5736 5743 5747 5748
13761	852.6762	2555.0067	2553.2864	1.7203	0	1	96	7	R.YTQSGGVRPFGISTLVVGFDPNDK.V

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430. gi\|220697454\|gb\|EED53795.1\| **Mass:** 57088 **Score:** 40 **Queries matched:** 25 **emPAI:** 0.06

peptide N-myristoyl transferase (Nmt1) [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
133	**743.4720**	**742.4647**	**741.3116**	**1.1532**	**0**	**9**	**23**	**1**	**K.DMASYR.F** 131
822	987.4330	986.4257	985.5808	0.8449	1	3	99	7	K.LKDATITPK.M
889	1001.4440	1000.4367	1000.5665	-0.1298	2	5	57	6	K.KDAAEALRK.M 890
923	506.0506	1010.0867	1010.5760	-0.4893	0	16	4.2	2	K.LLENNPALK.N 925
1396	554.5126	1107.0107	1105.5437	1.4670	2	6	36	3	-.MSDPKDTKGK.A 1405
4486	753.2766	1504.5387	1504.8171	-0.2784	0	15	5.4	3	K.MTISELLTGLSVGGK.N 4487 4494 4495 4497
5471	534.6422	1600.9047	1598.9429	1.9618	1	4	63	9	R.LLLLMNDALIQAKK.A
7556	887.2651	1772.5157	1769.9974	2.5183	2	4	64	8	K.VTEINFLCIHKKLR.S
8538	**624.8285**	**1871.4637**	**1868.9665**	**2.4972**	**1**	**2**	**91**	**4**	**K.LLENNPALKNELAGMDK.K**
9396	**986.2366**	**1970.4587**	**1971.9861**	**-1.5274**	**2**	**0**	**1.3e+02**	**3**	**K.GKAPQAEDTQAGSSEQKLK.D**
9446	**660.1419**	**1977.4037**	**1978.0306**	**-0.6269**	**0**	**11**	**11**	**1**	**K.NHLPSTTSTPGLRPMEIK.D**
9466	660.7132	1979.1177	1980.9305	-1.8128	0	4	58	7	R.YSQSFLHWALMSPGWR.K
11614	**752.3335**	**2253.9787**	**2253.1470**	**0.8317**	**0**	**40**	**0.014**	**1**	**K.ITDFFSFYNLPSTVIQHPK.H** 11610
12252	782.4152	2344.2237	2344.1766	0.0471	2	6	34	2	K.MAEKLLENNPALKNELAGMDK.K 12250 12251

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431. gi\|220697382\|gb\|EED53723.1\| **Score:** 39 **Queries matched:** 4

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
76	**691.7500**	**690.7427**	**690.3813**	**0.3614**	**1**	**13**	**11**	**3**	**R.RQYPK.Q**
853	496.9296	991.8447	991.4869	0.3578	1	39	0.02	2	R.QALSMRDR.Q
4433	500.8192	1499.4357	1500.7718	-1.3361	1	4	67	9	R.QGMPSGEIERLLR.L
10343	1039.6941	2077.3737	2075.9840	1.3897	2	6	37	4	R.QALSMRDRQGMPSGEIER.L

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432. gi\|220700631\|gb\|EED56969.1\| **Mass:** 96403 **Score:** 39 **Queries matched:** 12 **emPAI:** 0.03

phospholipase PldA, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
435	438.9266	875.8387	875.4171	0.4216	0	14	7.1	5	K.VCIVDDR.V
983	**343.0915**	**1026.2527**	**1026.6298**	**-0.3771**	**2**	**9**	**19**	**5**	**R.LDQVLKRR.A**
2865	663.2146	1324.4147	1325.7554	-1.3407	1	6	36	7	R.INKTPALEALEK.E
3042	**672.0646**	**1342.1147**	**1343.6504**	**-1.5356**	**0**	**7**	**30**	**3**	**K.DTVAHTTMLNGGK.M** 3068 3069
3985	**723.8266**	**1445.6387**	**1443.7147**	**1.9241**	**0**	**7**	**30**	**4**	**K.QGHLYDPYQPVK.D**
4730	**766.7951**	**1531.5757**	**1532.7623**	**-1.1866**	**0**	**11**	**13**	**2**	**K.ANFVQEELYVHGK.V**

8170	**611.2819**	**1830.8237**	**1830.9839**	**-0.1602**	**2**	**2**	**95**	**8**	**R.AYDRINKTPALEALEK.E**
8696	630.0209	1887.0407	1886.8832	0.1575	1	4	56	4	R.QPEATGTRAIMDYQYK.S
11388	740.2889	2217.8447	2217.1277	0.7170	1	39	0.016	1	K.TPALEALEKEAGVTYNDIQR.G 11389

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433. gi|220694211|gb|EED50555.1| **Mass:** 108949 **Score:** 39 **Queries matched:** 16 **emPAI:** 0.03

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
64	686.5530	685.5457	685.4123	0.1335	0	9	27	9	R.IEVAVR.W
810	493.3681	984.7217	985.5920	-0.8703	0	39	0.02	2	R.LSSQGLLIR.G 812
1044	520.6721	1039.3297	1039.4207	-0.0910	0	7	32	4	R.GTSGDDADFR.T
1048	521.6276	1041.2407	1040.4927	0.7480	0	6	40	4	K.EGYLFDAAR.N
2745	437.5432	1309.6077	1310.6367	-1.0290	1	9	19	4	K.EGYLFDAARNR.R
4714	510.9072	1529.6997	1528.7933	0.9064	1	9	20	5	K.RGCLGVLANTGHFK.T
5377	797.2286	1592.4427	1591.8359	0.6069	1	3	76	5	K.FFRDQPDTLVAGVK.G
9921	678.8085	2033.4037	2034.9945	-1.5908	0	3	74	3	R.YCNAVAFSTHGLLAAGLDR.V
11234	732.8909	2195.6507	2195.1488	0.5020	2	3	71	5	K.FFRDQPDTLVAGVKGQYVR.I
11966	768.8232	2303.4477	2301.1601	2.2877	1	4	47	5	R.TLSADSQHTKAAALAVFQDEAK.L 11967
12453	**793.4769**	**2377.4087**	**2376.1096**	**1.2991**	**1**	**(4)**	**48**	**1**	**K.ACLAADAGQQAGKPTQAEMMRR.F**
12573	799.2449	2394.7127	2392.1046	2.6082	1	6	34	2	K.ACLAADAGQQAGKPTQAEMMRR.F
14533	**898.6955**	**2693.0647**	**2693.3997**	**-0.3350**	**1**	**1**	**86**	**5**	**R.ILPSHDIQEISRENHHTKPLSSR.E** 14524

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434. gi|220697584|gb|EED53925.1| **Mass:** 48782 **Score:** 39 **Queries matched:** 8 **emPAI:** 0.14

methionine aminopeptidase, type II, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
602	**464.0976**	**926.1807**	**926.5549**	**-0.3742**	**0**	**11**	**10**	**10**	**K.NLLNVINK.N** 604
1051	522.0461	1042.0777	1042.5407	-0.4630	0	17	3.1	2	K.LDLNGQGGAAK.A
6166	**828.2176**	**1654.4207**	**1652.7754**	**1.6453**	**2**	**0**	**1.5e+02**	**4**	**K.DDNLYRTTNEEKR.Y**
10667	**708.7422**	**2123.2047**	**2121.9650**	**1.2397**	**1**	**0**	**1.2e+02**	**8**	**R.MNNDFLQEYRQGAEVHR.Q**
11042	**725.0885**	**2172.2437**	**2170.1481**	**2.0956**	**0**	**29**	**0.17**	**1**	**K.TIKPGQTLTEIAEGIEESVR.A** 11028
14522	**898.1942**	**2691.5607**	**2690.3989**	**1.1618**	**0**	**7**	**24**	**2**	**K.YLLGLNNLVSSGIVQDYPPLCDIK.G**

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435. gi|220698460|gb|EED54800.1| **Score:** 38 **Queries matched:** 13

ribosomal protein S15, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
273	410.5556	819.0967	818.4147	0.6820	0	12	13	1	R.HLQEHR.N
772	**976.9700**	**975.9627**	**975.4733**	**0.4894**	**1**	**1**	**1.4e+02**	**5**	**R.AGSAETRER.R**
953	509.6606	1017.3067	1015.4822	1.8245	0	10	21	10	R.DTADPQLEK.E
967	511.4011	1020.7877	1020.6556	0.1321	2	9	19	7	R.LLVHKRQK.L
2050	614.8086	1227.6027	1227.6935	-0.0908	1	8	24	9	R.NAQEAISRIVK.I

3183	679.6256	1357.2367	1356.6721	0.5647	1	11	14	2	R.RHDPFLMAQSR.Q 3171 3177 3179 3193
6590	**562.4759**	**1684.4057**	**1683.9016**	**0.5042**	**2**	**2**	**93**	**5**	**R.KAANLSRQQALAEER.E**
10633	1060.1936	2118.3727	2117.9979	0.3748	0	38	0.019	2	R.LNYFVTPEGLQEAMEYSK.A 10632

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436. gi|220701477|gb|EED57815.1| **Mass:** 111194 **Score:** 38 **Queries matched:** 8 **emPAI:** 0.03

Sec23/Sec24 family protein [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1662	**575.9396**	**1149.8647**	**1149.6254**	**0.2393**	**0**	**11**	**14**	**2**	**R.QINLELAGHR.K**
3885	**479.6542**	**1435.9407**	**1433.8215**	**2.1192**	**2**	**7**	**33**	**8**	**R.QINLELAGHRK.E**
4620	761.2316	1520.4487	1518.8042	1.6445	0	2	1e+02	9	R.LFLIDVSQESVNR.G
5360	**796.4001**	**1590.7857**	**1590.7435**	**0.0422**	**1**	**3**	**81**	**1**	**R.CRAYINPFMTFR.S** 5354
10681	**709.2229**	**2124.6467**	**2123.0171**	**1.6296**	**1**	**0**	**1.1e+02**	**9**	**R.EDTSAEGSLTSLAGLRAPYW.-**
11580	**751.1795**	**2250.5167**	**2248.2249**	**2.2918**	**0**	**38**	**0.019**	**1**	**K.KPEPALLPALNAAMSALQATGGK.I**
12666	804.2039	2409.5897	2408.2886	1.3011	2	2	78	6	R.LFLIDVSQESVNRGFLKGVCK.G

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437. gi|220697844|gb|EED54184.1| **Mass:** 38373 **Score:** 38 **Queries matched:** 9 **emPAI:** 0.09

protein phosphatase 2A catalytic subunit Pph21, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
342	**846.8470**	**845.8397**	**845.4065**	**0.4332**	**0**	**6**	**57**	**8**	**R.AGEPMVSR.R**
903	502.0581	1002.1017	1001.5076	0.5941	1	5	64	10	R.AGEPMVSRR.T
3966	722.7681	1443.5217	1442.6653	0.8564	0	8	24	6	K.YTFLQFDPCPR.A
6854	852.6761	1703.3377	1702.8137	0.5240	0	2	92	9	R.NVVTIFSAPNYCYR.C
10820	1072.7021	2143.3897	2142.9681	0.4217	0	38	0.019	2	R.IGGPNPDTNYLFMGDYVDR.G 10849
14248	885.4742	2653.4007	2651.2728	2.1279	0	8	20	1	R.GAGYTFGQDISEAFNHNNGLTLVAR.A 14239 14250

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438. gi|220700656|gb|EED56994.1| **Mass:** 81812 **Score:** 38 **Queries matched:** 21 **emPAI:** 0.04

metallopeptidase MepB [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
62	685.4680	684.4607	684.4534	0.0073	0	8	23	5	K.KPSLLK.H 63
340	846.6320	845.6247	843.4926	2.1321	1	0	2e+02	7	K.RLIEASR.K
574	917.5850	916.5777	916.5090	0.0687	1	16	5.4	3	R.SRLTAGGQK.E 573
1156	531.7741	1061.5337	1059.4832	2.0505	0	8	34	10	K.NETLDPESR.R
2552	430.1202	1287.3387	1286.7306	0.6081	2	12	9.4	5	R.SRLTAGGQKEIK.S 2542 2545 2548 2550 2561
4043	484.7652	1451.2737	1450.6688	0.6049	1	8	24	4	K.NDIEARGETFDGK.Y
7099	**864.7591**	**1727.5037**	**1726.7832**	**0.7205**	**0**	**6**	**32**	**1**	**K.GGSQDEMTSLTEFLGR.E**
7863	**900.8121**	**1799.6097**	**1798.8447**	**0.7650**	**0**	**10**	**16**	**1**	**K.AEAELDEFFIETVMR.E**
7864	900.8486	1799.6827	1797.8872	1.7955	0	6	37	3	R.QLHFGIFDMTVHEPK.S
8961	**639.3315**	**1914.9727**	**1911.9901**	**2.9826**	**1**	**2**	**88**	**3**	**K.LVDAVLNKNETLDPESR.R**
13620	**845.2932**	**2532.8577**	**2531.2867**	**1.5710**	**0**	**33**	**0.062**	**1**	**K.EQAGDKPEPAEQIPDEVIANLIR.T** 13616

13834	**857.0519**	**2568.1337**	**2565.1668**	**2.9669**	**0**	**5**	**39**	**1**	**R.DFVEAPSQMLENWCWTPSQLK.S**
14131	**877.9382**	**2630.7927**	**2629.4778**	**1.3150**	**2**	**2**	**67**	**4**	**R.RYPATALVCNFTKPTPKKPSLLK.H**

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439. gi\|220691491\|gb\|EED47839.1\| **Mass:** 62807 **Score:** 38 **Queries matched:** 9 **emPAI:** 0.05

arylsulfatase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1351	**549.7991**	**1097.5837**	**1096.6716**	**0.9121**	**1**	**38**	**0.026**	**1**	**R.LERLIQLGR.V** 1350
2627	432.8292	1295.4657	1292.6183	2.8474	1	6	43	4	K.EIAPCSRGFEK.N
9548	664.4942	1990.4607	1991.9808	-1.5201	0	6	38	2	K.MEVFAAMVDLIDQNIQR.V
9677	**669.1185**	**2004.3337**	**2006.0771**	**-1.7434**	**2**	**7**	**29**	**1**	**R.AIRQGSWKALYMTAPLGK.D**
10651	707.8335	2120.4787	2120.0758	0.4029	1	7	27	5	R.KMEVFAAMVDLIDQNIQR.V
10758	713.3189	2136.9347	2136.0707	0.8640	1	(6)	33	4	R.KMEVFAAMVDLIDQNIQR.V
13888	860.9069	2579.6987	2578.2995	1.3992	2	8	18	3	R.AGSARKMEVFAAMVDLIDQNIQR.V
13889	861.0735	2580.1987	2578.2995	1.8992	2	(8)	19	4	R.AGSARKMEVFAAMVDLIDQNIQR.V

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440. gi\|220700052\|gb\|EED56391.1\| **Mass:** 67233 **Score:** 38 **Queries matched:** 6 **emPAI:** 0.05

carbon catabolite repression protein CreD, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
148	749.6270	748.6197	747.4167	1.2031	0	8	27	5	R.YLDLPK.T 146
781	489.8611	977.7077	976.5705	1.1372	1	5	56	6	K.YAKDIIVR.K
1400	554.7066	1107.3987	1104.6655	2.7332	2	7	32	6	R.KYAKDIIVR.K
4029	**725.8276**	**1449.6407**	**1450.7086**	**-1.0679**	**1**	**3**	**84**	**5**	**K.TLTRCLQDTDTK.G**
15611	1021.5755	3061.7047	3059.5775	2.1272	0	38	0.018	1	K.GLTIGQIVSQLIESHDLTLNPEDPDSIR.N

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441. gi\|220698436\|gb\|EED54776.1\| **Mass:** 22732 **Score:** 37 **Queries matched:** 7 **emPAI:** 0.15

glycolipid transfer protein HET-C2, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
232	800.4920	799.4847	799.5167	-0.0320	0	18	3	4	K.IVSILQK.F 233
1315	546.4631	1090.9117	1090.5771	0.3346	0	16	4	1	R.GLDFTAQALR.R 1316
1339	548.7561	1095.4977	1095.5196	-0.0219	0	37	0.027	1	K.TGEELASSFR.E
2408	637.4486	1272.8827	1272.6826	0.2001	0	1	1.3e+02	6	K.VFSVAVGAAPNNK.N
7187	580.7772	1739.3097	1737.9890	1.3208	2	6	39	1	K.TKKHTASEGLLWLVR.G

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442. gi\|220691415\|gb\|EED47763.1\| **Mass:** 60276 **Score:** 37 **Queries matched:** 16 **emPAI:** 0.05

actin interacting protein 2 [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2032	613.6701	1225.3257	1223.6662	1.6595	0	11	13	2	R.NHLFPLDLGAK.G
3134	676.7521	1351.4897	1352.7048	-1.2151	0	7	29	3	R.NGSISAEHGLGLAK.K 3153 3157

3518	696.2946	1390.5747	1389.8204	0.7543	1	5	53	10	R.GHTRLVLKPQNK.E
3768	712.6971	1423.3797	1422.6780	0.7017	0	37	0.029	1	K.LGFVGDDDSFPVR.A
5050	781.6581	1561.3017	1560.7976	0.5041	0	5	53	3	K.AIEPWVYEWIQK.R
6681	**564.6949**	**1691.0627**	**1689.7920**	**1.2707**	**1**	**5**	**48**	**4**	**K.KEFIGYSQDETMVK.L** 6666
7929	903.8086	1805.6027	1803.8825	1.7202	0	8	24	2	K.SHLSEILSAFELMDGR.S
9011	**640.8849**	**1919.6327**	**1917.9216**	**1.7111**	**1**	**2**	**83**	**9**	**K.EFIGYSQDETMVKLMK.Q**
10906	718.8502	2153.5287	2154.0640	-0.5353	0	6	31	1	R.AVVGYGHMGDSNLHLNISVR.E 10926
11914	**766.7952**	**2297.3637**	**2296.1595**	**1.2042**	**2**	**5**	**36**	**2**	**K.LMKQLKDLYDPNGIMNPYK.Y**
14148	**879.4529**	**2635.3367**	**2636.4724**	**-1.1357**	**0**	**3**	**54**	**1**	**K.QLFIGAEGTIGVITGLSILCPPRPK.A**
14399	891.5249	2671.5527	2672.3129	-0.7602	1	5	32	8	R.AVVGYGHMGDSNLHLNISVREYNK.E

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443. gi|220694306|gb|EED50650.1| **Mass:** 26582 **Score:** 37 **Queries matched:** 6 **emPAI:** 0.13

orotate phosphoribosyltransferase [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
3001	669.9466	1337.8787	1337.7343	0.1444	0	6	39	10	K.NNVLSFGSFILK.S
3253	**682.5441**	**1363.0737**	**1362.6892**	**0.3845**	**0**	**9**	**20**	**1**	**K.DHGEGGNIVGAPLK.G**
5290	793.6526	1585.2907	1584.8835	0.4072	2	8	25	4	K.LGDKIGESEIQRLK.D 5291
10370	**694.3952**	**2080.1637**	**2078.0837**	**2.0801**	**0**	**31**	**0.11**	**1**	**R.ESPYFFTSSLLHTAPLLR.A** 10363

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444. gi|46370483|gb|AAS90018.1| **Mass:** 46640 **Score:** 36 **Queries matched:** 5 **emPAI:** 0.07

OmtA [Aspergillus flavus]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
10520	1051.0501	2100.0857	2100.0595	0.0262	0	36	0.032	1	R.ILLDEMIMPDLLAQDSQR.F
10814	715.2352	2142.6837	2140.0657	2.6181	1	2	79	1	R.FMNQIDMTVVLTLNGKER.S
11009	**1085.1611**	**2168.3077**	**2167.2034**	**1.1043**	**1**	**1**	**91**	**1**	**-.MALPNKAALVGLANTLSEQVK.C**
12437	792.6655	2374.9747	2375.1824	-0.2077	1	2	79	6	K.SRILLDEMIMPDLLAQDSQR.F
15454	**999.9832**	**2996.9277**	**2997.4225**	**-0.4948**	**2**	**7**	**19**	**1**	**R.GCAQRFIFEEVAPGQYAHTDASKMLR.V**

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445. gi|220693839|gb|EED50184.1| **Mass:** 44863 **Score:** 36 **Queries matched:** 12 **emPAI:** 0.07

conserved hypothetical protein [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
478	894.5330	893.5257	892.5018	1.0239	1	2	1e+02	10	K.YVKDLAGK.A 479
962	**510.6231**	**1019.2317**	**1017.4978**	**1.7339**	**0**	**7**	**41**	**8**	**K.AEQLAEETK.S**
1118	528.1031	1054.1917	1053.6155	0.5762	2	8	24	8	R.TPLRNARAR.Y
2657	650.5141	1299.0137	1299.7511	-0.7373	2	3	88	8	K.GKLDVDTAVKVR.D
3738	**710.0426**	**1418.0707**	**1416.6674**	**1.4034**	**0**	**36**	**0.038**	**1**	**K.TPEPDEAFGWLR.D**
4703	**765.2751**	**1528.5357**	**1527.7576**	**0.7781**	**2**	**5**	**50**	**6**	**M.LSRSSRFATSCTR.Q**
6111	551.1805	1650.5197	1648.8420	1.6777	2	10	16	4	K.DLAGKAKESGFGNLDK.L 6098
7234	581.2545	1740.7417	1737.7516	2.9902	0	3	77	9	K.EMGSAYGPQAQEEVDK.T

10285	**690.4332**	**2068.2777**	**2069.0793**	**-0.8016**	**2**	**3**	**74**	**6**	**K.TIVQTANQTEAYFKEAKK.K**
12688	**805.3652**	**2413.0737**	**2410.1474**	**2.9263**	**2**	**3**	**64**	**2**	**R.LKEMGSAYGPQAQEEVDKTWK.Q**

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446. gi|220696817|gb|EED53158.1| **Mass:** 46296 **Score:** 36 **Queries matched:** 9 **emPAI:** 0.07

phosphoserine aminotransferase [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
1228	538.0931	1074.1717	1072.5149	1.6568	0	8	27	3	K.VDGQQAEAQK.K
2266	629.7576	1257.5007	1257.6565	-0.1557	1	5	60	4	R.VIKGGNVDEAEK.A
2843	**661.2866**	**1320.5587**	**1319.6755**	**0.8833**	**0**	**9**	**20**	**1**	**R.SEIAANILNTMK.A** 2821
8282	**923.4576**	**1844.9007**	**1844.0117**	**0.8890**	**0**	**36**	**0.035**	**1**	**K.LGLPIAPTILDYCVTAK.N**
10413	1043.7766	2085.5387	2086.1058	-0.5671	2	2	80	6	K.KLLATFPDKVDGQQAEAQK.K
10579	704.0982	2109.2727	2107.1313	2.1414	1	3	74	4	R.ASNYNAIPVSGAEKLVAYLK.E
14781	**916.7462**	**2747.2167**	**2744.3367**	**2.8800**	**2**	**(3)**	**51**	**4**	**K.ADMIYEAADAYPEVYKVVPDKSVR.S** 14782

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447. gi|220699236|gb|EED55575.1| **Mass:** 20455 **Score:** 36 **Queries matched:** 3 **emPAI:** 0.16

transmembrane protein 14, putative [Aspergillus flavus NRRL3357]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
12857	812.5345	2434.5817	2433.2751	1.3066	0	36	0.033	1	R.TGQTYGDELGLLASIVLSGSSIPR.A 12852 12876

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448. gi|1762235|gb|AAC23536.1| **Mass:** 193373 **Score:** 36 **Queries matched:** 30 **emPAI:** 0.02

polyketide synthase PKSL2 [Aspergillus parasiticus]

Query	**Observed**	**Mr(expt)**	**Mr(calc)**	**Delta**	**Miss**	**Score**	**Expect**	**Rank**	**Peptide**
85	704.1170	703.1097	702.4024	0.7073	1	17	4.8	2	R.SRALEK.H
113	723.4480	722.4407	723.3551	-0.9144	0	36	0.036	2	R.FDSLSR.Q
701	482.3616	962.7087	962.5219	0.1869	1	2	1.2e+02	8	K.KILSMESR.G 700
1295	**544.6236**	**1087.2327**	**1088.5284**	**-1.2957**	**0**	**5**	**63**	**8**	**R.TNGIMAPNQK.A**
1381	553.0001	1103.9857	1103.5870	0.3988	1	20	1.9	3	R.CVAATLGTRR.S
1615	**571.0941**	**1140.1737**	**1139.7251**	**0.4486**	**2**	**2**	**89**	**9**	**K.GARRIILVSR.R**
2354	634.0501	1266.0857	1265.6074	0.4783	0	1	1.1e+02	10	R.EIGMAAGSEFVR.A
2989	669.2391	1336.4637	1335.7108	0.7529	0	7	35	8	R.EYVLDLVNIMK.Y 2982
5312	794.7321	1587.4497	1586.7736	0.6761	1	2	97	9	R.MHDVDKHNLLGHR.T 5292
5931	819.4726	1636.9307	1637.7719	-0.8412	0	4	62	2	K.TQAATQAEWMSTIGK.Q
6789	851.0226	1700.0307	1698.9338	1.0969	1	7	31	2	R.GEGAAVVILKNMAEAVK.N
7327	876.6786	1751.3427	1750.9802	0.3625	2	3	70	2	R.NADIVRISDGIPRVAR.L
7630	593.9559	1778.8457	1778.0090	0.8367	0	6	37	9	K.HEPLPSPLLVDIAIHK.V
7898	902.2686	1802.5227	1801.9574	0.5654	1	2	93	3	K.EEIEAFALNLNNKGIK.T
8231	**614.1242**	**1839.3507**	**1839.9512**	**-0.6005**	**1**	**14**	**5.9**	**1**	**K.NMAEAVKNGDHILATLK.G**
8846	952.0921	1902.1697	1903.0679	-0.8982	1	0	1.3e+02	2	K.NWAALVHSASPLAPTIKK.I
9022	**641.2489**	**1920.7247**	**1919.9424**	**0.7823**	**1**	**2**	**86**	**4**	**R.RSQGVNTIAMQWTSWR.E**

9853	676.3122	2025.9147	2025.1696	0.7451	1	5	37	2	R.VLAPKIAGSLTLNMLFPPK.T 9848
10102	**683.9772**	**2048.9097**	**2048.1378**	**0.7719**	**1**	**2**	**85**	**1**	**R.VIKADTATSLAQAPLHGLSR.I**
10211	1031.3806	2060.7467	2059.1690	1.5777	2	5	45	5	R.RKNWAALVHSASPLAPTIK.K 10188
10658	708.4279	2122.2617	2122.0841	0.1777	2	3	60	2	R.RSLKTQAATQAEWMSTIGK.Q 10657
11927	**767.4425**	**2299.3057**	**2298.1036**	**1.2021**	**2**	**5**	**45**	**3**	**R.SEHTTRMHDVDKHNLLGHR.T**
12452	**793.4269**	**2377.2587**	**2378.3468**	**-1.0880**	**2**	**0**	**1.1e+02**	**7**	**K.AVMSVQKGILPPQANLKTLNTR.V**
15395	991.4799	2971.4177	2970.3454	1.0724	1	1	90	10	K.NIENFDASFFNISPKEAEQMDPQQR.L

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449. gi\|220688427\|gb\|EED44780.1\| **Mass:** 121340 **Score:** 36 **Queries matched:** 20 **emPAI:** 0.03

polyketide synthase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
85	704.1170	703.1097	702.4024	0.7073	1	17	4.8	2	R.SRALEK.H
113	723.4480	722.4407	723.3551	-0.9144	0	36	0.036	2	R.FDSLSR.Q
701	482.3616	962.7087	962.5219	0.1869	1	2	1.2e+02	8	K.KILSMESR.G 700
1295	544.6236	1087.2327	1088.5284	-1.2957	0	5	63	8	R.TNGIMAPNQK.A
1381	553.0001	1103.9857	1103.5870	0.3988	1	20	1.9	3	R.CVAATLGTRR.S
2140	**414.9342**	**1241.7807**	**1239.6499**	**2.1308**	**0**	**10**	**16**	**1**	**K.YIQTGPAIYSK.E**
2354	634.0501	1266.0857	1265.6074	0.4783	0	1	1.1e+02	10	R.EIGMAAGSEFVR.A
2434	**638.9301**	**1275.8457**	**1275.6241**	**0.2216**	**1**	**3**	**89**	**5**	**K.VDASSEIPRMR.W** 2463
6789	851.0226	1700.0307	1698.9338	1.0969	1	7	31	2	R.GEGAAVVILKNMAEAVK.D
7630	593.9559	1778.8457	1778.0090	0.8367	0	6	37	9	K.HEPLPSPLLVDIAIHK.I
7898	902.2686	1802.5227	1801.9574	0.5654	1	2	93	3	K.EEIEAFALNLNNKGIK.T
8250	614.8005	1841.3797	1840.9353	0.4445	1	3	81	2	K.NMAEAVKDGDHILATLK.G
9259	**651.9549**	**1952.8427**	**1951.8959**	**0.9468**	**1**	**1**	**1.1e+02**	**9**	**R.RSQGDNTIAMQWTSWR.E**
9303	654.1135	1959.3187	1959.8237	-0.5050	0	4	60	4	-.MEANDSPHDVAVVGMGCR.L
9853	676.3122	2025.9147	2025.1696	0.7451	1	5	37	2	R.VLAPKIAGSLTLNMLFPPK.T 9848
10572	**1054.8326**	**2107.6507**	**2109.0161**	**-1.3653**	**1**	**4**	**54**	**2**	**R.RSLETQAATQAEWMSTVGK.Q**
12452	793.4269	2377.2587	2378.3468	-1.0880	2	0	1.1e+02	7	K.AVMSVQKGILPPQANLKTLNTR.V

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450. gi\|220699699\|gb\|EED56038.1\| **Mass:** 37093 **Score:** 36 **Queries matched:** 11 **emPAI:** 0.09

phosphatidylinositol transporter, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
294	831.4050	830.3977	830.4134	-0.0157	0	31	0.19	2	K.EDQNVVK.N 296 304
1094	**525.3511**	**1048.6877**	**1048.4825**	**0.2052**	**0**	**6**	**50**	**3**	**K.EFGTDDLPR.T**
2495	641.7091	1281.4037	1280.6798	0.7239	1	4	63	8	K.LGKIDLNAMYK.I
2865	663.2146	1324.4147	1323.6306	0.7841	0	36	0.042	1	R.SELEQLGYTER.L
3450	**692.5236**	**1383.0327**	**1382.6751**	**0.3576**	**0**	**1**	**1.3e+02**	**10**	**R.MLQNLVTEYEK.L** 3453
4411	**748.7076**	**1495.4007**	**1495.7085**	**-0.3077**	**0**	**8**	**23**	**1**	**K.LLETCCTIMDLK.G**
8623	628.6299	1882.8677	1879.9569	2.9108	2	8	23	1	R.KAGKLLETCCTIMDLK.G

9014	**641.0115**	**1920.0127**	**1918.9822**	**1.0305**	**1**	**7**	**29**	**1**	**R.MLQNLVTEYEKLADPR.L**

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451. gi\|220696458\|gb\|EED52800.1\| **Mass:** 48514 **Score:** 35 **Queries matched:** 11 **emPAI:** 0.14
aspartate transaminase, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
138	745.5370	744.5297	744.4130	0.1168	1	12	14	5	R.ERLEAK.G
1226	**537.9831**	**1073.9517**	**1072.6175**	**1.3342**	**2**	**6**	**51**	**3**	**R.IAEMRKGLR.E**
1527	**565.1746**	**1128.3347**	**1126.6346**	**1.7001**	**0**	**28**	**0.31**	**1**	**K.VILGSDSPAIR.E** 1511 1528
1746	585.6301	1169.2457	1166.5536	2.6921	1	9	19	7	R.TMSGRIAEMR.K
3867	478.5692	1432.6857	1430.7307	1.9551	0	27	0.3	1	R.AGAFHFVSAPGATAK.N
4585	759.5126	1517.0107	1515.7569	1.2538	0	6	37	8	R.NDPSINNEYLPIK.G
13518	**841.6612**	**2521.9617**	**2521.2271**	**0.7346**	**0**	**35**	**0.035**	**1**	**R.ISMAGLNTHNIDYFAEAVDSVVR.E** 13538
14138	**878.6472**	**2632.9197**	**2630.2415**	**2.6783**	**2**	**1**	**90**	**9**	**R.ERRHFPFFDTAYQGFASGDLNR.D**

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452. gi\|220692426\|gb\|EED48773.1\| **Mass:** 55898 **Score:** 35 **Queries matched:** 5 **emPAI:** 0.06
oligosaccharyl transferase subunit (alpha), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
359	428.6501	855.2857	853.5021	1.7836	0	7	27	4	R.VILPEGAR.N
1527	565.1746	1128.3347	1127.6411	0.6936	2	15	5.7	2	K.VGGLEVRDRK.A 1528
4215	**737.7961**	**1473.5777**	**1472.7915**	**0.7862**	**0**	**35**	**0.049**	**1**	**K.YFAIDLPEPLAPK.S**
12850	1217.9406	2433.8667	2431.1867	2.6800	0	3	60	3	K.LPSTNVPDYTTTSGLKPGSDPER.Q

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453. gi\|220694178\|gb\|EED50522.1\| **Mass:** 47405 **Score:** 35 **Queries matched:** 7 **emPAI:** 0.07
Arp2/3 complex subunit (Arp3), putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
665	**956.0490**	**955.0417**	**955.4512**	**-0.4094**	**1**	**7**	**28**	**7**	**K.EFARYDR.E**
695	481.4921	960.9697	960.4737	0.4960	1	12	12	3	R.ASEARSGGAR.S
3151	**677.8726**	**1353.7307**	**1353.7292**	**0.0015**	**0**	**35**	**0.046**	**1**	**R.DITYFVQSLLR.D**
8632	**629.2142**	**1884.6207**	**1884.9271**	**-0.3064**	**0**	**2**	**94**	**4**	**R.HGPWFGGSLLGQTPEFR.S**
10515	**700.8335**	**2099.4787**	**2100.0348**	**-0.5561**	**1**	**3**	**67**	**1**	**K.HTVTSPNGRSVNIDVGYER.F**
12995	**819.6592**	**2455.9557**	**2454.2979**	**1.6578**	**2**	**2**	**82**	**6**	**R.LLKHTVTSPNGRSVNIDVGYER.F**
15588	**1019.2759**	**3054.8057**	**3055.4563**	**-0.6506**	**0**	**3**	**48**	**2**	**R.GTEDLDFFIGDEALAAANGPGYGINYPIR.H**

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454. gi\|220700573\|gb\|EED56911.1\| **Mass:** 70711 **Score:** 35 **Queries matched:** 20 **emPAI:** 0.05
structure-specific recognition protein, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
239	803.7220	802.7147	801.4782	1.2365	1	6	49	8	K.KVIMPSK.D
915	503.9706	1005.9267	1004.6131	1.3136	2	7	36	8	K.IFRGLSGKK.V

1221	537.6926	1073.3707	1070.5471	2.8237	0	6	48	9	R.FYIPGTVMK.T
2162	**623.4551**	**1244.8957**	**1243.7322**	**1.1635**	**2**	**4**	**65**	**1**	**R.GLSGKKVIMPSK.D**
4225	**738.1476**	**1474.2807**	**1475.6575**	**-1.3768**	**0**	**0**	**1.5e+02**	**7**	**K.AGMGEHQFSNINR.E**
5755	812.4071	1622.7997	1621.7988	1.0010	1	2	1e+02	8	R.EEQQPLEEFFKAK.N
5757	812.4766	1622.9387	1621.7195	1.2192	1	8	22	4	R.GRFDIDMYESSFR.L
9158	647.7345	1940.1817	1940.8752	-0.6935	0	9	18	1	R.SSGVIQLDGFDQEDFER.L 9150
11685	**756.5332**	**2266.5777**	**2265.0875**	**1.4903**	**1**	**4**	**45**	**1**	**R.LESFSKMESFDNIYLDLSK.Q** 11686
13004	820.5772	2458.7097	2457.2540	1.4557	0	35	0.037	1	K.AEIGDVAGDTFATFLDVLHLTPR.G 13001
13849	**858.2332**	**2571.6777**	**2571.2084**	**0.4694**	**1**	**12**	**8**	**1**	**K.LDEEISLELNMTDELMETRYK.D** 13850 13853 13861 13868
15011	938.8859	2813.6357	2814.3303	-0.6945	2	3	49	1	K.LDEEISLELNMTDELMETRYKDK.L
16084	1099.1385	3294.3937	3295.4205	-1.0267	1	2	61	3	K.NEMSDDAGALLAAALDNDVMGSSDDEGVRADR.G

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455. gi\|220691595\|gb\|EED47943.1\| **Mass:** 159466 **Score:** 35 **Queries matched:** 48 **emPAI:** 0.02

exonuclease Kem1, putative [Aspergillus flavus NRRL3357]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
187	**774.4690**	**773.4617**	**772.4595**	**1.0022**	**1**	**8**	**39**	**10**	**R.WIQAKK.N**
691	481.0391	960.0637	960.5604	-0.4966	1	13	9.7	10	R.SSSLLAKQK.L
1793	**589.6161**	**1177.2177**	**1176.6291**	**0.5886**	**0**	**35**	**0.055**	**1**	**K.FPEFIAGIQR.N**
1961	**607.0206**	**1212.0267**	**1211.5492**	**0.4775**	**1**	**4**	**62**	**5**	**R.DFELDMNGKK.M**
1999	610.1726	1218.3307	1218.6244	-0.2937	0	17	4.1	7	K.FLEQLADDLR.L 2003 2004
2343	633.7021	1265.3897	1264.5836	0.8061	1	5	48	6	R.RGDSGWEFSPK.A
3086	**450.2845**	**1347.8317**	**1346.7194**	**1.1123**	**1**	**13**	**8.6**	**2**	**R.KFLEQLADDLR.L** 3075 3080 3084
3715	**708.8436**	**1415.6727**	**1414.8256**	**0.8471**	**2**	**7**	**31**	**4**	**R.SSSLLAKQKLGQR.V**
4284	**494.0359**	**1479.0857**	**1476.7936**	**2.2921**	**2**	**8**	**25**	**6**	**R.FRTALDAEVAKEK.A** 4266 4273 4279
4885	773.6951	1545.3757	1544.6815	0.6942	0	2	1.1e+02	3	K.NGGENNSESQERPK.S 4866
5399	**532.6422**	**1594.9047**	**1596.7671**	**-1.8624**	**0**	**7**	**27**	**3**	**R.EYLELEFQELER.T**
5489	802.1671	1602.3197	1602.8730	-0.5532	1	5	46	5	R.VVYAQDSGKVPIATR.G
6125	**551.4962**	**1651.4667**	**1650.7645**	**0.7022**	**1**	**3**	**79**	**5**	**R.GAVAGMGNGRGNGFSQR.G**
6414	**558.6409**	**1672.9007**	**1672.7764**	**0.1243**	**1**	**2**	**87**	**9**	**K.KNGGENNSESQERPK.S**
7079	**863.4756**	**1724.9367**	**1725.7814**	**-0.8447**	**0**	**2**	**81**	**1**	**K.MGGYINEQGVINMER.L**
7716	**893.3696**	**1784.7247**	**1783.9944**	**0.7303**	**2**	**4**	**64**	**1**	**K.VNGLIAAVKGREPEFGK.E**
7749	895.0496	1788.0847	1785.9454	2.1393	0	12	8.8	1	R.VFVGYPFLQEAYVVR.V 7746
8447	**930.7326**	**1859.4507**	**1859.8842**	**-0.4335**	**1**	**2**	**80**	**2**	**R.FFEAEYSGERWIQAK.K**
8464	621.6845	1862.0317	1863.8871	-1.8553	2	1	1e+02	10	R.GAVAGMGNGRGNGFSQRGR.G
9130	**646.2875**	**1935.8407**	**1933.1071**	**2.7337**	**0**	**1**	**1.2e+02**	**5**	**R.LGTIIGPVEAMVHVQLLK.G**
9219	**650.5142**	**1948.5207**	**1946.1175**	**2.4032**	**2**	**4**	**54**	**4**	**K.IKPKKLFFMAIDGVAPR.A**
10314	691.6772	2072.0097	2073.2132	-1.2035	1	5	45	3	R.RLGTIIGPVEAMVHVQLLK.G
10487	699.6505	2095.9297	2096.1014	-0.1717	2	3	60	8	K.EHLLTPEEKARNGFGASLK.F
10565	**703.2715**	**2106.7927**	**2104.1065**	**2.6862**	**2**	**1**	**97**	**7**	**K.AADPQPLDFPPTLPARDRK.F**
11927	767.4425	2299.3057	2297.1685	2.1372	1	1	93	9	K.LIEQDADQLIQNQPAMQAKK.V

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      12079    773.3412  2317.0017  2318.0426  -1.0409   2     2         83   5   K.YYTGKFEWGLDNHEEMRK.L
      12121    775.4349  2323.2827  2322.1348   1.1480   1     4         49   3   K.EILPKMGGYINEQGVINMER.L 12120
      12998    819.7819  2456.3237  2454.2664   2.0573   1     3         61   3   K.KPKELEHQNFYLLHLCMVR.E
      13005    820.6559  2458.9457  2459.3053  -0.3596   2     3         59   3   R.NESMVITVLDPGSRSSSLLAKQK.L
      13473    839.8552  2516.5437  2514.2841   2.2596   2     2         80   3   K.FFRWLSERYPAISMLIAENR.I
      13988    869.3905  2605.1497  2607.0878  -1.9381   1     2         75   3   K.LPAKQNDDSDDEEDEEASMAVQR.I 13990
      15432    996.8355  2987.4847  2984.5047   2.9800   2     6         22   1   R.GIASWPWFFQYHYAPMISDVKKGLK.A
      15435    997.3699  2989.0877  2989.3570  -0.2693   2     6         28   1   K.LPAKQNDDSDDEEDEEASMAVQRIIR.K
      15895   1068.4415  3202.3027  3203.6550  -1.3523   2     5         29   1   K.KGLKADTNFQLGQPFRPYDQLMGVLPDR.S 15892 15896
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456.   gi|220690781|gb|EED47130.1|     Mass: 50181     Score: 35     Queries matched: 16    emPAI: 0.07
       tubulin beta subunit [Aspergillus flavus NRRL3357]
      Query    Observed   Mr(expt)   Mr(calc)    Delta Miss Score Expect Rank   Peptide
       2501    642.1186  1282.2227  1281.6097  0.6130   0     5      43    2   R.MMATFSVAPSPK.V
       3286    456.4409  1366.3007  1364.5714  1.7294   0     8      22    5   R.NMMAAANFHNGR.F
       5292    793.6841  1585.3537  1584.8181  0.5356   0    12      10    2   R.AVLVDLEPGTMDAVR.A 5308 5312
       5478    801.6526  1601.2907  1600.8131  0.4777   0   (11)     12    3   R.AVLVDLEPGTMDAVR.A 5454 5463 5470 5477 5483 5490 5497
      13862    858.7655  2573.2747  2572.3319  0.9428   0    38   0.018    1   K.LASPSYGDLNHLVSAVMSGVTVSLR.F 13857
      16147   1110.7329  3329.1767  3326.5218  2.6550   0     2      63    4   R.EAESCDCLQGFQITHSLGGGTGSGMGTLLISK.I
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457.   gi|220694223|gb|EED50567.1|     Mass: 38399     Score: 35     Queries matched: 16    emPAI: 0.09
       KH domain RNA-binding protein [Aspergillus flavus NRRL3357]
      Query    Observed   Mr(expt)   Mr(calc)     Delta Miss Score  Expect Rank   Peptide
       1308   1090.3540  1089.3467  1089.5666  -0.2199   1     3    1e+02    9   R.DETGVKAGVSK.V
       1441    558.1746  1114.3347  1113.5891   0.7457   2     8       27    7   K.TRRSQLPQE.-
       2303    631.6381  1261.2617  1260.6826   0.5791   0     6       46    8   R.GTGTILYNPAVR.A
       2765    657.2466  1312.4787  1311.7511   0.7277   0    35    0.057    1   R.VLTVTGPLQGTAR.A 2759
       2789    658.6941  1315.3737  1315.6732  -0.2995   1     7       34   10   K.NVADLRDETGVK.A 2795
       2851    661.8026  1321.5907  1319.7310   1.8597   1     1  1.1e+02   10   K.AGVSKVVPGVHDR.V
       4801    770.3821  1538.7497  1538.7987  -0.0490   1     8       22    2   K.HIQDASGVRMVAQK.E
       5299    529.5762  1585.7067  1585.7294  -0.0226   0     6       38   10   K.TEEEYAQSMLTLR.A
       6556    561.5859  1681.7357  1678.8018   2.9339   1     7       28    7   R.MVAQKEMLPQSTER.I
      13233    829.2805  2484.8197  2485.2370  -0.4173   1     6       35    5   K.EMLPQSTERIVEVQGTPEGIEK.A 13235
      15972   1083.8202  3248.4387  3249.6049  -1.1662   2     4       39    8   R.MFTIMGSAQANEKALYLLYENLEAEKTR.R
      16082   1098.7679  3293.2817  3290.5799   2.7018   0     3       51    2   R.GYPLVTEDGEEIQTQNISIPADMVGCIIGR.A 16079
```

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458.   gi|220698074|gb|EED54414.1|     Mass: 11906     Score: 34     Queries matched: 5   emPAI: 0.29
       NADH-ubiquinone oxidoreductase 12 kda subunit, putative [Aspergillus flavus NRRL3357]
      Query  Observed    Mr(expt)    Mr(calc)    Delta Miss Score Expect Rank  Peptide
```

17	643.3960	642.3887	642.2465	0.1422	0	12	10	1	R.SMMSR.L 18
1556	566.6856	1131.3567	1130.5972	0.7596	0	34	0.07	1	M.PTPESAAFLAK.K
2531	**643.7626**	**1285.5107**	**1284.6938**	**0.8169**	**1**	**5**	**46**	**6**	**R.DAIIREQWVR.S**
7196	871.0721	1740.1297	1738.8784	1.2513	2	5	44	4	R.EGVNHLEKCGALREK.Y
