

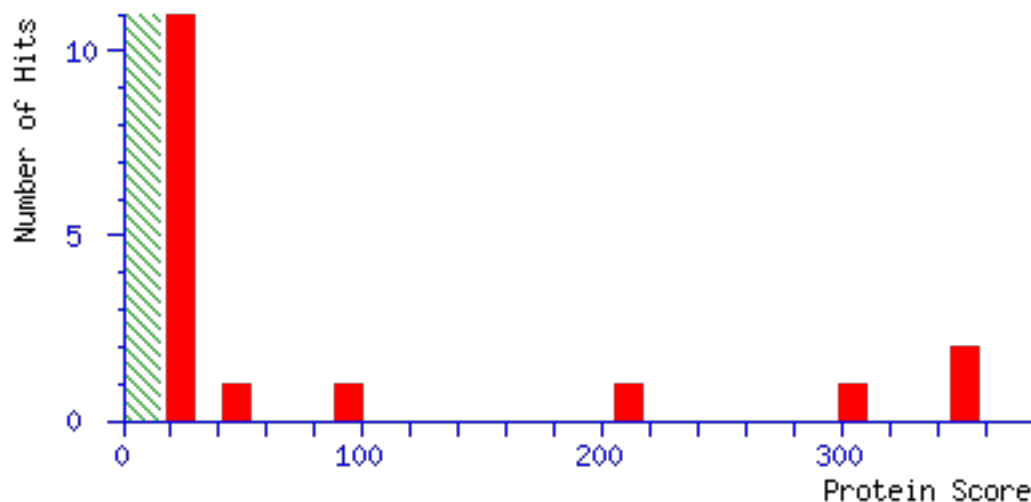
Cambridge Centre for Proteomics Mascot Search Results

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_4.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 09:58:48 GMT

Protein hits : [3::sp|P02930|TOLC ECOLI](#) Outer membrane protein TolC OS=Escheric
[1::sp|cRAP087|P02769|ALBU BOVIN](#) Serum albumin OS=Bos taurus GN=ALB PE=1
[1::sp|cRAP022|P00766|CTRA BOVIN](#) Chymotrypsinogen A OS=Bos taurus PE=1 S
[1::sp|P0AEX9|MALE ECOLI](#) Maltose/maltodextrin-binding periplasmi
[1::sp|cRAP008|P00722|BGAL ECOLI](#) Beta-galactosidase OS=Escherichia coli
[1::sp|cRAP109|P02788|TRFL HUMAN](#) Lactotransferrin OS=Homo sapiens GN=LTF
[1::sp|cRAP108|P02787|TRFE HUMAN](#) Serotransferrin OS=Homo sapiens GN=TF P
[1::sp|cRAP051|P02534|K1M1 SHEEP](#) Keratin, type I microfibrillar 48 kDa,
[1::sp|cRAP081|P68082|MYG HORSE](#) Myoglobin OS=Equus caballus GN=MB PE=1
[1::sp|cRAP112|P00761|TRYP PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1
[1::sp|cRAP117|000000|rLys-C](#)
[1::sp|cRAP033|P08263|GSTA1 HUMAN](#) Glutathione S-transferase A1 OS=Homo sa
[1::sp|cRAP090|P00791|PEPA PIG](#) Pepsin A OS=Sus scrofa GN=PGA PE=1 SV=3
[1::sp|cRAP052|P25690|K1M2 SHEEP](#) Keratin, type I microfibrillar, 47.6 kD
[1::sp|cRAP044|O76011|KRT34 HUMAN](#) Keratin, type I cuticular Ha4 OS=Homo s
[1::sp|cRAP053|P35908|K22E HUMAN](#) Keratin, type II cytoskeletal 2 epiderm
[1::sp|cRAP021|P02741|CRP HUMAN](#) C-reactive protein OS=Homo sapiens GN=C

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 (mammals) ... fishes) ... Takifugu rubripes (Japanese Pufferfish) ... Danio rerio (zebra fish) ... Schizosaccharomyces pombe (fission yeast) ... Pneumocystis carinii ... Other Fungi ... Viridiplantae (green plants) ... Mycobacterium tuberculosis complex ... Other Actinobacteria (class) ... Firmicutes (gram-positive bacteria) ... Agrobacterium tumefaciens ... Campylobacter jejuni ... Escherichia coli ... Neisseria meningitidis ... Species information unavailable				

Error tolerant

- [3::sp|P02930|TOLC ECOLI](#) **Mass:** 53708 **Score:** 351 **Matches:** 19(19) **Sequences:** Outer membrane protein TolC OS=Escherichia coli (strain K12) OX=83333 GN=tolC PE=1 S...
 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
206	388.7127	775.4108	775.4116	-0.99	1	20	0.0097	1	U	Y.YPELA
1096	426.2219	850.4292	850.4297	-0.63	0	(27)	0.002	1	U	L.RQITG
1097	426.2219	850.4293	850.4297	-0.49	0	29	0.0013	1	U	L.RQITG
2468	482.7402	963.4658	963.4662	-0.38	1	(33)	0.00055	1	U	Y.NFVGA
2469	482.7403	963.4660	963.4662	-0.20	1	43	5.8e-05	1	U	Y.NFVGA
2954	501.7582	1001.5018	1001.5029	-1.12	2	(20)	0.0097	1	U	L.GTLNE
2955	501.7591	1001.5036	1001.5029	0.70	2	29	0.0012	1	U	L.GTLNE

7214	665.8032	1329.5919	1329.5936	-1.30	1	41	7.9e-05	1	U	L.DLTAS
7215	665.8049	1329.5953	1329.5936	1.27	1	(34)	0.00047	1	U	L.DLTAS
8552	745.8632	1489.7119	1489.7121	-0.12	0	89	1.6e-09	1	U	Y.RDANG
8553	745.8643	1489.7140	1489.7121	1.28	0	(60)	1.2e-06	1	U	Y.RDANG
8556	746.3559	1490.6972	1490.6961	0.79	0	(62)	1.3e-06	1	U	Y.RDANG
8557	746.3564	1490.6982	1490.6961	1.43	0	(71)	1.6e-07	1	U	Y.RDANG
9396	804.9225	1607.8304	1607.8307	-0.18	2	(34)	0.00049	1	U	L.RQITG
9397	804.9243	1607.8340	1607.8307	2.02	2	43	5.1e-05	1	U	L.RQITG
9404	805.4158	1608.8171	1608.8147	1.48	2	(27)	0.0025	1	U	L.RQITG
9405	805.4180	1608.8214	1608.8147	4.14	2	(27)	0.0023	1	U	L.RQITG
10802	936.4578	1870.9011	1870.9020	-0.51	1	62	1.7e-06	1	U	L.ANEVT
10803	936.4586	1870.9026	1870.9020	0.28	1	(62)	1.8e-06	1	U	L.ANEVT

2. [1::sp|cRAP087|P02769|ALBU_BOVIN](#) Mass: 71244 Score: 344 Matches: 19(19) Seq
 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
346	396.6899	791.3653	791.3636	2.16	1	21	0.0083	1		Y.LQQCP
1087	426.2109	850.4073	850.4072	0.10	1	(28)	0.002	1	U	L.VNELT
1089	426.2110	850.4075	850.4072	0.31	1	40	0.00012	1	U	L.VNELT
1241	434.7146	867.4146	867.4160	-1.66	0	31	0.00074	1	U	L.KTVME
1242	434.7151	867.4157	867.4160	-0.40	0	(22)	0.0068	1	U	L.KTVME
2615	487.7327	973.4508	973.4505	0.36	1	(34)	0.00044	1	U	F.KDLGE
2616	487.7330	973.4515	973.4505	1.04	1	(27)	0.0019	1	U	F.KDLGE
2617	487.7333	973.4520	973.4505	1.55	1	37	0.00019	1	U	F.KDLGE
3807	532.7198	1063.4250	1063.4240	0.94	0	20	0.0097	1		L.ECADD
5427	590.8274	1179.6402	1179.6400	0.17	2	(40)	0.0001	1	U	Y.GFQNA
5428	590.8283	1179.6421	1179.6400	1.73	2	46	2.3e-05	1	U	Y.GFQNA
6212	414.5204	1240.5393	1240.5394	-0.11	0	(27)	0.002	1	U	F.AEDKD
6213	414.5204	1240.5393	1240.5394	-0.03	0	(26)	0.003	1	U	F.AEDKD
6214	621.2781	1240.5417	1240.5394	1.89	0	36	0.00023	1	U	F.AEDKD
6215	621.2794	1240.5442	1240.5394	3.86	0	(33)	0.00049	1	U	F.AEDKD
7747	697.3353	1392.6561	1392.6555	0.45	0	(78)	2.1e-08	1	U	Y.ICDNQ
7748	697.3373	1392.6600	1392.6555	3.25	0	78	1.7e-08	1	U	Y.ICDNQ
9879	563.5621	1687.6644	1687.6640	0.21	0	(33)	0.00047	1	U	F.VDKCC
9880	844.8431	1687.6716	1687.6640	4.49	0	34	0.00042	1	U	F.VDKCC

3. [1::sp|cRAP022|P00766|CTRA_BOVIN](#) Mass: 26220 Score: 305 Matches: 21(21) Seq
 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
732	412.7300	823.4455	823.4440	1.91	1	46	2.3e-05	1	U	L.KLSTA
2944	501.2537	1000.4928	1000.4938	-0.93	0	(25)	0.0029	1	U	Y.TNANT
2945	501.2558	1000.4970	1000.4938	3.29	0	(20)	0.0095	1	U	Y.TNANT
2950	501.7446	1001.4746	1001.4778	-3.18	0	(27)	0.0018	1	U	Y.TNANT
2951	501.7450	1001.4754	1001.4778	-2.32	0	36	0.00026	1	U	Y.TNANT
3172	508.7849	1015.5553	1015.5550	0.30	1	53	5.2e-06	1	U	L.TINND
3174	508.7855	1015.5564	1015.5550	1.44	1	(52)	6.3e-06	1	U	L.TINND

4582	561.7940	1121.5735	1121.5717	1.58	1	52	6.7e-06	1	U	W.QVSLQ
4583	561.7941	1121.5737	1121.5717	1.79	1	(40)	9.5e-05	1	U	W.QVSLQ
4600	562.2850	1122.5554	1122.5557	-0.29	1	(50)	1e-05	1	U	W.QVSLQ
7111	440.5649	1318.6730	1318.6728	0.12	0	(20)	0.0095	1	U	F.DQGSS
7112	440.5650	1318.6732	1318.6728	0.25	0	(23)	0.0054	1	U	F.DQGSS
7114	660.3449	1318.6753	1318.6728	1.84	0	(41)	7.2e-05	1	U	F.DQGSS
7116	660.3459	1318.6772	1318.6728	3.33	0	42	6.1e-05	1	U	F.DQGSS
10177	869.9571	1737.8997	1737.9009	-0.69	1	(29)	0.0013	1	U	Y.TNANT
10178	869.9603	1737.9061	1737.9009	2.97	1	(40)	9.7e-05	1	U	Y.TNANT
10180	870.4512	1738.8878	1738.8849	1.63	1	42	0.00011	1	U	Y.TNANT
10181	870.4521	1738.8897	1738.8849	2.76	1	(24)	0.0056	1	U	Y.TNANT
10182	870.4526	1738.8907	1738.8849	3.32	1	(23)	0.0086	1	U	Y.TNANT
10355	892.4410	1782.8674	1782.8689	-0.85	0	34	0.00097	1	U	L.SRIVN
10356	892.4437	1782.8728	1782.8689	2.15	0	(22)	0.014	1	U	L.SRIVN

4. [1::sp|P0AEX9|MALE_ECOLI](#) Mass: 43360 Score: 212 Matches: 11(11) Sequences:
Maltose/maltodextrin-binding periplasmic protein OS=Escherichia coli (strain K12) OX
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
48	382.1852	762.3559	762.3548	1.40	1	(23)	0.0052	1	U	F.NLQEP
50	382.1854	762.3563	762.3548	1.96	1	26	0.0027	1	U	F.NLQEP
854	417.2421	832.4696	832.4695	0.20	0	34	0.00044	1	U	Y.GVTVL
2814	496.2583	990.5021	990.5022	-0.09	0	(21)	0.0073	1	U	L.AEITP
2815	496.2589	990.5032	990.5022	1.02	0	23	0.0048	1	U	L.AEITP
3731	530.3079	1058.6012	1058.6012	0.00	0	(35)	0.0003	1	U	L.IAYPI
3732	530.3082	1058.6018	1058.6012	0.59	0	47	2.2e-05	1	U	L.IAYPI
4378	552.8002	1103.5858	1103.5863	-0.43	1	35	0.0003	1	U	L.LAEIT
4381	552.8017	1103.5888	1103.5863	2.35	1	(32)	0.00065	1	U	L.LAEIT
5052	578.8080	1155.6015	1155.6023	-0.65	1	32	0.00063	1	U	W.EEIPA
8645	500.5914	1498.7525	1498.7346	11.9	2	21	0.0093	1	U	L.KAKGK

5. [1::sp|cRAP008|P00722|BGAL_ECOLI](#) Mass: 117321 Score: 98 Matches: 3(3) Sequences:
Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ 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
4756	568.2723	1134.5300	1134.5305	-0.48	0	35	0.00033	1	U	Y.GQDSR
8382	736.3793	1470.7441	1470.7467	-1.74	2	63	5e-07	1	U	W.LGLGP
8383	736.3817	1470.7487	1470.7467	1.41	2	(50)	9.5e-06	1	U	W.LGLGP

6. [1::sp|cRAP109|P02788|TRFL_HUMAN](#) Mass: 80014 Score: 40 Matches: 2(2) Sequences:
Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6
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
1658	453.2406	904.4666	904.4728	-6.81	2	21	0.0077	1	U	W.NIPMGL
2955	501.7591	1001.5036	1001.5029	0.70	1	21	0.0077	2	U	F.GSPSQ

7. [1::sp|cRAP108|P02787|TRFE HUMAN](#) **Mass:** 79294 **Score:** 30 **Matches:** 1(1) **Seque**
 Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3
 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
3367	515.7284	1029.4422	1029.4477	-5.32	1	33	0.00082	1	U	L.EKAVA

8. [1::sp|cRAP051|P02534|K1M1 SHEEP](#) **Mass:** 48070 **Score:** 26 **Matches:** 1(1) **Seque**
 Keratin, type I microfibrillar 48 kDa, component 8C-1 OS=Ovis aries 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
171	387.2204	772.4262	772.4079	23.7	0	29	0.0014	1	U	L.AEIRGDL.

9. [1::sp|cRAP081|P68082|MYG HORSE](#) **Mass:** 17072 **Score:** 25 **Matches:** 2(2) **Sequen**
 Myoglobin OS=Equus caballus GN=MB 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
7734	696.8355	1391.6565	1391.6602	-2.69	1	25	0.0033	1	U	F.GADAQQ
7735	696.8356	1391.6566	1391.6602	-2.61	1	(23)	0.0061	1	U	F.GADAQQ

10. [1::sp|cRAP112|P00761|TRYP PIG](#) **Mass:** 25078 **Score:** 25 **Matches:** 2(2) **Sequenc**
 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
6405	629.3331	1256.6516	1256.6513	0.21	1	25	0.0029	1	U	Y.VNWIQQ
6406	629.3343	1256.6541	1256.6513	2.25	1	(21)	0.0079	1	U	Y.VNWIQQ

11. [1::sp|cRAP117|000000|rLys-C](#) **Mass:** 28023 **Score:** 24 **Matches:** 1(1) **Sequences**
 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
4666	565.2777	1128.5409	1128.5523	-10.14	0	24	0.0035	1	U	L.NNGNS

12. [1::sp|cRAP033|P08263|GSTA1 HUMAN](#) **Mass:** 25672 **Score:** 23 **Matches:** 2(2) **Sequ**
 Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3
 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
10880	943.4330	1884.8515	1884.8494	1.13	1	28	0.0071	1	U	L.MFQQVP
10883	943.4371	1884.8597	1884.8494	5.47	1	(20)	0.039	1	U	L.MFQQVP

13. [1::sp|cRAP090|P00791|PEPA_PIG](#) Mass: 41635 Score: 21 Matches: 1(1) Sequen
 Pepsin A OS=Sus scrofa GN=PGA PE=1 SV=3
 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
5971	611.2783	1220.5420	1220.5231	15.5	0	21	0.0096	1	U	F.EGMDVP

14. [1::sp|cRAP052|P25690|K1M2_SHEEP](#) Mass: 47345 Score: 21 Matches: 1(1) Sequen
 Keratin, type I microfibrillar, 47.6 kDa OS=Ovis aries PE=3 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
5699	599.8569	1197.6993	1197.6829	13.7	2	21	0.0073	1	U	L.NGLRRI

15. [1::sp|cRAP044|O76011|KRT34_HUMAN](#) Mass: 50818 Score: 21 Matches: 2(2) Sequen
 Keratin, type I cuticular Ha4 OS=Homo sapiens GN=KRT34 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
2734	493.2877	984.5608	984.5604	0.40	0	21	0.0083	1	U	L.VVNIDNAK
2735	493.2879	984.5613	984.5604	0.94	0	(20)	0.0091	1	U	L.VVNIDNAK

16. [1::sp|cRAP053|P35908|K22E_HUMAN](#) Mass: 65678 Score: 20 Matches: 1(1) Sequen
 Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 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
327	395.2396	788.4646	788.4466	22.8	1	20	0.009	1	U	L.MNVKLAL.

17. [1::sp|cRAP021|P02741|CRP_HUMAN](#) Mass: 25194 Score: 20 Matches: 1(1) Sequen
 C-reactive protein OS=Homo sapiens GN=CRP 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
10289	589.3019	1764.8838	1764.8418	23.8	1	20	0.012	1	U	Y.TVGAEA

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 : 12081

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