

Accession	Name	Species	Confidence	Found	Avg 115:11EF	115:11495% CI 115:114
gi 3156070	acyl-CoA synthetase long-c	Mus muscl	99	27	0.9849	1.024 [0.9618, 1.0881]
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence Score
	3 EVAELAECIGSGLIQJ	0.219			1	99 48
	3 LVDVEEMNYLASJ	0.197			1	99 53
	3 SAVLEDDJLLVYYYDDVR	0.263			1	99 47

Accession	Name	Species	Confidence	Found	Avg 115:11EF	115:11495% CI 115:114
gi 6679937	similar to glyceraldehyde-3-	Mus muscl	99	21	1.0013	1.0414 [0.9614, 1.1214]
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence Score
	3 VIISAPSADAPMFVMGVNF	0.254			1	99 36
	2 GAAQNIIPASTGAAJ	0.16			1	99 45
	3 VPTPNVSVVDLTCR	0.175			0	99 40

Accession	Name	Species	Confidence	Found	Avg 115:11EF	115:11495% CI 115:114
gi 6679237	pyruvate carboxylase	Mus muscl	99	19	0.9997	1.0256 [0.9748, 1.0764]
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence Score
	3 DFTATFGPLDSLNTN	0.198			0	92 30
	2 IEGRPGASLPPLNLJ	0.177			1	99 46
	3 GLAPVQAYLHIPDIJ	0.192			1	99 45

Accession	Name	Species	Confidence	Found	Avg 115:11EF	115:11495% CI 115:114
gi 3198218	malate dehydrogenase 2, N	Mus muscl	99	18	0.9731	1.0362 [0.9391, 1.1333]
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence Score
	3 MIAEAIPELJ	0.145			1	97 34
	3 VDFPQDQLATLTGR	0.163			0	99 49
	3 FVFSLV DAMNGJ	0.172			1	99 43

Accession	Name	Species	Confidence	Found	Avg 115:11EF	115:11495% CI 115:114
gi 3198064	ATP synthase, H+ transpor	Mus muscl	99	17	0.9928	1.039 [0.9555, 1.1225]
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence Score
	3 FLSQPFQVAEVFTGHMGJ	0.232			1	99 43
	3 AIAELGIYPAVDPLDSTSR	0.212			0	99 52
	3 VVDLLAPYAJ	0.128			1	99 50

Accession	Name	Species	Confidence	Found	Avg 115:11EF	115:11495% CI 115:114
gi 3198167	heat shock protein 1 (chape	Mus muscl	99	13	0.9488	1.0246 [0.9260, 0.1146]
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence Score
	3 CEFQDAYVLLSEJ	0.192			1	99 35
	2 CIPALDSLJPANEDQJ	0.241			2	99 36
	3 ISSVQSIVPALEIANAHR	0.21			0	99 33

Accession	Name	Species	Confidence	Found	Avg 115:11EF	115:11495% CI 115:114
gi 6671539	aldolase 1, A isoform	Mus muscl	99	12	1.0007	1.0354 [0.9665, 1.1043]
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence Score
	2 GILAADESTGSIAJ	0.163			1	99 52
	3 GVVPLAGTNGETTTQGLD	0.243			0	99 42
	2 ALANSLACQGJ	0.145			1	99 39

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11495% CI 114:114
gi 1807933	aconitase 2, mitochondrial	Mus muscl	99	11	0.9082	1.0807 [0.8404, 0.1310]
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence Score

2	IVYGHLLDDPANQEIER	0.211	0	99	41
3	DVGGIVLANACGPCIGQW	0.248	0	99	52

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11:95% CI	114
gi 1414963	fatty acid binding protein 4,	Mus muscl	99	10	0.9071	1.0528	[0.8616, 0.9
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
	3 LVSENFDDYMJ	0.162			1	99	52
	3 LGVEFDEITADDR	0.149			0	99	46
	2 LVVECVMJ	0.127			1	81	27

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11:95% CI	114
gi 6754524	lactate dehydrogenase 1, A	Mus muscl	99	9	0.8815	1.033	[0.8533, 0.9
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
	2 VIGSGCNLDSAR	0.145			0	99	47
	2 SADTLWGIQJ	0.139			1	99	42
	2 VTLTPEEEAR	0.121			0	81	34

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11:95% CI	114
gi 6671509	actin, beta, cytoplasmic	Mus muscl	99	8	0.9434	1.0331	[0.9132, 0.9
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
	3 DLTDYLMJ	0.137			1	99	38
	2 EITALAPSTMJ	0.145			1	99	38
	2 VAPEEHPVLLTEAPLNPJ	0.239			1	99	32

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11:95% CI	114
gi 6679299	prohibitin	Mus muscl	99	7	0.8603	1.1385	[0.7557, 0.9
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
	3 NITYLPAGQSVLLQLPQ	0.193			0	78	30
	3 JLEAAEDIAYQLSR	0.18			1	99	44
	2 ILFRPVASQLPR	0.143			0	99	32

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11:95% CI	114
gi 6678413	triosephosphate isomerase	Mus muscl	99	7	0.8521	1.0942	[0.7787, 0.9
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
	3 VSHALAEGLGVIACIGEJ	0.215			1	99	34
	3 DLGATWVVLGHSER	0.154			0	92	28
	2 SNVNDGVAQSTR	0.128			0	99	40

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11:95% CI	114
gi 5187306	eukaryotic translation elong	Mus muscl	99	7	0.9351	1.0643	[0.8786, 0.9
Rslt	Matched Sequence	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
	3 VETGVLJPGMVVTFAPVN'	0.477			2	99	34
	2 IGGIGTVPVGR	0.095			0	99	34
	2 QLIVGVNJ	0.102			1	99	37

Avg 116:11EF 116:11±95% CI 11±		Avg 117:11EF 117:11±95% CI 11±		Biological F Molecular Function	
0.995 1.0201 [0.9754, 1.0446]		1.0343 1.0167 [1.0173, 1.0515]			
Dist Score 114:115	% Error 11±116:115	% Error 11±117:115	% Error 11±	Cycle	Exp
21	0.917 2.6532	0.9605 2.6668	0.9165 2.6646	127	2
26	0.9368 2.3091	0.9559 2.3344	0.8978 2.3409	69	2
24	0.8488 2.981	1.0079 2.9106	0.8758 2.9758	92	4

Avg 116:11EF 116:11±95% CI 11±		Avg 117:11EF 117:11±95% CI 11±		Biological F Molecular Function	
1.0311 1.0284 [1.0026, 1.0542]		1.0171 1.0245 [0.9927, 1.0420]			
Dist Score 114:115	% Error 11±116:115	% Error 11±117:115	% Error 11±	Cycle	Exp
15	0.8619 2.5468	1.0193 2.4911	0.8307 2.5812	56	2
21	0.8369 2.4641	1.0068 2.3906	0.8256 2.4879	1247	4
20	0.8683 2.3515	0.96 2.3336	0.8165 2.3964	35	4

Avg 116:11EF 116:11±95% CI 11±		Avg 117:11EF 117:11±95% CI 11±		Biological F Molecular Function	
1.0085 1.025 [0.9839, 1.0561]		1.0169 1.0362 [0.9814, 1.0537]			
Dist Score 114:115	% Error 11±116:115	% Error 11±117:115	% Error 11±	Cycle	Exp
9	0.8995 2.8318	0.991 2.8164	0.8776 2.8547	92	2
23	0.9249 2.4522	0.9729 2.4596	0.8989 2.4732	1296	2
23	0.8463 2.6183	0.8995 2.6243	0.846 2.6299	122	2

Avg 116:11EF 116:11±95% CI 11±		Avg 117:11EF 117:11±95% CI 11±		Biological F Molecular Function	
0.9757 1.0515 [0.9280, 1.0750]		1.0038 1.0362 [0.9687, 1.0401]			
Dist Score 114:115	% Error 11±116:115	% Error 11±117:115	% Error 11±	Cycle	Exp
10	0.9186 2.9925	0.9566 3.0109	0.8302 3.086	36	4
17	0.7788 3.8868	0.85 3.8736	0.6617 4.0187	69	3
20	0.9354 2.5276	0.9347 2.5697	0.8509 2.5972	139	4

Avg 116:11EF 116:11±95% CI 11±		Avg 117:11EF 117:11±95% CI 11±		Biological F Molecular Function	
0.9914 1.0539 [0.9407, 1.0671]		1.0292 1.013 [1.0160, 1.0426]			
Dist Score 114:115	% Error 11±116:115	% Error 11±117:115	% Error 11±	Cycle	Exp
21	0.888 2.7147	0.9294 2.729	0.8477 2.7554	139	2
27	0.8686 3.0237	0.9633 2.9968	0.8478 3.057	118	2
21	0.9396 2.595	1.0028 2.5953	0.9154 2.6233	60	2

Avg 116:11EF 116:11±95% CI 11±		Avg 117:11EF 117:11±95% CI 11±		Biological F Molecular Function	
0.9802 1.0287 [0.9529, 1.0505]		1.0287 1.0346 [0.9943, 1.0642]			
Dist Score 114:115	% Error 11±116:115	% Error 11±117:115	% Error 11±	Cycle	Exp
12	0.9396 2.8389	0.9897 2.8468	0.87 2.8976	81	2
17	0.9794 2.2128	0.9756 2.2431	0.9325 2.2407	1290	3
14	0.905 3.4697	1.0259 3.4302	0.8555 3.5245	63	3

Avg 116:11EF 116:11±95% CI 11±		Avg 117:11EF 117:11±95% CI 11±		Biological F Molecular Function	
1.032 1.0339 [0.9982, 1.0696]		1.0079 1.0255 [0.9829, 1.0337]			
Dist Score 114:115	% Error 11±116:115	% Error 11±117:115	% Error 11±	Cycle	Exp
28	0.8237 2.5117	0.9486 2.4624	0.7864 2.5583	1272	4
22	0.8177 7.5543	1.0114 7.4539	0.7242 7.6696	25	4
17	0.8956 2.067	0.9929 2.0499	0.8751 2.087	1235	4

Avg 116:11EF 116:11±95% CI 11±		Avg 117:11EF 117:11±95% CI 11±		Biological F Molecular Function	
0.9692 1.1284 [0.8589, 1.0979]		0.8538 1.0877 [0.7850, 0.9287]			
Dist Score 114:115	% Error 11±116:115	% Error 11±117:115	% Error 11±	Cycle	Exp

21	0.9083	2.8175	0.9473	2.8318	0.7955	2.9199	1277	4
22	0.6933	4.819	0.8875	4.6542	0.6371	4.9305	87	2

Avg 116:11EF 116:11!95% CI 11(Avg 117:11EF 117:11!95% CI 11!Biological F Molecular Function

0.9912	1.0197 [0.9721, 1.0673]	0.9367	1.0518 [0.8905, 0.9852]
--------	-------------------------	--------	-------------------------

Dist Score	114:115	% Error 11:116:115	% Error 11:117:115	% Error 11:Cycle	Exp			
26	0.9694	2.4151	0.9908	2.4317	0.968	2.4218	19	3
23	0.9405	3.137	0.9947	3.1411	0.9674	3.1341	50	2
8	0.9602	2.5337	1.05	2.5236	0.9292	2.5558	1293	2

Avg 116:11EF 116:11!95% CI 11(Avg 117:11EF 117:11!95% CI 11: Biological F Molecular Function

0.9697	1.1161 [0.8688, 1.1161]	0.8452	1.0366 [0.8154, 0.8762]
--------	-------------------------	--------	-------------------------

Dist Score	114:115	% Error 11:116:115	% Error 11:117:115	% Error 11:Cycle	Exp			
25	0.9059	2.3916	0.9976	2.3779	0.8536	2.428	1237	3
14	0.8704	2.3102	0.9869	2.2805	0.855	2.3303	1304	3
8	0.8822	2.4105	0.9928	2.3852	0.8221	2.456	1243	2

Avg 116:11EF 116:11t95% CI 11tAvg 117:11EF 117:11t95% CI 11tBiological F Molecular Function

0.9832	1.0514 [0.9351, 1.1677]	0.8962	1.0514 [0.8524, 0.9422]
--------	-------------------------	--------	-------------------------

Dist Score	114:115	% Error 11:116:115	% Error 11:117:115	% Error 11:Cycle	Exp			
13	0.9553	2.3568	0.9843	2.3749	0.9087	2.3905	42	2
16	0.9428	2.4391	1.0113	2.4372	0.9197	2.4622	1282	2
16	0.9281	2.2936	1.026	2.2743	0.9052	2.3191	1302	4

Avg 116:11EF 116:11!95% CI 11(Avg 117:11EF 117:11!95% CI 11!Biological F Molecular Function

0.9584	1.0684 [0.8970, 1.0684]	0.777	1.1336 [0.6855, 0.8808]
--------	-------------------------	-------	-------------------------

Dist Score	114:115	% Error 11:116:115	% Error 11:117:115	% Error 11:Cycle	Exp			
8	0.8915	3.6434	0.8415	3.7595	0.676	3.9353	157	2
21	0.8965	3.2363	0.9894	3.2161	0.8066	3.3164	35	3
13	0.8836	4.0899	0.9429	4.0908	0.8493	4.1039	1298	3

Avg 116:11EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11: Biological F Molecular Function

0.9823 1.0522 [0.9335, 1.1010] 0.8255 1.0682 [0.7728, 0.8818]

Dist Score	114:115	% Error 11:116:115	% Error 11:117:115	% Error 11:Cycle	Exp			
15	0.749	3.3003	1.0097	3.1092	0.7766	3.291	112	3
9	0.8102	3.4248	0.9772	3.355	0.8174	3.4332	20	2
13	0.8537	2.4443	0.9774	2.4112	0.8335	2.4671	1199	2

Avg 116:11EF 116:11!95% CI 11(Avg 117:11EF 117:11!95% CI 11: Biological F Molecular Function

Model	Mean	95% CI	Model	Mean	95% CI
Model 1	0.9771	1.0196 [0.9583, 0.9999]	Model 2	0.8968	1.083 [0.8281, 0.9712]

Dist Score	114:115	% Error 11:116:115	% Error 11:117:115	% Error 11:Cycle	Exp			
20	0.8269	3.1572	0.9482	3.1008	0.7674	3.2382	75	3
13	0.957	2.6827	0.9929	2.6917	0.9358	2.6949	1277	2
12	0.991	2.2866	1.0049	2.3048	0.9807	2.2961	1257	3

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
9.152	1003.157	2	2004.299	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
4.938	900.0756	2	1798.137	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
6.664	822.1863	3	2463.537	c:\pe sciex	x:\katrin\protein_rodent0705.fasta

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
3.993	834.5311	3	2500.571	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
26.341	829.5571	2	1657.1	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
2.535	851.0489	2	1700.083	c:\pe sciex	x:\katrin\protein_rodent0705.fasta

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
6.609	900.0565	2	1798.098	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
30.308	617.4365	3	1849.288	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
8.789	679.4791	3	2035.416	c:\pe sciex	x:\katrin\protein_rodent0705.fasta

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
2.607	468.3288	3	1401.965	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
4.975	569.0318	3	1704.074	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
10.08	808.5274	2	1615.04	c:\pe sciex	x:\katrin\protein_rodent0705.fasta

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
10.025	771.159	3	2310.455	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
8.499	1066.685	2	2131.355	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
4.284	459.6646	3	1375.972	c:\pe sciex	x:\katrin\protein_rodent0705.fasta

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
5.81	630.7201	3	1889.139	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
29.859	744.4888	3	2230.445	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
4.539	683.7937	3	2048.359	c:\pe sciex	x:\katrin\protein_rodent0705.fasta

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
28.398	811.0381	2	1620.062	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
1.811	806.172	3	2415.494	c:\pe sciex	x:\katrin\protein_rodent0705.fasta
25.351	710.9705	2	1419.926	c:\pe sciex	x:\katrin\protein_rodent0705.fasta

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
------	-------------	-------------	-------------	-----------	------------

28.811	671.7462	3	2012.217	c:\pe sciex x:\katrin\protein_rodent0705.fasta
6.246	768.1285	3	2301.364	c:\pe sciex x:\katrin\protein_rodent0705.fasta

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
1.358	868.5135	2	1735.013	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
3.56	812.4816	2	1622.949	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
30.062	422.622	3	1264.844	c:\pe sciex x:\katrin\protein_rodent0705.fasta	

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
25.494	696.9301	2	1391.846	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
31.009	703.9703	2	1405.926	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
25.945	644.9118	2	1287.809	c:\pe sciex x:\katrin\protein_rodent0705.fasta	

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
2.983	643.9162	2	1285.818	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
29.157	725.4896	2	1448.965	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
30.866	748.1742	3	2241.501	c:\pe sciex x:\katrin\protein_rodent0705.fasta	

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
11.333	667.1172	3	1998.33	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
2.517	632.4173	3	1894.23	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
30.516	514.3689	3	1540.085	c:\pe sciex x:\katrin\protein_rodent0705.fasta	

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
8.099	704.8053	3	2111.394	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
1.394	562.0249	3	1683.053	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
22.322	696.4241	2	1390.834	c:\pe sciex x:\katrin\protein_rodent0705.fasta	

Time	Precursor I	Precursor z	Precursor I	Data File	FASTA File
5.411	737.8	4	2947.171	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
28.746	585.4129	2	1168.811	c:\pe sciex x:\katrin\protein_rodent0705.fasta	
27.142	579.9322	2	1157.85	c:\pe sciex x:\katrin\protein_rodent0705.fasta	

0.969759	0.969692	0.954388	0.974117	0.917063	0.945341	0.920682
0.958059	0.962418	0.961649	0.968425	0.932557	0.955137	0.903404
0.967636	0.992634	0.919155	0.972722	0.827424	0.93329	0.858231

0.961846	0.972817	0.878145	0.970866	0.85218	0.920105	0.829034
0.970506	0.978391	0.971609	0.968029	0.830155	0.999821	0.816856
0.955786	0.958788	0.939613	0.976652	0.865582	0.940801	0.831713

0.973076	0.974956	0.930805	0.955965	0.897765	0.946122	0.860506
0.967308	0.981823	0.924428	0.961374	0.911226	0.916027	0.880178
0.973835	0.961614	0.958146	0.969014	0.857055	0.896255	0.85251

0.972159	0.972958	0.982167	0.968166	0.917846	0.965654	0.826111
1	0.95495	0.901695	1	0.81554	0.802598	0.692916
0.972448	0.968318	0.977853	0.969599	0.939389	0.943904	0.852026

0.969733	0.973986	0.963037	0.96814	0.884122	0.918953	0.842612
0.970324	0.990941	0.936515	0.975005	0.850529	0.910392	0.834167
0.978051	0.97364	0.972294	0.976803	0.943857	1.001414	0.918374

0.972042	0.972042	0.943836	0.96815	0.9396	0.960981	0.866517
0.969029	1	0.95681	0.993316	0.949067	0.933464	0.926267
0.99778	0.982768	0.856987	0.988306	0.918824	0.894599	0.860321

0.980338	0.992422	0.968132	0.975316	0.813671	0.925383	0.772845
0.952367	0.973412	0.816074	0.982331	0.800022	0.847921	0.730835
0.965776	0.970184	0.953169	0.972176	0.891531	0.975487	0.876897

0.969371	0.970721	0.891949	0.980315	0.907037	0.870429	0.803362
0.984752	0.964957	0.797668	0.965564	0.707522	0.733639	0.6375

0.947627	0.958156	0.94245	0.968608	0.958748	0.974559	0.978559
0.946388	0.958861	0.832455	0.957522	0.928265	0.863569	0.966049
0.963487	0.954386	0.940264	0.946521	0.969357	1.034464	0.921543

0.968608	0.978204	0.929761	0.978079
0.99108	1	0.976711	1
0.917588	0.994296	0.911962	0.976486

0.956482	0.972165	0.96187	0.965225	0.939889	0.973877	0.902213
0.969374	0.96742	0.971391	0.973957	0.944704	1.015451	0.925914
0.968343	0.984344	0.916725	0.959702	0.913013	0.955519	0.882539

0.985392	0.986365	0.942717	0.983991	0.890621	0.804263	0.674373
0.994256	0.992308	0.931832	1	0.898261	0.929102	0.812853
0.959694	0.992575	0.863828	0.963172	0.854329	0.820596	0.824141

1	1	0.973272	0.99252	0.749	0.982712	0.770791
0.958576	0.941534	0.874391	0.911108	0.824864	0.907513	0.790986
0.967406	0.967819	0.929108	0.975926	0.853336	0.938306	0.840482

0.998173	0.985522	0.951283	0.989117
0.962516	0.957585	0.911921	0.959175
0.951172	0.956817	0.959666	0.971968

0.892348	0.94459	0.894106	0.056757	0.010943	0.032247
----------	---------	----------	----------	----------	----------

0.849306	0.953576	0.825868	0.017887	0.041365	0.007918
----------	----------	----------	----------	----------	----------

0.888682	0.919468	0.864398	0.028205	0.025111	0.014239
----------	----------	----------	----------	----------	----------

0.890925	0.904052	0.790351	0.066168	0.088532	0.08537
----------	----------	----------	----------	----------	---------

0.892836	0.943586	0.865051	0.04727	0.050263	0.046372
----------	----------	----------	---------	----------	----------

0.93583	0.929681	0.884368	0.01547	0.033353	0.036418
---------	----------	----------	---------	----------	----------

0.835074	0.916264	0.793526	0.049367	0.06427	0.075195
----------	----------	----------	----------	---------	----------

0.952123 0.957531 0.955384

0.021331 0.08671 0.029967

0.932535 0.981616 0.903556

0.017077 0.030706 0.021719

0.809067 0.942844 0.800753

0.053932 0.037804 0.035858

0.887873 0.939321 0.857736

0.045902 0.022717 0.054458

Accession	Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114:11	Avg 116:11
gil3156070	acyl-CoA s	Mus muscl	99	37	0.9654	1.0406	[0.9278, 1.0	1.0905
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score	Dist Score
	6 EVAELAE	0.039			1	99	54	24
	5 LAQGEYIA	0.027			1	99	47	21
	5 SQIDELYA	0.03			1	99	46	16

Accession	Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114:11	Avg 116:11
gil6679937	similar to g	Mus muscl	99	21	0.9591	1.0552	[0.9089, 1.0	1.1236
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score	Dist Score
	5 VIISAPSAI	0.034			1	99	34	15
	5 LISWYDNI	0.028			0	99	40	15
	5 VPTPNVS	-0.885			0	97	25	10

Accession	Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114:11	Avg 116:11
gil6679237	pyruvate c	Mus muscl	99	47	0.9836	1.0288	[0.9560, 1.0	1.1077
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score	Dist Score
	5 IEGRPGA	0.037			1	99	43	17
	5 AEAEQA	0.032			0	99	55	29
	5 VFDYSEY	0.021			0	99	46	25

Accession	Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114:11	Avg 116:11
gil3198218	malate deh	Mus muscl	99	21	0.9479	1.1048	[0.8580, 1.0	1.0445
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score	Dist Score
	5 VDFPQDQ	0.003			0	99	41	16
	4 IQEAGTEV	0.019			1	99	39	15
	5 VNVPVIGC	0.025			1	99	43	19

Accession	Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114:11	Avg 116:11
gil3198064	ATP synth	Mus muscl	99	20	0.9765	1.1231	[0.8695, 1.0	1.0992
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score	Dist Score
	5 VVDLLAPY	0.008			1	99	35	13
	5 FTQAGSE	0.011			0	99	35	17
	5 VLDSGAPI	0.027			1	99	44	21

Accession	Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114:11	Avg 116:11
gil3198167	heat shock	Mus muscl	99	19	1.0283	1.0124	[1.0157, 1.0	1.1218
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score	Dist Score
	5 AAVEEGIV	0.02			0	99	41	14
	5 VGLQVVA	0.015			1	99	40	15
	4 VTDALNA	0.014			0	97	44	10

Accession	Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114:11	Avg 116:11
gil6671539	aldolase 1,	Mus muscl	99	13	0.9944	1.036	[0.9598, 1.0	1.1278
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score	Dist Score
	5 GVVPLAG	0.043			0	99	49	28
	4 ALANSLAC	0.025			1	99	41	19
	4 ALQASAL	0.02			1	93	34	9

Accession	Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114:11	Avg 116:11
gil1414963	fatty acid b	Mus muscl	99	15	0.9724	1.0252	[0.9485, 0.9	1.1105
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score	Dist Score

5	LVSSENFI	0.022		1	99	56	29
5	LGVEFDEI	0.029		0	99	47	24
4	NTEISFJ	-0.007		1	99	34	11

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11F	95% CI	114	Avg 116:11
gil6754524	lactate deh	Mus muscl	99	12	0.9396	1.1101	[0.8464, 1.0		1.1028
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score		Dist Score
	4	VIGSGCNI	0.025		0	99	44		23
	5	SLNPELG	0.174		2	99	29		12
	4	VTLTPEEE	0.021		0	93	37		9

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11F	95% CI	114	Avg 116:11
gil6671509	actin, beta,	Mus muscl	99	11	0.9889	1.1438	[0.8646, 1.0		1.1357
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score		Dist Score
	4	AGFAGDD	0.037		0	99	46		20
	5	VAPEEHP	0.039		1	99	35		17
	5	YPIEHGIV	14.068	PIE	M(Oxidatio	1	97	31	10

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11F	95% CI	114	Avg 116:11
gil6679299	prohibitin	Mus muscl	99	9	0.9346	1.1998	[0.7790, 1.0		1.0883
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score		Dist Score
	5	JLEAAEDI	0.02		1	99	43		21

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11F	95% CI	114	Avg 116:11
gil6678413	triosephos	Mus muscl	99	9	0.9443	1.0509	[0.8986, 0.9		1.1174
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score		Dist Score
	4	SNVNDGV	0.028		0	99	40		15
	5	FFVGGNV	0.02		1	99	33		12
	6	VVLAYEP	1.034		1	99	36		19

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11F	95% CI	114	Avg 116:11
gil5187306	eukaryotic	Mus muscl	99	11	1.0051	1.0572	[0.9507, 1.0		1.1518
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score		Dist Score
	5	IGGIGTVP	0.015		0	99	36		13
	5	VETGVLJF	0.057		2	99	36		19
	4	STTTGHLI	0.023		1	59	27		7

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0316 [1.0571, 1.0344 [0.9405, 1.0063]
114:115 % Error 11:116:115 % Error 11:117:115 % Error 11' Cycle Exp Time
0.9373 3.0614 1.1106 2.9835 0.9771 3.0486 104 4 7.531
0.9984 2.4796 1.0644 2.4803 1.023 2.4775 19 2 1.322
0.94 2.4449 1.0684 2.4162 0.9945 2.4287 222 2 16.01

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0312 [1.0896, 1.0963 1.0567 [0.9114, 1.0176]
114:115 % Error 11:116:115 % Error 11:117:115 % Error 11' Cycle Exp Time
0.8747 3.3089 1.1743 3.1467 0.8704 3.3362 268 4 19.4
0.9144 2.8448 1.0911 2.8008 0.9582 2.8357 263 2 18.981
0.9838 3.4335 1.154 3.3926 1.0799 3.4033 214 3 15.47

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0231 [1.0827, 1.09723 1.0379 [0.9368, 1.0092]
114:115 % Error 11:116:115 % Error 11:117:115 % Error 11' Cycle Exp Time
0.9923 2.709 1.1551 2.6636 1.0701 2.6824 107 2 7.687
0.9827 2.5763 1.0893 2.5586 1.0218 2.5686 106 4 7.669
0.9924 2.7179 1.0957 2.7018 0.9913 2.729 305 4 22.078

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.1451 [0.9121, 1.09382 1.1085 [0.8464, 1.0400]
114:115 % Error 11:116:115 % Error 11:117:115 % Error 11' Cycle Exp Time
1.0228 1.9872 1.1089 1.98 0.9968 2.0083 303 2 21.878
1.0443 2.4371 1.0993 2.4419 1.0929 2.4288 1494 2 33.356
1.0465 2.5459 1.0686 2.5635 1.0391 2.5565 3 2 0.161

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0809 [1.0169, 1.0966 1.0911 [0.8853, 1.0540]
114:115 % Error 11:116:115 % Error 11:117:115 % Error 11' Cycle Exp Time
1.025 2.1022 1.2043 2.0556 1.0384 2.1079 280 3 20.253
0.9251 3.0022 1.1002 2.9602 0.9348 3.0121 293 4 21.21
1.0319 2.6947 1.181 2.6598 1.0685 2.6896 233 3 16.841

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0265 [1.0929, 1.0344 1.0265 [1.0077, 1.0618]
114:115 % Error 11:116:115 % Error 11:117:115 % Error 11' Cycle Exp Time
0.9932 2.6221 1.112 2.5939 1.0542 2.5998 300 4 21.716
1.0367 2.4454 1.1201 2.4405 1.0975 2.4308 78 2 5.586
1.0274 2.7224 1.0883 2.725 1.0511 2.7219 1515 3 35.127

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0191 [1.1067, 1.0049 1.0564 [0.9512, 1.0615]
114:115 % Error 11:116:115 % Error 11:117:115 % Error 11' Cycle Exp Time
0.8693 9.6892 1.1533 9.5991 0.8656 9.7067 183 4 13.24
0.9518 2.246 1.121 2.2084 1.0228 2.2273 1497 4 33.668
1.0057 2.32 1.1018 2.3109 1.038 2.3164 1492 3 33.235

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0395 [1.0683, 1.0307 1.0233 [1.0072, 1.0546]
114:115 % Error 11:116:115 % Error 11:117:115 % Error 11' Cycle Exp Time

0.9871	2.35	1.0848	2.3389	0.9952	2.3551	174	3	12.568
0.9419	2.2473	1.0862	2.2235	0.972	2.2518	250	2	18.037
1.0142	2.721	1.0401	2.7315	1.0555	2.7157	1514	2	35.002

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.0781 [1.0230, 1.1232] 0.9655 1.0687 [0.9035, 1.0318]

114:115	% Error 11	116:115	% Error 11	117:115	% Error 11	Cycle	Exp	Time
0.978	2.5621	1.0988	2.5454	1.0104	2.5589	1501	2	33.933
0.9425	3.3951	1.1162	3.3531	1.0023	3.3799	53	4	3.835
0.9757	2.4263	1.1238	2.3991	1.0129	2.4214	1510	4	34.739

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.095 [1.0372, 1.1528] 1.0203 1.0666 [0.9566, 1.0883]

114:115	% Error 11	116:115	% Error 11	117:115	% Error 11	Cycle	Exp	Time
1.0297	2.725	1.1088	2.7213	1.0329	2.7321	1465	3	31.015
1.0089	2.9656	1.1999	2.9013	1.0865	2.9367	120	2	8.625
1.042	2.8565	1.1665	2.8252	1.0004	2.8969	181	2	13.04

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.1469 [0.9489, 1.3449] 0.9237 1.1951 [0.7729, 1.1039]

114:115	% Error 11	116:115	% Error 11	117:115	% Error 11	Cycle	Exp	Time
0.9121	3.5571	1.129	3.4622	0.9514	3.5468	215	2	15.505

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.0308 [1.0840, 1.0076] 0.9441 1.0957 [0.8617, 1.0345]

114:115	% Error 11	116:115	% Error 11	117:115	% Error 11	Cycle	Exp	Time
0.943	2.6832	1.1386	2.6242	1.0058	2.6643	1423	2	27.515
0.9799	2.4946	1.1591	2.4407	1.0042	2.4953	180	2	12.968
0.9176	4.0893	1.164	3.9748	0.9129	4.1049	67	2	4.8

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.0465 [1.1007, 1.0023] 1.0222 1.0635 [0.9612, 1.0871]

114:115	% Error 11	116:115	% Error 11	117:115	% Error 11	Cycle	Exp	Time
1.0222	2.8799	1.117	2.8719	1.0621	2.8743	64	3	4.614
0.9751	3.5879	1.1963	3.474	1.0256	3.569	320	2	23.109
0.9822	2.4898	1.1183	2.4659	1.0235	2.4831	1464	4	30.955

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
1003.067	2	2004.12	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.970395
753.9399	2	1505.865	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.964567
784.9582	2	1567.902	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.949363

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
626.094	4	2500.347	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.951729
962.4693	2	1922.924	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.953039
567.3487	3	1699.024	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.99108

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
617.3876	3	1849.141	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.959745
846.4395	2	1690.865	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.960785
833.4044	2	1664.794	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.944082

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
852.9647	2	1703.915	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.968002
681.4111	2	1360.808	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.955089
479.2996	3	1434.877	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.959794

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
688.9348	2	1375.855	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.982902
527.2975	3	1578.871	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.963757
736.4525	3	2206.336	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.974125

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
915.0242	2	1828.034	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.967504
600.9118	2	1199.809	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.972552
552.8238	2	1103.633	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.994672

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
806.1013	3	2415.282	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.895656
710.9122	2	1419.81	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.958592
545.3591	2	1088.704	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.997756

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
-------------	-------------	-------------	-----------	------------	--

868.4432	2	1734.872	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.974244
812.4171	2	1622.82	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.958233
563.8197	2	1125.625	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.935401

Precursor I Precursor I Data File FASTA File

696.8689	2	1391.723	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.877589
566.6	4	2262.371	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.975883
644.8615	2	1287.709	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.886199

Precursor I Precursor I Data File FASTA File

560.7956	2	1119.577	c:\pe sciex x:\katrin\protein_rodent0705.fasta	1
561.3333	4	2241.304	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.971586
750.3937	3	2248.159	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.971744

Precursor I Precursor I Data File FASTA File

632.3659	3	1894.076	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.960827
----------	---	----------	--	----------

Precursor I Precursor I Data File FASTA File

696.3723	2	1390.73	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.970224
621.859	2	1241.703	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.961306
473.7915	4	1891.137	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.984262

Precursor I Precursor I Data File FASTA File

585.3702	2	1168.726	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.972137
737.696	4	2946.755	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.976581
470.2841	3	1407.83	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.968064

0.97325 0.966323 0.974942
0.954192 0.966852 0.96002
0.97178 0.957407 0.957345

0.934551 1.102695 0.978799
1.009255 1.078522 1.029248
0.918315 1.052597 0.979727

1 0.908904 0.974226
0.925389 0.905299 0.970258
0.985737 0.877347 0.995861

0.832478 1.067326 0.847966
0.941722 1.067413 1.004661
0.989133 1.027109 1.090991

0.994059 0.946471 0.966468
0.991621 0.947137 0.955112
0.968607 0.913296 0.963313

0.958046 1.099803 1.040399
0.952142 1.040434 0.98418
0.967273 1.033131 0.985882

0.976305 0.946419 0.973969
0.962898 0.948016 0.962937
0.964156 0.917653 0.957576

1.014102 1.074955 0.994415
1.03583 1.08231 1.092944
1.041766 1.01706 1.032008

1 0.963754 0.978298
0.98369 0.843801 0.921877
0.993087 0.931484 0.974662

1.007474 1.160649 1.015865
0.906354 0.943742 0.876059
1.012197 1.107741 1.048676

0.964355 0.925777 0.965689
0.950195 0.948529 0.975475
0.988069 0.896545 0.961712

0.996443 1.067516 1.055658
1.061093 1.118136 1.126699
1.034266 0.987491 1.023061

0.95915 0.804406 0.954963
0.964268 0.982574 0.960443
1 0.942547 0.978312

0.811754 0.967233 0.861821
0.946197 1.142281 1.018742
1.003443 1.038498 1.015488

0.947854	0.937212	0.989694
0.994077	0.859031	0.959634
0.945437	0.948545	0.961337

1.014583	1.072621	1.03913
0.907937	0.938638	0.938321
1.003433	1.043519	1.073251

0.993796	0.878027	0.960723
0.952267	0.946822	0.969451
0.985696	0.896134	0.964302

1	0.932511	0.990269
0.98296	0.893805	0.961201
0.961353	0.973781	0.974131

1.0297	1.033968	1.022849
0.997226	1.091069	1.06245
1.053263	1.181581	1.013697

0.980277	0.891639	0.9673
----------	----------	--------

0.971471	0.923063	0.976288
0.956947	0.970737	0.96699
0.951588	0.95707	0.941429

0.94179	1.081865	1.010787
0.984364	1.175803	1.014739
0.949107	1.170706	0.903154

1	0.918009	0.965567
0.977284	0.936854	0.97005
1	0.92066	0.96381

0.954041	1.077938	0.995925	0.048501	0.025054	0.028863
----------	----------	----------	----------	----------	----------

0.921111	1.053949	0.981206	0.080336	0.023244	0.123199
----------	----------	----------	----------	----------	----------

0.959154	1.057789	1.003487	0.007626	0.036568	0.031978
----------	----------	----------	----------	----------	----------

1.030566	1.058108	1.039789	0.014564	0.035739	0.049723
----------	----------	----------	----------	----------	----------

0.975342	1.070711	0.9802	0.059792	0.113096	0.091669
----------	----------	--------	----------	----------	----------

1.030601	1.057715	1.068473	0.03248	0.065872	0.052994
----------	----------	----------	---------	----------	----------

0.920465	1.049337	0.965351	0.098401	0.088026	0.089674
----------	----------	----------	----------	----------	----------

0.975318 1.018259 1.016901

0.058619 0.070472 0.070158

1.02673 1.102206 1.032999

0.028136 0.074434 0.025912

0.95842 1.142791 0.976227

0.022764 0.052825 0.063314

0.975175 1.06888 1.006056

0.041764 0.033648 0.033031

Accession number	Protein name	Confidence	Peptide sequence	Ratio 0min:5min	% Error 0min:5min	Ratio 15min:5min n	% Error 15min:5min n	Ratio 45min:5min n	% Error 45min:5min n	Average 0min:5min	Average 15min:5min n	Average 45min:5min n	Stdev 0min:5min	Stdev 15min:5min n	Stdev 45min:5min n
Replicate 1															
gil31560705	acyl-CoA synthetase long-chain family member 1	99													
			EVAELAEICGSLGIQJ	0.9171	2.6532	0.9453	2.6668	0.9207	2.6646						
			LVDVEEMNYLASJ	0.9326	2.3091	0.9551	2.3344	0.9034	2.3409						
			SAVLEDDJLLVYYDDVR	0.8274	2.9810	0.9333	2.9106	0.8582	2.9758	0.8923	0.9446	0.8941	0.0568	0.0109	0.0322
gil6679937	similar to glyceraldehyde-3-phosphate dehydr	99													
			VIISAPSADAPMFVMGVNHE	0.8522	2.5468	0.9201	2.4911	0.8290	2.5812						
			GAAQNIIPASTGA AJ	0.8302	2.4641	0.9998	2.3906	0.8169	2.4879						
			VP TPNVSVVDLT CR	0.8656	2.3515	0.9408	2.3336	0.8317	2.3964	0.8493	0.9536	0.8259	0.0179	0.0414	0.0079
gil6679237	pyruvate carboxylase	99													
			DFTATFGPLDSL NTR	0.8978	2.8318	0.9461	2.8164	0.8605	2.8547						
			IEGRPGASLPPLNLJ	0.9112	2.4522	0.9160	2.4596	0.8802	2.4732						
			GLAPVQAYLHIPDIJ	0.8571	2.6183	0.8963	2.6243	0.8525	2.6299	0.8887	0.9195	0.8644	0.0282	0.0251	0.0142
gil31982186	malate dehydrogenase 2, NAD (mitochondrial)	99													
			MIAEAIPELJ	0.9178	2.9925	0.9657	3.0109	0.8261	3.0860						
			VDFFPDQLATLTGR	0.8155	3.8868	0.8026	3.8736	0.6929	4.0187						
			FVFSLVDAMNGJ	0.9394	2.5276	0.9439	2.5697	0.8520	2.5972	0.8909	0.9041	0.7904	0.0662	0.0885	0.0854
gil31980648	ATP synthase, H+ transporting mitochondrial F	99													
			FLSQPFQVAEVFTGHMGJ	0.8841	2.7147	0.9190	2.7290	0.8426	2.7554						
			AI AELGIYPAVDPLDSTSR	0.8505	3.0237	0.9104	2.9968	0.8342	3.0570						
			VVDLLAPYAJ	0.9439	2.5950	1.0014	2.5953	0.9184	2.6233	0.8928	0.9436	0.8651	0.0473	0.0503	0.0464
gil31981679	heat shock protein 1 (chaperonin)	99													
			CEFQDAYVLLSEJ	0.9396	2.8389	0.9610	2.8468	0.8665	2.8976						
			CIPALDSLJPANEDQJ	0.9491	2.2128	0.9335	2.2431	0.9263	2.2407						
			ISSVQSIVPALEIAN AHR	0.9188	3.4697	0.8946	3.4302	0.8603	3.5245	0.9358	0.9297	0.8844	0.0155	0.0334	0.0364
gil6671539	aldolase 1, A isoform	99													
			GILAADESTGSIAJ	0.8137	2.5117	0.9254	2.4624	0.7728	2.5583						
			GVVPLAGTNGETTTQGLDC	0.8000	7.5543	0.8479	7.4539	0.7308	7.6696						
			ALANSLACQ GJ	0.8915	2.0670	0.9755	2.0499	0.8769	2.0870	0.8351	0.9163	0.7935	0.0494	0.0643	0.0752
gil14149635	fatty acid binding protein 4, adipocyte	99													
			LVSSNFDDY MJ	0.9587	2.4151	0.9746	2.4317	0.9786	2.4218						
			LGVEFDEITADDR	0.9283	3.1370	0.8636	3.1411	0.9660	3.1341						
			LVVECV MJ	0.9694	2.5337	1.0345	2.5236	0.9215	2.5558	0.9521	0.9575	0.9554	0.0213	0.0867	0.0300
gil6671509	actin, beta, cytoplasmic	99													
			DLTDYLMJ	0.9399	2.3568	0.9739	2.3749	0.9022	2.3905						
			EITALAPSTMJ	0.9447	2.4391	1.0155	2.4372	0.9259	2.4622						
			VAPEEHPLYLLTEAPLN PJ	0.9130	2.2936	0.9555	2.2743	0.8825	2.3191	0.9325	0.9816	0.9036	0.0171	0.0307	0.0217
gil6678413	triosephosphate isomerase 1	99													
			VSHALAEGLGVACIGEJ	0.7490	3.3003	0.9827	3.1092	0.7708	3.2910						
			DLGATWVVLGHSE R	0.8249	3.4248	0.9075	3.3550	0.7910	3.4332						
			SNVNDGVAQSTR	0.8533	2.4443	0.9383	2.4112	0.8405	2.4671	0.8091	0.9428	0.8008	0.0539	0.0378	0.0359
	average									0.8879	0.9393	0.8577			
	stdev									0.0459	0.0227	0.0545			
Replicate 2															
gil31560705	acyl-CoA synthetase long-chain family member 1	99													
			EVAELAEICGSLGIQJ	0.9346	3.0614	1.1027	2.9835	1.1296	3.0486						
			LAQGEYIAPEJ	1.0093	2.4796	1.0785	2.4803	1.0364	2.4775						
			SQIDELYATIJ	0.9183	2.4449	1.0526	2.4162	1.0983	2.4287	0.9540	1.0779	1.0881	0.0485	0.0251	0.0474
gil6679937	similar to glyceraldehyde-3-phosphate dehydr	99													
			VIISAPSADAPMFVMGVNHE	0.8325	3.3089	1.0673	3.1467	1.0314	3.3362						
			LISWYDNEYGYSNR	0.9417	2.8448	1.0674	2.8008	1.1209	2.8357						
			VP TPNVSVVDLT CR	0.9891	3.4335	1.0271	3.3926	1.1899	3.4033	0.9211	1.0539	1.1141	0.0803	0.0232	0.0795
gil6679237	pyruvate carboxylase	99													

gij31982186	malate dehydrogenase 2, NAD (mitochondrial)	99	IEGRPGASLPLNLJ	0.9580	2.7090	1.0998	2.6636	1.2181	2.6824	0.9592	1.0578	1.0926	0.0076	0.0366	0.1149
			AEAEAQAELSFPFR	0.9521	2.5763	1.0404	2.5586	1.0670	2.5686						
			VFDYSEYWEGAR	0.9673	2.7179	1.0331	2.7018	0.9926	2.7290						
gij31980648	ATP synthase, H+ transporting mitochondrial F	99	VDFPQDQLATLTGR	1.0141	1.9872	1.0750	1.9800	1.0209	2.0083	1.0306	1.0581	1.0788	0.0146	0.0357	0.0510
			IQEAGTEVVJ	1.0358	2.4371	1.0823	2.4419	1.1167	2.4288						
			VNVFVIGGHAGJ	1.0418	2.5459	1.0171	2.5635	1.0989	2.5565						
gij31981679	heat shock protein 1 (chaperonin)	99	VVDLLAPYAJ	1.0075	2.1022	1.1606	2.0556	1.0778	2.1079	0.9753	1.0707	1.0623	0.0598	0.1131	0.0258
			FTQAGSEVSALLGR	0.9064	3.0022	0.9437	2.9602	1.0326	3.0121						
			VLDSGAPIJIPVGPETLGR	1.0122	2.6947	1.1077	2.6598	1.0766	2.6896						
gij6671539	aldolase 1, A isoform	99	AAVEEGIVLGGGCALLR	0.9964	2.6221	1.0675	2.5939	1.1276	2.5998	1.0306	1.0577	1.0913	0.0325	0.0659	0.0408
			VGLQVVAVVJ	1.0611	2.4454	1.1181	2.4405	1.0991	2.4308						
			VTDALNATR	1.0343	2.7224	0.9875	2.7250	1.0471	2.7219						
gij14149635	fatty acid binding protein 4, adipocyte	99	GVVPLAGTNGETTTQGLDC	0.8118	9.6892	0.9672	9.5991	1.0362	9.7067	0.9205	1.0493	1.0321	0.0984	0.0880	0.0139
			ALANSLACQGJ	0.9462	2.2460	1.1423	2.2084	1.0167	2.2273						
			ALQASALJ	1.0034	2.3200	1.0385	2.3109	1.0435	2.3164						
gij6671509	actin, beta, cytoplasmic	99	LVSSNFDDYMJ	1.0146	2.3500	1.0726	2.3389	1.1651	2.3551	0.9753	1.0183	1.0815	0.0586	0.0705	0.0966
			LGVFEDEITADDR	0.9079	2.2473	0.9386	2.2235	1.1036	2.2518						
			NTEISFJ	1.0034	2.7210	1.0435	2.7315	0.9757	2.7157						
gij6678413	triosephosphate isomerase 1	99	AGFAGDDAPR	1.0297	2.7250	1.0340	2.7213	1.0666	2.7321	1.0267	1.1022	1.0323	0.0281	0.0744	0.0426
			VAPEEHVLLTEAPLNPJ	0.9972	2.9656	1.0911	2.9013	1.0456	2.9367						
			YPIEHGIVTNWDDMEJ	1.0533	2.8565	1.1816	2.8252	0.9847	2.8969						
			SNVNDGVAQSTR	0.9418	2.6832	1.0819	2.6242	1.0798	2.6643	0.9584	1.1428	1.0724	0.0228	0.0528	0.0133
			FFVGGNWJ	0.9844	2.4946	1.1758	2.4407	1.0804	2.4953						
			VVLAYEPVWAIGTGJ	0.9491	4.0893	1.1707	3.9748	1.0570	4.1049						
	average									0.9752	1.0689	1.0746			
	stdev									0.0418	0.0336	0.0262			
Replicate 3															
gij31560705	acyl-CoA synthetase long-chain family member 1	99	LVDVEEMNYLASJ	0.9111	2.7466	0.9928	2.7413	1.1296	2.6622	0.9220	1.0073	1.0881	0.0119	0.0191	0.0474
			LAQGEYIAPEJ	0.9202	2.2291	1.0002	2.2351	1.0364	2.1839						
			SQIDELYATIJ	0.9346	1.8025	1.0289	1.7932	1.0983	1.7505						
gij6679937	similar to glyceraldehyde-3-phosphate dehydr	99	VIIISAPSADAPMFVMGVNHE	0.7957	2.1504	0.9121	2.0699	1.0314	2.0269	0.8370	0.9285	1.1141	0.0640	0.0437	0.0795
			LVINGJPITIFQERDPTNIJ	0.8045	2.1208	0.8955	2.1074	1.1209	2.0062						
			LISWYDNEYGYSNR	0.9107	2.9006	0.9781	2.8859	1.1899	2.8179						
gij6679237	pyruvate carboxylase	99	LDNASAFQGAVISPHYDSL	0.9695	3.2148	0.9694	3.2748	1.2181	3.0653	0.8704	0.8932	1.0926	0.0862	0.0729	0.1149
			SSSAPVASPNVR	0.8134	1.9495	0.8859	1.9338	1.0670	1.8440						
			VVEIAPATHLDPQLR	0.8282	1.7655	0.8242	1.7637	0.9926	1.7169						
gij31982186	malate dehydrogenase 2, NAD (mitochondrial)	99	VDFPQDQLATLTGR	0.8427	1.8613	0.8905	1.8605	1.0209	1.8077	0.8714	0.9262	1.0788	0.0342	0.0332	0.0510
			GYLGEQLPDCLJ	0.8622	2.8277	0.9320	2.8409	1.1167	2.6991						
			MIAEAIPELJ	0.9093	1.8318	0.9561	1.8488	1.0989	1.7722						
gij31980648	ATP synthase, H+ transporting mitochondrial F	99	IMNVIGEPIDER	0.9108	1.9074	0.9152	1.8972	1.0778	1.8513	0.8879	0.9269	1.0623	0.0625	0.0147	0.0258
			IMDPNIVGNEHYDVAR	0.8172	3.4193	0.9221	3.3762	1.0326	3.3071						
			EGNDLYHEMIESGVINLJ	0.9357	4.1837	0.9434	4.2412	1.0766	4.0517						
gij31981679	heat shock protein 1 (chaperonin)	99	VGGTSDVEVNEJ	0.9434	1.5597	0.9787	1.5683	1.1276	1.5091						
			CEFQDAYVLLSEJ	0.9564	2.5929	0.9916	2.5967	1.0991	2.5283						

gil6671539	aldolase 1, A isoform	99	NAGVEGSLIVEJ	0.8830	1.5881	0.9300	1.5961	1.0471	1.5343	0.9276	0.9668	1.0913	0.0392	0.0325	0.0408
			GILAADESTGSIAJ	0.7948	2.2150	0.9237	2.1686	1.0362	2.0846						
			ADDGRFPQVIJ	0.7883	3.3327	0.9344	3.2479	1.0167	3.1447						
			IGEHTPSALAIMENANVLAR	0.7875	2.1275	0.8919	2.0878	1.0435	2.0456	0.7902	0.9167	1.0321	0.0040	0.0221	0.0139
gil14149635	fatty acid binding protein 4, adipocyte	99	JVAGMAJPNMIISVNGDLVT	0.8288	3.5477	0.8941	3.4784	1.1651	3.2972						
			LGVEFDEITADDRJ	0.8972	1.8111	0.9724	1.8034	1.1036	1.7435						
			LVSSENFDDUMJ	0.8755	1.8780	0.9572	1.8708	0.9757	1.8467	0.8671	0.9413	1.0815	0.0350	0.0415	0.0966
			DSYVGDEAQSJ	0.8908	3.0467	0.9081	3.0926	1.0666	2.9308						
gil6671509	actin, beta, cytoplasmic	99	AGFAGDDAPR	0.8737	1.4813	0.8677	1.4907	1.0456	1.4465						
			QEYDESGPSIVHR	0.9618	3.5605	0.8810	3.6023	0.9847	3.5272	0.9088	0.8856	1.0323	0.0467	0.0206	0.0426
			VVLAYEPVWAIGTGJ	0.8887	2.5954	0.9599	2.5954	1.0798	2.5032						
			SNVNDGVAQSTR	0.8867	2.8333	0.9339	2.8141	1.0804	2.7639						
gil6678413	triosephosphate isomerase 1	99	IAVAAQNCYJ	0.8957	1.8697	0.9390	1.8765	1.0570	1.8154	0.8904	0.9442	1.0724	0.0047	0.0138	0.0133
	average														
	stdev														

Accession Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114	Avg 116:11
gil3156070 acyl-CoA s	Mus muscl	99	38	0.8831	1.0338	[0.8542, 0.9]	0.9606
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
14 LVDVEEM	-0.003				1	99	52
13 LAQGEYIA	0.007				1	99	42
14 SQIDELYA	0.01				1	99	41

Accession Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114	Avg 116:11
gil6679937 similar to g	Mus muscl	99	24	0.8711	1.0386	[0.8388, 0.9]	0.9623
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
14 VIISAPSAI	-0.006				1	99	40
14 LVINGJPIT	-0.002				2	99	47
14 LISWYDNI	0.008				0	99	41

Accession Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114	Avg 116:11
gil6679237 pyruvate c	Mus muscl	99	49	0.8692	1.0208	[0.8515, 0.9]	0.9466
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
14 LDNASAF	-0.01				1	99	46
12 SSSAPVA	0.019				0	99	46
14 VVEIAPAT	0.003				0	99	41

Accession Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114	Avg 116:11
gil3198218 malate deh	Mus muscl	99	25	0.8813	1.0507	[0.8388, 0.9]	0.9449
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
14 VDFPQDQ	-0.017				0	99	47
14 GYLGPEQ	-0.013				1	99	43
14 MIAEAIPEI	-0.015				1	99	40

Accession Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114	Avg 116:11
gil3198064 ATP synth	Mus muscl	99	17	0.8751	1.0317	[0.8483, 0.9]	0.9565
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
14 IMNVIGEP	-0.004				0	99	46
14 IMDPNIVG	0.005				0	99	44
14 EGNDLYH	0.167				1	99	31

Accession Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114	Avg 116:11
gil3198167 heat shock	Mus muscl	99	27	0.898	1.0303	[0.8716, 0.9]	0.9543
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
12 VGGTSDV	0.007				1	99	52
14 CEFQDAY	-0.008				1	99	50
14 NAGVEGS	0.005				1	99	46

Accession Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114	Avg 116:11
gil6671539 aldolase 1,	Mus muscl	99	18	0.8877	1.0275	[0.8639, 0.9]	0.9627
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score
14 GILAADES	0.003				1	99	50
14 ADDGRPF	0.012				1	99	45
14 IGEHTPSA	0.009				0	78	30

Accession Name	Species	Confidence	Found	Avg 114:11	EF 114:11	95% CI 114	Avg 116:11
gil1414963 fatty acid b	Mus muscl	99	15	0.9003	1.0401	[0.8656, 0.9]	0.9703
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence	Score

14	JVAGMAJF	0.167	2	99	44	23
14	LGVEFDEI	-0.008	1	99	41	17
14	LVSSENFI	0.02	2	97	31	10

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11EF 95% CI	Avg 116:11
gil6754524	lactate dehyd	Mus muscu	99	15	0.8826	1.0213 [0.8641, 0.9591]	0.9876

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11EF 95% CI	Avg 116:11
gil6671509	actin, beta,	Mus muscu	99	12	0.8766	1.0304 [0.8508, 0.9591]	0.937
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence Score	Dist Score
12	DSYVGDE	0.001			1	99	51
12	AGFAGDD	0.017			0	99	32
12	QEYDESG	0.023			0	99	32

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11EF 95% CI	Avg 116:11
gil6678413	triosephosph	Mus muscu	99	13	0.8566	1.0466 [0.8184, 0.9591]	0.9642
Rslt	Matched S	Delta Mass	Zone	Mod	Cust AA	Confidence Score	Dist Score
15	VVLAYEP\	-0.006			1	99	53
11	SNVNDGV	0.008			0	99	45
13	IAVAAQNC	0.011			1	99	38

Accession	Name	Species	Confidence	Found	Avg 114:11EF	114:11EF 95% CI	Avg 116:11
gil5187306	eukaryotic	Mus muscu	99	11	0.9054	1.0285 [0.8803, 0.9591]	0.9527

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0145 [0.9468, 0.1 1.0482 1.02 [1.0276, 1.0691]
114:115 % Error 11' 116:115 % Error 11' 117:115 % Error 11' Cycle Exp Time
0.9042 2.7466 0.9863 2.7413 1.1212 2.6622 384 4 27.793
0.916 2.2291 0.9723 2.2351 1.0357 2.1839 350 4 25.258
0.9292 1.8025 1.0221 1.7932 1.0872 1.7505 299 4 21.635

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.019 [0.9444, 0.1 1.0469 1.0188 [1.0277, 1.0666]
114:115 % Error 11' 116:115 % Error 11' 117:115 % Error 11' Cycle Exp Time
0.7959 2.1504 1.0109 2.0699 1.0621 2.0269 334 2 24.112
0.8049 2.1208 0.902 2.1074 1.1223 2.0062 249 2 17.958
0.8869 2.9006 0.9889 2.8859 1.107 2.8179 366 4 26.488

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0156 [0.9321, 0.1 1.0522 1.016 [1.0356, 1.0690]
114:115 % Error 11' 116:115 % Error 11' 117:115 % Error 11' Cycle Exp Time
0.9554 3.2148 0.9579 3.2748 1.2058 3.0653 351 4 25.4
0.8166 1.9495 0.9149 1.9338 1.0751 1.844 125 4 9.043
0.8591 1.7655 0.9354 1.7637 1.0257 1.7169 154 4 11.139

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0176 [0.9285, 0.1 1.0593 1.0247 [1.0338, 1.0855]
114:115 % Error 11' 116:115 % Error 11' 117:115 % Error 11' Cycle Exp Time
0.8914 1.8613 0.9635 1.8605 1.0676 1.8077 392 4 28.37
0.8698 2.8277 0.9219 2.8409 1.1225 2.6991 233 4 16.855
0.9213 1.8318 0.9529 1.8488 1.0955 1.7722 290 4 20.983

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0371 [0.9223, 0.1 1.0482 1.0583 [0.9904, 1.1093]
114:115 % Error 11' 116:115 % Error 11' 117:115 % Error 11' Cycle Exp Time
0.8867 1.9074 0.9758 1.8972 1.047 1.8513 307 3 22.196
0.8581 3.4193 0.9808 3.3762 1.0309 3.3071 145 4 10.487
0.9357 4.1837 0.952 4.2412 1.102 4.0517 457 3 33.112

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0419 [0.9159, 0.1 1.0654 1.0225 [1.0419, 1.0894]
114:115 % Error 11' 116:115 % Error 11' 117:115 % Error 11' Cycle Exp Time
0.9288 1.5597 0.9727 1.5683 1.1162 1.5091 257 3 18.597
0.9354 2.5929 0.999 2.5967 1.075 2.5283 413 3 29.883
0.8883 1.5881 0.9378 1.5961 1.055 1.5343 37 4 2.669

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0164 [0.9472, 0.1 1.0351 1.0179 [1.0170, 1.0536]
114:115 % Error 11' 116:115 % Error 11' 117:115 % Error 11' Cycle Exp Time
0.7971 2.215 0.9355 2.1686 1.0399 2.0846 53 3 3.806
0.789 3.3327 0.9409 3.2479 1.0158 3.1447 7 4 0.508
0.8565 2.1275 0.9998 2.0878 1.053 2.0456 373 3 26.978

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11' Biological F Molecular Function
1.0281 [0.9438, 0.1 1.0537 1.0463 [1.0071, 1.1025]
114:115 % Error 11' 116:115 % Error 11' 117:115 % Error 11' Cycle Exp Time

0.8073	3.5477	0.9568	3.4784	1.1762	3.2972	231	2	16.654
0.8939	1.8111	0.9839	1.8034	1.1085	1.7435	221	4	15.983
0.8698	1.878	0.952	1.8708	0.9637	1.8467	71	4	5.125

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.0193 [0.9689, 1.0707] 1.0247 1.015 [1.0095, 1.0401]

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.016 [0.9223, 0.9997] 1.0513 1.0136 [1.0372, 1.0657]

114:115	% Error 11`	116:115	% Error 11`	117:115	% Error 11`	Cycle	Exp	Time
0.8908	3.0467	0.9081	3.0926	1.0666	2.9308	179	3	12.948
0.8919	1.4813	0.9265	1.4907	1.0416	1.4465	256	3	18.524
0.9416	3.5605	0.9533	3.6023	1.0076	3.5272	291	2	21.021

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.0428 [0.9247, 1.0609] 1.0466 1.0683 [0.9797, 1.1181]

114:115	% Error 11`	116:115	% Error 11`	117:115	% Error 11`	Cycle	Exp	Time
0.8928	2.5954	0.9631	2.5954	1.0832	2.5032	10	4	0.723
0.8681	2.8333	0.9778	2.8141	1.0514	2.7639	4752	3	87.042
0.8968	1.8697	0.9511	1.8765	1.0504	1.8154	82	4	5.921

EF 116:11±95% CI 11(Avg 117:11EF 117:11±95% CI 11`Biological F Molecular Function
1.0259 [0.9286, 0.9992] 1.05 1.0329 [1.0166, 1.0845]

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
899.9828	2	1797.951	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.94094
753.926	2	1505.837	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.968012
784.9469	2	1567.879	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.952987

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
834.4436	3	2500.309	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.973736
682.9108	4	2727.614	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.949864
962.4563	2	1922.898	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.949522

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
878.4768	3	2632.409	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.968642
658.3697	2	1314.725	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.97671
601.6854	3	1802.034	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.952738

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
852.9548	2	1703.895	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.935094
889.4719	2	1776.929	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.955124
701.9137	2	1401.813	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.939494

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
765.4126	2	1528.811	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.997828
663.0039	3	1985.99	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.915758
588.1	4	2348.371	c:\pe sciex x:\katrin\protein_rodent0705.fasta		1

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
761.4118	2	1520.809	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.970208
945.4851	2	1888.956	c:\pe sciex x:\katrin\protein_rodent0705.fasta		1
752.4421	2	1502.87	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.96194

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
810.9597	2	1619.905	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.988134
815.9682	2	1629.922	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.974662
751.0742	3	2250.201	c:\pe sciex x:\katrin\protein_rodent0705.fasta		0.918365

Precursor I	Precursor Z	Precursor I	Data File	FASTA File	
-------------	-------------	-------------	-----------	------------	--

690.7	4	2758.771	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.991485
948.5014	2	1894.988	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.954841
627.3305	3	1878.97	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.951714

Precursor I Precursor Z Precursor I Data File FASTA File

743.8746	2	1485.735	c:\pe sciex x:\katrin\protein_rodent0705.fasta	1
560.7906	2	1119.567	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.959979
554.2835	3	1659.829	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.993519

Precursor I Precursor Z Precursor I Data File FASTA File

946.0528	2	1890.091	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.954361
696.3621	2	1390.71	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.986669
713.4037	2	1424.793	c:\pe sciex x:\katrin\protein_rodent0705.fasta	0.961502

0.933814	0.939935	0.940837
0.963574	0.991224	0.964252
0.947453	0.953726	0.957139

0.911099	0.992765	1.129632
0.920219	1.0002	1.036429
0.934627	1.028867	1.098314

0.973958	0.878805	0.945805
0.950362	0.943465	0.949186
0.924712	0.914574	0.993997

0.795719	0.912138	1.031399
0.804478	0.895454	1.120911
0.910695	0.978058	1.189942

0.95454	0.966027	0.96427
0.980563	0.949451	0.97321
0.988264	0.870795	0.956354

0.969515	0.969428	1.218092
0.813391	0.885871	1.067038
0.828217	0.824214	0.992581

0.989132	0.914164	0.94585
0.963553	0.974117	0.958555
0.951894	0.955139	0.954852

0.842701	0.890475	1.020885
0.862191	0.932008	1.116678
0.909298	0.956148	1.098903

0.971468	0.911171	1
0.961543	0.904037	0.963094
1	0.991002	0.976919

0.91076	0.915234	1.07775
0.817241	0.922143	1.032563
0.9357	0.943434	1.076565

0.955225	0.961143	0.965016
0.978038	0.970809	1
0.967727	0.95965	0.960503

0.943369	0.978727	1.127641
0.956405	0.991616	1.099139
0.882988	0.929973	1.047124

0.990935	0.978443	0.987378
0.975574	0.96879	0.976407
0.998804	0.891045	0.989789

0.794847	0.923707	1.036167
0.788262	0.934357	1.016667
0.787522	0.891934	1.043497

0.965797	0.902512	0.956716
0.951368	0.940292	0.9472
0.945511	0.950724	0.957307

0.828772	0.894105	1.165141
0.897163	0.972445	1.103643
0.875505	0.957248	0.975723

1	1	1
0.979991	0.917795	0.983787
0.972635	0.898906	0.95049

0.8908	0.9081	1.0666
0.873687	0.867699	1.045635
0.961817	0.881036	0.984659

0.958721	0.955508	0.955725
0.965973	0.922596	0.992608
0.962724	0.950443	0.968762

0.888739	0.959872	1.079814
0.886699	0.933892	1.080391
0.895661	0.938967	1.056987

0.921982	1.007277	1.088125	0.011862	0.019064	0.04743
----------	----------	----------	----------	----------	---------

0.836964	0.92855	1.114084	0.064003	0.043679	0.079492
----------	---------	----------	----------	----------	----------

0.870374	0.893171	1.09257	0.086178	0.072882	0.114903
----------	----------	---------	----------	----------	----------

0.871397	0.92621	1.078822	0.034239	0.033218	0.050956
----------	---------	----------	----------	----------	----------

0.8879	0.926937	1.062293	0.062451	0.014699	0.025754
--------	----------	----------	----------	----------	----------

0.927587	0.966772	1.091302	0.03917	0.032514	0.040826
----------	----------	----------	---------	----------	----------

0.79021	0.916666	1.03211	0.004032	0.022071	0.013867
---------	----------	---------	----------	----------	----------

0.867147 0.941266 1.081502

0.034953 0.041544 0.096631

0.908768 0.885611 1.032298

0.046732 0.020586 0.042568

0.890367 0.944244 1.072397

0.004698 0.01377 0.013349

0.87727 0.93367 1.07455

0.041091 0.035039 0.026163