

Accession number	Protein name	Confidence	Peptide sequence	Ratio	% Error	Ratio	% Error	Ratio	% Error	Average	Average	Average	Stdev	Stdev	Stdev
				0min:5min	0min:5min	15min:5min	15min:5min	45min:5min	45min:5min	0min:5min	15min:5min	45min:5min	0min:5min	15min:5min	45min:5min
				n	n	n	n	n	n				n	n	n
Replicate 1															
gi 31560705	acyl-CoA synthetase long-chain family member 1	99	EVAELAECIGSGLIQJ	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						
			SAVLDDJLLVYYDDVR	0.8274	2.9810	0.9333	2.9106	0.8582	2.9758	0.8923	0.9446	0.8941	0.0568	0.0109	0.0322
gi 6679937	similar to glyceraldehyde-3-phosphate dehydr	99	VIISAPSADAPMFVMGVNHE	0.8522	2.5468	0.9201	2.4911	0.8290	2.5812						
			GAAQNIIPASTGAAJ	0.8302	2.4641	0.9998	2.3906	0.8169	2.4879						
			VPTPNVSVVDLTCR	0.8656	2.3515	0.9408	2.3336	0.8317	2.3964	0.8493	0.9536	0.8259	0.0179	0.0414	0.0079
gi 6679237	pyruvate carboxylase	99	DFTATFGPLDSLNTNR	0.8978	2.8318	0.9461	2.8164	0.8605	2.8547						
			IEGRPGASLPLNLJ	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
gi 31982186	malate dehydrogenase 2, NAD (mitochondrial)	99	MIAEAIPELJ	0.9178	2.9925	0.9657	3.0109	0.8261	3.0860						
			VDFPQDQLATLTGR	0.8155	3.8868	0.8026	3.8736	0.6929	4.0187						
			FVFSLV DAMNGJ	0.9394	2.5276	0.9439	2.5697	0.8520	2.5972	0.8909	0.9041	0.7904	0.0662	0.0885	0.0854
gi 31980648	ATP synthase, H+ transporting mitochondrial F	99	FLSQPFQVAEFTGHMGJ	0.8841	2.7147	0.9190	2.7290	0.8426	2.7554						
			AIAELGIYPAVDPLDSTSR	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
gi 31981679	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						
			ISSVQSI VPALEIANHR	0.9188	3.4697	0.8946	3.4302	0.8603	3.5245	0.9358	0.9297	0.8844	0.0155	0.0334	0.0364
gi 6671539	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						
			ALANSLACQGJ	0.8915	2.0670	0.9755	2.0499	0.8769	2.0870	0.8351	0.9163	0.7935	0.0494	0.0643	0.0752
gi 14149635	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
gi 6671509	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						
			VAPEEHPVLLTEAPLN 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
gi 6678413	triosephosphate isomerase 1	99	VSHALAEGLGVACIGEJ	0.7490	3.3003	0.9827	3.1092	0.7708	3.2910						
			DLGATWVVLGH SER	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

gi 31560705	acyl-CoA synthetase long-chain family member 1	99	EVAELAECIGSGLIQJ	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			
gi 6679937	similar to glyceraldehyde-3-phosphate dehydrogenase	99	VIIISAPSADAPMFVMGVNHE	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									
			VPTPNVSVVDLTCCR	0.9891	3.4335	1.0271	3.3926	1.1899	3.4033	0.9211	1.0539	1.1141	0.0803	0.0232	0.0795			
gi 6679237	pyruvate carboxylase	99	IEGRPGASLPLNLJ	0.9580	2.7090	1.0998	2.6636	1.2181	2.6824									
			AEAEAQAEEELSFP	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	0.9592	1.0578	1.0926	0.0076	0.0366	0.1149			
gi 31982186	malate dehydrogenase 2, NAD (mitochondrial)	99	VDFPQDQLATLTGR	1.0141	1.9872	1.0750	1.9800	1.0209	2.0083									
			IQEAGTEVVJ	1.0358	2.4371	1.0823	2.4419	1.1167	2.4288									
			VNVPVIGGHAGJ	1.0418	2.5459	1.0171	2.5635	1.0989	2.5565	1.0306	1.0581	1.0788	0.0146	0.0357	0.0510			
gi 31980648	ATP synthase, H+ transporting mitochondrial F1F0 complex, epsilon subunit	99	VVDLLAPYAJ	1.0075	2.1022	1.1606	2.0556	1.0778	2.1079									
			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	0.9753	1.0707	1.0623	0.0598	0.1131	0.0258			
gi 31981679	heat shock protein 1 (chaperonin)	99	AAVEEGIVLGGGCALLR	0.9964	2.6221	1.0675	2.5939	1.1276	2.5998									
			VGLQVVAVJ	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	1.0306	1.0577	1.0913	0.0325	0.0659	0.0408			
gi 6671539	aldolase 1, A isoform	99	GVVPLAGTNGETTTQGLD	0.8118	9.6892	0.9672	9.5991	1.0362	9.7067									
			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	0.9205	1.0493	1.0321	0.0984	0.0880	0.0139			
gi 14149635	fatty acid binding protein 4, adipocyte	99	LVSSNFDDYMJ	1.0146	2.3500	1.0726	2.3389	1.1651	2.3551									
			LGVEFDEITADDR	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	0.9753	1.0183	1.0815	0.0586	0.0705	0.0966			
gi 6671509	actin, beta, cytoplasmic	99	AGFAGDDAPR	1.0297	2.7250	1.0340	2.7213	1.0666	2.7321									
			VAPEEHPVLLTEAPLN	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	1.0267	1.1022	1.0323	0.0281	0.0744	0.0426			
gi 6678413	triosephosphate isomerase 1	99	SNVNDGVAQSTR	0.9418	2.6832	1.0819	2.6242	1.0798	2.6643									
			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	0.9584	1.1428	1.0724	0.0228	0.0528	0.0133			
	average									0.9752	1.0689	1.0746						
	stdev									0.0418	0.0336	0.0262						

Replicate 3

gi 31560705	acyl-CoA synthetase long-chain family member 1	99	LVDVEEMNYLASJ	0.9111	2.7466	0.9928	2.7413	1.1296	2.6622									
			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	0.9220	1.0073	1.0881	0.0119	0.0191	0.0474			
gi 6679937	similar to glyceraldehyde-3-phosphate dehydr	99	VIISAPSADAPMFVMGVNHE	0.7957	2.1504	0.9121	2.0699	1.0314	2.0269									
			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	0.8370	0.9285	1.1141	0.0640	0.0437	0.0795			
gi 6679237	pyruvate carboxylase	99	LDNASAFQGAIVSPHYDSL	0.9695	3.2148	0.9694	3.2748	1.2181	3.0653									
			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	0.8704	0.8932	1.0926	0.0862	0.0729	0.1149			
gi 31982186	malate dehydrogenase 2, NAD (mitochondrial)	99	VDFPQDQLATLTGR	0.8427	1.8613	0.8905	1.8605	1.0209	1.8077									
			GYLGPQLPDCIJ	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	0.8714	0.9262	1.0788	0.0342	0.0332	0.0510			
gi 31980648	ATP synthase, H+ transporting mitochondrial F	99	IMNVIGEPIDER	0.9108	1.9074	0.9152	1.8972	1.0778	1.8513									
			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	0.8879	0.9269	1.0623	0.0625	0.0147	0.0258			
gi 31981679	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									
			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			
gi 6671539	aldolase 1, A isoform	99	GILAADESTGSIAJ	0.7948	2.2150	0.9237	2.1686	1.0362	2.0846									
			ADDGRPPQVIJ	0.7883	3.3327	0.9344	3.2479	1.0167	3.1447									
			IGEHTPSALAIMENANVLR	0.7875	2.1275	0.8919	2.0878	1.0435	2.0456	0.7902	0.9167	1.0321	0.0040	0.0221	0.0139			
gi 14149635	fatty acid binding protein 4, adipocyte	99	JVAGMAJPNMIIISVNGDLVT	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									
			LVSSNFDDUMJ	0.8755	1.8780	0.9572	1.8708	0.9757	1.8467	0.8671	0.9413	1.0815	0.0350	0.0415	0.0966			
gi 6671509	actin, beta, cytoplasmic	99	DSYVGDEAQSJ	0.8908	3.0467	0.9081	3.0926	1.0666	2.9308									
			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			
gi 6678413	triosephosphate isomerase 1	99	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									
			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									0.8773	0.9337	1.0746						
	stdev									0.0411	0.0350	0.0262						