

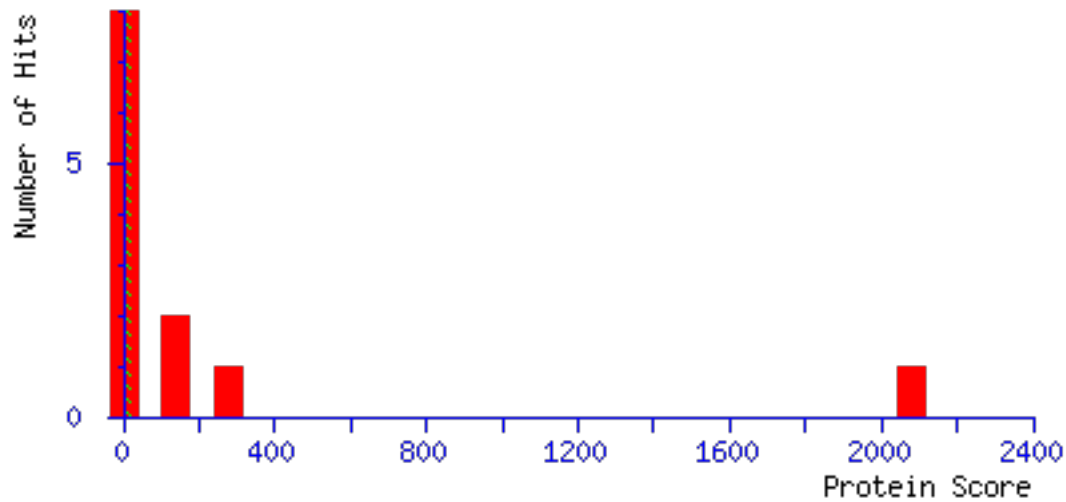
Cambridge Centre for Proteomics Mascot Search Results

User : anja
 Email : aa2030@cam.ac.uk
 Search title : P378 (\\prot-filesvr1\data\CORE\PARAMETERS\Mascot_search_parameters\Yagnesh\M291_Ben_Luisi_tolc_arca_velos_xlink_ox_chymo_041218.par), submitted from Daemon on CCP-PC158
 MS data file : \\prot-filesvr1\data\CORE\RAW_DATA_2018_Velos\P378_Ben_Luisi\P378_Band_1_Xlinked_BSA.mgf
 Database 1 : cRAP 20181217 (120 sequences; 39582 residues)
 Database 2 : M291_ARCA ARCA_20181203 (1 sequences; 238 residues)
 Database 3 : M291_TOLC TOLC_20181203 (1 sequences; 493 residues)
 Timestamp : 19 Dec 2018 at 09:56:35 GMT

Protein hits : [1::sp|cRAP087|P02769|ALBU BOVIN](#) Serum albumin OS=Bos taurus GN=ALB PE=1
[1::sp|cRAP002|P02768|ALBU HUMAN](#) Serum albumin OS=Homo sapiens GN=ALB PE=1
[1::sp|cRAP022|P00766|CTRA BOVIN](#) Chymotrypsinogen A OS=Bos taurus PE=1 SV=1
[1::sp|cRAP112|P00761|TRYP PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1
[1::sp|cRAP004|P04745|AMY1 HUMAN](#) Alpha-amylase 1 OS=Homo sapiens GN=AMY1
[1::sp|cRAP015|P02666|CASB BOVIN](#) Beta-casein OS=Bos taurus GN=CSN2 PE=1
[1::sp|cRAP091|Q10735|PEPB PIG](#) Pepsin B (Fragment) OS=Sus scrofa GN=PG
[1::sp|cRAP046|O76013|KRT36 HUMAN](#) Keratin, type I cuticular Ha6 OS=Homo s
[1::sp|cRAP056|P15241|K2M2 SHEEP](#) Keratin, type II microfibrillar, compon
[1::sp|cRAP003|P00883|ALDOA RABIT](#) Fructose-bisphosphate aldolase A OS=Ory
[1::sp|cRAP020|P01031|CO5 HUMAN](#) Complement C5 OS=Homo sapiens GN=C5 PE=1
[1::sp|cRAP071|Q9NSB2|KRT84 HUMAN](#) Keratin, type II cuticular Hb4 OS=Homo

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 15 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Protein Family Summary	Peptide Summary	Select Summary (protein hits)	Select Summary (unassigned)	Exp
Significance threshold p<				
Standard scoring MudPIT scoring				
Show pop-ups Suppress pop-ups				
Preferred taxonomy All entries .. Archaea (Archaeobacteria) .. Eukaryota (eucaryotes) Alveolata (alveolates and relatives) bony vertebrates lobe-finned fish and tetrapod clade Mammalia (mammals) Mus musculus (house mouse) Rattus norvegicus (brown rat) Other Mammalia (other mammals) fishes) Takifugu rubripes (Japanese Pufferfish) Danio rerio (zebra fish) Schizosaccharomyces pombe (fission yeast) Pneumocystis carinii Other Fungi Viridiplantae (green plants and algae) Mycobacterium tuberculosis complex Other Actinobacteria (class) Firmicutes (gram-positive bacteria) Agrobacterium tumefaciens Campylobacter jejuni Escherichia coli Neisseria meningitidis (meningococcus) Species information unavailable				

Error tolerant

- [1::sp|cRAP087|P02769|ALBU_BOVIN](#) **Mass:** 71244 **Score:** 2077 **Matches:** 292 (292) **S**
 Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
265	396.6889	791.3633	791.3636	-0.39	1	(23)	0.0045	1		Y.LQQ
266	396.6889	791.3633	791.3636	-0.39	1	23	0.0045	1		Y.LQQ
268	396.6892	791.3639	791.3636	0.39	1	(22)	0.0059	1		Y.LQQ
271	396.6895	791.3643	791.3636	0.92	1	(23)	0.0046	1		Y.LQQ
278	397.1806	792.3466	792.3476	-1.31	1	(23)	0.0053	1		Y.LQQ
401	404.6950	807.3753	807.3763	-1.14	0	(24)	0.0041	1	U	Y.QEA
402	404.6950	807.3755	807.3763	-0.99	0	(24)	0.0043	1	U	Y.QEA

<u>407</u>	404.6956	807.3767	807.3763	0.52	0	36	0.00027	1	U	Y.QEA
<u>408</u>	404.6957	807.3768	807.3763	0.67	0	(32)	0.00063	1	U	Y.QEA
<u>411</u>	404.6958	807.3771	807.3763	1.04	0	(20)	0.0099	1	U	Y.QEA
<u>426</u>	405.2235	808.4325	808.4331	-0.68	1	30	0.00097	1	U	Y.STV
<u>427</u>	405.2245	808.4345	808.4331	1.75	1	(30)	0.0011	1	U	Y.STV
<u>610</u>	415.2607	828.5068	828.5069	-0.07	2	23	0.0047	1	U	L.SLI
<u>820</u>	426.2104	850.4062	850.4072	-1.19	1	(32)	0.0007	1	U	L.VNE
<u>823</u>	426.2106	850.4067	850.4072	-0.63	1	(41)	9.6e-05	1	U	L.VNE
<u>824</u>	426.2106	850.4067	850.4072	-0.63	1	(41)	8.5e-05	1	U	L.VNE
<u>825</u>	426.2106	850.4067	850.4072	-0.63	1	(26)	0.0034	1	U	L.VNE
<u>826</u>	426.2107	850.4068	850.4072	-0.56	1	(29)	0.0016	1	U	L.VNE
<u>828</u>	426.2107	850.4068	850.4072	-0.56	1	(21)	0.0094	1	U	L.VNE
<u>829</u>	426.2108	850.4069	850.4072	-0.35	1	(20)	0.011	1	U	L.VNE
<u>830</u>	426.2108	850.4071	850.4072	-0.11	1	(22)	0.0079	1	U	L.VNE
<u>831</u>	426.2110	850.4074	850.4072	0.24	1	(20)	0.012	1	U	L.VNE
<u>832</u>	426.2112	850.4079	850.4072	0.81	1	(20)	0.011	1	U	L.VNE
<u>834</u>	426.2138	850.4129	850.4072	6.71	1	53	4.7e-06	1	U	L.VNE
<u>835</u>	426.2139	850.4133	850.4072	7.13	1	(34)	0.00037	1	U	L.VNE
<u>961</u>	434.7152	867.4158	867.4160	-0.26	0	(27)	0.0019	1	U	L.KTV
<u>962</u>	434.7153	867.4160	867.4160	-0.05	0	(39)	0.00011	1	U	L.KTV
<u>963</u>	434.7153	867.4161	867.4160	0.09	0	42	6.9e-05	1	U	L.KTV
<u>964</u>	434.7154	867.4163	867.4160	0.30	0	(34)	0.00043	1	U	L.KTV
<u>1079</u>	442.7122	883.4099	883.4109	-1.20	0	(24)	0.0041	1	U	L.KTV
<u>1080</u>	442.7134	883.4123	883.4109	1.49	0	(24)	0.0042	1	U	L.KTV
<u>1288</u>	457.2246	912.4347	912.4341	0.61	1	(44)	4.7e-05	1	U	Y.ANK
<u>1289</u>	457.2246	912.4347	912.4341	0.67	1	50	1.1e-05	1	U	Y.ANK
<u>1368</u>	461.2374	920.4603	920.4603	-0.02	1	(29)	0.0014	1	U	Y.QEA
<u>1369</u>	461.2374	920.4603	920.4603	-0.02	1	(24)	0.0039	1	U	Y.QEA
<u>1373</u>	461.2379	920.4612	920.4603	0.96	1	35	0.00033	1	U	Y.QEA
<u>1813</u>	487.7313	973.4480	973.4505	-2.60	1	(30)	0.0012	1	U	F.KDL
<u>1814</u>	487.7321	973.4496	973.4505	-0.96	1	(42)	6.9e-05	1	U	F.KDL
<u>1815</u>	487.7321	973.4496	973.4505	-0.96	1	(30)	0.00098	1	U	F.KDL
<u>1816</u>	487.7321	973.4496	973.4505	-0.96	1	(23)	0.005	1	U	F.KDL
<u>1817</u>	487.7321	973.4497	973.4505	-0.77	1	(24)	0.0038	1	U	F.KDL
<u>1818</u>	487.7322	973.4499	973.4505	-0.59	1	(34)	0.00041	1	U	F.KDL
<u>1819</u>	487.7324	973.4502	973.4505	-0.28	1	(31)	0.00077	1	U	F.KDL
<u>1820</u>	487.7324	973.4503	973.4505	-0.22	1	(28)	0.0017	1	U	F.KDL
<u>1821</u>	487.7325	973.4504	973.4505	-0.09	1	(44)	4.3e-05	1	U	F.KDL
<u>1822</u>	487.7325	973.4505	973.4505	-0.03	1	(34)	0.00044	1	U	F.KDL
<u>1823</u>	487.7325	973.4505	973.4505	-0.03	1	(30)	0.0011	1	U	F.KDL
<u>1824</u>	487.7326	973.4506	973.4505	0.09	1	(30)	0.00095	1	U	F.KDL
<u>1825</u>	487.7326	973.4506	973.4505	0.09	1	(31)	0.0008	1	U	F.KDL
<u>1826</u>	487.7326	973.4507	973.4505	0.23	1	(22)	0.0072	1	U	F.KDL
<u>1827</u>	487.7327	973.4508	973.4505	0.30	1	(36)	0.00024	1	U	F.KDL
<u>1828</u>	487.7327	973.4508	973.4505	0.30	1	(49)	1.3e-05	1	U	F.KDL
<u>1829</u>	487.7327	973.4508	973.4505	0.30	1	(32)	0.00063	1	U	F.KDL
<u>1830</u>	487.7327	973.4508	973.4505	0.30	1	(44)	4.5e-05	1	U	F.KDL
<u>1831</u>	487.7327	973.4508	973.4505	0.36	1	(28)	0.0016	1	U	F.KDL
<u>1832</u>	487.7327	973.4509	973.4505	0.42	1	(43)	5.7e-05	1	U	F.KDL
<u>1833</u>	487.7328	973.4511	973.4505	0.60	1	(29)	0.0012	1	U	F.KDL
<u>1834</u>	487.7329	973.4512	973.4505	0.73	1	(25)	0.003	1	U	F.KDL
<u>1835</u>	487.7330	973.4514	973.4505	0.91	1	(36)	0.00026	1	U	F.KDL
<u>1836</u>	487.7330	973.4514	973.4505	0.97	1	(26)	0.0026	1	U	F.KDL
<u>1837</u>	487.7331	973.4516	973.4505	1.16	1	(40)	0.00011	1	U	F.KDL
<u>1838</u>	487.7331	973.4516	973.4505	1.16	1	(36)	0.00029	1	U	F.KDL
<u>1839</u>	487.7331	973.4516	973.4505	1.16	1	(35)	0.00031	1	U	F.KDL
<u>1841</u>	487.7332	973.4518	973.4505	1.34	1	53	5.6e-06	1	U	F.KDL

1842	487.7332	973.4519	973.4505	1.49	1	(31)	0.00088	1	U	F.KDL
1843	487.7334	973.4522	973.4505	1.80	1	(31)	0.00077	1	U	F.KDL
1844	487.7341	973.4536	973.4505	3.17	1	(35)	0.00031	1	U	F.KDL
2056	498.7293	995.4441	995.4447	-0.68	1	51	8.1e-06	1	U	F.SAL
2057	498.7294	995.4443	995.4447	-0.44	1	(21)	0.0086	1	U	F.SAL
2059	498.7296	995.4445	995.4447	-0.20	1	(48)	1.4e-05	1	U	F.SAL
2615	525.2421	1048.4696	1048.4681	1.38	0	22	0.0067	1	U	L.KEC
2636	526.2822	1050.5499	1050.5498	0.10	1	(33)	0.00056	1	U	F.KAD
2637	526.2824	1050.5503	1050.5498	0.44	1	(44)	4.2e-05	1	U	F.KAD
2638	526.2826	1050.5507	1050.5498	0.90	1	51	8.2e-06	1	U	F.KAD
2639	526.2829	1050.5512	1050.5498	1.37	1	(34)	0.00038	1	U	F.KAD
2649	526.7447	1051.4748	1051.4757	-0.81	0	(34)	0.0007	1	U	L.IKQ
2650	526.7448	1051.4751	1051.4757	-0.58	0	56	4.8e-06	1	U	L.IKQ
2654	526.7453	1051.4760	1051.4757	0.35	0	(28)	0.0028	1	U	L.IKQ
2655	526.7453	1051.4760	1051.4757	0.35	0	(50)	1.6e-05	1	U	L.IKQ
2656	526.7454	1051.4763	1051.4757	0.58	0	(33)	0.00081	1	U	L.IKQ
2658	526.7455	1051.4765	1051.4757	0.81	0	(22)	0.01	1	U	L.IKQ
2659	526.7458	1051.4770	1051.4757	1.28	0	(46)	4.8e-05	1	U	L.IKQ
2660	526.7459	1051.4771	1051.4757	1.40	0	(30)	0.002	1	U	L.IKQ
2661	526.7461	1051.4777	1051.4757	1.97	0	(29)	0.0022	1	U	L.IKQ
2663	526.7462	1051.4779	1051.4757	2.10	0	(26)	0.0047	1	U	L.IKQ
2664	526.7464	1051.4782	1051.4757	2.45	0	(26)	0.0053	1	U	L.IKQ
2666	526.7468	1051.4790	1051.4757	3.15	0	(24)	0.0078	1	U	L.IKQ
2676	527.2358	1052.4570	1052.4597	-2.54	0	(47)	2.7e-05	1	U	L.IKQ
2677	527.2366	1052.4587	1052.4597	-0.93	0	(43)	8.8e-05	1	U	L.IKQ
2678	527.2376	1052.4605	1052.4597	0.82	0	(46)	4.5e-05	1	U	L.IKQ
2681	527.7269	1053.4392	1053.4437	-4.28	0	(28)	0.0019	1	U	L.IKQ
2777	532.7198	1063.4251	1063.4240	1.06	0	(33)	0.0005	1		L.ECA
2778	532.7199	1063.4253	1063.4240	1.17	0	(26)	0.0024	1		L.ECA
2779	532.7201	1063.4256	1063.4240	1.51	0	49	1.3e-05	1		L.ECA
2782	532.7205	1063.4264	1063.4240	2.20	0	(25)	0.0029	1		L.ECA
2783	532.7208	1063.4271	1063.4240	2.90	0	(27)	0.0022	1		L.ECA
2918	538.7560	1075.4975	1075.4974	0.08	2	40	0.00012	1	U	Y.YAN
2953	541.2883	1080.5620	1080.5604	1.49	0	(34)	0.00044	1	U	L.SQK
2954	541.2885	1080.5623	1080.5604	1.82	0	35	0.00035	1	U	L.SQK
3207	558.8289	1115.6432	1115.6438	-0.57	1	(25)	0.0033	1	U	F.VEV
3208	558.8292	1115.6438	1115.6438	-0.03	1	(41)	8.8e-05	1	U	F.VEV
3209	558.8297	1115.6447	1115.6438	0.85	1	(26)	0.0023	1	U	F.VEV
3210	558.8306	1115.6467	1115.6438	2.61	1	42	6.5e-05	1	U	F.VEV
3712	589.2620	1176.5094	1176.5081	1.09	1	(33)	0.00047	1		L.LEC
3714	589.2626	1176.5106	1176.5081	2.13	1	35	0.00035	1		L.LEC
3745	590.8271	1179.6397	1179.6400	-0.24	2	(41)	7.6e-05	1	U	Y.GFQ
3746	590.8276	1179.6407	1179.6400	0.59	2	(35)	0.00034	1	U	Y.GFQ
3747	590.8279	1179.6412	1179.6400	1.00	2	(40)	9.1e-05	1	U	Y.GFQ
3752	591.3184	1180.6223	1180.6240	-1.48	2	43	5.3e-05	1	U	Y.GFQ
3753	591.3185	1180.6224	1180.6240	-1.38	2	(37)	0.00021	1	U	Y.GFQ
3754	591.3209	1180.6273	1180.6240	2.75	2	(30)	0.00097	1	U	Y.GFQ
3792	593.7947	1185.5748	1185.5740	0.69	1	(27)	0.0023	1	U	L.KTV
3793	593.7954	1185.5763	1185.5740	1.92	1	30	0.0012	1	U	L.KTV
3844	596.8202	1191.6258	1191.6248	0.89	1	(41)	7.3e-05	1	U	L.KHL
3848	596.8209	1191.6272	1191.6248	2.01	1	(42)	6.7e-05	1	U	L.KHL
3864	597.3107	1192.6069	1192.6088	-1.57	1	43	5.6e-05	1	U	L.KHL
3865	597.3126	1192.6106	1192.6088	1.50	1	(34)	0.00041	1	U	L.KHL
3866	597.3302	1192.6458	1192.6492	-2.81	2	(37)	0.00019	1	U	Y.VPK
3867	597.3311	1192.6475	1192.6492	-1.39	2	45	3.2e-05	1	U	Y.VPK
3868	398.5568	1192.6485	1192.6492	-0.63	2	(21)	0.0082	1	U	Y.VPK
3869	398.5570	1192.6491	1192.6492	-0.07	2	(29)	0.0012	1	U	Y.VPK

<u>3872</u>	398.5573	1192.6500	1192.6492	0.68	2	(29)	0.0012	1	U	Y.VPK
<u>3875</u>	597.3330	1192.6515	1192.6492	1.90	2	(44)	4.3e-05	1	U	Y.VPK
<u>4074</u>	606.7965	1211.5783	1211.5822	-3.22	2	22	0.011	1	U	Y.QEA
<u>4075</u>	606.7968	1211.5791	1211.5822	-2.62	2	(20)	0.016	1	U	Y.QEA
<u>4266</u>	409.5448	1225.6126	1225.6125	0.07	1	(22)	0.0058	1	U	L.CKV
<u>4267</u>	613.8141	1225.6136	1225.6125	0.93	1	(29)	0.0013	1	U	L.CKV
<u>4269</u>	613.8146	1225.6147	1225.6125	1.83	1	30	0.00096	1	U	L.CKV
<u>4447</u>	414.5201	1240.5386	1240.5394	-0.64	0	40	0.00011	1	U	F.AED
<u>4449</u>	621.2773	1240.5401	1240.5394	0.60	0	(32)	0.0007	1	U	F.AED
<u>4450</u>	414.5207	1240.5402	1240.5394	0.69	0	(23)	0.005	1	U	F.AED
<u>4451</u>	621.2782	1240.5418	1240.5394	1.99	0	(35)	0.00035	1	U	F.AED
<u>4453</u>	621.2789	1240.5432	1240.5394	3.07	0	(22)	0.0067	1	U	F.AED
<u>4463</u>	621.7694	1241.5241	1241.5234	0.61	0	(36)	0.00026	1	U	F.AED
<u>4464</u>	621.7696	1241.5246	1241.5234	1.00	0	(30)	0.0012	1	U	F.AED
<u>5083</u>	654.8684	1307.7223	1307.7197	1.96	0	(29)	0.0012	1	U	L.KHK
<u>5084</u>	654.8684	1307.7223	1307.7197	1.96	0	(27)	0.0018	1	U	L.KHK
<u>5085</u>	654.8698	1307.7251	1307.7197	4.10	0	(32)	0.00067	1	U	L.KHK
<u>5086</u>	654.8702	1307.7258	1307.7197	4.66	0	33	0.00052	1	U	L.KHK
<u>5225</u>	663.8907	1325.7668	1325.7667	0.09	0	(34)	0.00042	1	U	Y.TRK
<u>5226</u>	663.8908	1325.7669	1325.7667	0.18	0	36	0.00023	1	U	Y.TRK
<u>5703</u>	697.3328	1392.6511	1392.6555	-3.16	0	(63)	5.8e-07	1	U	Y.ICD
<u>5704</u>	697.3329	1392.6512	1392.6555	-3.06	0	(58)	1.8e-06	1	U	Y.ICD
<u>5706</u>	697.3348	1392.6550	1392.6555	-0.34	0	(77)	2.6e-08	1	U	Y.ICD
<u>5707</u>	697.3348	1392.6550	1392.6555	-0.34	0	(66)	3e-07	1	U	Y.ICD
<u>5708</u>	697.3348	1392.6551	1392.6555	-0.26	0	(68)	2.1e-07	1	U	Y.ICD
<u>5709</u>	697.3350	1392.6554	1392.6555	-0.09	0	(63)	6.3e-07	1	U	Y.ICD
<u>5710</u>	697.3350	1392.6555	1392.6555	0.00	0	80	1.1e-08	1	U	Y.ICD
<u>5711</u>	697.3351	1392.6556	1392.6555	0.09	0	(65)	4.1e-07	1	U	Y.ICD
<u>5712</u>	697.3352	1392.6559	1392.6555	0.27	0	(72)	8.3e-08	1	U	Y.ICD
<u>5713</u>	697.3352	1392.6559	1392.6555	0.27	0	(35)	0.00042	1	U	Y.ICD
<u>5714</u>	697.3353	1392.6560	1392.6555	0.36	0	(39)	0.00016	1	U	Y.ICD
<u>5715</u>	697.3353	1392.6561	1392.6555	0.45	0	(60)	1.3e-06	1	U	Y.ICD
<u>5716</u>	697.3354	1392.6562	1392.6555	0.53	0	(68)	2e-07	1	U	Y.ICD
<u>5717</u>	697.3354	1392.6562	1392.6555	0.53	0	(67)	2.5e-07	1	U	Y.ICD
<u>5718</u>	697.3354	1392.6562	1392.6555	0.53	0	(63)	6.4e-07	1	U	Y.ICD
<u>5719</u>	697.3354	1392.6562	1392.6555	0.53	0	(36)	0.00033	1	U	Y.ICD
<u>5720</u>	465.2260	1392.6563	1392.6555	0.58	0	(57)	2.3e-06	1	U	Y.ICD
<u>5721</u>	697.3355	1392.6563	1392.6555	0.62	0	(55)	3.7e-06	1	U	Y.ICD
<u>5722</u>	697.3355	1392.6563	1392.6555	0.62	0	(57)	2.1e-06	1	U	Y.ICD
<u>5723</u>	697.3355	1392.6563	1392.6555	0.62	0	(54)	4.5e-06	1	U	Y.ICD
<u>5724</u>	697.3355	1392.6563	1392.6555	0.62	0	(45)	3.8e-05	1	U	Y.ICD
<u>5725</u>	697.3355	1392.6565	1392.6555	0.70	0	(75)	4.2e-08	1	U	Y.ICD
<u>5726</u>	697.3356	1392.6566	1392.6555	0.79	0	(63)	5.8e-07	1	U	Y.ICD
<u>5727</u>	697.3356	1392.6567	1392.6555	0.88	0	(47)	2.2e-05	1	U	Y.ICD
<u>5728</u>	697.3356	1392.6567	1392.6555	0.88	0	(42)	6.7e-05	1	U	Y.ICD
<u>5729</u>	697.3356	1392.6567	1392.6555	0.88	0	(38)	0.00017	1	U	Y.ICD
<u>5730</u>	697.3357	1392.6568	1392.6555	0.96	0	(70)	1.1e-07	1	U	Y.ICD
<u>5731</u>	697.3357	1392.6568	1392.6555	0.96	0	(62)	7.1e-07	1	U	Y.ICD
<u>5732</u>	697.3357	1392.6569	1392.6555	1.05	0	(60)	1.3e-06	1	U	Y.ICD
<u>5733</u>	465.2264	1392.6572	1392.6555	1.25	0	(50)	1.2e-05	1	U	Y.ICD
<u>5734</u>	697.3360	1392.6574	1392.6555	1.41	0	(32)	0.00071	1	U	Y.ICD
<u>5735</u>	697.3361	1392.6576	1392.6555	1.49	0	(67)	2.5e-07	1	U	Y.ICD
<u>5736</u>	697.3361	1392.6577	1392.6555	1.58	0	(44)	5e-05	1	U	Y.ICD
<u>5737</u>	697.3362	1392.6579	1392.6555	1.75	0	(61)	9.7e-07	1	U	Y.ICD
<u>5738</u>	697.3362	1392.6579	1392.6555	1.75	0	(41)	9.4e-05	1	U	Y.ICD
<u>5739</u>	697.3364	1392.6582	1392.6555	1.93	0	(46)	2.5e-05	1	U	Y.ICD
<u>5740</u>	697.3364	1392.6583	1392.6555	2.03	0	(62)	6.8e-07	1	U	Y.ICD

<u>5741</u>	697.3365	1392.6584	1392.6555	2.11	0	(62)	6.6e-07	1	U	Y.ICD
<u>5742</u>	697.3367	1392.6588	1392.6555	2.37	0	(46)	2.6e-05	1	U	Y.ICD
<u>5744</u>	697.3368	1392.6590	1392.6555	2.54	0	(59)	1.4e-06	1	U	Y.ICD
<u>5745</u>	697.3369	1392.6593	1392.6555	2.71	0	(62)	5.9e-07	1	U	Y.ICD
<u>5746</u>	697.3370	1392.6594	1392.6555	2.82	0	(59)	1.4e-06	1	U	Y.ICD
<u>5747</u>	697.3370	1392.6595	1392.6555	2.90	0	(60)	1.1e-06	1	U	Y.ICD
<u>5748</u>	697.3371	1392.6596	1392.6555	2.99	0	(71)	7.6e-08	1	U	Y.ICD
<u>5749</u>	697.3371	1392.6596	1392.6555	2.99	0	(57)	2.1e-06	1	U	Y.ICD
<u>5750</u>	697.3372	1392.6598	1392.6555	3.07	0	(52)	7.2e-06	1	U	Y.ICD
<u>5751</u>	697.3372	1392.6598	1392.6555	3.07	0	(32)	0.00061	1	U	Y.ICD
<u>5752</u>	697.3373	1392.6600	1392.6555	3.25	0	(47)	2.1e-05	1	U	Y.ICD
<u>5753</u>	697.3375	1392.6604	1392.6555	3.50	0	(73)	5.3e-08	1	U	Y.ICD
<u>5754</u>	697.3380	1392.6615	1392.6555	4.29	0	(36)	0.00027	1	U	Y.ICD
<u>5755</u>	697.3380	1392.6615	1392.6555	4.29	0	(44)	3.9e-05	1	U	Y.ICD
<u>5756</u>	697.3383	1392.6620	1392.6555	4.65	0	(63)	4.9e-07	1	U	Y.ICD
<u>5757</u>	697.3388	1392.6631	1392.6555	5.44	0	(50)	1.1e-05	1	U	Y.ICD
<u>5758</u>	697.3403	1392.6660	1392.6555	7.54	0	(34)	0.00044	1	U	Y.ICD
<u>5767</u>	697.8306	1393.6467	1393.6395	5.17	0	(64)	6.3e-07	1	U	Y.ICD
<u>5768</u>	697.8386	1393.6626	1393.6395	16.6	0	(38)	0.00025	1	U	Y.ICD
<u>5769</u>	697.8391	1393.6637	1393.6395	17.3	0	(41)	9.5e-05	1	U	Y.ICD
<u>5781</u>	698.3221	1394.6297	1394.6235	4.46	0	(25)	0.005	1	U	Y.ICD
<u>5782</u>	698.3231	1394.6316	1394.6235	5.78	0	(35)	0.00058	1	U	Y.ICD
<u>5987</u>	711.4097	1420.8049	1420.8038	0.80	1	(41)	8.6e-05	1	U	L.LKH
<u>5989</u>	711.4114	1420.8083	1420.8038	3.21	1	47	2.1e-05	1	U	L.LKH
<u>6026</u>	713.8177	1425.6208	1425.6194	0.99	1	38	0.00034	1		L.ECA
<u>6578</u>	756.9333	1511.8520	1511.8559	-2.57	1	24	0.0044	1	U	F.AVE
<u>6581</u>	505.2538	1512.7396	1512.7395	0.07	2	42	8.1e-05	1	U	Y.LQQ
<u>6901</u>	784.8098	1567.6049	1567.6065	-0.99	0	(37)	0.0002	1	U	F.QEC
<u>6902</u>	784.8112	1567.6079	1567.6065	0.88	0	(53)	5.1e-06	1	U	F.QEC
<u>6903</u>	784.8116	1567.6086	1567.6065	1.34	0	(42)	7e-05	1	U	F.QEC
<u>6904</u>	523.5436	1567.6091	1567.6065	1.65	0	(38)	0.00017	1	U	F.QEC
<u>6905</u>	784.8119	1567.6092	1567.6065	1.74	0	66	2.5e-07	1	U	F.QEC
<u>6906</u>	784.8124	1567.6102	1567.6065	2.36	0	(53)	4.5e-06	1	U	F.QEC
<u>6907</u>	784.8126	1567.6106	1567.6065	2.59	0	(24)	0.0042	1	U	F.QEC
<u>6908</u>	784.8128	1567.6111	1567.6065	2.91	0	(40)	9.9e-05	1	U	F.QEC
<u>6909</u>	523.5444	1567.6113	1567.6065	3.05	0	(34)	0.00036	1	U	F.QEC
<u>6924</u>	785.2917	1568.5689	1568.5905	-13.75	0	(24)	0.0039	1	U	F.QEC
<u>6926</u>	785.3070	1568.5993	1568.5905	5.63	0	(48)	1.4e-05	1	U	F.QEC
<u>6927</u>	785.3092	1568.6038	1568.5905	8.50	0	(39)	0.00013	1	U	F.QEC
<u>6950</u>	524.9354	1571.7843	1571.7831	0.72	2	(21)	0.0082	1	U	F.DEH
<u>6956</u>	787.3917	1572.7689	1572.7671	1.11	2	(49)	1.4e-05	1	U	F.DEH
<u>6959</u>	787.3923	1572.7701	1572.7671	1.89	2	(50)	1.1e-05	1	U	F.DEH
<u>6960</u>	787.3926	1572.7707	1572.7671	2.28	2	(47)	2.1e-05	1	U	F.DEH
<u>6962</u>	787.3931	1572.7716	1572.7671	2.83	2	53	5e-06	1	U	F.DEH
<u>7037</u>	792.4542	1582.8939	1582.8930	0.55	2	24	0.0035	1	U	F.AVE
<u>7052</u>	792.9479	1583.8813	1583.8770	2.71	2	(21)	0.0083	1	U	F.AVE
<u>7433</u>	827.8024	1653.5902	1653.5858	2.67	0	47	2.2e-05	1	U	L.EEC
<u>7434</u>	827.8031	1653.5916	1653.5858	3.55	0	(39)	0.00013	1	U	L.EEC
<u>7645</u>	563.5613	1687.6620	1687.6640	-1.20	0	(50)	1.1e-05	1	U	F.VDK
<u>7646</u>	563.5615	1687.6626	1687.6640	-0.88	0	(35)	0.00029	1	U	F.VDK
<u>7648</u>	844.8390	1687.6634	1687.6640	-0.36	0	(44)	3.9e-05	1	U	F.VDK
<u>7649</u>	844.8391	1687.6635	1687.6640	-0.29	0	(60)	1.1e-06	1	U	F.VDK
<u>7650</u>	844.8392	1687.6638	1687.6640	-0.14	0	(41)	8.6e-05	1	U	F.VDK
<u>7651</u>	844.8392	1687.6639	1687.6640	-0.07	0	68	1.7e-07	1	U	F.VDK
<u>7652</u>	563.5626	1687.6659	1687.6640	1.08	0	(33)	0.0005	1	U	F.VDK
<u>7653</u>	563.5626	1687.6659	1687.6640	1.08	0	(24)	0.0038	1	U	F.VDK
<u>7654</u>	563.5628	1687.6666	1687.6640	1.52	0	(36)	0.00024	1	U	F.VDK

<u>7655</u>	563.5629	1687.6668	1687.6640	1.63	0	(25)	0.0034	1	U	F.VDK
<u>7656</u>	563.5632	1687.6677	1687.6640	2.16	0	(47)	2.2e-05	1	U	F.VDK
<u>7657</u>	844.8415	1687.6684	1687.6640	2.60	0	(63)	5e-07	1	U	F.VDK
<u>7658</u>	844.8415	1687.6684	1687.6640	2.60	0	(60)	1.1e-06	1	U	F.VDK
<u>8178</u>	886.4200	1770.8254	1770.8247	0.42	2	(41)	0.00014	1	U	L.IKQ
<u>8179</u>	591.2828	1770.8267	1770.8247	1.15	2	59	2.1e-06	1	U	L.IKQ
<u>8180</u>	591.2832	1770.8278	1770.8247	1.76	2	(36)	0.00046	1	U	L.IKQ
<u>8181</u>	886.4221	1770.8296	1770.8247	2.77	2	(43)	8.1e-05	1	U	L.IKQ
<u>8419</u>	922.4374	1842.8603	1842.8492	6.06	1	22	0.013	1	U	L.AKY
<u>8470</u>	621.6175	1861.8306	1861.8298	0.43	0	(27)	0.0067	1	U	F.AKT
<u>8472</u>	931.9230	1861.8315	1861.8298	0.90	0	48	5.2e-05	1	U	F.AKT
<u>8473</u>	621.6180	1861.8323	1861.8298	1.32	0	(36)	0.00089	1	U	F.AKT
<u>8754</u>	993.4120	1984.8094	1984.8077	0.85	1	(47)	4.1e-05	1	U	Y.NGV
<u>8755</u>	662.6109	1984.8109	1984.8077	1.58	1	(29)	0.0027	1	U	Y.NGV
<u>8756</u>	993.4128	1984.8110	1984.8077	1.65	1	(62)	1.2e-06	1	U	Y.NGV
<u>8757</u>	662.6124	1984.8155	1984.8077	3.89	1	(30)	0.0019	1	U	Y.NGV
<u>8758</u>	993.9040	1985.7934	1985.7917	0.85	1	66	5.4e-07	1	U	Y.NGV
<u>8759</u>	993.9075	1985.8005	1985.7917	4.41	1	(55)	6.3e-06	1	U	Y.NGV
<u>8760</u>	994.3953	1986.7760	1986.7758	0.11	1	(45)	4.7e-05	1	U	Y.NGV
<u>8761</u>	994.3973	1986.7801	1986.7758	2.20	1	(64)	7.4e-07	1	U	Y.NGV
<u>8890</u>	508.7299	2030.8906	2030.8891	0.73	1	(22)	0.021	1	U	F.AED
<u>8892</u>	1016.4551	2030.8957	2030.8891	3.26	1	45	0.00011	1	U	F.AED
<u>8980</u>	1034.9038	2067.7931	2067.7972	-2.00	1	59	1.1e-06	1	U	Y.EAT
<u>8984</u>	690.2737	2067.7992	2067.7972	0.97	1	(22)	0.0061	1	U	Y.EAT
<u>8992</u>	1034.9094	2067.8043	2067.7972	3.42	1	(48)	1.7e-05	1	U	Y.EAT
<u>8995</u>	1034.9098	2067.8050	2067.7972	3.78	1	(49)	1.3e-05	1	U	Y.EAT
<u>8997</u>	1034.9102	2067.8058	2067.7972	4.14	1	(48)	1.5e-05	1	U	Y.EAT
<u>9139</u>	706.3677	2116.0812	2116.0800	0.56	1	36	0.00029	1	U	L.SHK
<u>9141</u>	706.3680	2116.0823	2116.0800	1.07	1	(30)	0.0011	1	U	L.SHK
<u>9143</u>	1059.0502	2116.0858	2116.0800	2.72	1	(24)	0.0041	1	U	L.SHK
<u>9144</u>	1059.0518	2116.0890	2116.0800	4.22	1	(33)	0.00052	1	U	L.SHK
<u>9447</u>	744.0607	2229.1602	2229.1641	-1.75	2	(33)	0.00052	1	U	F.LSH
<u>9448</u>	1115.5892	2229.1639	2229.1641	-0.08	2	(48)	1.4e-05	1	U	F.LSH
<u>9455</u>	744.0634	2229.1684	2229.1641	1.95	2	(25)	0.0033	1	U	F.LSH
<u>9456</u>	1115.5939	2229.1732	2229.1641	4.08	2	51	7.3e-06	1	U	F.LSH
<u>9543</u>	758.9571	2273.8496	2273.8446	2.22	0	40	9.5e-05	1	U	Y.GDM
<u>9544</u>	758.9576	2273.8509	2273.8446	2.79	0	(29)	0.0012	1	U	Y.GDM
<u>9545</u>	1137.9329	2273.8512	2273.8446	2.90	0	(23)	0.0046	1	U	Y.GDM
<u>9546</u>	1137.9330	2273.8514	2273.8446	3.01	0	(38)	0.00014	1	U	Y.GDM
<u>9547</u>	758.9593	2273.8562	2273.8446	5.12	0	(27)	0.0019	1	U	Y.GDM
<u>9548</u>	759.2898	2274.8475	2274.8286	8.33	0	(31)	0.00077	1	U	Y.GDM
<u>9578</u>	764.2867	2289.8384	2289.8395	-0.48	0	(26)	0.0028	1	U	Y.GDM
<u>9579</u>	1145.9276	2289.8407	2289.8395	0.51	0	(39)	0.00014	1	U	Y.GDM
<u>9580</u>	1145.9287	2289.8429	2289.8395	1.47	0	(34)	0.00042	1	U	Y.GDM
<u>9581</u>	764.2883	2289.8430	2289.8395	1.52	0	(21)	0.0084	1	U	Y.GDM
<u>9582</u>	764.2884	2289.8433	2289.8395	1.68	0	(24)	0.0042	1	U	Y.GDM
<u>9583</u>	1145.9294	2289.8443	2289.8395	2.11	0	(27)	0.0022	1	U	Y.GDM
<u>9584</u>	764.2889	2289.8450	2289.8395	2.40	0	(21)	0.0088	1	U	Y.GDM
<u>9585</u>	764.2894	2289.8463	2289.8395	2.96	0	(35)	0.0003	1	U	Y.GDM
<u>9952</u>	796.6513	2386.9321	2386.9286	1.45	1	22	0.0081	1	U	Y.GDM
<u>10293</u>	890.0890	2667.2451	2667.2486	-1.31	2	42	0.00019	1	U	L.SHK
<u>10296</u>	890.0927	2667.2561	2667.2486	2.80	2	(32)	0.0018	1	U	L.SHK
<u>10353</u>	941.7993	2822.3761	2822.3796	-1.24	1	34	0.0005	1	U	L.EKS
<u>10356</u>	941.8046	2822.3919	2822.3796	4.34	1	(23)	0.005	1	U	L.EKS
<u>10411</u>	971.1553	2910.4442	2910.3779	22.8	1	(26)	0.0041	1	U	L.EKS
<u>10428</u>	979.4959	2935.4659	2935.4637	0.76	2	(32)	0.00091	1	U	L.LEK
<u>10430</u>	979.4963	2935.4670	2935.4637	1.13	2	38	0.00021	1	U	L.LEK

2. [1::sp|cRAP002|P02768|ALBU_HUMAN](#) Mass: 71317 Score: 281 Matches: 60 (60) Seq

Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

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

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptid
265	396.6889	791.3633	791.3636	-0.39	1	(23)	0.0045	1		Y.LQQC
266	396.6889	791.3633	791.3636	-0.39	1	23	0.0045	1		Y.LQQC
268	396.6892	791.3639	791.3636	0.39	1	(22)	0.0059	1		Y.LQQC
271	396.6895	791.3643	791.3636	0.92	1	(23)	0.0046	1		Y.LQQC
278	397.1806	792.3466	792.3476	-1.31	1	(23)	0.0053	1		Y.LQQC
2655	526.7453	1051.4760	1051.5008	-23.55	1	(21)	0.015	2	U	L.IKQN
2659	526.7458	1051.4770	1051.5008	-22.62	1	21	0.014	2	U	L.IKQN
2768	532.2493	1062.4841	1062.4838	0.31	0	26	0.0023	1	U	L.KECC
2777	532.7198	1063.4251	1063.4240	1.06	0	(33)	0.0005	1		L.ECAD
2778	532.7199	1063.4253	1063.4240	1.17	0	(26)	0.0024	1		L.ECAD
2779	532.7201	1063.4256	1063.4240	1.51	0	49	1.3e-05	1		L.ECAD
2782	532.7205	1063.4264	1063.4240	2.20	0	(25)	0.0029	1		L.ECAD
2783	532.7208	1063.4271	1063.4240	2.90	0	(27)	0.0022	1		L.ECAD
3154	555.2856	1108.5567	1108.5665	-8.84	0	22	0.0062	1	U	L.SQRF
3712	589.2620	1176.5094	1176.5081	1.09	1	(33)	0.00047	1		L.LECA
3714	589.2626	1176.5106	1176.5081	2.13	1	35	0.00035	1		L.LECA
5703	697.3328	1392.6511	1392.6555	-3.15	0	(30)	0.0011	2	U	Y.ICEN
5704	697.3329	1392.6512	1392.6555	-3.05	0	(30)	0.0011	2	U	Y.ICEN
5706	697.3348	1392.6550	1392.6555	-0.33	0	(30)	0.0012	2	U	Y.ICEN
5707	697.3348	1392.6550	1392.6555	-0.33	0	(25)	0.0039	2	U	Y.ICEN
5708	697.3348	1392.6551	1392.6555	-0.25	0	(27)	0.0026	2	U	Y.ICEN
5709	697.3350	1392.6554	1392.6555	-0.07	0	(25)	0.0035	2	U	Y.ICEN
5710	697.3350	1392.6555	1392.6555	0.01	0	(37)	0.00027	2	U	Y.ICEN
5711	697.3351	1392.6556	1392.6555	0.10	0	(25)	0.0042	2	U	Y.ICEN
5712	697.3352	1392.6559	1392.6555	0.28	0	40	0.00012	2	U	Y.ICEN
5715	697.3353	1392.6561	1392.6555	0.46	0	(30)	0.0013	2	U	Y.ICEN
5716	697.3354	1392.6562	1392.6555	0.54	0	(27)	0.0026	2	U	Y.ICEN
5717	697.3354	1392.6562	1392.6555	0.54	0	(38)	0.00019	2	U	Y.ICEN
5718	697.3354	1392.6562	1392.6555	0.54	0	(29)	0.0016	2	U	Y.ICEN
5720	465.2260	1392.6563	1392.6555	0.59	0	(33)	0.00055	2	U	Y.ICEN
5721	697.3355	1392.6563	1392.6555	0.63	0	(23)	0.0057	2	U	Y.ICEN
5722	697.3355	1392.6563	1392.6555	0.63	0	(31)	0.001	2	U	Y.ICEN
5723	697.3355	1392.6563	1392.6555	0.63	0	(28)	0.0018	2	U	Y.ICEN
5724	697.3355	1392.6563	1392.6555	0.63	0	(21)	0.01	2	U	Y.ICEN
5725	697.3355	1392.6565	1392.6555	0.72	0	(32)	0.0007	2	U	Y.ICEN
5726	697.3356	1392.6566	1392.6555	0.80	0	(32)	0.00072	2	U	Y.ICEN
5727	697.3356	1392.6567	1392.6555	0.89	0	(24)	0.0053	2	U	Y.ICEN
5728	697.3356	1392.6567	1392.6555	0.89	0	(20)	0.012	2	U	Y.ICEN
5730	697.3357	1392.6568	1392.6555	0.97	0	(37)	0.00026	2	U	Y.ICEN
5731	697.3357	1392.6568	1392.6555	0.97	0	(32)	0.00074	2	U	Y.ICEN

5732	697.3357	1392.6569	1392.6555	1.06	0	(33)	0.00058	2	U	Y.ICEN
5733	465.2264	1392.6572	1392.6555	1.26	0	(26)	0.0029	2	U	Y.ICEN
5735	697.3361	1392.6576	1392.6555	1.51	0	(36)	0.00027	2	U	Y.ICEN
5737	697.3362	1392.6579	1392.6555	1.76	0	(28)	0.0019	2	U	Y.ICEN
5740	697.3364	1392.6583	1392.6555	2.04	0	(23)	0.0051	2	U	Y.ICEN
5741	697.3365	1392.6584	1392.6555	2.12	0	(32)	0.00064	2	U	Y.ICEN
5744	697.3368	1392.6590	1392.6555	2.55	0	(22)	0.0073	2	U	Y.ICEN
5745	697.3369	1392.6593	1392.6555	2.73	0	(32)	0.0006	2	U	Y.ICEN
5746	697.3370	1392.6594	1392.6555	2.83	0	(28)	0.0017	2	U	Y.ICEN
5747	697.3370	1392.6595	1392.6555	2.91	0	(30)	0.00095	2	U	Y.ICEN
5748	697.3371	1392.6596	1392.6555	3.00	0	(26)	0.0027	2	U	Y.ICEN
5749	697.3371	1392.6596	1392.6555	3.00	0	(22)	0.0061	2	U	Y.ICEN
5750	697.3372	1392.6598	1392.6555	3.08	0	(27)	0.0022	2	U	Y.ICEN
5751	697.3372	1392.6598	1392.6555	3.08	0	(21)	0.0086	2	U	Y.ICEN
5753	697.3375	1392.6604	1392.6555	3.52	0	(33)	0.00058	2	U	Y.ICEN
5754	697.3380	1392.6615	1392.6555	4.31	0	(25)	0.0032	2	U	Y.ICEN
5756	697.3383	1392.6620	1392.6555	4.66	0	(30)	0.00097	2	U	Y.ICEN
5767	697.8306	1393.6467	1393.6395	5.19	0	(33)	0.00076	3	U	Y.ICEN
6026	713.8177	1425.6208	1425.6194	0.99	1	38	0.00034	1		L.ECAD
6581	505.2538	1512.7396	1512.7395	0.07	2	29	0.0016	2	U	Y.LQQC

3. [1::sp|cRAP022|P00766|CTRA_BOVIN](#) Mass: 26220 Score: 113 Matches: 6(6) Sequen

Chymotrypsinogen A OS=Bos taurus PE=1 SV=1

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

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
570	412.7286	823.4427	823.4440	-1.56	1	37	0.00018	1	U	L.KLSTA
571	412.7290	823.4434	823.4440	-0.61	1	(36)	0.00024	1	U	L.KLSTA
2127	501.2543	1000.4940	1000.4938	0.23	0	(24)	0.0036	1	U	Y.TNANT
2128	501.2548	1000.4951	1000.4938	1.33	0	26	0.0028	1	U	Y.TNANT
2299	508.7846	1015.5547	1015.5550	-0.29	1	(34)	0.00045	1	U	L.TINND
2301	508.7848	1015.5551	1015.5550	0.12	1	50	1.1e-05	1	U	L.TINND

4. [1::sp|cRAP112|P00761|TRYP_PIG](#) Mass: 25078 Score: 94 Matches: 6(6) Sequen

Trypsin OS=Sus scrofa PE=1 SV=1

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

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
899	429.7369	857.4592	857.4607	-1.70	0	35	0.00031	1	U	W.IQQTI
900	429.7376	857.4607	857.4607	0.01	0	(21)	0.0084	1	U	W.IQQTI
2908	538.2629	1074.5113	1074.5094	1.77	1	23	0.0062	1	U	Y.QVSLN
4623	629.3330	1256.6515	1256.6513	0.12	1	35	0.00029	1	U	Y.VNWIQ
4624	629.3336	1256.6526	1256.6513	0.99	1	(29)	0.0012	1	U	Y.VNWIQ
4639	629.8279	1257.6412	1257.6353	4.67	1	(20)	0.0094	1	U	Y.VNWIQ

5. [1::sp|cRAP004|P04745|AMY1_HUMAN](#) Mass: 58415 Score: 48 Matches: 3(3) Sequen

Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1049	440.2263	878.4380	878.4246	15.2	0	(22)	0.007	1	U	F.GNGRVTEF
1053	440.2273	878.4400	878.4246	17.5	0	22	0.0067	1	U	F.GNGRVTEF
1601	477.2058	952.3970	952.3774	20.6	0	26	0.0025	1	U	Y.DNGSNQVA

6. [1::sp|cRAP015|P02666|CASB BOVIN](#) Mass: 25148 Score: 25 Matches: 5(5) Sequen
Beta-casein OS=Bos taurus GN=CSN2 PE=1 SV=2
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
842	426.7284	851.4422	851.4496	-8.77	1	(27)	0.0018	1	U	-.MKVLIL.A
846	426.7287	851.4428	851.4496	-8.04	1	(21)	0.0085	1	U	-.MKVLIL.A
848	426.7287	851.4429	851.4496	-7.90	1	(21)	0.0085	1	U	-.MKVLIL.A
850	426.7288	851.4430	851.4496	-7.83	1	(23)	0.0047	1	U	-.MKVLIL.A
852	426.7290	851.4434	851.4496	-7.26	1	28	0.0017	1	U	-.MKVLIL.A

7. [1::sp|cRAP091|Q10735|PEPB PIG](#) Mass: 7794 Score: 23 Matches: 1(1) Sequen
Pepsin B (Fragment) OS=Sus scrofa GN=PGB PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
144	387.7339	773.4533	773.4469	8.24	0	23	0.0047	1	U	-.MERIIL.R

8. [1::sp|cRAP046|O76013|KRT36 HUMAN](#) Mass: 53354 Score: 21 Matches: 1(1) Sequen
Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT36 PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4593	419.1909	1254.5509	1254.5728	-17.41	1	21	0.014	1	U	L.AETEA

Proteins matching the same set of peptides:

- [1::sp|cRAP045|Q92764|KRT35 HUMAN](#) Mass: 51640 Score: 17 Matches: 1(1) Sequen
Keratin, type I cuticular Ha5 OS=Homo sapiens GN=KRT35 PE=2 SV=5

9. [1::sp|cRAP056|P15241|K2M2 SHEEP](#) Mass: 55472 Score: 21 Matches: 1(1) Sequen
Keratin, type II microfibrillar, component 7C OS=Ovis aries PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
5195	662.3223	1322.6300	1322.6210	6.81	1	21	0.022	1	U	L.QKAKQD

Proteins matching the same set of peptides:

- [1::sp|cRAP072|P78386|KRT85 HUMAN](#) Mass: 57306 Score: 21 Matches: 1(1) Sequen

Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1

[1::sp|cRAP057|P25691|K2M3 SHEEP](#) Mass: 56418 Score: 18 Matches: 1(1) Sequ

Keratin, type II microfibrillar, component 5 OS=Ovis aries PE=1 SV=1

[1::sp|cRAP069|Q9NSB4|KRT82 HUMAN](#) Mass: 57985 Score: 18 Matches: 1(1) Sequ

Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3

10. [1::sp|cRAP003|P00883|ALDOA RABIT](#) Mass: 39774 Score: 19 Matches: 1(1) Sequ

Fructose-bisphosphate aldolase A OS=Oryctolagus cuniculus GN=ALDOA PE=1 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
7630	421.9577	1683.8018	1683.7773	14.5	1	21	0.016	1	U	W.GGKKE

11. [1::sp|cRAP020|P01031|CO5 HUMAN](#) Mass: 189897 Score: 18 Matches: 1(1) Sequ

Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
771	424.2264	846.4383	846.4521	-16.22	0	21	0.0087	1	U	L.IEKQKL

12. [1::sp|cRAP071|Q9NSB2|KRT84 HUMAN](#) Mass: 65942 Score: 18 Matches: 1(1) Sequ

Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=2 SV=2

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
9290	544.5241	2174.0673	2174.1114	-20.26	2	20	0.023	1	U	L.GGARV

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Chymotrypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Deamidated \(NQ\)](#), [DTSSP Cross link \(K\)](#), [DTSSP Cross link di oxidation \(K\)](#), [DTSSP Cross link single oxidation \(K\)](#), [DTSSP Cross link tri oxidation \(K\)](#), [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Fragment Mass Tolerance: ± 0.8 Da
Max Missed Cleavages : 2
Instrument type : ESI-TRAP
Number of queries : 10609

Mascot: <http://www.matrixscience.com/>