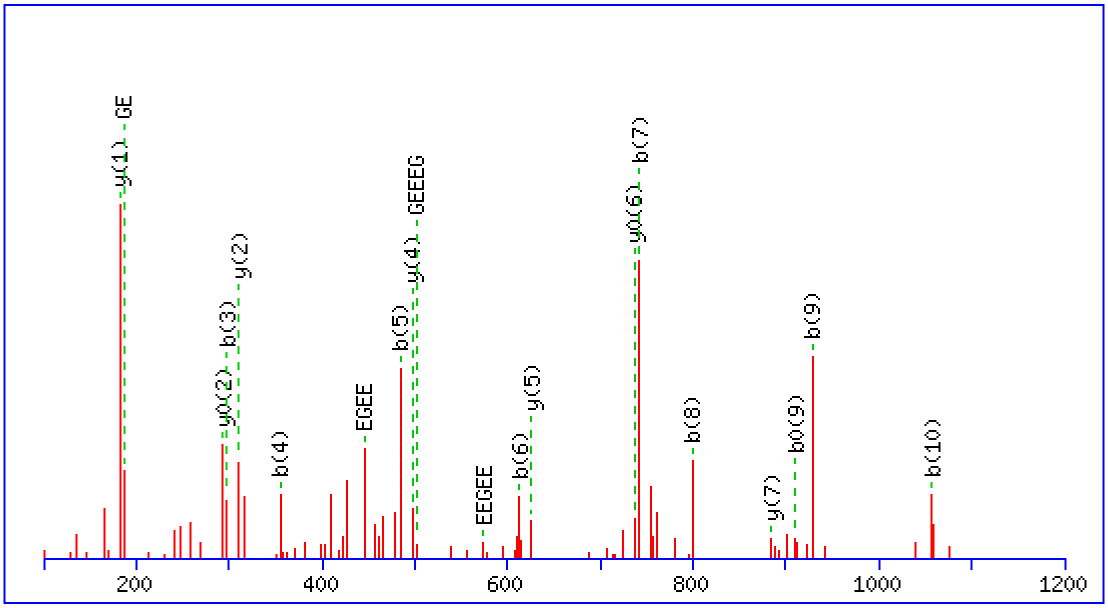
Figure S1 (Fig 4A Synthetic)

MS/MS Fragmentation of **EGEGEEEGEEY**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1
Match to Query 1231: 1237.393368 from(619.703960,2+)

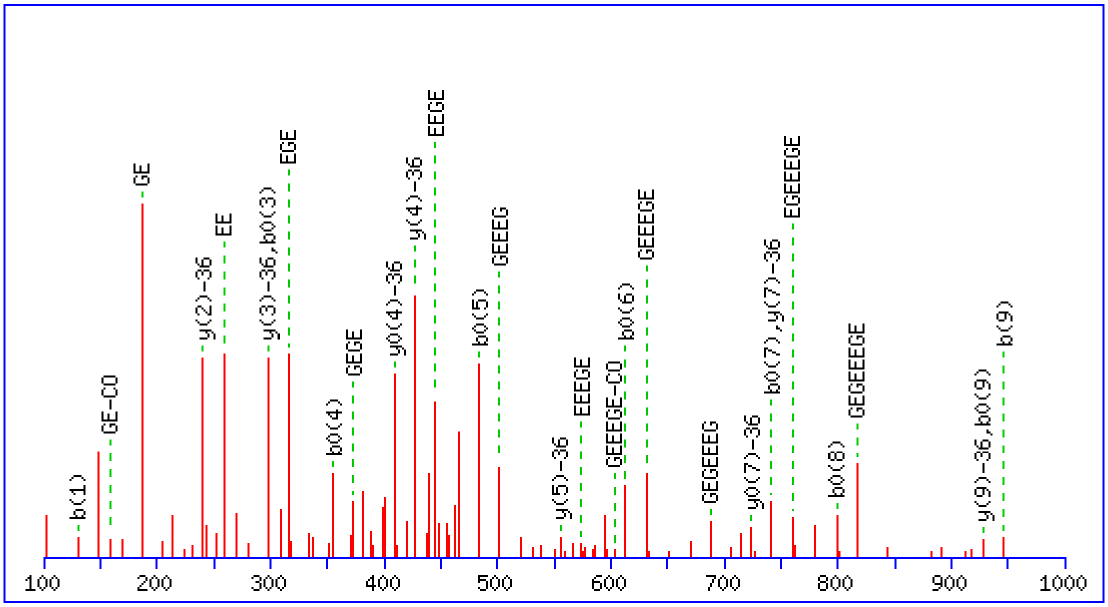


Monoisotopic mass of neutral peptide Mr(calc): 1237.4258
Variable modifications:
E441 : -H2O (E)
Ions Score: 79 **Expect:** 2.7e-008
Matches (Bold Red): 31/111 fragment ions using 27 most intense peaks

#	b	b^0	Seq.	y	y^0	#
1	112.0393	94.0287	E			11
2	169.0608	151.0502	G	1127.4011	1109.3906	10
3	**298.1034**	280.0928	E	1070.3797	1052.3691	9
4	**355.1248**	337.1143	G	941.3371	923.3265	8
5	**484.1674**	466.1569	E	**884.3156**	866.3050	7
6	**613.2100**	595.1995	E	755.2730	**737.2624**	6
7	**742.2526**	724.2420	E	**626.2304**	608.2198	5
8	**799.2741**	781.2635	G	**497.1878**	479.1773	4
9	**928.3167**	**910.3061**	E	440.1664	422.1558	3
10	**1057.3593**	1039.3487	E	**311.1238**	**293.1132**	2
11			Y	**182.0812**		1

Figure S2 (Fig 4B Synthetic)

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1
Match to Query 373: 1092.347928 from(547.181240,2+)

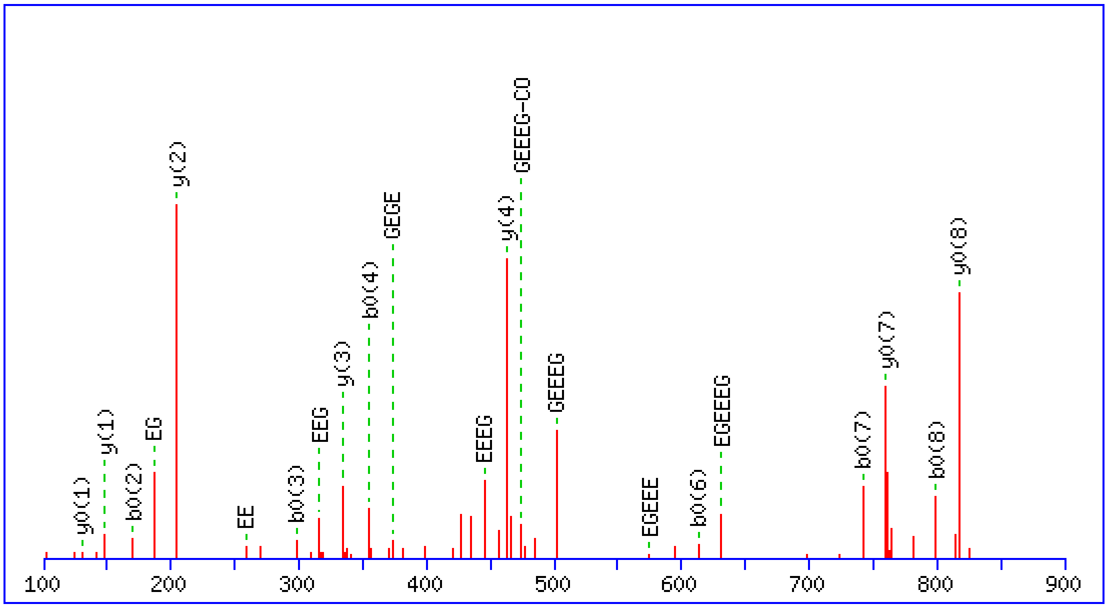


Monoisotopic mass of neutral peptide Mr(calc): 1092.3857
Variable modifications:
neutral loss 36.0211
Ions Score: 69 **Expect:** 1.6e-006
Matches (Bold Red): 58/92 fragment ions using 43 most intense peaks

#	b	b^0	Seq.	y	y^0	#
1	**130.0499**	112.0393	**E**			**10**
2	**187.0713**	169.0608	**G**	**928.3292**	910.3187	**9**
3	**316.1139**	**298.1034**	**E**	871.3078	853.2972	**8**
4	**373.1354**	**355.1248**	**G**	**742.2652**	**724.2546**	**7**
5	**502.1780**	**484.1674**	**E**	685.2437	667.2331	**6**
6	**631.2206**	**613.2100**	**E**	**556.2011**	538.1906	**5**
7	**760.2632**	**742.2526**	**E**	**427.1585**	**409.1480**	**4**
8	**817.2846**	**799.2741**	**G**	**298.1159**	280.1054	**3**
9	**946.3272**	**928.3167**	**E**	**241.0945**	223.0839	**2**
10			**E**	112.0519	94.0413	**1**

Figure S3 (Fig 4C Synthetic)

MS/MS Fragmentation of **EGEGEEEGE**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1
Match to Query 435: 963.294228 from(482.654390,2+)



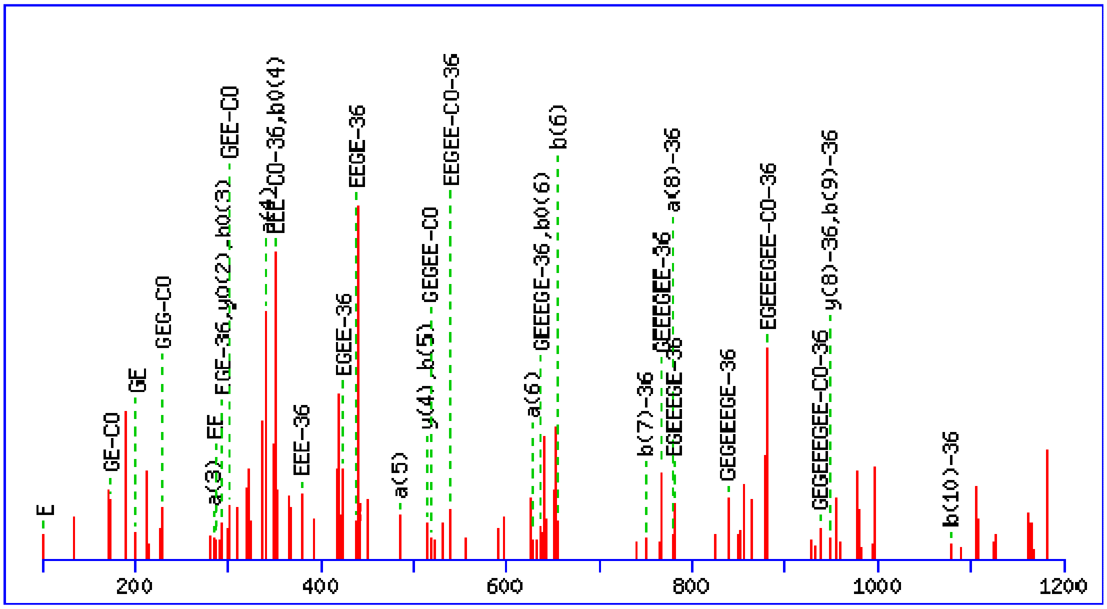
Monoisotopic mass of neutral peptide Mr(calc): 963.3305
Ions Score: 61 **Expect:** 6.2e-006
Matches (Bold Red): 46/74 fragment ions using 44 most intense peaks

#	b	b^0	Seq.	y	y^0	#
1	**130.0499**	112.0393	E			9
2	**187.0713**	**169.0608**	G	835.2952	**817.2846**	8
3	**316.1139**	**298.1034**	E	778.2737	**760.2632**	7
4	**373.1354**	**355.1248**	G	649.2311	**631.2206**	6
5	**502.1780**	484.1674	E	592.2097	**574.1991**	5
6	**631.2206**	**613.2100**	E	**463.1671**	**445.1565**	4
7	**760.2632**	**742.2526**	E	**334.1245**	**316.1139**	3
8	**817.2846**	**799.2741**	G	**205.0819**	**187.0713**	2
9			E	**148.0604**	**130.0499**	1

Figure S4

MS/MS Fragmentation of **EGEGEEEGEEY**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1

Match to Query 2293: 1293.618448 from(647.816500,2+)



Monoisotopic mass of neutral peptide Mr(calc): 1293.5010
Variable modifications:
E441 : -H2O (E)
E443 : Methyl (DE)
E445 : Methyl (DE)
E446 : Methyl (DE)
E449 : Methyl (DE)
Ions Score: 14 **Expect:** 0.017
Matches (Bold Red): 47/142 fragment ions using 92 most intense peaks

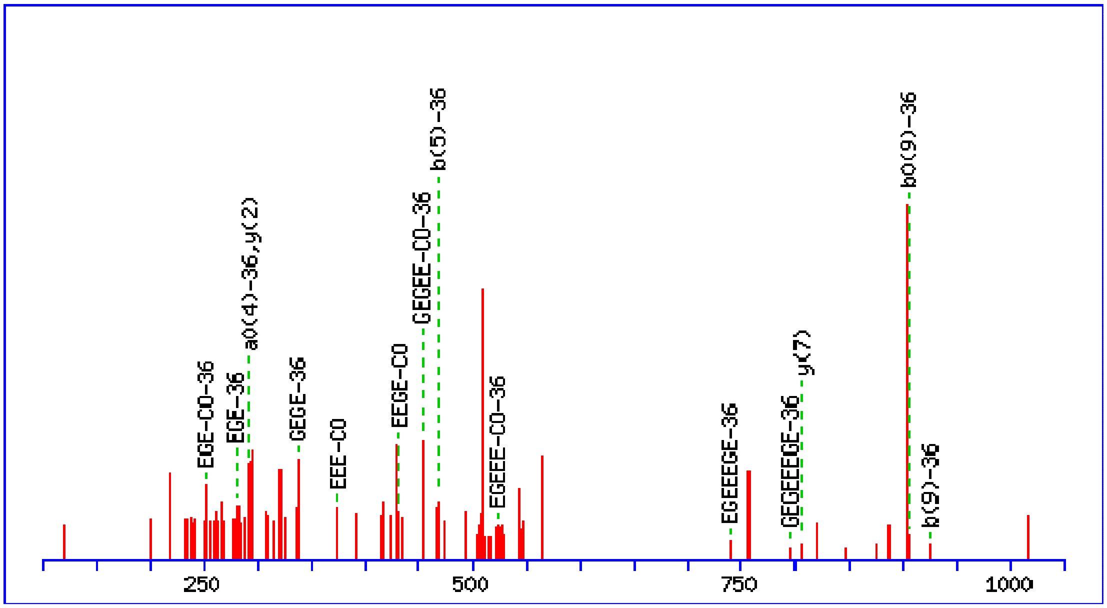
#	Immon.	a	a^0	b	b^0	Seq.	y	y^0	#
1	**102.0550**	84.0444	66.0338	112.0393	94.0287	E			11
2	30.0338	141.0659	123.0553	169.0608	151.0502	G	1147.4552	1129.4446	10
3	116.0706	**284.1241**	266.1135	312.1190	**294.1085**	E	1090.4337	1072.4232	9
4	30.0338	**341.1456**	323.1350	369.1405	**351.1299**	G	**947.3755**	929.3649	8
5	116.0706	**484.2038**	466.1933	**512.1987**	494.1882	E	890.3540	872.3434	7
6	116.0706	**627.2621**	609.2515	**655.2570**	**637.2464**	E	747.2958	729.2852	6
7	66.0464	720.2961	702.2855	**748.2910**	730.2805	E	604.2375	586.2269	5
8	30.0338	**777.3176**	759.3070	805.3125	787.3019	G	**511.2035**	493.1929	4
9	116.0706	920.3758	902.3653	**948.3707**	930.3602	E	454.1820	436.1714	3
10	**102.0550**	1049.4184	1031.4078	**1077.4133**	1059.4028	E	311.1238	**293.1132**	2

11	136.0757					**Y**	182.0812		**1**

Figure S5

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1

Match to Query 2186: 1120.573428 from(561.286714,2+)



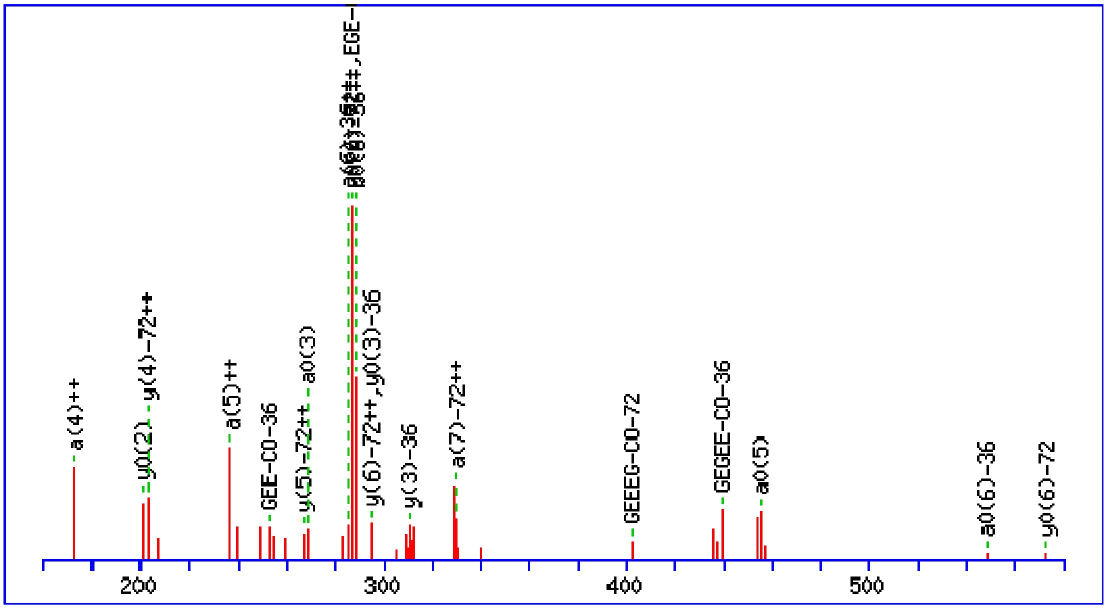
Monoisotopic mass of neutral peptide Mr(calc): 1120.4169
Variable modifications:
E446 : Methyl (DE)
C-term : Methyl (C-term)
Ions Score: 15 **Expect:** 0.049
Matches (Bold Red): 22/120 fragment ions using 45 most intense peaks

#	Immon.	a	a^0	b	b^0	Seq.	y	y^0	#
1	102.0550	102.0550	84.0444	130.0499	112.0393	**E**			**10**
2	30.0338	159.0764	141.0659	187.0713	169.0608	**G**	956.3605	938.3500	**9**
3	66.0464	**252.1105**	234.0999	**280.1054**	262.0948	**E**	899.3391	881.3285	**8**
4	30.0338	309.1319	**291.1214**	**337.1268**	319.1163	**G**	**806.3050**	788.2945	**7**
5	102.0550	438.1745	420.1639	**466.1694**	448.1589	**E**	749.2836	731.2730	**6**
6	116.0706	581.2328	563.2222	609.2277	591.2171	**E**	620.2410	602.2304	**5**
7	102.0550	710.2754	692.2648	**738.2703**	720.2597	**E**	477.1827	459.1722	**4**
8	30.0338	767.2968	749.2863	**795.2917**	777.2812	**G**	348.1401	330.1296	**3**
9	102.0550	896.3394	878.3288	**924.3343**	**906.3238**	**E**	**291.1187**	273.1081	**2**
10	102.0550					**E**	162.0761	144.0655	**1**

Figure S6

MS/MS Fragmentation of **EGEGEEEGE**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1

Match to Query 303: 977.471552 from(326.823851,3+)



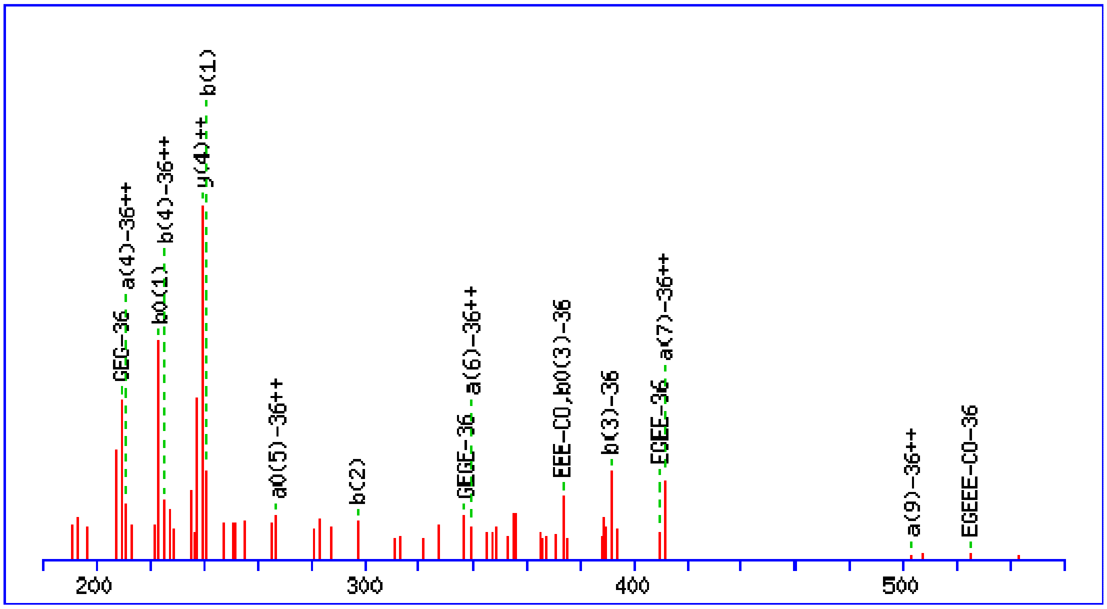
Monoisotopic mass of neutral peptide Mr(calc): 977.3713
Variable modifications:
C-term : Methyl (C-term)
Ions Score: 20 **Expect:** 0.0067
Matches (Bold Red): 22/147 fragment ions using 27 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	102.055	130.05	65.5286	**112.039**	56.5233	E					9
2	30.0338	187.071	94.0393	**169.061**	85.034	G	777.294	389.151	759.283	380.145	8
3	102.055	316.114	158.561	**298.103**	149.555	E	720.272	360.64	702.262	351.635	7
4	30.0338	373.135	**187.071**	**355.125**	**178.066**	G	591.23	**296.119**	**573.219**	**287.113**	6
5	102.055	502.178	251.593	484.167	242.587	E	534.208	**267.608**	516.198	258.603	5
6	66.0464	595.212	**298.11**	577.202	**289.104**	E	405.166	**203.086**	387.155	**194.081**	4
7	66.0464	688.246	344.627	670.236	335.621	E	**312.132**	156.569	**294.121**	147.564	3
8	30.0338	745.268	373.137	727.257	364.132	G	219.098	**110.052**	**201.087**	**101.047**	2
9	102.055					E	**162.076**	81.5417	144.066	72.5364	1

Figure S7

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1

Match to Query 700: 1217.464112 from(406.821371,3+)

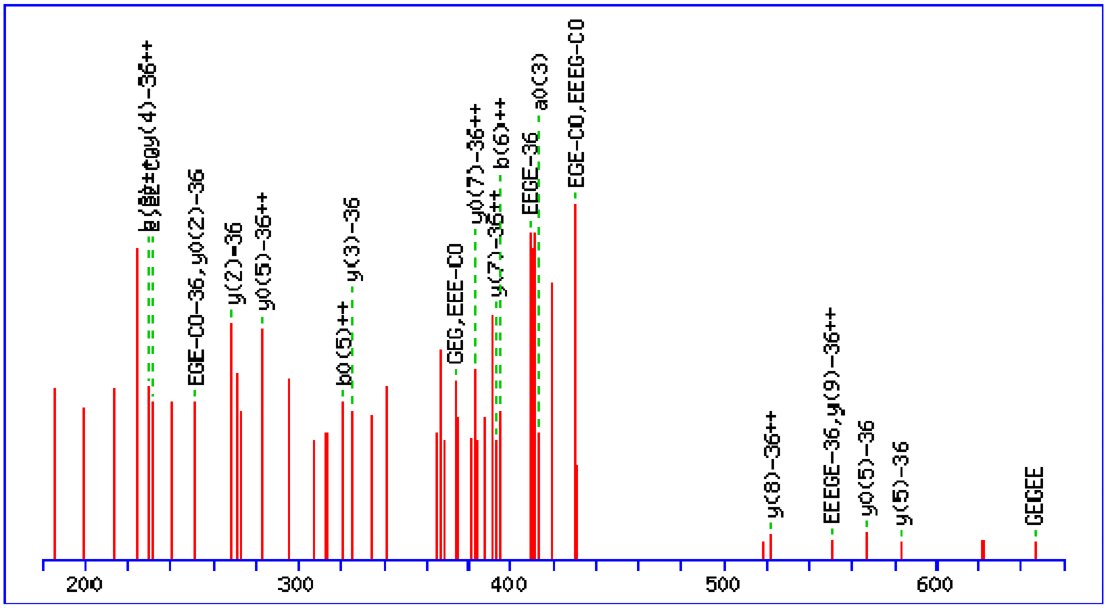


Monoisotopic mass of neutral peptide Mr(calc): 1217.4333
Variable modifications:
E441 : +E-H2O (E)
E447 : Methyl (DE)
Ions Score: 27 **Expect:** 0.005
Matches (Bold Red): 17/174 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^0	y^{0++}	#
1	231.0975	**241.0819**	**121.0446**	**223.0713**	**112.0393**	E					10
2	30.0338	**298.1034**	149.5553	280.0928	140.5500	G	942.3449	471.6761	924.3343	462.6708	9
3	66.0464	**391.1374**	**196.0723**	**373.1268**	**187.0671**	E	885.3234	443.1654	867.3129	434.1601	8
4	30.0338	448.1589	**224.5831**	**430.1483**	215.5778	G	792.2894	396.6483	774.2788	387.6431	7
5	102.055	577.2015	**289.1044**	559.1909	280.0991	E	735.2679	**368.1376**	717.2574	**359.1323**	6
6	102.055	706.2440	353.6257	688.2335	**344.6204**	E	606.2253	303.6163	588.2148	294.6110	5
7	116.0706	849.3023	**425.1548**	831.2917	416.1495	E	477.1827	**239.0950**	459.1722	**230.0897**	4
8	30.0338	906.3238	453.6655	888.3132	444.6602	G	334.1245	167.5659	**316.1139**	158.5606	3
9	102.055	1035.366	518.1868	1017.356	509.1815	E	277.1030	**139.0552**	**259.0925**	**130.0499**	2
10	102.055					E	148.0604	74.5339	**130.0499**	65.5286	1

Figure S8

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1
Match to Query 828: 1277.547002 from(426.849001,3+)

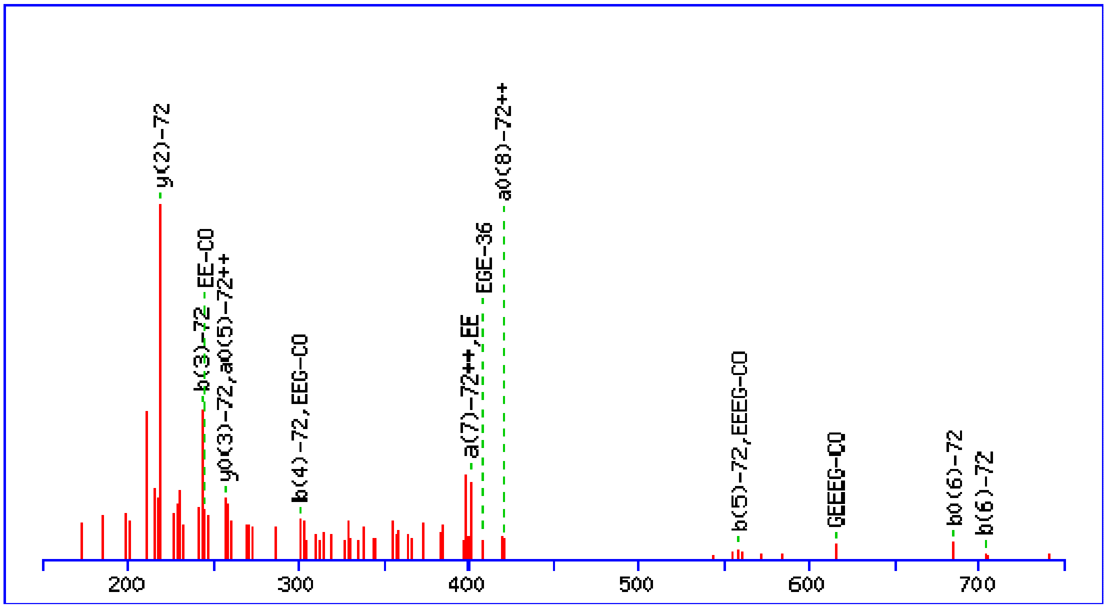


Monoisotopic mass of neutral peptide Mr(calc): 1277.4908
Variable modifications:
E441 : Methyl (DE)
E443 : +E (E)
E445 : Methyl (DE)
E450 : Methyl (DE)
C-term : Methyl (C-term)
Ions Score: 20 **Expect:** 0.008
Matches (Bold Red): 27/174 fragment ions using 38 most intense peaks

#	Immon.	b	b++	b0	b0++	Seq.	y	y++	y0	y0++	#
1	116.0706	144.0655	72.5364	126.055	63.5311	**E**					**10**
2	30.0338	**201.087**	101.0471	**183.0764**	92.0419	**G**	1099.4188	**550.213**	1081.4082	541.2077	**9**
3	**231.0975**	459.1722	**230.0897**	**441.1616**	**221.0844**	**E**	1042.3973	**521.7023**	1024.3867	512.697	**8**
4	30.0338	516.1936	258.6005	498.1831	249.5952	**G**	784.3121	**392.6597**	766.3016	**383.6544**	**7**
5	116.0706	659.2519	**330.1296**	641.2413	**321.1243**	**E**	727.2907	**364.149**	709.2801	**355.1437**	**6**
6	102.055	788.2945	**394.6509**	770.2839	385.6456	**E**	**584.2324**	292.6198	**566.2219**	**283.6146**	**5**
7	102.055	917.3371	**459.1722**	899.3265	450.1669	**E**	**455.1898**	**228.0985**	437.1793	**219.0933**	**4**
8	30.0338	974.3585	487.6829	956.348	478.6776	**G**	**326.1472**	163.5773	**308.1367**	154.572	**3**
9	66.0464	1067.3926	534.1999	1049.382	525.1946	**E**	**269.1258**	135.0665	**251.1152**	126.0612	**2**
10	116.0706					**E**	176.0917	88.5495	158.0812	79.5442	**1**

Figure S9

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1
Match to Query 748: 1249.372222 from(417.457407,3+)



Monoisotopic mass of neutral peptide Mr(calc): 1249.4973

Variable modifications:

E445 : +E (E)

E446 : Methyl (DE)

C-term : Methyl (C-term)

Ions Score: 24 **Expect:** 0.013

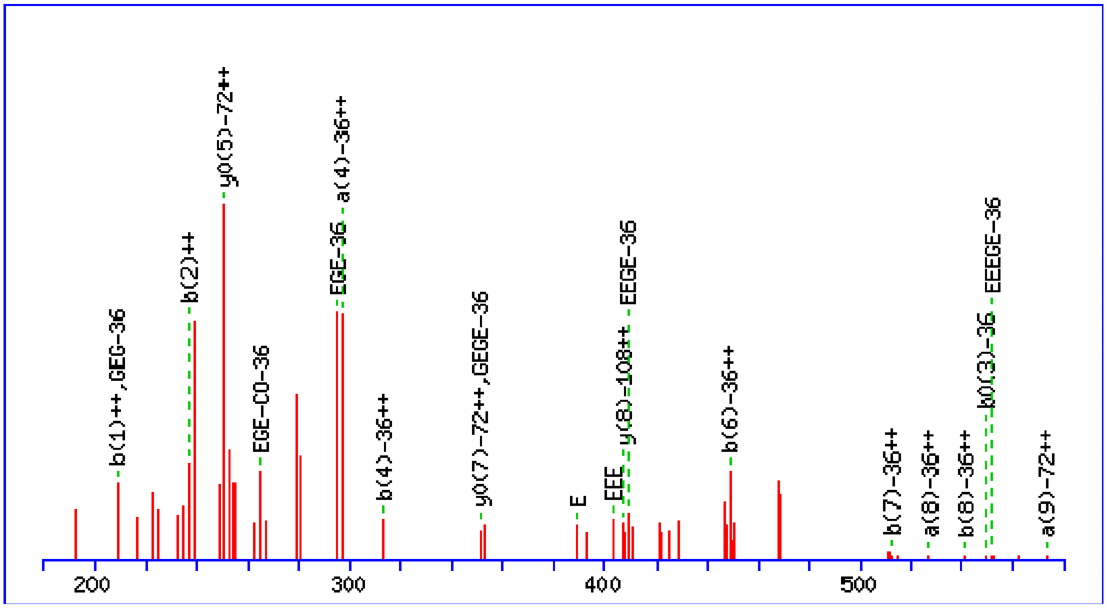
Matches (Bold Red): 17/174 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	66.0464	94.0413	47.5243	76.0307	38.519	E					10
2	30.0338	**151.0628**	76.035	133.0522	67.0297	G	1013.386	507.1966	995.3754	498.1914	9
3	66.0464	**244.0968**	122.552	226.0862	113.5468	E	956.3645	478.6859	938.354	469.6806	8
4	30.0338	**301.1183**	151.0628	283.1077	142.0575	G	863.3305	**432.1689**	845.3199	423.1636	7
5	231.0975	**559.2035**	280.1054	541.1929	**271.1001**	E	806.309	403.6582	788.2985	394.6529	6
6	116.0706	**702.2617**	351.6345	**684.2511**	342.6292	E	548.2239	274.6156	530.2133	265.6103	5
7	102.055	831.3043	416.1558	813.2937	**407.1505**	E	405.1656	**203.0864**	**387.155**	**194.0812**	4
8	30.0338	888.3258	444.6665	870.3152	435.6612	G	276.123	138.5651	**258.1125**	129.5599	3
9	66.0464	981.3598	491.1835	963.3492	482.1783	E	**219.1016**	**110.0544**	**201.091**	**101.0491**	2
10	66.0464					E	**126.0675**	63.5374	108.057	54.5321	1

Figure S10

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1

Match to Query 1024: 1392.581352 from(465.193784,3+)

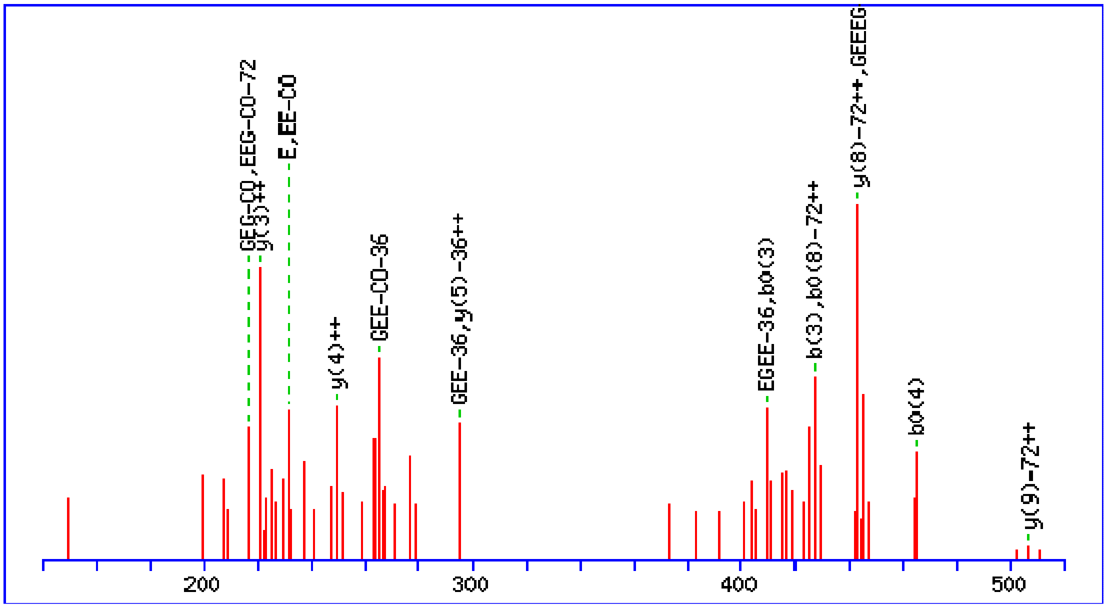


Monoisotopic mass of neutral peptide Mr(calc): 1392.5555
Variable modifications:
E441 : +2E2Me (E)
E445 : Methyl (DE)
Ions Score: 33 **Expect:** 0.0032
Matches (Bold Red): 25/174 fragment ions using 35 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	**388.184**	416.1789	**208.5931**	398.1684	199.5878	**E**					**10**
2	30.0338	473.2004	**237.1038**	455.1898	228.0986	**G**	870.3278	435.6675	852.3172	426.6622	**9**
3	66.0464	566.2344	283.6209	**548.2239**	274.6156	**E**	813.3063	**407.1568**	795.2958	398.1515	**8**
4	30.0338	623.2559	**312.1316**	605.2453	**303.1263**	**G**	720.2723	360.6398	702.2617	**351.6345**	**7**
5	116.0706	766.3141	383.6607	748.3036	374.6554	**E**	663.2508	**332.129**	645.2402	**323.1238**	**6**
6	102.055	895.3567	**448.182**	877.3462	**439.1767**	**E**	520.1926	260.5999	502.182	**251.5946**	**5**
7	102.055	1024.3993	**512.7033**	1006.3888	503.698	**E**	391.15	**196.0786**	373.1394	**187.0733**	**4**
8	30.0338	1081.4208	**541.214**	1063.4102	532.2088	**G**	262.1074	131.5573	244.0968	122.552	**3**
9	66.0464	1174.4548	587.7311	1156.4443	578.7258	**E**	205.0859	103.0466	187.0753	94.0413	**2**
10	66.0464					**E**	112.0519	56.5296	94.0413	47.5243	**1**

Figure S11

MS/MS Fragmentation of **EGEGEEEGEEY**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1
Match to Query 1012: 1380.528072 from(461.176024,3+)

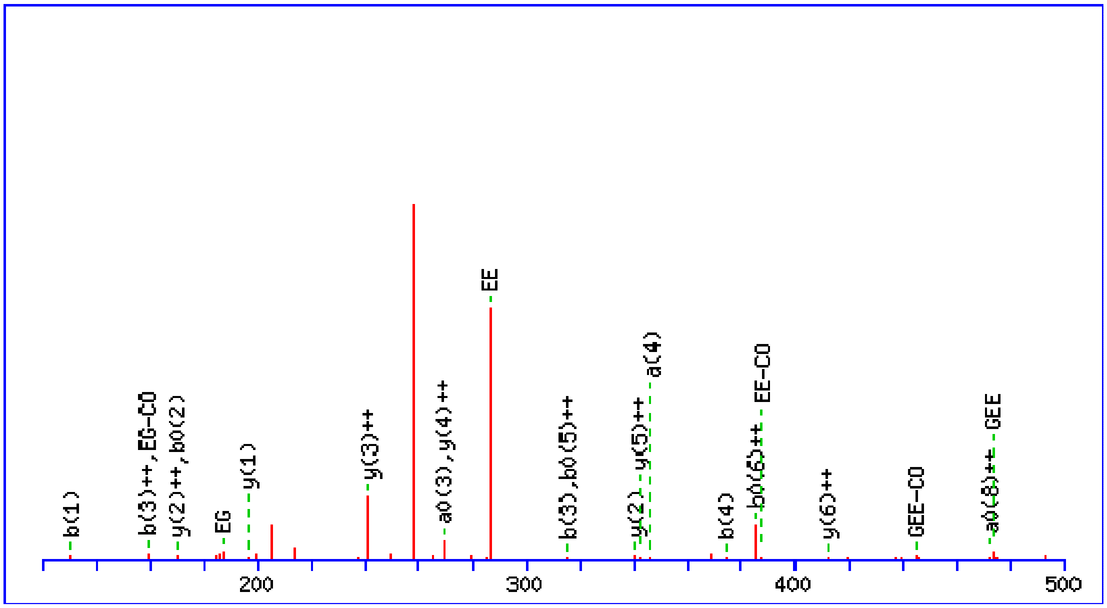


Monoisotopic mass of neutral peptide Mr(calc): 1380.5092
Variable modifications:
E441 : +E-H2O (E)
E445 : Methyl (DE)
Ions Score: 34 **Expect:** 0.00038
Matches (Bold Red): 17/201 fragment ions using 13 most intense peaks

#	Immon.	b	b++	b0	b0++	Seq.	y	y++	y0	y0++	#
1	**231.0975**	241.0819	121.0446	**223.0713**	112.0393	E					11
2	30.0338	298.1034	149.5553	**280.0928**	140.55	G	1069.3997	535.2035	1051.3891	526.1982	10
3	102.055	**427.146**	214.0766	**409.1354**	205.0713	E	1012.3782	**506.6927**	994.3676	497.6875	9
4	30.0338	484.1674	242.5873	**466.1569**	233.5821	G	883.3356	**442.1714**	865.325	**433.1662**	8
5	116.0706	627.2257	**314.1165**	609.2151	**305.1112**	E	826.3141	413.6607	808.3036	404.6554	7
6	66.0464	720.2597	360.6335	702.2491	351.6282	E	683.2559	**342.1316**	665.2453	333.1263	6
7	66.0464	813.2937	**407.1505**	795.2832	**398.1452**	E	590.2219	**295.6146**	572.2113	286.6093	5
8	30.0338	870.3152	435.6612	852.3046	**426.656**	G	497.1878	**249.0975**	479.1773	240.0923	4
9	102.055	999.3578	500.1825	981.3472	491.1773	E	440.1664	**220.5868**	422.1558	211.5815	3
10	102.055	1128.4004	564.7038	1110.3898	555.6986	E	**311.1238**	156.0655	293.1132	147.0602	2
11	136.0757					Y	182.0812	91.5442			1

Figure S12

MS/MS Fragmentation of **EGEGEEEGEEY**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1
Match to Query 1143: 1468.543662 from(490.514554,3+)



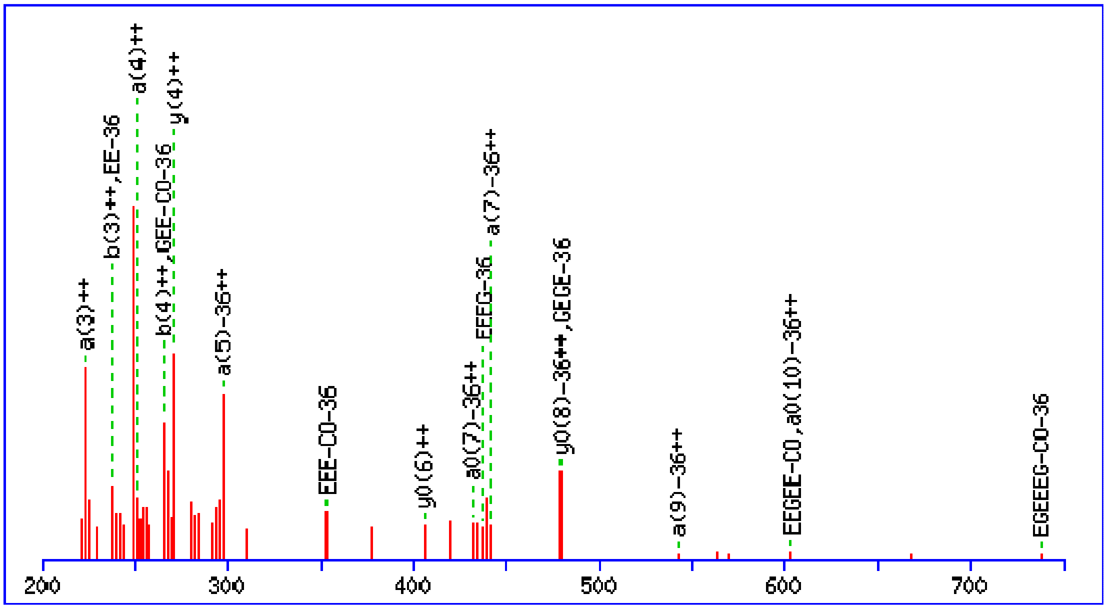
Monoisotopic mass of neutral peptide Mr(calc): 1468.5729
Variable modifications:
E445 : +1E1Me (E)
E446 : Methyl (DE)
E447 : Methyl (DE)
E449 : Methyl (DE)
E450 : Methyl (DE)
C-term : Methyl (C-term)
Ions Score: 32 **Expect:** 0.00026
Matches (Bold Red): 34/201 fragment ions using 38 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	102.055	**130.0499**	65.5286	112.0393	56.5233	E					11
2	30.0338	**187.0713**	94.0393	**169.0608**	85.034	G	1340.5376	670.7725	1322.5271	661.7672	10
3	102.055	**316.1139**	**158.5606**	298.1034	149.5553	E	1283.5162	642.2617	1265.5056	633.2564	9
4	30.0338	**373.1354**	**187.0713**	355.1248	178.0661	G	1154.4736	577.7404	1136.463	568.7351	8
5	245.1132	645.2362	323.1218	627.2257	**314.1165**	E	1097.4521	549.2297	1079.4415	540.2244	7
6	116.0706	788.2945	394.6509	770.2839	**385.6456**	E	825.3513	**413.1793**	807.3407	404.174	6
7	116.0706	931.3527	466.18	913.3422	457.1747	E	682.293	**341.6501**	664.2825	332.6449	5
8	30.0338	988.3742	494.6907	970.3636	485.6854	G	539.2348	**270.121**	521.2242	261.1157	4
9	116.0706	1131.4324	566.2199	1113.4219	557.2146	E	482.2133	**241.6103**	464.2027	232.605	3
10	116.0706	1274.4907	637.749	1256.4801	628.7437	E	**339.1551**	**170.0812**	321.1445	161.0759	2
11	136.0757					Y	**196.0968**	98.552			1

Figure S13

MS/MS Fragmentation of **EGEGEEEGEEY**
Found in **sp|P68369|TBA1A_MOUSE**, Tubulin alpha-1A chain OS=Mus musculus GN=TUBA1A PE=1 SV=1

Match to Query 1170: 1482.711102 from(495.237034,3+)



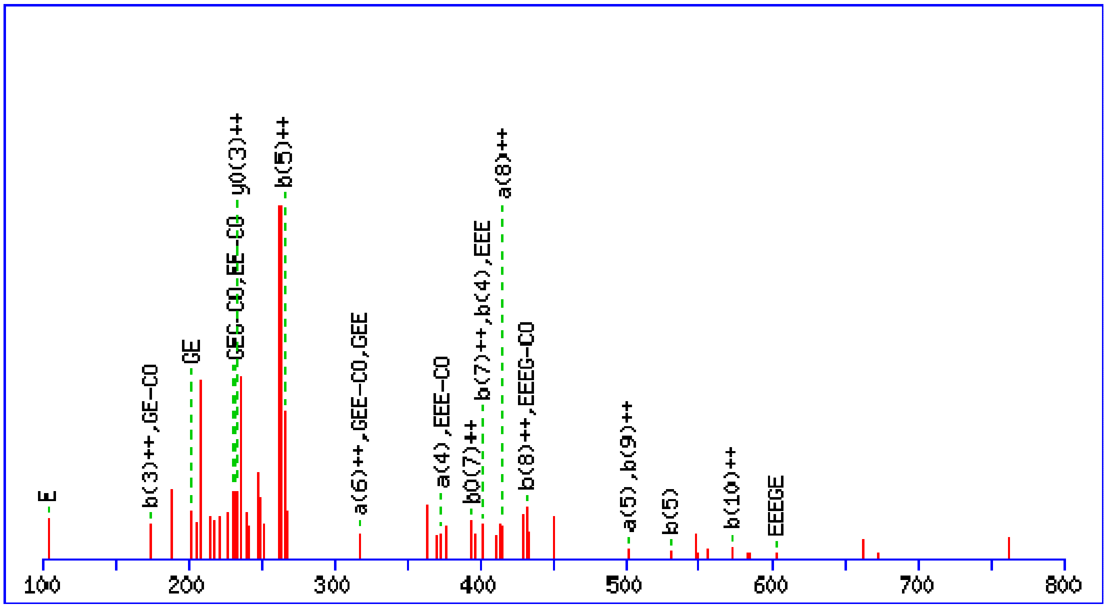
Monoisotopic mass of neutral peptide Mr(calc): 1482.6011
Variable modifications:
E441 : Methyl (DE)
E443 : +1E1Me (E)
E446 : Methyl (DE)
E447 : Methyl (DE)
E449 : Methyl (DE)
E450 : Methyl (DE)
C-term : Methyl (C-term)
Ions Score: 23 **Expect:** 0.0032
Matches (Bold Red): 22/201 fragment ions using 24 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	116.0706	144.0655	72.5364	126.055	63.5311	E					11
2	30.0338	201.087	101.0471	**183.0764**	92.0419	G	1304.5291	652.7682	1286.5185	643.7629	10
3	245.1132	473.1878	**237.0976**	**455.1773**	**228.0923**	E	1247.5076	624.2574	1229.497	615.2522	9
4	30.0338	530.2093	**265.6083**	512.1987	256.603	G	975.4068	488.207	957.3962	**479.2017**	8
5	66.0464	623.2433	**312.1253**	605.2328	**303.12**	E	918.3853	459.6963	900.3747	**450.691**	7
6	116.0706	766.3016	383.6544	748.291	374.6491	E	825.3513	**413.1793**	807.3407	**404.174**	6
7	116.0706	909.3598	**455.1836**	891.3493	**446.1783**	E	682.293	**341.6501**	664.2825	332.6449	5
8	30.0338	966.3813	483.6943	948.3707	474.689	G	539.2348	**270.121**	521.2242	**261.1157**	4
9	116.0706	1109.4395	555.2234	1091.429	546.2181	E	482.2133	**241.6103**	464.2027	232.605	3
10	116.0706	1252.4978	626.7525	1234.4872	617.7472	E	339.1551	**170.0812**	321.1445	161.0759	2
11	136.0757					Y	196.0968	98.552			1

Figure S14

MS/MS Fragmentation of **EGEGEEEGEEY**
Found in **sp|P81947|TBA1B_BOVIN**, Tubulin alpha-1B chain OS=Bos taurus GN=TUBA1B PE=1 SV=2

Match to Query 1039: 1339.723522 from(447.574507,3+)



Monoisotopic mass of neutral peptide Mr(calc): 1339.5303

Variable modifications:

E441 : Methyl (DE)

E443 : Methyl (DE)

E447 : Methyl (DE)

E449 : Methyl (DE)

E450 : Methyl (DE)

C-term : Methyl (C-term)

Ions Score: 26 **Expect:** 0.00063

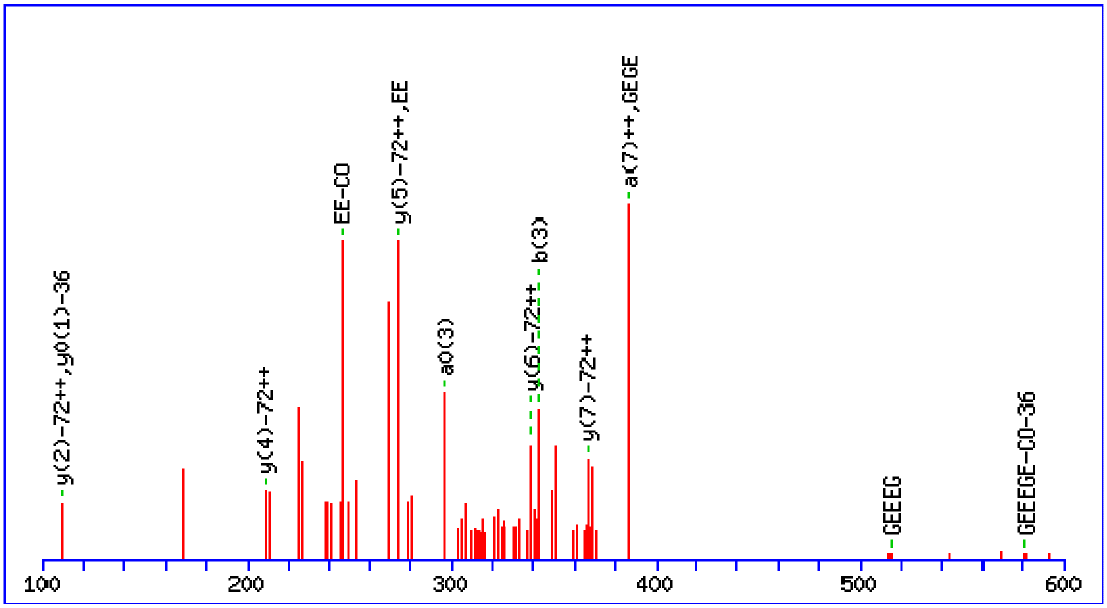
Matches (Bold Red): 40/201 fragment ions using 40 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	116.071	144.066	72.5364	126.055	63.5311	**E**					**11**
2	30.0338	**201.087**	101.047	183.076	92.0419	**G**	1197.479	599.243	1179.47	590.238	**10**
3	116.071	344.145	**172.576**	326.135	163.571	**E**	1140.457	570.733	1122.45	561.727	**9**
4	30.0338	**401.167**	**201.087**	383.156	192.082	**G**	997.399	499.204	979.389	490.198	**8**
5	**102.055**	**530.209**	**265.608**	512.199	256.603	**E**	940.378	470.693	922.368	461.688	**7**
6	**102.055**	659.252	**330.129**	641.241	321.124	**E**	811.336	406.171	793.325	397.166	**6**
7	116.071	802.310	**401.659**	784.299	**392.653**	**E**	682.293	341.650	664.283	332.645	**5**
8	30.0338	859.332	**430.169**	841.321	421.164	**G**	539.235	270.121	521.224	261.116	**4**
9	116.071	1002.389	**501.699**	984.379	492.693	**E**	482.213	241.610	464.203	**232.605**	**3**
10	116.071	1145.448	**573.228**	1127.44	564.222	**E**	339.155	170.081	321.145	161.076	**2**
11	136.076					**Y**	196.097	98.552			**1**

Figure S15

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P81947|TBA1B_BOVIN**, Tubulin alpha-1B chain OS=Bos taurus GN=TUBA1B PE=1 SV=2

Match to Query 634: 1148.317382 from(383.772460,3+)

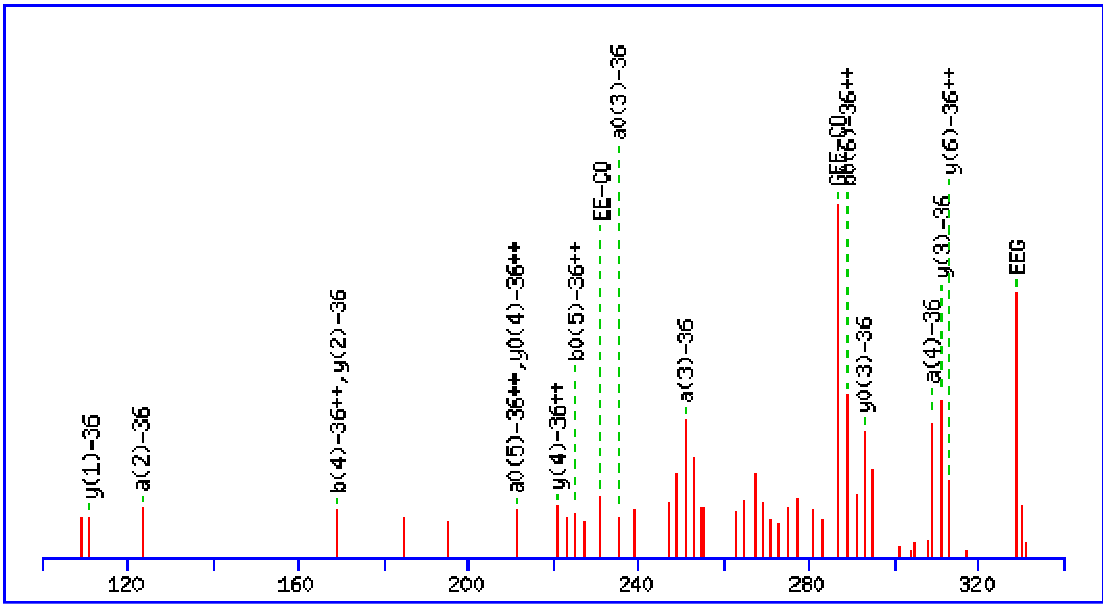


Monoisotopic mass of neutral peptide Mr(calc): 1148.4608
Variable modifications:
E441 : Methyl (DE)
E443 : Methyl (DE)
E447 : Methyl (DE)
C-term : Methyl (C-term)
Ions Score: 20 **Expect:** 0.011
Matches (Bold Red): 15/174 fragment ions using 25 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	116.071	144.066	72.5364	126.055	63.5311	E					10
2	30.0338	201.087	**101.047**	183.076	92.0419	G	934.368	467.688	916.357	458.682	9
3	116.071	**344.145**	172.576	326.135	163.571	E	877.346	439.177	859.336	**430.171**	8
4	30.0338	401.167	**201.087**	383.156	192.082	G	734.288	**367.648**	716.277	358.642	7
5	102.055	530.209	**265.608**	512.199	256.603	E	677.267	**339.137**	659.256	**330.132**	6
6	102.055	659.252	**330.129**	641.241	321.124	E	548.224	**274.616**	530.213	**265.610**	5
7	116.071	802.3010	401.659	784.299	392.653	E	419.181	**210.094**	401.171	**201.089**	4
8	30.0338	859.332	**430.169**	841.321	421.164	G	276.123	138.565	258.113	129.559	3
9	66.0464	952.366	476.687	934.355	467.681	E	219.102	**110.054**	201.091	**101.049**	2
10	66.0464					E	126.068	63.5374	**108.057**	54.5321	1

Figure S16

MS/MS Fragmentation of **EGEGEEEGE**
Found in **sp|P81947|TBA1B_BOVIN**, Tubulin alpha-1B chain OS=Bos taurus GN=TUBA1B PE=1 SV=2
Match to Query 328: 977.249562 from(326.749854,3+)



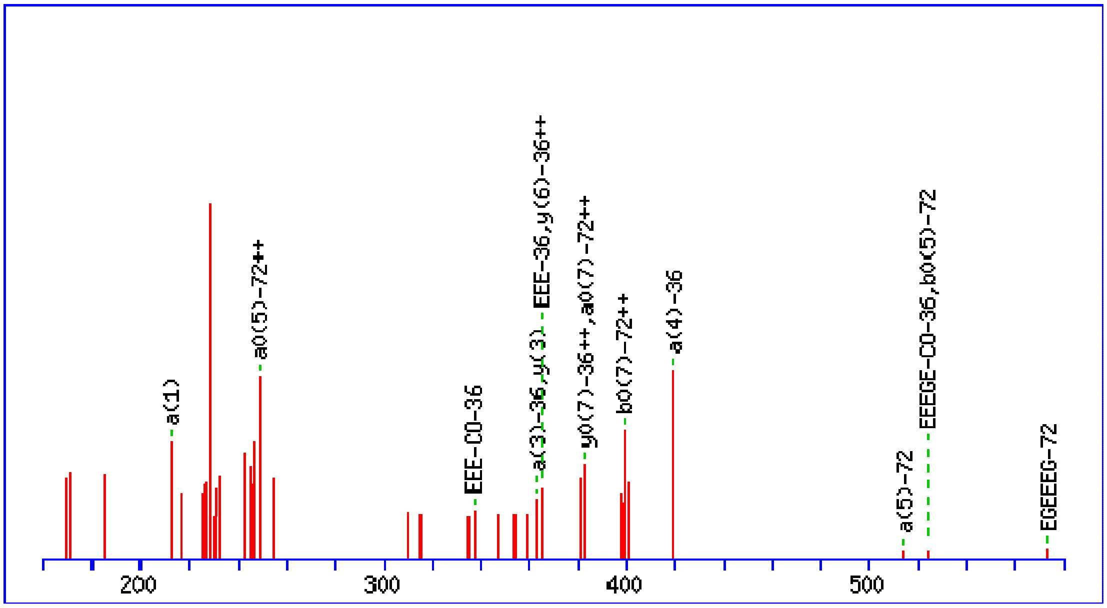
Monoisotopic mass of neutral peptide Mr(calc): 977.3713
Variable modifications:
E447 : Methyl (DE)
Ions Score: 34 **Expect:** 0.00028
Matches (Bold Red): 19/147 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	66.0464	94.0413	47.5243	76.0307	38.519	E					9
2	30.0338	151.063	76.035	133.052	67.0297	G	813.302	407.155	795.292	398.15	8
3	102.055	280.105	**140.556**	262.095	131.551	E	756.281	378.644	738.27	369.639	7
4	30.0338	337.127	**169.067**	319.116	**160.062**	G	627.238	**314.123**	609.228	305.118	6
5	102.055	466.169	233.588	448.159	**224.583**	E	570.217	**285.612**	552.206	276.607	5
6	102.055	595.212	298.109	577.202	**289.104**	E	441.174	**221.091**	423.164	**212.085**	4
7	116.071	738.270	369.639	720.259	360.634	E	**312.132**	156.569	**294.121**	147.564	3
8	30.0338	795.292	398.149	777.281	389.144	G	**169.073**	85.0403	151.063	76.035	2
9	66.0464					E	**112.052**	56.5296	94.0413	47.5243	1

Figure S17

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P81947|TBA1B_BOVIN**, Tubulin alpha-1B chain OS=Bos taurus GN=TUBA1B PE=1 SV=2

Match to Query 815: 1245.608142 from(416.202714,3+)



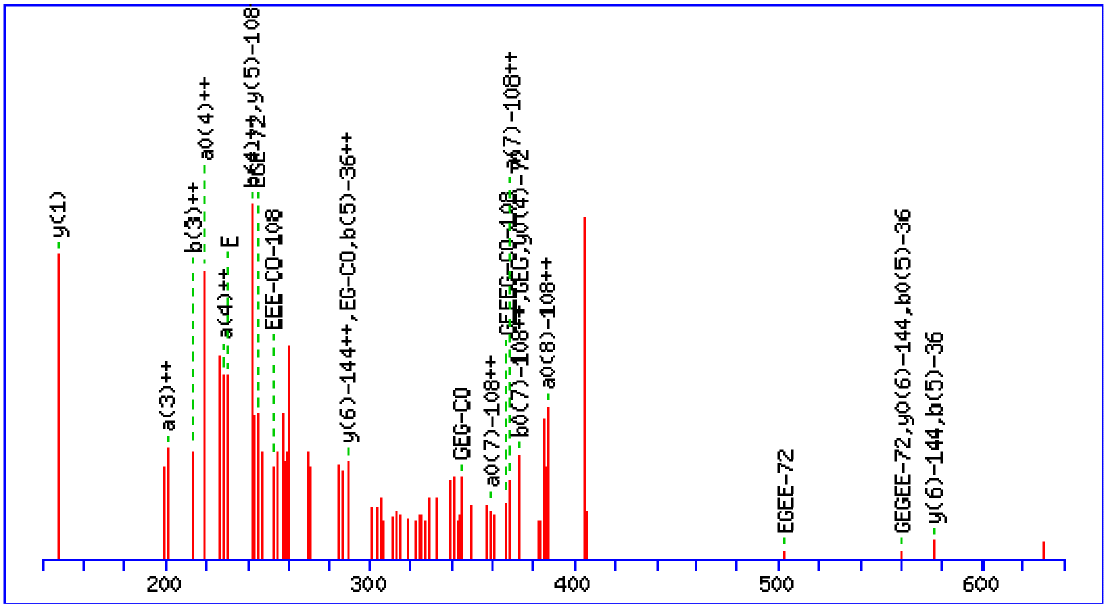
Monoisotopic mass of neutral peptide Mr(calc): 1245.4772
Variable modifications:
E441 : +E-H2O (E)
E446 : Methyl (DE)
E450 : Methyl (DE)
C-term : Methyl (C-term)
Ions Score: 26 **Expect:** 0.008
Matches (Bold Red): 16/174 fragment ions using 14 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	231.098	241.082	**121.045**	223.071	112.039	E					10
2	30.0338	298.103	**149.555**	280.093	140.550	G	934.368	467.688	916.357	458.682	9
3	66.0464	391.137	**196.072**	373.127	**187.067**	E	877.346	439.177	859.336	430.171	8
4	30.0338	448.159	**224.583**	430.148	215.578	G	784.312	**392.659**	766.302	**383.654**	7
5	66.0464	541.193	**271.100**	**523.182**	262.095	E	727.291	**364.149**	709.280	**355.144**	6
6	116.071	684.251	342.629	666.241	333.624	E	634.257	317.632	616.246	**308.627**	5
7	102.055	813.294	**407.151**	795.283	**398.145**	E	491.198	246.103	473.188	**237.098**	4
8	30.0338	870.315	435.661	852.305	426.656	G	**362.156**	181.582	344.145	172.576	3
9	102.055	999.358	500.183	981.347	491.177	E	305.134	**153.071**	287.124	144.066	2
10	116.071					E	176.092	88.5495	158.081	79.5442	1

Figure S18

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P81947|TBA1B_BOVIN**, Tubulin alpha-1B chain OS=Bos taurus GN=TUBA1B PE=1 SV=2

Match to Query 741: 1203.646452 from(402.215484,3+)

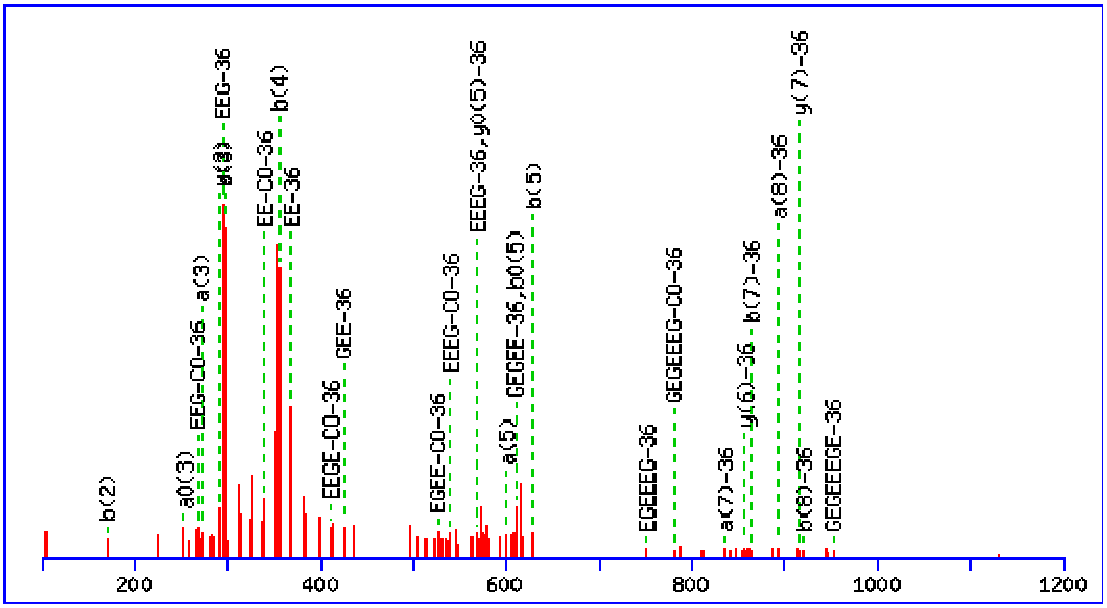


Monoisotopic mass of neutral peptide Mr(calc): 1203.4554
Variable modifications:
E441 : -H2O (E)
E443 : +E (E)
Ions Score: 16 **Expect:** 0.005
Matches (Bold Red): 31/174 fragment ions using 42 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	102.055	112.039	56.5233	94.0287	47.518	**E**					**10**
2	30.0338	169.061	85.034	**151.050**	76.0287	**G**	949.346	475.177	931.336	466.171	**9**
3	**231.098**	427.146	**214.077**	409.135	205.071	**E**	892.325	446.666	874.314	437.661	**8**
4	30.0338	484.167	**242.587**	466.157	233.582	**G**	634.239	**317.623**	616.229	308.618	**7**
5	66.0464	**577.202**	**289.104**	**559.191**	280.099	**E**	**577.218**	**289.113**	**559.208**	280.107	**6**
6	66.0464	670.236	335.621	652.225	326.616	**E**	484.184	**242.596**	466.173	233.590	**5**
7	66.0464	763.269	382.138	745.259	**373.133**	**E**	391.150	**196.079**	**373.139**	187.073	**4**
8	30.0338	820.291	410.649	802.280	401.644	**G**	298.116	149.562	280.105	140.556	**3**
9	66.0464	913.325	457.166	895.315	448.161	**E**	**241.095**	121.051	223.084	112.046	**2**
10	102.055					**E**	**148.060**	74.5339	130.049	65.5286	**1**

Figure S19

MS/MS Fragmentation of **EGEGEEEGEE**
Found in **sp|P81947|TBA1B_BOVIN**, Tubulin alpha-1B chain OS=Bos taurus GN=TUBA1B PE=1 SV=2
Match to Query 1741: 1245.454268 from(623.727134,2+)

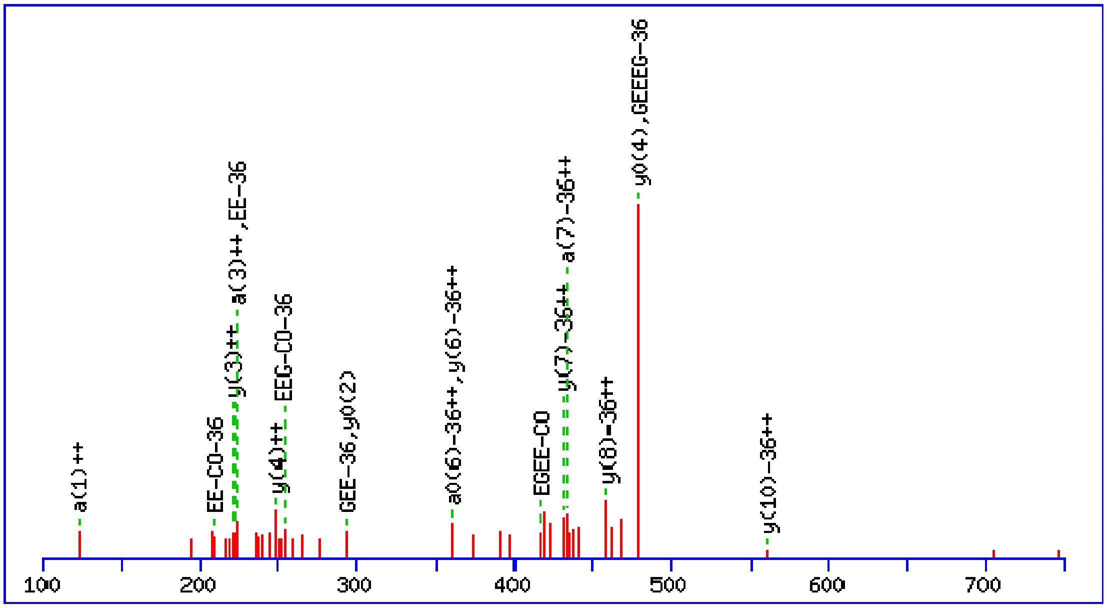


Monoisotopic mass of neutral peptide Mr(calc): 1245.4646
Variable modifications:
E441 : -H2O (E)
E445 : +1E1Me (E)
E447 : Methyl (DE)
E449 : Methyl (DE)
Ions Score: 22 **Expect:** 0.029
Matches (Bold Red): 32/120 fragment ions using 59 most intense peaks

#	Immon.	b	b^0	Seq.	y	y^0	#
1	102.055	112.0393	94.0287	**E**			**10**
2	30.0338	**169.0608**	151.0502	**G**	1099.4188	1081.4082	**9**
3	102.055	**298.1034**	280.0928	**E**	1042.3973	1024.3868	**8**
4	30.0338	**355.1248**	337.1143	**G**	**913.3547**	895.3442	**7**
5	245.113	**627.2257**	**609.2151**	**E**	**856.3333**	838.3227	**6**
6	66.0464	720.2597	702.2491	**E**	584.2324	**566.2219**	**5**
7	116.071	**863.3180**	845.3074	**E**	491.1984	473.1878	**4**
8	30.0338	**920.3394**	902.3289	**G**	348.1401	330.1296	**3**
9	116.071	1063.3977	1045.3871	**E**	**291.1187**	273.1081	**2**
10	102.055			**E**	148.0604	130.0499	**1**

Figure S20

MS/MS Fragmentation of **EGEGEEEGEEY**
Found in **sp|P81947|TBA1B_BOVIN**, Tubulin alpha-1B chain OS=Bos taurus GN=TUBA1B PE=1 SV=2
Match to Query 1165: 1426.505332 from(476.501107,3+)



Monoisotopic mass of neutral peptide Mr(calc): 1426.5385
Variable modifications:
E441 : +1E1Me (E)
E443 : Methyl (DE)
E445 : Methyl (DE)
Ions Score: 42 **Expect:** 6.6e-005
Matches (Bold Red): 18/201 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^0	y^{0++}	#
1	245.113	273.108	137.058	255.098	128.052	**E**					**11**
2	30.0338	330.129	165.568	312.119	156.563	**G**	1119.423	**560.216**	1101.413	551.210	**10**
3	116.071	473.188	237.098	455.177	**228.092**	**E**	1062.402	531.705	1044.391	522.699	**9**
4	30.0338	530.209	265.608	512.199	256.603	**G**	919.344	**460.176**	901.334	451.170	**8**
5	116.071	673.268	337.137	655.257	328.132	**E**	862.323	**431.665**	844.312	422.659	**7**
6	66.0464	766.302	383.654	748.291	374.649	**E**	719.265	**360.136**	701.254	351.131	**6**
7	102.055	895.344	448.176	877.334	**439.170**	**E**	626.230	313.619	608.219	**304.614**	**5**
8	30.0338	952.366	476.687	934.355	**467.681**	**G**	497.188	**249.098**	**479.177**	**240.092**	**4**
9	102.055	1081.408	541.208	1063.397	532.203	**E**	440.166	**220.587**	422.156	211.582	**3**
10	102.055	1210.450	605.729	1192.440	596.724	**E**	311.124	156.066	**293.113**	147.060	**2**
11	136.076					**Y**	182.081	91.5442			**1**

Table S1. List of common contaminants that were excluded from the search

```
>cont|000001| gi|68|emb|CAA44927.1| alpha lactalbumin [Bos taurus (contaminant)]
EQLTKCEVFRELKDLKGYGGVSLPEWVCTAFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLD
DDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>cont|000002| gi|67549|pir||TRBOTR trypsin (EC 3.4.21.4) precursor - bovine [Bos taurus (contaminant)]
VDDDDKIVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSY
NSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNM
FCAGYLEGGKDSCQGDSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN
>cont|000003| gi|89257|pir||A23473 chymotrypsin-like proteinase (EC 3.4.21.-) - pig (tentative sequence) (fragments) [Sus scrofa
(contaminant)]
CGVPAIKPALBIVBGZBAVPGSWPWZVSLZBSBGFHFCGGSLISZMNNDLTLLKLASPAQYTTRIGPVCLASGDEALPEXLPC
VMICAGASGASSCQGDSGGPLVCEKGDTWXLXGIVSWGSXXCB
>cont|000004| gi|115114|sp|P00974|BPT1_BOVIN Pancreatic trypsin inhibitor precursor (Basic protease inhibitor) (BPI) (BPTI)
(Aprotinin) [Bos taurus (contaminant)]
MKMSRLCLSVALLVLLGTLAASTPGCDTSNQAKAQRPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFK
SAEDCMRTCGGAIGPWENL
>cont|000005| gi|115115|sp|P04815|BPT2_BOVIN Spleen trypsin inhibitor I precursor (SI-I) (Contains: Spleen trypsin inhibitor II
(SI-II); Spleen trypsin inhibitor III (SI-III)) [Bos taurus (contaminant)]
MKMSRLCLSIALLVLLGTLAASTPGCDTSNQAKAQRPDFCLEPPYTGPCKAKMIRYFYNAKAGFCETFVYGGCKAKSNNFR
SAEDCMRTCGGAIGPRENL
>cont|000006| gi|115660|sp|P02666|CASB_BOVIN Beta-casein precursor [Bos taurus (contaminant)]
MKVLILACLVALALARELEELNVPGEIVESLSSSEESITRINKKIEKFQSEEQQQTEDELQDKIHPFAQTQSLVYPFPGPIPNSLP
QNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPKHKEMPFPKYPVEPFTESQSLTLTDVENLHLPLPLLQSWMHQPHQPLPP
TVMFPPQSVLSLSQSKVLPVPQKAVPYPQRDMPIQAFLLYQEPVLGPVRGPFPIIV
>cont|000007| gi|117616|sp|P00767|CTRB_BOVIN Chymotrypsinogen B (Contains: Chymotrypsin B chain A; Chymotrypsin B chain
B; Chymotrypsin B chain C) [Bos taurus (contaminant)]
CGVPAIQPVLSGLARIVNGEDAVPGSWPWQVSLQDSTGFHFCGGSLISEDWVVTAAHCGVTTSDVVVAGEFDQGLETEDTQ
VLKIGKVFKNPKFSILTVRNDITLLKLATPAQFSETVSAVCLPSADEDFPAGMLCATTGWGKTKYNALKTPDKLQQATLPIVS
NTDCRKYWGSRVTDVMICAGASGVSSCMGDSGGPLVCQKNGAWTLAGIVSWGSSTCSTSTPAVYARVTALMPWVQETLA
AN
>cont|000008| gi|124854|sp|P00996|IPK1_BOVIN Pancreatic secretory trypsin inhibitor [Bos taurus (contaminant)]
NILGREAKCTNEVNGCPRIYNPVCGTDGVTYSNECLLCMENKERQTPVLIQKSGPC
>cont|000009| gi|162805|gb|AAA30431.1| beta-casein [Bos taurus (contaminant)]
MKVLILACLVALALARELEELNVPGEIVESLSSSEESITRINKKIEKFQSEEQQQTEDELQDKIHPFAQTQSLVYPFPGPIHNSLP
QNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPKHKEMPFPKYPVEPFTESQSLTLTDVENLHLPLPLLQSWMHQPHQPLPP
TVMFPPQSVLSLSQSKVLPVPQKAVPYPQRDMPIQAFLLYQEPVLGPVRGPFPIIV
>cont|000010| gi|217533|dbj|BAA00313.1| alpha-s1-casein [Bos taurus (contaminant)]
GTQYTDAPSFSDIPNPIG
>cont|000011| gi|230373|pdb|1TPA|I Chain I, Anhydro-Trypsin (E.C.3.4.21.4) Complex With Pancreatic Trypsin Inhibitor [Bos taurus
(contaminant)]
RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA
>cont|000012| gi|230594|pdb|2KAI|A Chain A, Kallikrein A (E.C.3.4.21.8) Complex With Bovine Pancreatic Trypsin Inhibitor [Bos
taurus (contaminant)]
IIGGRECEKNSHPWQVAIYHYSSFQCGGVLVNPKWVLTAAHCKNDNYEVWLGRHNLFENENTAQFFGVTADFPHPGFNLS
>cont|000013| gi|231268|pdb|7PTI|  Bovine Pancreatic Trypsin Inhibitor (BPTI) Mutant (Cys 30 Replaced By Ala, Cys 51 Replaced
By Ala) (C30A, C51A) [Bos taurus (contaminant)]
RPDFCLEPPYTGPCKARIIRYFYNAKAGLAQTFVYGGCRAKRNNFKSAEDAMRTCGGA
>cont|000014| gi|295774|emb|CAA29664.1| alpha-lactalbumin [Bos taurus (contaminant)]
MMSFVSLLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPEWVCTAFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCK
DDQNPHSSNICNISCDKFLDDDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>cont|000015| gi|346472|pir||A45109 chymotrypsin (EC 3.4.21.1) homolog p31 - pig (fragment) [Sus scrofa (contaminant)]
XGVPAIPPVLSGLSRIVNGEEAVPG
>cont|000016| gi|418636|pir||LABOZ alpha-lactalbumin - bovine (tentative sequence) [Bos taurus (contaminant)]
EQLTKCEVFQELKDLKGYGGVSLPEWVCTTFHTSGYDTEAIVQNNDSTEYGLFQINNKIWCKNDQDPHSSNICNISCDKFLD
DDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>cont|000017| gi|418694|pir||ABBOS serum albumin precursor (validated) - bovine [Bos taurus (contaminant)]
MKWVTFISLLLLFSSAYSRGVFRRDTHKSEIAHRFKDLGEEQFKGLVLIAFSQYLQQCPFDEHVKLVNELTEFAKTCVADESH
AGCEKSLHTLFGDELCKVASLRETYGDMADCCEKQEPERNECFLSHKDDSPDLPKLKPDPNTLCDEFKADEKKFWGKYLYE
IARRHPYFYAPELLYYANKYNGVFQDCCQAEDKGACLLPKIETMREKVLASSARQRLRCASIQKFGERALKAWSVARLSQK
FPKAEFVEVTKLVTDLTKVHKECCHGDLLECADDRADLAKYICDNQDTISSKLKECCDKPLLEKSHCIAEVEKDAIPENLPPL
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TADFAEDKDVCKNYQEAKDAFLGSFLYEYSRRHPEYAVSVLLRLAKEYEATLEECCAKDDPHACYSTVFDKLKHLVDEPQ
NLIKQNCDQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESERMPCTEDYLSLILNRLCVLHEKTP
VSEKVTKCCTESLVNRRPCFSALTPDETYVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQLKTVMENF
VAFVDKCCAADDKEACFAVEGPKLVVSTQTALA
>cont|000018| gi|442692|pdb|1BTI|  Bovine Pancreatic Trypsin Inhibitor (Bpti) Mutant With Phe 22 Replaced By Ala (F22a) [Bos
taurus (contaminant)]
RPDFCLEPPYTGPCKARIIRYAYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA
>cont|000019| gi|442882|pdb|1FAN|  Bovine Pancreatic Trypsin Inhibitor (Bpti) Mutant With Phe 45 Replaced By Ala (F45a) [Bos
taurus (contaminant)]
RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNAKSAEDCMRTCGGA
>cont|000020| gi|443137|pdb|1NAG|  Bovine Pancreatic Trypsin Inhibitor (Bpti) Mutant With Asn 43 Replaced By Gly (N43g) [Bos
taurus (contaminant)]
RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRGNFKSAEDCMRTCGGA
>cont|000021| gi|459292|gb|AAB29137.1| beta-casein A3 [Bos taurus (contaminant)]
MKVLILACLVALALARELEELNVPGEIVESLSSSEESITRINKKIEKFQSEEQQQTEDELQDKIHPFAQTQSLVYPFPGPIPNSLP
QNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPKQKEMPFPKYPVEPFTESQSLTLTDVENLHLPLPLLQSWMHQPHQPLPP
TVMFPPQSVLSLSQSKVLPVPQKAVPYPQRDMPIQAFLLYQEPVLGPVRGPFPIIV
>cont|000022| gi|462378|sp|P00976|IBPC_BOVIN Colostrum trypsin inhibitor (Colostrum BPI) [Bos taurus (contaminant)]
FQTPPDLCQLPQARGPCKAALLRYFYNSTSNACEPFTYGGCQGNNBNFETTEMCLRICEPPQQTDKS
>cont|000023| gi|494360|pdb|1MCT|A Chain A, Trypsin (E.C.3.4.21.4) Complexed With Inhibitor From Bitter Gourd [Sus scrofa
(Contaminant)]
IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDN
DIMLIKLSSPATLNSRVATVSLPRSCAAAGTECLISGWGNTKSSGSSYPSLLQCLKAPVLSNSSCKSSYPGQITGNMICVGFLQ
GGKDSCQGDSGGPVVCNGQLQGIVSWGYGCAQKNKPGVYTKVCNYVNWIQQTIAAN
>cont|000024| gi|664893|emb|CAA28886.1| trypsin ihibitor precursor [Bos taurus (contaminant)]
SVALLVLLGTLAASTPGCDTSNQAKAQRPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRT
CGGAIGPWENL
>cont|000025| gi|999626|pdb|1EPT|A Chain A, Porcine E-Trypsin (E.C.3.4.21.4) [Sus scrofa (contaminant)]
IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYK
>cont|000027| gi|1827748|pdb|1MTN|A Chain A, Bovine Alpha-Chymotrypsin:bpti Crystallization [Bos taurus (contaminant)]
CGVPAIQPVLSGL
>cont|000028| gi|1827749|pdb|1MTN|B Chain B, Bovine Alpha-Chymotrypsin:bpti Crystallization [Bos taurus (contaminant)]
IVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTSDVVVAGEFDQGSSSEKIQKLKIAKVFKNSKYNS
LTINNDITLLKLSTAASFSQTVSAVCLPSASDDFAAGTTCVTTGWGLTRY
>cont|000029| gi|1840093|gb|AAB47256.1| kappa-casein [Bison bison (contaminant)]
KNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEASPEVIESPPEINTVQVTSTAV
>cont|000030| gi|1840101|gb|AAB47260.1| kappa-casein [Bos taurus (contaminant)]
KNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEDSPEVIESPPEINTVQVTSTAV
>cont|000031| gi|1840103|gb|AAB47261.1| kappa-casein [Bos taurus (contaminant)]
KNQDKTEIPTINTIASGEPTSTPTIEAVESTVATLEASPEVIESPPEINTVQVTSTAV
>cont|000032| gi|1942351|pdb|1AKS|A Chain A, Crystal Structure Of The First Active Autolysate Form Of The Porcine Alpha
Trypsin [Sus scrofa (contaminant)]
IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDN
DIMLIKLSSPATLNSRVATVSLPRSCAAAGTECLISGWGNTK
>cont|000033| gi|2136705|pir||S66289 alpha 1 antichymotrypsin - bovine (fragment) [Bos taurus (contaminant)]
ARANFRDSEAARSLINDYVKNKTQGKKEELFKYLSPRTELVLVNYIYFKAQWKTPFDPKHTEQAEFHVSDNKTVEVPMMTL
DLETPYFRDEELGCTLVELTYTSNDSALFILPDEGKMRDLEAKLTPETLTRWRNSLQPRRIHELYLPKFSIKSNYELNDILSQL
GIRKIFANADLSGITGTADLVVSQVVHGAALDVDEEGTEGAAATGISMERTILRIIVRVNRPFLIAIVLKDTQSIIFLGKVTNPSE
A
>cont|000034| gi|2136706|pir||S66290 alpha 1 antichymotrypsin - bovine (fragment) [Bos taurus (contaminant)]
ARVSQMGIKKIFTDADLSGITGTADLVVSQVVHGAALDVDEEGTEGAAATGIGIERTFLRIIVRVNRPFLIAVVLKDTQSIIFLG
KVTNPSEA
>cont|000035| gi|2190337|emb|CAA41735.1| serum albumin [Bos taurus (contaminant)]
MKWVTFISLLLLFSSAYSRGVFRRDTHKSEIAHRFKDLGEEHFKGLVLIAFSQYLQQCPFDEHVKLVNELTEFAKTCVADESH
AGCEKSLHTLFGDELCKVASLRETYGDMADCCEKQEPERNECFLSHKDDSPDLPKLKPDPNTLCDEFKADEKKFWGKYLYE
IARRHPYFYAPELLYYANKYNGVFQECCQAEDKGACLLPKIETMREKVLTSSARQRLRCASIQKFGERALKAWSVARLSQK
FPKAEFVEVTKLVTDLTKVHKECCHGDLLECADDRADLAKYICDNQDTISSKLKECCDKPLLEKSHCIAEVEKDAIPENLPPL
TADFAEDKDVCKNYQEAKDAFLGSFLYEYSRRHPEYAVSVLLRLAKEYEATLEECCAKDDPHACYSTVFDKLKHLVDEPQ
NLIKQNCDQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESERMPCTEDYLSLILNRLCVLHEKTP
VSEKVTKCCTESLVNRRPCFSALTPDETYVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQLKTVMENF
VAFVDKCCAADDKEACFAVEGPKLVVSTQTALA
>cont|000036| gi|2499861|sp|Q29463|TRY2_BOVIN Anionic trypsin precursor [Bos taurus (contaminant)]
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MHPLLILAFVGAAVAFPSDDDDKIVGGYTCAENSVPYQVSLNAGYHFCGGSLINDQWVVSAAHCYQYHIQVRLGEYNIDVL
EGGEQFIDASKIIRHPKYSSWTLDNDILLIKLSTPAVINARVSTLLLPSACASAGTECLISGWGNTLSSGVNYPDLLQCLVAPLL
SHADCEASYPGQITNNMICAGFLEGGKDSCQGDSGGPVACNGQLQGIVSWGYGCAQKGKPGVYTKVCNYVDWIQETIAAN
S
>cont|000037| gi|2554812|pdb|1AFQ|C Chain C, Crystal Structure Of Bovine Gamma-Chymotrypsin Complexed With A Synthetic
Inhibitor [Bos taurus (contaminant)]
NTPDRLQQASLPLLSNTNCKKYWGTKIKDAMICAGASGVSSCMGDSGGPLVCKKNGAWTLVGIVSWGSSTCSTSTPGVYA
RVTALVNWVQQTLAAN
>cont|000038| gi|2625062|gb|AAB86612.1| kappa-casein [Bison bison (contaminant)]
NNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQPTTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPT
TEAVESTVATLEASPEVIESPPEINTVQVTSTAV
>cont|000039| gi|2625080|gb|AAB86621.1| kappa-casein [Boselaphus tragocamelus (contaminant)]
NNQFLPYPYYAKSVAVRSPAQILQWQVLSNTVPAKSCQDQPTTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASVEPTSTST
TEAIVNTVATQEASSEVIASAPETNTVEVTPTVV
>cont|000040| gi|2914482|pdb|1TFX|A Chain A, Complex Of The Second Kunitz Domain Of Tissue Factor Pathway Inhibitor With
Porcine Trypsin [Sus scrofa (contaminant)]
IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDN
DIMLIKLSSPATLNSRVATVSLPRSCAAAGTECLISGWGNTKSSGSSYPSLLQCLKAPVLSDSSCKSSYPGQITGNMICVGFLE
GGKDSCQGDSGGPVVCNGQLQGIVSWGYGCAQKNKPGVYTKVCNYVNWIQQTIAAN
>cont|000041| gi|3024051|sp|P79263|ITIH4_PIG Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy chain H4) (Inter-
alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Major acute phase protein)
(MAP) [Sus scrofa (contaminant)]
MKTLSPTGYGLLLVLPLLLAVLQSTTAHKNDINIYSLTVDSKVSSRFAHTVVTSRVVNKGSAVQEATFQMELPKKAFITNFS
MIIDGVTYPGNIKEKAAAQEQYSAVARGESAGLVRATGRKTEQFQVAVSVAPAAKVTFELVYEELLARHLGVYELLLKIQP
QQLVKHLQMDIHIFEPQGISFLETESTFMTNELAEALTISQNKTKAHIRFKPTLSQQQKSPEQQETVLDGNFIVRYDVNRTVTG
GSIQIENGYFVHYFAPEVWSAIPKNVIFVIDTSGSMRGRKIQQTREALIKILGDLGSRDQFNLVSFSGEAPRRRAVAASAENVE
EAKSYAAEIHAQGGTNINDAMLMAVQLLERANREELLPARSVTFIILLTDGDPTVGETNPSKIQKNVREAIDGQHSLFCLGFG
FDVPYAFLEKMALENGGLARRIYEDSDSALQLEDFYQEVANPLLRLVAFEYPSNAVEEVTQDNFRLFFKGSELVVAGKLRD
QSPDVLSAKVRGQLHMENVTFVMESRVAEQEAEFLSPKYIFHSFMERLWAYLTIQQLLAQTVSASDAEKKALEARALSLSL
NYSFVTPLTSMVITKPEGQEQSQVAEKPVENGNRQGNTHSGHSSFQFHSVGDRTSRLTGGSSVDPVFSHRRGWKGQAQGFE
KMSYLPPRLGPPGPLQPTRFSHPFSRITLDRVLPEVLSVPDETSHDMDSRIIGATIPPPPARIQAPSVILPLPGQSVDQLCVDLKH
SQGPVKLLSDPGQGVEVTGHYEREKARFSWIEVTFKHPPLQVRASLEHIVVIRNRQSSAYKWKETLYSVMPGLKITMDKAGL
LLLSSPNRVTIGLLSWDGPGKGLRLLLRDTDHFSSQISGTFGQFYQDVVWGPPAAADDSKRTVTVQGHDHSATRELKLDYQ
EGSPGKEISCWTVVL
>cont|000042| gi|3098477|gb|AAC15663.1| inter-alpha-trypsin inhibitor heavy-chain H1 [Sus scrofa (contaminant)]
GHVLFRPTVGQQQSCSTCST
>cont|000044| gi|4139559|pdb|3TGI|I Chain I, Wild-Type Rat Anionic Trypsin Complexed With Bovine Pancreatic Trypsin Inhibitor
(Bpti) [Bos taurus (contaminant)]
RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGAIGPWENL
>cont|000045| gi|4191560|gb|AAD09813.1| beta-casein H [Bos taurus (contaminant)]
LEELNVPGEIVESLSSSEESITRINKKIEKFQSEEQQQTE
>cont|000046| gi|4887006|gb|AAD32140.1|AF123251_1 kappa-casein precursor [Bos taurus (contaminant)]
RCEKDERFFSDKIAKYIPIQYVLSRYPSYGLNYYQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQP
TTMACHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPITEAVESTVATLEDSPEVIESPPEINTVQVTSTAV
>cont|000047| gi|6435821|pdb|1QLQ|A Chain A, Bovine Pancreatic Trypsin Inhibitor (Bpti) Mutant With Altered Binding Loop
Sequence [Bos taurus (contaminant)]
RPDFCLEPPYAGACRARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000048| gi|6451687|dbj|BAA86919.1| alpha lactalbumin [Bos taurus (contaminant)]
GLMPGPLRLFPQIKGGEQCGDPISESWGVTKMMSFVSLLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPECEFPAILL
CPIIHPLHSFP
>cont|000049| gi|6715447|gb|AAF26420.1|AF217654_1 parvalbumin [Bos taurus (contaminant)]
RFIVKGFSPDGRDLSVKET
>cont|000050| gi|7288120|dbj|BAA92833.1| alpha-lactalbumin [Bos taurus (contaminant)]
MMSFVSLLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPECEFPAILLCPIIHPLHSFP
>cont|000051| gi|7441524|pir||S72220 alpha-S1-casein - bovine (fragments) [Bos taurus (contaminant)]
FVAPFPEVFRQFYQLDAYPSGAWYYVPLGTQY
>cont|000052| gi|7528205|gb|AAF63191.1| kappa-casein [Bos grunniens (contaminant)]
RCEKDERFFSDKIAKYIPIQYVLSRYLSYGLNYYQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQP
TTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGERTSTPTTEAVESTVATLEASPEVIESPPEINTVQVTSTAV
>cont|000053| gi|7546571|pdb|3BTE|I Chain I, The Crystal Structures Of The Complexes Between Bovine Beta- Trypsin And Ten P1
Variants Of Bpti. [Bos taurus (contaminant)]
RPDFCLEPPYTGPCEARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
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>cont|000054| gi|7546595|pdb|3BTM|I Chain I, The Crystal Structures Of The Complexes Between Bovine Beta- Trypsin And Ten P1 Variants Of Bpti [Bos taurus (contaminant)]
RPDFCLEPPYTGPCMARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000055| gi|7546599|pdb|3BTT|I Chain I, The Crystal Structures Of The Complexes Between Bovine Beta- Trypsin And Ten P1 Variants Of Bpti [Bos taurus (contaminant)]
RPDFCLEPPYTGPCTARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000056| gi|7546601|pdb|3BTW|I Chain I, The Crystal Structures Of The Complexes Between Bovine Beta- Trypsin And Ten P1 Variants Of Bpti [Bos taurus (contaminant)]
RPDFCLEPPYTGPCWARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000057| gi|8099320|gb|AAF72096.1|AF092513_1 kappa-casein [Bos indicus x Bos taurus (contaminant)]
RCEKDERFFSDKIAKYIPIQYVLSRYPSYGLNYYQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQP
TTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEDSPEVIESPPEINTVQVTSTAV
>cont|000058| gi|9955853|emb|CAC05490.1| alpha-1-antichymotrypsin 2 [Sus scrofa (contaminant)]
MSLFLALGLLVAGLCSRVHCVPADDPASKIVTLKDQIKKLPAHNTAVVSSNTDFAFSLYKQLALTNPHENVIFSPLSVSMALA
FLSLGARGPTLTELLEGLKFNLTKTPEAEIHQGFQHLLSTLDRSSNLLQLRLGNAMFIDEQLELLDKFVQDAHELYHSEAFPTN
FQDLEAARRLINDYVKNKTEGKIVDLFKKLDPLTKVVLVNYIYFKAKWKTPFNPNLTTEADFHVSKNRTVRVPMMGIRALT
VPYFRDEELACTVVELPYTSNDSALFILPDDGRMAAVEAKLLPETLRRWRDFLQPRWIVELYLPKFSISSDYRLHEILPQLGIE
EIFGDNANLSGITNTKPLKVSQVVHSAVLDVNEEGTEAAAATGIDINVRSLERIALHFNRPFLFVIISKDIQSIIFLGKVTKP
>cont|000059| gi|9968805|emb|CAC06755.1| alpha-1-antichymotrypsin 2 [Sus scrofa (contaminant)]
VDLFKKLDPLTKVVLVNYIYFKAKWKTPFNPNLTTEADFHVSKNRTVRVPMMGIRALTVPYFRDEELACTVVELPYTSNDS
ALFILPDDGRMAAVEAKLLPETLRRWRDFLQPRWIVELYLPKFSISSDYRLHEILPQLGIEEIFGDNANLSGITNTKPLKVSQVV
HSAVLDVNEEGTEAAAATGIDINVRSLERIALHFNRPFLFVIISKDIQSIIFLGKVTKP
>cont|000060| gi|9968807|emb|CAC06756.1| alpha-1-antichymotrypsin 3 [Sus scrofa (contaminant)]
PKLFDEHATFSVMVLVNYIYFNAKWKTPFDPEHTIESTFHVSKNRTVKVPMMSLRGLETPYFRDEELACTVVELPYTSNDSA
LFILPDDGRMAAVEAKLLPETLRRWRDSLQPRRIDALYLPRFSVSGDYQLKDTLKQLGIQKVFTHEADLSGVTGDNKLGVSK
VIHKAVLDVGEEGTEAAAATGIEMMTSTLQSLTVIFSRP
>cont|000061| gi|12084466|pdb|1F6R|A Chain A, Crystal Structure Of Apo-Bovine Alpha-Lactalbumin [Bos taurus (contaminant)]
EQLTKCEVFRELKDLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLD
DDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>cont|000062| gi|13096612|pdb|1G3B|A Chain A, Bovine Beta-Trypsin Bound To Meta-Amidino Schiff Base Magnesium(Ii) Chelate [Bos taurus (contaminant)]
DDDDKIVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYN
SNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFC
AGYLEGGKDSCQGDSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN
>cont|000063| gi|13399516|pdb|1EJM|B Chain B, Crystal Structure Of The Bpti Ala16leu Mutant In Complex With Bovine Trypsin [Bos taurus (contaminant)]
RPDFCLEPPYTGPCRLRIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000064| gi|13661026|emb|CAC37028.1| beta casein B [Bos taurus (contaminant)]
KIHPFAQTQSLVYPFPGPIHNSLPQNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPKHKEMPFPKYPVEPFTERQSLTLTDVE
NLHLPLPLLQSWMHQPHQPLPPTVMFPPQSVLSLSQSKVLPVPQKAVPYPQRDMPIQAFLLV
>cont|000065| gi|22552661|gb|AAM25909.1| kappa-casein long form [Bos grunniens (contaminant)]
RCEKDERFFSDKIAKYIPIQYVLSRYPSYGLNYYQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQP
TTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEASPEASPEVIESPPEINTVQVTSTAV
>cont|000066| gi|22552663|gb|AAM25910.1| kappa-casein short form [Bos grunniens (contaminant)]
RCEKDERFFSDKIAKYIPIQYVLSRYPSYGLNYYQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQP
TTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEASPEVIESPPEINTVQVTSTAV
>cont|000067| gi|27805979|ref|NP_776803.1| lactalbumin, alpha [Bos taurus (contaminant)]
MMSFVSLLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCK
DDQNPHSSNICNISCDKFLDDDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>cont|000068| gi|27806743|ref|NP_776414.1| inter-alpha-trypsin inhibitor (protein HC), light [Bos taurus (contaminant)]
MRSLSGLLLLLTACLAVNASSVPTLPDDIQVQENFDLSRIYGKWFNVAVGSTCPWLKRFKEKMTMSTVVLIAGPTSKEISVT
NTHRRKGVCESISGTYEKTSADGKFLYHKAKWNITMESYVVHTNYDEYAIFLTKKLSRRHGPTITVKLYGREPQLRESLLEEF
REVALGVGIPEDAIFTMPDRGECVPGEQDPVPTPLSRARRAVLTQEEEGSGAGQPVTNFSKKADSCQLDYSQGPCLGLFKRY
FYNGTSMACETFLYGGCMGNGNNFLSEKECLQTCRTVEACNLPIVQGPCRSYIQLWAFDAVKGKCVRFSYGGCKGNGNKF
YSEKECKEYCGIPGEADEELLRFSN
>cont|000069| gi|27806789|ref|NP_776392.1| transthyretin (prealbumin, amyloidosis type I) [Bos taurus (contaminant)]
MASFRLFLLCLAGLVFVSEAGSVGAGEPKCPLMVKVLDAVRGSPAANVGVKVFKKAADETWEPFASGKTSESGELHGLTTE
DKFVEGLYKVELDTKSYWKSLGISPFHEFAEVVFTANDSGPRHYTIAALLSPYSYSTTALVSSPKA
>cont|000070| gi|27806941|ref|NP_776307.1| serine (or cysteine) proteinase inhibitor, clade A (alpha-1antiproteinase, antitrypsin), member 1 [Bos taurus (contaminant)]
MALSITRGLLLLAALCCLAPISLAGVLQGHAVQETDDTSHQEAACHKIAPNLANFAFSIYHHLAHQSNTSNIFFSPVSIASAFA
MLSLGAKGNTHTEILKGLGFNLTELAEAEIHKGFQHLLHTLNQPNHQLQLTTGNGLFINESAKLVDTFLEDVKNLYHSEAFSI

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NFRDAEEAKKKINDYVEKGSHGKIVELVKVLDPNTVFALVNYISFKGKWEKPFEMKHTTERDFHVDEQTTVKVPMMNRLG
MFDLHYCDKLASWVLLLDYVGNVTACFILPDLGKLQQLEDKLNNELLAKFLEKKYASSANLHLPKLSISETYDLKSVLGDV
GITEVFSDRADLSGITKEQPLKVSKALHKAALTIDEKGTEAVGSTFLEAIPMSLPPDVEFNRPFLCILYDRNTKSPLFVGKVVN
PTQA
>cont|000071| gi|27806963|ref|NP_776953.1| casein alpha-S2 [Bos taurus (contaminant)]
MKFFIFTCLLAVALAKNTMEHVSSSEESIISQETYKQEKNMAINPSKENLCSTFCKEVVRNANEEEYSIGSSSEESAEVATEEV
KITVDDKHYQKALNEINQFYQKFPQYLQYLYQGPIVLNPWDQVKRNAVPITPTLNREQLSTSEENSKKTVDMESTEVFTKKT
KLTEEEKNRLNFLKKISQRYQKFALPQYLKTVYQHQKAMKPWIQPKTKVIPYVRYL
>cont|000072| gi|27807205|ref|NP_777093.1| serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),
member 7 [Bos taurus (contaminant)]
MPLFSLVLLILGLHCAPPNSCEGKITSCLSPQQNATLYKMSSINADFAFNLYRRFTVEIPDQNIFFSPVSIPAGLAMLSLGACSST
QTQILEGLGFNLTDTPVAEIQQGFQHLICSLNFPKKELELQMGNALFIGKQLKPLEKFLDDVKNLYETEVFSTDFSNVSAAQQ
EINSHVEKQTKGKIVGLIQDLKPNTITVLVNYLCFKAQWANPFDPSKTEEGSSFLVDKTTTVQVPMMHQMEQYYHLVDTEL
NCTVLQMDYSKNALALFVLPKEGQMEWVEGAMSSKTLKKWNRLLRKGWVDLFVPKFSISATYDLGDILLKMGIQDAFAD
NADFSGLTKDNGLKVSNVAHKAMFYIGEKGTEAVPEVRFLNQPETTLLHPIIQFDRSFLLLILEKNTRSILFLGKVVDPTEA
>cont|000073| gi|27807487|ref|NP_777193.1| serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),
member 3 [Bos taurus (contaminant)]
MRAERTSFLLALGLLVAGIPSVHCLPENVVVKDQHRRVDGHTLASSNTDFAFSLYKQLPLKNPNKNVILSPLSVSIALAFLSL
GARGSTLTEILEGLKFNLTEIQEKEIHHSVLYSSEAFPTNFRDSEAARSLINDYVKNKTQGKIEELFKYLSPRTELVLVNYIYFK
AQWKTPFDPKHTEQAEFHVSDNKTVEVPMMTLDLETPYFRDEELGCTLVELTYTSNDSALFILPDEGKMRDLEAKLTPETLT
RWRNSLQPRRIHELYLPKFSIKSNYELNDILSQLGIRKIFANADLSGITGTADLVVSQVVHGAALDVDEEGTEGAAATGISME
RTILRIIVRVNRPFLIAIVLKDTQSIIFLGKVTNPSEA
>cont|000074| gi|27807517|ref|NP_777214.1| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 [Bos taurus
(contaminant)]
MDALSEANGTFALTLLKKLGEGNSKNVFISPLSISSALAMVLLGAKGNTAAQMCQTLSLNKSSGGGEDVHQGFQNLLSEVN
RRDTQYLLRTANRLFGEKTYDFLSSFKDSCHKFYQAEMEELDFVSATEQSRKHINTWVAEKTEGKIRDLLPANSVNPMTRLV
LVNAIYFKGNWDTQFNKEHTEERPFRVSKNVEKPVQMMFKKSTCKITYIGEISTQILVLPYVGQELNMVILLPSESTDLNTVE
KALTYEKFIAWTKPDVMDEEEVEVFLPRFTLEESYDMEEFLQELGMTDAFEETRADFSGMSSGRGLHLSKVMHKSFVEVTE
EGTEAAAATGAVVMMRCLMVVPRFNANHPFLFFIQHSKTGAILFCGRFCSP
>cont|000075| gi|27819626|ref|NP_777115.1| pancreatic anionic trypsinogen [Bos taurus (contaminant)]
MHPLLILAFVGAAVAFPSDDDDKIVGGYTCAENSVPYQVSLNAGYHFCGGSLINDQWVVSAAHCYQYHIQVRLGEYNIDVL
EGGEQFIDASKIIRHPKYSSWTLDNDILLIKLSTPAVINARVSTLALPSACASGSTECLISGWGNTLSSGVNYPDLLQCLEAPLL
SHADCEASYPGEITNNMICAGFLEGGKDSCQGDSGGPVACNGQLQGIVSWGYGCAQKGKPGVYTKVCNYVDWIQETIAAN
S
>cont|000076| gi|27881412|ref|NP_776719.1| casein kappa [Bos taurus (contaminant)]
MMKSFFLVVTILALTLPFLGAQEQNQEQPIRCEKDERFFSDKIAKYIPIQYVLSRYPSYGLNYYQQKPVALINNQFLPYPYYAK
PAAVRSPAQILQWQVLSNTVPAKSCQAQPTTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLE
DSPEVIESPPEINTVQVTSTAV
>cont|000077| gi|27923792|sp|Q9TSR4|LALBA_BOSMU Alpha-lactalbumin precursor (Lactose synthase B protein) [Bos grunniens
(contaminant)]
MMSFVSLLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCK
DDQNPHSSDICNISCDKFLDDDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL
>cont|000078| gi|28373262|pdb|1CO7|I Chain I, R117h Mutant Rat Anionic Trypsin Complexed With Bovine Pancreatic Trypsin
Inhibitor (Bpti) [Bos taurus (contaminant)]
KMSRLCLSVALLVLLGTLAASTPGCDTSNQAKAQRPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSA
EDCMRTCGGAIGPWENL
>cont|000079| gi|28374081|pdb|1NMM|B Chain B, Beta-1,4-Galactosyltransferase Mutant Cys342thr Complex With Alpha-
Lactalbumin And Glcnac [Bos taurus (contaminant)]
ASMTGGQQMGRGSSLTACPEESPLLVGPMLIEFNIPVDLKLVEQQNPKVKLGGRYTPMDCISPHKVAIIIPFRNRQEHLKYWL
YYLHPILQRQQLDYGIYVINQAGESMFNRAKLLNVGFKEALKDYDYNCFVFSDVDLIPMNDHNTYRCFSQPRHISVAMDKF
GFSLPYVQYFGGVSALSKQQFLSINGFPNNYWGWGGEDDDIYNRLAFRGMSVSRPNAVIGKTRMIRHSRDKKNEPNPQRFD
RIAHTKETMLSDGLNSLTYMVLEVQRYPLYTKITVDIGTPS
>cont|000080| gi|28603766|ref|NP_788819.1| serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),
member 5 [Bos taurus (contaminant)]
MRLCLFLCLVLLGPRMATLRRSQKKKIQEVPPAVTTAPPGSRDFVFDLYRALAAAAPAQNIFFSPLSITVSLAMLSLGAQSNT
KAQILEGLGIGPGEGSEEELHSASQRLLRELQQPQDSLQLSLGNALFTKPRLPIQEAFLGAMRTLYLADTFPTNFEDPEGAKKK
INDYVAKQTKGKIVDLIKSLDGTQVMVMVNYIFFKAKWETSFNLKSTHEQDFYVTPETVVRVPMMKQQDQFYYLLDRNLS
CKVVGVPYQGNATAFFILPREGEMEQVENGLKEKTLKKWLRMPMKRRLELYLPKFSIEGSYQLEEVLPKLGIRDIFTSDADL
TGISNHSSIRVSEMVHKAVVEVDESGTQAAAATGMVITFKSARLGSQRIVFNRPFLVLIVKNSKHILFLGKVTRP
>cont|000081| gi|115646|sp|P02662|CAS1_BOVIN Alpha-S1-casein precursor [Bos taurus (contaminant)]
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MKLLILTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVAPFPEVFGKEKVNELSKDIGSESTEDQAMEDIKQMEAESISSSE
EIVPNSVEQKHIQKEDVPSERYLGYLEQLLRLKKYKVPQLEIVPNSAEERLHSMKEGIHAQQKEPMIGVNQELAYFYPELFRQ
FYQLDAYPSGAWYYVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW
>cont|000082| gi|117615|sp|P00766|CTRA_BOVIN Chymotrypsinogen A (Contains: Chymotrypsin A chain A; Chymotrypsin A
chain B; Chymotrypsin A chain C) [Bos taurus (contaminant)]
CGVPAIQPVLSGLSRIVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTSDVVVAGEFDQGSSSEKIQ
KLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDDFAAGTTCVTTGWGLTRYTNANTPDRLQQASLPLLS
NTNCKKYWGTKIKDAMICAGASGVSSCMGDSGGPLVCKKNGAWTLVGIVSWGSSTCSTSTPGVYARVTALVNWVQQTLA
AN
>cont|000083| gi|124857|sp|P00998|IPK1_PIG Pancreatic secretory trypsin inhibitor [Sus scrofa (contaminant)]
TSPQREATCTSEVSGCPKIYNPVCGTDGITYSNECVLCSENKKRQTPVLIQKSGPC
>cont|000085| gi|229725|pdb|1BPT|  Bovine Pancreatic Trypsin Inhibitor (BPTI) Mutant (Tyr 23 Replaced By Ala) (Y23A) [Bos
taurus (contaminant)]
RPDFCLEPPYTGPCKARIIRYFANAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA
>cont|000086| gi|230338|pdb|1TAB|E Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I) [Bos taurus
(contaminant)]
IVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYNSNTLN
NDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYL
EGGKDSCQGDSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN
>cont|000087| gi|230595|pdb|2KAI|B Chain B, Kallikrein A (E.C.3.4.21.8) Complex With Bovine Pancreatic Trypsin Inhibitor [Bos
taurus (contaminant)]
ADGKDYSHDLMLLRLQSPAKITDAVKVLELPTQEPELGSTCEASGWGSIEPGPDDFEFPDEIQCVQLTLLQNTFCADAHPDK
VTESMLCAGYLPGGKDTCMGDSGGPLICNGMWQGITSWGHTPCGSANKPSIYTKLIFYLDWIDDTITENP
>cont|000088| gi|230765|pdb|2TLD|E Chain E, Bovine Trypsin (E.C.3.4.21.4) Complex With A Modified SSI (Streptomyces
Subtilisin Inhibitor) With Met 70 Replaced By Gly And Met 73 Replaced By Lys (SSI(M70G,M73K)) [Bos taurus (contaminant)]
IVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYNSNTLN
NDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGLE
GGDSCQGDSGGPVVCSGKLQGIVSWGSGCAKNKPGVYTKVCNYVSWIKQTIASN
>cont|000089| gi|231307|pdb|8PTI|  Bovine Pancreatic Trypsin Inhibitor (BPTI) Mutant (Tyr 35 Replaced By Gly) (Y35G) [Bos
taurus (contaminant)]
RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVGGGCRAKRNNFKSAEDCMRTCGGA
>cont|000090| gi|250415|gb|AAB22365.1| extracellular matrix stabilizing factor, ESF=inter-alpha-trypsin inhibitor homolog (cattle,
fetal bovine serum, Peptide Partial, 14 aa) [Bos taurus (contaminant)]
XVLGQEEEGXXDGQ
>cont|000091| gi|284626|pir||S23202 kappa-casein - bovine [Bos taurus (contaminant)]
EEQNQEQPIRCEKDERFWQVLSNTVPAKSCQAQPTTMSNTVPAKSCQAQPTTM
>cont|000092| gi|423225|pir||S31220 82K protein - bovine [Bos taurus (contaminant)]
SLPGRAVDGIEVYSTKVNXK
>cont|000093| gi|423226|pir||S31221 86K protein - bovine [Bos taurus (contaminant)]
SISGESGERTEDVDQVTVYK
>cont|000094| gi|442595|pdb|1AAL|A Chain A, Bovine Pancreatic Trypsin Inhibitor (Bpti, Basic) Mutant With Cys 30 Replaced By
Val And Cys 51 Replaced By Ala (C30v,C51a) [Bos taurus (contaminant)]
RPDFCLEPPYTGPCKARIIRYFYNAKAGLVQTFVYGGCRAKRNNFKSAEDAMRTCGGA
>cont|000095| gi|999628|pdb|1EPT|C Chain C, Porcine E-Trypsin (E.C.3.4.21.4) [Sus scrofa (contaminant)]
SSGSSYPSLLQCLKAPVLSNSSCKSSYPGQITGNMICVGFLQGGKDSCQGDSGGPVVCNGQLQGIVSWGYGCAQKNKPGVY
TKVCNYVNWIQQTIAAN
>cont|000096| gi|1351320|sp|P49142|TTHY_PETBR Transthyretin precursor (Prealbumin) [Petaurus breviceps (contaminant)]
MAFHSLLLLCLAGLLFVSEAGPVAHGGEDSKCPLMVKVLDAVRGRPAVNVDVKVFKKTEKQTWELFASGKTNDNGEIHEL
TSDDKFGEGLYKVEFDTISYWKALGVSPFHEYADVVFTANDAGHRHYTIAAQLSPYSFSTTAIVSNPTE
>cont|000097| gi|1351907|sp|P02769|ALBU_BOVIN Serum albumin precursor (Allergen Bos d 6) (BSA) [Bos taurus (contaminant)]
MKWVTFISLLLLFSSAYSRGVFRRDTHKSEIAHRFKDLGEEHFKGLVLIAFSQYLQQCPFDEHVKLVNELTEFAKTCVADESH
AGCEKSLHTLFGDELCKVASLRETYGDMADCCEKQEPERNECFLSHKDDSPDLPKLKPDPNTLCDEFKADEKKFWGKYLYE
IARRHPYFYAPELLYYANKYNGVFQECCQAEDKGACLLPKIETMREKVLASSARQRLRCASIQKFGERALKAWSVARLSQK
FPKAEFVEVTKLVTDLTKVHKECCHGDLLECADDRADLAKYICDNQDTISSKLKECCDKPLLEKSHCIAEVEKDAIPENLPPL
TADFAEDKDVCKNYQEAKDAFLGSFLYEYSRRHPEYAVSVLLRLAKEYEATLEECCAKDDPHACYSTVFDKLKHLVDEPQ
NLIKQNCDQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESERMPCTEDYLSLILNRLCVLHEKTP
VSEKVTKCCTESLVNRRPCFSALTPDETYVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQLKTVMENF
VAFVDKCCAADDKEACFAVEGPKLVVSTQTALA
>cont|000098| gi|1364186|emb|CAA27065.1| unnamed protein product [Bos taurus (contaminant)]
RPDFCLEPPYTGPCKAKMIRYFYNAKAGFCETFVYGGCKAKSNNFRSAEDCMRTCGGA
>cont|000099| gi|1703026|sp|P50447|A1AT_PIG Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase)
[Sus scrofa (contaminant)]
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MASSSTWGLLLLAGLCCLVPISLAEGLQGHAVQETDVPRHDHEQHQEAACHRIAPNLADFAFSLYRQVARQSNTSNIFLSPV
TIARAFAMLSLGTKGATHAEILEGLQFNLTEKAEAEIHEGFQHLLHTLNQPDNQLQLTTGNGLFIDEKAKLVPKFLEDVKNLY
HSEAFSINFRDTEEAKKCINDYVEKGSQGKIVDLVDELDKDTVFALVNYIFFKGKWEKPFEVEQTTEEDFHVDEETTVKVPM
MNRLGMFDLHHCDKLSSWVLLMDYVATATAFFILPDQGKLHQLEDMLTKEIRAKFLEKRYPSSANLHLPKLTISGTYDLKS
LLGNLGITKVFSDEADLSGVTEEQPLKLSKALHRAVLTIDEKGTEATGATILEAIPMSIPPNVKFNKPFLFLIYDTKTKAVLFM
GKVMNPTQK
>cont|000100| gi|1827750|pdb|1MTN|C Chain C, Bovine Alpha-Chymotrypsin:bpti Crystallization [Bos taurus (contaminant)]
ANTPDRLQQASLPLLSNTNCKKYWGTKIKDAMICAGASGVSSCMGDSGGPLVCKKNGAWTLVGIVSWGSSTCSTSTPGVY
ARVTALVNWVQQTLAAN
>cont|000101| gi|2392548|pdb|1TAW|A Chain A, Bovine Trypsin Complexed To Appi [Bos taurus (contaminant)]
IVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYNSNTLN
NDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSTSSCKSAYPGQITSNMFCAGYL
EGGKDSCQGDSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN
>cont|000102| gi|2497580|sp|Q29100|UPTI_PIG Uterine plasmin/trypsin inhibitor precursor (UPTI) [Sus scrofa (contaminant)]
MSRLCLSAALLLLLLGALVASTPGDEESSLVRAGPPGFCREPPYTGPCSAHFVRYFYNATTGLCQSFVYGGCRGKQNNFMDE
KECLHTCDTCAKAQGKRGNCASEMLKSTRPQGWAVAAFQMG
>cont|000104| gi|2507586|sp|P04366|AMBP_PIG AMBP protein precursor (Contains: Alpha-1-microglobulin; Inter-alpha-trypsin
inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (EI-14)) [Sus scrofa (contaminant)]
AVSASPVLTLPNDIQVQENFDLSRIYGKWFHVAVGSTCPWLKRFKDKMTMGTLMLGEGATEREISVTKTHRRKGICEVISGA
YEKTSTDGKFLYHKSKWNITMESYVVHTNYDEYAIFLTKKFSRRHGPTLTAKLYGREPQLRESLLEEFREVALGVGIPEDSIF
TMPDRGECVPGEQEPEPTLLSRARRAVLPQEEEGSGAGQPVADFSKKEDSCQLGYSQGPCLGMIKRYFYNGSSMACETFHY
GGCMGNGNNFVSEKECLQTCRTVEACSLPIVSGPCRGFFQLWAFDAVQGKCVLFNYGGCQGNGNQFYSEKECKEYCGVPG
EEDEELLRSSN
>cont|000105| gi|2625070|gb|AAB86616.1| kappa-casein [Bos grunniens (contaminant)]
NNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQPTTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPT
TEAVESTVATLEASPEASPEVIESPPEINTVQVTSTAV
>cont|000106| gi|2801548|gb|AAB97519.1| kappa-casein [Bos taurus (contaminant)]
KNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEDSPEVIEGPPEINTVQVTSTAV
>cont|000107| gi|3024032|sp|Q29052|ITIH1_PIG Inter-alpha-trypsin inhibitor heavy chain H1 precursor (ITI heavy chain H1) (Inter-
alpha-inhibitor heavy chain 1) [Sus scrofa (contaminant)]
MDGTMGLQGLLCLCLASHLALQAMPTQGSPTDSTKGNKAVNGVVIRSLKVNCKVTSRFAHYVVTSQVVNNTNKPKEVAF
DVEIPKTAFISDFAITADENTFVGDIKDKVTAWKQYRKAAISGENSGLVRASGRTMEQFTIHVTIGPRSKATFQLTYEEVLRRK
LTQYDIVIKVKPKQLVQHFEIDVDIFEPQGISKLDAQASFLSKEAAAQLIKKSFSGKKGHVLFRPTVGQQQSCSTCSTTLLNGD
FKVTYDVNREKLCDLLVANNYFAHFFAPQNLTKLNKNVVFVIDISSSMEGQKVKQTKEALLKILSDLKPGDYFDLVLFGSAV
QSWRGSLVQASTANLDAARSYVRQFSLAGSTNLNGGLLRGIEILNKAQGSLPEFSNRASILIMLTDGEPTEGVTDRSQILKNV
RDAIRGRFPLYNLGFGHDVEWNFLEVRALENNGRAQRIYEDHDSAQQLQGFYDQVANPLLKDVELQYPADAVLALTQHRH
KQYYEGSEITVAGRIADNKLSSFKADVQASGDQGFKTTCLVDEEEMKKLLQERGHMLENYVERLWAYLTIQELLAKRMKL
EWAEKASVSAKALQMSLDYQFVTPLTSMTIRGMADKDGLEPVIDKPLEDSQPLEMLGPRRKFVLSASQPSPTHPSSSIQKLPD
RVTGVDTDPHFIIRVPQKEDTLCFNINEEPGVVLSLVQDPDTGFSVNGQLIGNEARCPGKHEGTYFGRLGIANPATGFQLEVTP
QNITLNPGSGGPVFSWRDQASLRQDEVVVTINRKRNLGVVREDGGTFEVVLHRLWKGSAIHQDFLGFYVLDSHRMSARTHG
LLAQFFHPFDYKVSDIHPGSDPTKTDATMVVKNRQLTVTRGLQKDYSKDPRHGLKVTCWFIHNNGDGLIDGVHTDYIVPDIF
>cont|000108| gi|3024050|sp|O02668|ITIH2_PIG Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (Inter-
alpha-inhibitor heavy chain 2) [Sus scrofa (contaminant)]
MKGLTCFLLCFLLSEAQGFEIPTNGLSEFAEYGDLAELALGKFHVVPGNRRSQEGVDQVTLYSYKVQSTITSRMANTVIQTK
VVNHSPEPQDVVFDIQIPKGAFISNFSMTVDGTKFTSSIKEKTVGRALYWQARAKGKTAGLVRSRALDMENFKTEVNIAPGA
KVQFELHYQEVKWRNLGSYEHRIHLQPGRLAKHLEVDVQIIEPQGLRFLHVLDTFDGHFDGVPVVVKGQQKAHVAFKPTVA
QQRKCPSCSETAVDGELVVMYDVNREQKAGELQLFNGYFVHFFAPESMDPIPKNILFVIDVSGSMWGIKMKQTVEAMKTIL
DDLRAEDQFSLVDFNHNIRTWRNDLVSATKTQVADAKTYIEKIQPSGGTNINEALLRAIFILNEANNLGLLDPNSVSLIILVSD
GDPTVGELQLSKIQKNVKQNIQDNVSLFSLGIGFDVDYDFLKRLSNDNRGMAQRIYGNQDTASQLKKFYNQVSTPLLRNVQ
FNYPQASVTDVTQNSFPNYFGGSEIVVAGKFNPEKLEQLQGIITATSANVELVLETLAEMDGLEAFLAKDRHADPDFTKKLW
AYLTINQLLDERSRAPSAAVKKKITKSILQMSLDHHIVTPLTAMVVENEAGDERMLADAPPQDQSCCSGTLNYGRKVTPNSL
PSWVNPLPTPRVPLPAVGPSVIEATPPPHVMRVENDPHFIIYLPRSQQNICFNIDSEPGKILNLVSDPESGIVINGQLISAKKLKD
GKLSTYFGKIGFYFQHEDVKVEISTETISLSRGSRVSVLSWSDSALVLNQRVHISVKKEKTVTVTLDQEVSFSVLLHRVWKKH
PINVDFLGIYIPPTTKFSPKAHGLIGQFMHEPEIRIFNERPGKDPEKPEASMEVKGQTLVVTRGLQKDYRTDRVFGTDVPCWFV
HNSGKGFIDGHYKDYLVPLLYSFLKRP
>cont|000109| gi|3098478|gb|AAC15664.1| inter-alpha-trypsin inhibitor heavy-chain H1 [Sus scrofa (contaminant)]
SAVQSWRGSLVQASTANLDAARSYVRQFSLAG
>cont|000110| gi|4261799|gb|AAD14099.1|1683174_1 alpha-s1 casein [Bos taurus (contaminant)]
LFRQFYQLDAYPSGAWYYVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW
>cont|000111| gi|4887004|gb|AAD32139.1|AF123250_1 kappa-casein precursor [Bos taurus (contaminant)]
HCEKDERFFSDKIAKYIPIQYVLSRYPSYGLNYYQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQP
TTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEDSPEVIESPPEINTVQVTSTAV
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>cont|000112| gi|6451694|dbj|BAA86914.1| alpha lactalbumin [Bos taurus (contaminant)]
GLMPGPLRLFPQIKGGEQCGDPISESWGVTKMMSFVSLLLVGILFHATQAEQLTKCEVFRELKDLKGYGGVSLPECEFPAILL
CPIIHPLHSFPP
>cont|000113| gi|7441526|pir||A59068 beta-casein variant CnH - bovine [Bos taurus (contaminant)]
RELEELNVPGEIVESLSSSEESITCINKKIEKFQSEEQQQTEDELQDKIHPFAQTQSLVYPFPGPIPNSLPQNIPPLTQTPVVVPPFI
QPEVMGVSKVKEAMAPKHKEMPFPKYPVEPFTESQSLTLTDVENLHLPPLLLQSWMHQPHQPLPPTVMFPPQSVLSLSQSKV
LPVPQKAVPYPQRDMPIQAFLLYQEPVLGPVRGPFPIIV
>cont|000114| gi|7546585|pdb|3BTD|I Chain I, The Crystal Structures Of The Complexes Between The Bovine Beta-Trypsin And Ten
P1 Variants Of Bpti. [Bos taurus (contaminant)]
RPDFCLEPPYTGPCDARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000115| gi|7546587|pdb|3BTF|I Chain I, The Crystal Structures Of The Complexes Between Bovine Beta- Trypsin And Ten P1
Variants Of Bpti. [Bos taurus (contaminant)]
RPDFCLEPPYTGPCFARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000116| gi|7546589|pdb|3BTG|I Chain I, The Crystal Structures Of The Complexes Between Bovine Beta- Trypsin And Ten P1
Variants Of Bpti [Bos taurus (contaminant)]
RPDFCLEPPYTGPCGARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000117| gi|7546591|pdb|3BTH|I Chain I, The Crystal Structures Of The Complexes Between Bovine Beta- Trypsin And Ten P1
Variants Of Bpti [Bos taurus (contaminant)]
RPDFCLEPPYTGPCHARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000118| gi|7546597|pdb|3BTQ|I Chain I, The Crystal Structures Of The Complexes Between Bovine Beta- Trypsin And Ten P1
Variants Of Bpti [Bos taurus (contaminant)]
RPDFCLEPPYTGPCQARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>cont|000119| gi|8099322|gb|AAF72097.1|AF105260_1 kappa-casein precursor [Bos taurus (contaminant)]
RCEKDERFFSDKIAKYIPIQYVLSRYPSYGLNYYQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQP
TTMARHPHPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPITEAVESTVATLEDSPEVIESPPEINTVQVTSTAV
>cont|000120| gi|8099324|gb|AAF72098.1|AF121023_1 kappa-casein precursor [Bos taurus x Bos indicus (contaminant)]
RCEKDERFFSDKIAKYIPIQYVLSRYPSYGLNYYQQKPVALINNQFLPYPYYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQP
TTMARHPHPHLAFMAIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEDSPEVIESPPEINTVQVTSTAV
>cont|000121| gi|9968809|emb|CAC06757.1| alpha-1-antichymotrypsin 1 [Sus scrofa (contaminant)]
NKTEGKIVELIKRLIPVTEAVLVNYIYFKAQWMTHFDPNLTTEADFYVSKNRTVRVPMMGIKNLTVPYFRDEELACTVVELP
YTSNDSTLFILPDDGRMAAVEAKLLPETLRRWRDSLQPRRIEALHLPRFSISSDYKLQEILPRLGIQKIFSEEADLSGITDTTPLC
VSQVVHSAVLDVDEEGTEGAASTGVVIERKSFENFIVRFDSPFLFARSS
>cont|000122|  spt|P13645| Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10) [Homo sapiens (contaminant)]
MSVRYSSSKHYSSSRSGGGGGGGGCGGGGGVSSLRISSSKGSLGGGFSSGGFSGGSFSRGSSGGGCFGGSSGGYGGLGGFGG
GSFHGSYGSSSFGGSYGGSFGGGNFGGGSFGGGSFGGGGFGGGGFGGGFGGGFGGDGGLLSGNEKVTMQNLNDRLASYLD
KVRALEESNYELEGKIKEWYEKHGNSHQGEPRDYSKYYKTIDDLKNQILNLTTDNANILLQIDNARLAADDFRLKYENEVAL
RQSVEADINGLRRVLDELTLTKADLEMQIESLTEELAYLKKNHEEEMKDLRNVSTGDVNVEMNAAPGVDLTQLLNNMRSQ
YEQLAEQNRKDAEAWFNEKSKELTTEIDNNIEQISSYKSEITELRRNVQALEIELQSQLALKQSLEASLAETEGRYCVQLSQIQ
AQISALEEQLQQIRAETECQNTEYQQLLDIKIRLENEIQTYRSLLEGEGSSGGGGRGGGSFGGGYGGGSSGGGSSGGGYGGGH
GGSSGGGYGGGSSGGGSSGGGYGGGSSSGGHGGGSSSGGHGGSSSGGYGGGSSGGGGGGYGGGSSGGGSSSGGGYGGGSS
SGGHKSSSSGSVGESSSKGPRY
>cont|000123|  spt|P11217| Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase) [Homo sapiens (contaminant)]
SRPLSDQEKRKQISVRGLAGVENVTELKKNFNRHLHFTLVKDRNVATPRDYYFALAHTVRDHLVGRWIRTQQHYYEKDPK
RIYYLSLEFYMGRTLQNTMVNLALENACDEATYQLGLDMEELEEIEEDAGLGNGGLGRLAACFLDSMATLGLAAYGYGIRY
EFGIFNQKISGGWQMEEADDWLRYGNPWEKARPEFTLPVHFYGHVEHTSQGAKWVDTQVVLAMPYDTPVPGYRNNVVNT
MRLWSAKAPNDFNLKDFNVGGYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVAATLQDIIRRFKSSKFGCRDPV
RTNFDAFPDKVAIQLNDTHPSLAIPELMRILVDLERMDWDKAWDVTVRTCAYTNHTVLPEALERWPVHLLETLLPRHLQIIY
EINQRFLNRVAAAFPGDVDRLRRMSLVEEGAVKRINMAHLCIAGSHAVNGVARIHSEILKKTIFKDFYELEPHKFQNKTNGIT
PRRWLVLCNPGLAEVIAERIGEDFISDLDQLRKLLSFVDDEAFIRDVAKVKQENKLKFAAYLEREYKVHINPNSLFDIQVKRIH
EYKRQLLNCLHVITLYNRIKREPNKFFVPRTVMIGGKAAPGYHMAKMIIRLVTAIGDVVNHDPAVGDRLRVIFLENYRVSLA
EKVIPAADLSEQISTAGTEASGTGNMKFMLNGALTIGTMDGANVEMAEEAGEENFFIFGMRVEDVDKLDQRGYNAQEYYD
RIPELRQVIEQLSSGFFSPKQPDLFKDIVNMLMHHDRFKVFADYEDYIKCQEKVSALYKNPREWTRMVIRNIATSGKFSSDRTI
AQYAREIWGVEPSRQRLPAPDEAI
>cont|000124|  spt|P81605| Dermcidin precursor (Preproteolysin) (Contains: Survival-promoting peptide; DCD-1) [Homo sapiens
(contaminant)]
MRFMTLLFLTALAGALVCAYDPEAASAPGSGNPCHEASAAQKENAGEDPGLARQAPKPRKQRSSLLEKGLDGAKKAVGGL
GKLGKDAVEDLESVGKGAVHDVKDVLDSVL
>cont|000125|  spt|P02538| Keratin, type II cytoskeletal 6A (Cytokeratin 6A) (CK 6A) (K6a keratin) [Homo sapiens (contaminant)]
ASTSTTIRSHSSSRRGFSANSARLPGVSRSGFSSVSVSRSRGSGGLGGACGGAGFGSRSLYGLGGSKRISIGGGSCAISGGYGSR
AGGSYGFGGAGSGFGFGGGAGIGFGLGGGAGLAGGFGGPGFPVCPPGGIQEVTVNQSLLTPLNLQIDPTIQRVRAEEREQIKT
LNNKFASFIDKVRFLEQQNKVLETKWTLLQEQGTKTVRQNLEPLFEQYINNLRRQLDSIVGERGRLDSELRGMQDLVEDFKN
KYEDEINKRTAAENEFVTLKKDVDAAYMNKVELQAKADTLTDEINFLRALYDAELSQMQTHISDTSVVLSMDNNRNLDLD
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SIIAEVKAQYEEIAQRSRAEAESWYQTKYEELQVTAGRHGDDLRNTKQEIAEINRMIQRLRSEIDHVKKQCANLQAAIADAE
QRGEMALKDAKNKLEGLEDALQKAKQDLARLLKEYQELMNVKLALDVEIATYRKLLEGEECRLNGEGVGQVNISVVQSTV
SSGYGGASGVGSGLGLGGGSSYSYGSGLGVGGGFSSSSGRAIGGGLSSVGGGSSTIKYTTTSSSSRKSYKH
>cont|000126|  spt|P48666| Keratin, type II cytoskeletal 6C (Cytokeratin 6C) (CK 6C) (K6c keratin) [Homo sapiens (contaminant)]
ASTSTTIRSHSSSRRGFSANSARLPGVSRSGFSSISVSRSRGSGGLGGACGGAGFGSRSLYGLGGSKRISIGGGSCAISGGYGSR
ARASYGFGGAGSGFGFGGGAGIGFDLGGGAGLAGGFGGPGFPVCPPGGIQEVTVNQSLLTPLNLQIDPAIQRVRAEEREQIKT
LNNKFASFIDKVRFLEQQNKVLETKWTLLQEQGTKTVRQNLEPLFEQYINNLRRQLDSIVGERGRLDSELRGMQDLVEDFKN
KYEDEINKRTAAENEFVTLKKDVDAAYMNKVELQAKADTLTDEINFLRALYDAELSQMQTHISDTSVVLSMDNNRNLDLD
SIIAEVKAQYEEIAQRSRAEAESWYQTKYEELQVTAGRHGDDLRNTKQEIAEINRMIQRLRSEIDHVKKQCANLQAAIADAE
QRGEMALKDAKNKLEGLEDALQKAKQDLARLLKEYQELMNVKLALDVEIATYRKLLEGEECRLNGEGVGQVNISVVQSTV
SSGYGGASGVGSGLGLGGGSSYSYGSGLGVGGGFSSSSGRAIGGGLSSVGGGSSTIKYTTTSSSSRKSYKH
>cont|000127|  spt|P48668| Keratin, type II cytoskeletal 6E (Cytokeratin 6E) (CK 6E) (K6e keratin) [Homo sapiens (contaminant)]
ASTSTTIRSHSSSRRGFSANSARLPGVSRSGFSSISVSRSRGSGGLGGACGGAGFGSRSLYGLGGSKRISIGGGSCAISGGYGSR
ARGSYGFGGAGSGFGFGGGAGIGFDLGGGAGLAGGFGGPGFPVCPPGGIQEVTVNQSLLTPLNLQIDPAIQRVRAEEREQIKT
LNNKFASFIDKVRFLEQQNKVLDTKWTLLQEQGTKTVRQNLEPLFEQYINNLRRQLDNIVGERGRLDSELRNMQDLVEDLK
NKYEDEINKRTAAENEFVTLKKDVDAAYMNKVELQAKADTLTDEINFLRALYDAELSQMQTHISDTSVVLSMDNNRNLDL
DSIIAEVKAQYEEIAQRSRAEAESWYQTKYEELQVTAGRHGDDLRNTKQEIAEINRMIQRLRSEIDHVKKQCASLQAAIADAE
QRGEMALKDAKNKLEGLEDALQKAKQDLARLLKEYQELMNVKLALDVEIATYRKLLEGEECRLNGEGIGQVNVSVVQSTI
SSGYGGASGVGSGLGLGGGSSYSYGSGLGIGGGFSSSSGRAIGGGLSSVGGGSSTIKYTTTSSSSRKSYKH
>cont|000129|  trm|Q8N175| Keratin 10 [Homo sapiens (contaminant)]
MSVRYSSSKHYSSSRSGGGGGGGGCGGGGGVSSLRISSSKGSLGGGFSSGGFSGGSFSRGSSGGGCFGGSSGGYGGLGGFGG
GSFRGSYGSSSFGGSYGGSFGGGSFGGGSFGGGSFGGGGFGGGGFGGGFGGGFGGDGGLLSGNEKVTMQNLNDRLASYLD
KVRALEESNYELEGKIKEWYEKHGNSHQGEPRDYSKYYKTIDDLKNQILNLTTDNANILLQIDNARLAADDFRLKYENEVAL
RQSVEADINGLRRVLDELTLTKADLEMQIESLTEELAYLKKNHEEEMKDLRNVSTGDVNVEMNAAPGVDLTQLLNNMRSQ
YEQLAEQNRKDAEAWFNEKSKELTTEIDNNIEQISSYKSEITELRRNVQALEIELQSQLALKQSLEASLAETEGRYCVQLSQIQ
AQISALEEQLQQIRAETECQNTEYQQLLDIKIRLENEIQTYRSLLEGEGSSGGGGRGGGSFGGGYGGGSSGGGSSGGGYGGGH
GGSSGGGYGGGSSGGGSSGGGYGGGSSSGGHGGSSSGGYGGGSSGGGGGGYGGGSSGGGSSSGGGYGGGSSSGGHKSSSS
GSVGESSSKGPRY
>cont|000130|  gb|AAA59199.1| keratin 10 [Homo sapiens (contaminant)]
GKYYKTIDDLKNQILNLTTDNANILLQIDNARLAADDFRLKYENEVALRQSVEADINGLRRVLDELTLTKADLEMQIESLTEE
LAYLKKNHEEEMKDLRNVSTGDVNVEMNAAPGVDLTQLLNNMRSQYEQLAEQNRKDAEAWFNEKSKELTTEIDNNIEQIS
SYKSEITELRRNVQALEIELQSQLALKQSLEASLAETEGRYCVQLSQIQAQISALEEQLQQIRAETECQNTEYQQLLDIKIRLEN
EIQTYRGLLEGEGSSGGGGRGGGSFGGGYGGGSSGGGSSGGGHGGSSGGGYGGGSSGGGSSGGGYGGGSSSGGHGGSSSG
GYGGGSSGGGGGGYGGGSSGGGSSSGGGYGGGSSSGGHKSSSSGSVGESSSKGPRY
>cont|000131|  gb|AAA59468.1| keratin-10 [Homo sapiens (contaminant)]
MQNLNDRLASYLDKVRALEESNYELEGKIKEWYEKHGNSHQGEPRDYSKYYKTIDDLKNQILNLTTDNANILLQIDNARLA
ADDFRLKYENEVALRQSVEADINGLRRVLDELTLTKADLEMQIESLTEYVAYLKKNHEEEMKDLRNVSTGDVNVEMNAAP
GIDLTQLLNNMRSQYEQLAEQNRKDAEAWVNEKSKELTTEIDNNIEQISSYKSEITELRRNVQRLEIELQSQLALKQSLEASLA
ETEGRYCVQLSQIQAQISALEEQLQQIRAETECQNTEYQQLLDIKIRLENEIQTYRSLLEGEGSSRSGGRGGGSFGGGYGGGTS
GGGTSGGGYGGGHGGSSGGGYGGGTSGGGTSGGGLRGELHGGHAHSTGGYGGGNSGGGGGGLRGRHSGGGSSSGGGYG
GGSSSGGHKSSSSGSVGESSSKGPRY
>cont|000132|  sp|P04264| K2C1_HUMAN Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair
alpha protein) [Homo sapiens (contaminant)]
MSRQFSSRSGYRSGGGFSSGSAGIINYQRRTTSSSTRRSGGGGGRFSSCGGGGGSFGAGGGFGSRSLVNLGGSKSISISVARGG
GRGSGFGGGYGGGGFGGGGFGGGGFGGGGIGGGGFGGFGSGGGGFGGGGFGGGGYGGGYGPVCPPGGIQEVTINQSLLQP
LNVEIDPEIQKVKSREREQIKSLNNQFASFIDKVRFLEQQNQVLQTKWELLQQVDTSTRTHNLEPYFESFINNLRRRVDQLKS
DQSRLDSELKNMQDMVEDYRNKYEDEINKRTNAENEFVTIKKDVDGAYMTKVDLQAKLDNLQQEIDFLTALYQAELSQM
QTQISETNVILSMDNNRSLDLDSIIAEVKAQNEDIAQKSKAEAESLYQSKYEELQITAGRHGDSVRNSKIEISELNRVIQRLRSEI
DNVKKQISNLQQSISDAEQRGENALKDAKNKLNDLEDALQQAKEDLARLLRDYQELMNTKLALDLEIATYRTLLEGEESRM
SGECAPNVSVSVSTSHTTISGGGSRGGGGGGYGSGGSSYGSGGGSYGSGGGGGGGRGSYGSGGSSYGSGGGSYGSGGGGG
GHGSYGSGSSSGGYRGGSGGGGGGSSGGRGSGGGSSGGSIGGRGSSSGGVKSSGGSSSVRFVSTTYSGVTR
>cont|000133|  pir|KRHU0| keratin 10, type I, cytoskeletal - human [Homo sapiens (contaminant)]
MSVRYSSSKHYSSSRSGGGGGGGGCGGGGGVSSLRISSSKGSLGGGFSSGGFSGGSFSRGSSGGGCFGGSSGGYGGLGGFGG
GSFHGSYGSSSFGGSYGGSFGGGNFGGGSFGGGSFGGGGFGGGGFGGGFGGGFGGDGGLLSGNEKVTMQNLNDRLASYLD
KVRALEESNYELEGKIKEWYEKHGNSHQGEPRDYSKYYKTIDDLKNQILNLTTDNANILLQIDNARLAADDFRLKYENEVAL
RQSVEADINGLRRVLDELTLTKADLEMQIESLTEELAYLKKNHEEEMKDLRNVSTGDVNVEMNAAPGVDLTQLLNNMRSQ
YEQLAEQNRKDAEAWFNEKSKELTTEIDNNIEQISSYKSEITELRRNVQALEIELQSQLALKQSLEASLAETEGRYCVQLSQIH
AQISALEEQLQQIRAETECQNTEYQQLLDIKIRLENEIQTYRSLLEGEGSSGGGGRGGGSFGGGYGGGSSGGGSSGGGYGGGH
GGSSGGGYGGGSSGGGSSGGGYGGGSSSGGHGGGSSSGGHGGSSSGGYGGGSSGGGGGGYGGGSSGGGSSSGGGYGGGSS
SGGHKSSSSGSVGESSSKGPRY
>cont|000134|  rf|NP_006112.2| keratin 1 [Homo sapiens (contaminant)]
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MSRQFSSRSGYRSGGGFSSGSAGIINYQRRTTSSSTRRSGGGGGRFSSCGGGGGSFGAGGGFGSRSLVNLGGSKSISISVARGG
GRGSGFGGGYGGGGFGGGGFGGGGFGGGGIGGGGFGGFGSGGGGFGGGGFGGGGYGGGYGPVCPPGGIQEVTINQSLLQP
LNVEIDPEIQKVKSREREQIKSLNNQFASFIDKVRFLEQQNQVLQTKWELLQQVDTSTRTHNLEPYFESFINNLRRRVDQLKS
DQSRLDSELKNMQDMVEDYRNKYEDEINKRTNAENEFVTIKKDVDGAYMTKVDLQAKLDNLQQEIDFLTALYQAELSQM
QTQISETNVILSMDNNRSLDLDSIIAEVKAQYEDIAQKSKAEAESLYQSKYEELQITAGRHGDSVRNSKIEISELNRVIQRLRSEI
DNVKKQISNLQQSISDAEQRGENALKDAKNKLNDLEDALQQAKEDLARLLRDYQELMNTKLALDLEIATYRTLLEGEESRM
SGECAPNVSVSVSTSHTTISGGGSRGGGGGGYGSGGSSYGSGGGSYGSGGGGGGGRGSYGSGGSSYGSGGGSYGSGGGGG
GHGSYGSGSSSGGYRGGSGGGGGGSSGGRGSGGGSSGGSIGGRGSSSGGVKSSGGSSSVRFVSTTYSGVTR
>cont|000135|  cra|hCP1609934.2| keratin 1 (epidermolytic hyperkeratosis) [Homo sapiens (contaminant)]
MSRQFSSRSGYRSGGGFSSGSAGIINYQRRTTSSSTRRSGGGGGRFSSCGGGGGSFGAGGGFGSRSLVNLGGSKSISISVARGG
GRGSGFGGGYGGGGFGGGGFGGGGFGGGGIGGGGFGGFGSGGGGFGGGGFGGGGYGGGYGPVCPPGGIQEVTINQSLLQP
LNVEIDPEIQKVKSREREQIKSLNNQFASFIDKVRFLEQQNQVLQTKWELLQQVDTSTRTHNLEPYFESFINNLRRRVDQLKS
DQSRLDSELKNMQDMVEDYRNKYEDEINKRTNAENEFVTIKKDVDGAYMTKVDLQAKLDNLQQEIDFLTALYQAELSQM
QTQISETNVILSMDNNRSLDLDSIIAEVKAQYEDIAQKSKAEAESLYQSKYEELQITAGRHGDSVRNSKIEISELNRVIQRLRSEI
DNVKKQISNLQQSISDAEQRGENALKDAKNKLNDLEDALQQAKEDLARLLRDYQELMNTKLALDLEIATYRTLLEGEESRM
SGECAPNVSVSVSTSHTTISGGGSRGGGGGGYGSGGSSYGSGGGSYGSGGGGGGGRGSYGSGGSSYGSGGGSYGSGGGGG
GHGSYGSGSSSGGYRGGSGGGGGGSSGGRGSGGGSSGGSIGGRGSSSGGVKSSGGSSSVKFVSTTYSGVTR
>cont|000136|  cra|hCP1812051| keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris) [Homo sapiens
(contaminant)]
MSVRYSSSKHYSSSRSGGGGGGGGCGGGGGVSSLRISSSKGSLGGGFSSGGFSGGSFSRGSSGGGCFGGSSGGYGGLGGFGG
GSFRGSYGSSSFGGSYGGSFGGGSFGGGSFGGGSFGGGGFGGGGFGGGFGGGFGGDGGLLSGNEKVTMQNLNDRLASYLD
KVRALEESNYELEGKIKEWYEKHGNSHQGEPRDYSKYYKTIDDLKNQILNLTTDNANILLQIDNARLAADDFRLKYENEVAL
RQSVEADINGLRRVLDELTLTKADLEMQIESLTEELAYLKKNHEEEMKDLRNVSTGDVNVEMNAAPGVDLTQLLNNMRSQ
YEQLAEQNRKDAEAWFNEKSKELTTEIDNNIEQISSYKSEITELRRNVQALEIELQSQLALKQSLEASLAETEGRYCVQLSQIQ
AQISALEEQLQQIRAETECQNTEYQQLLDIKIRLENEIQTYRSLLEGEGSSGGGGRGGGSFGGGYGGGSSGGGSSGGGYGGGH
GGSSGGGYGGGSSGGGSSGGGYGGGSSSGGHGGSSSGGYGGGSSGGGGGGYGGGSSGGGSSSGGGYGGGSSSGGHKSSSS
GSVGESSSKGPRSAETSWDTNKTRVIKTIIEEVAPDGRVLSSMVESETKKHYY
>cont|000137|  spt|P00760| Cationic trypsin precursor (EC 3.4.21.4) (Beta-trypsin) (Fragment) [Bos taurus (contaminant)]
FIFLALLGAAVAFPVDDDDKIVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGN
EQFISASKSIVHPSYNSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSS
CKSAYPGQITSNMFCAGYLEGGKDSCQGDSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN
>cont|000138|  spt|P79334| Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase) [Bos taurus (contaminant)]
SRPLTDQEKRKQISVRGLAGVENVTELKKNFNRHLHFTLVKDRNVATPRDYYFALAYTVRDHLVGRWIRTQQHYYEKDPK
RIYYLSLEFYIGRTLQNTMVNLALENACDEATYQLGLDMEELEEIEEDAGLGNGGLGRLAACFLDSMATLGLAAYGYGIRY
EFGIFNQKISGGWQMEEADDWLRYGNPWEKARPEFTLPVHFYGRVEHTSQGAKWVDTQVVLAMPYDTPVPGYRNNVVNT
MRLWSAKAPNDFNLKDFNVGGYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVAATLQDIIRRFKSSKFGCLDPV
RTNFDAFPDKVAIQLNDTHPSLAIPELMRILVDQERLEWEKAWEVTVKTCAYTNHTVLPEALERWPVHLIETLLPRHLQIIYEI
NQRFLNRVAAAFPGDVDRLRRMSLVEEGAVKRINMAHLCIAGSHAVNGVARIHSEILKKTIFKDFYELEPHKFQNKTNGITP
RRWLVMCNPGLAEIIAERIGEEYIADLDQLRKLLSYVDDESFIRDVAKVKQENKLKFSAYLEKEYKVHINPNSLFDIQVKRIH
EYKRQLLNCLHVITLYNRIKKEPNKFFVPRTVMIGGKAAPGYHMAKMIIKLITAIGDVVNHDPVVGDRLRVIFLENYRVSLAE
KVIPAADLSEQISTAGTEASGTGNMKFMLNGALTIGTMDGANVEMAEEAGEENFFIFGMRVEDVERLDQKGYNAQEYYDRI
PELRHVIDQLSSGFFSPKQPDLFKDIVNMLMHHDRFKVFADYEEYIKCQERVSALYKNPREWTRMVIRNIATSGKFSSDRTIA
QYAREIWGVEPTRQRMPAPDEKI
>cont|000139|  spt|P00489| Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase) [Oryctolagus cuniculus
(contaminant)]
SRPLSDQEKRKQISVRGLAGVENVTELKKNFNRHLHFTLVKDRNVATPRDYYFALAHTVRDHLVGRWIRTQQHYYEKDPK
RIYYLSLEFYMGRTLQNTMVNLALENACDEATYQLGLDMEELEEIEEDAGLGNGGLGRLAACFLDSMATLGLAAYGYGIRY
EFGIFNQKICGGWQMEEADDWLRYGNPWEKARPEFTLPVHFYGRVEHTSQGAKWVDTQVVLAMPYDTPVPGYRNNVVNT
MRLWSAKAPNDFNLKDFNVGGYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVAATLQDIIRRFKSSKFGCRDPV
RTNFDAFPDKVAIQLNDTHPSLAIPELMRVLVDLERLDWDKAWEVTVKTCAYTNHTVLPEALERWPVHLLETLLPRHLQIIY
EINQRFLNRVAAAFPGDVDRLRRMSLVEEGAVKRINMAHLCIAGSHAVNGVARIHSEILKKTIFKDFYELEPHKFQNKTNGIT
PRRWLVLCNPGLAEIIAERIGEEYISDLDQLRKLLSYVDDEAFIRDVAKVKQENKLKFAAYLEREYKVHINPNSLFDVQVKRI
HEYKRQLLNCLHVITLYNRIKKEPNKFVVPRTVMIGGKAAPGYHMAKMIIKLITAIGDVVNHDPVVGDRLRVIFLENYRVSL
AEKVIPAADLSEQISTAGTEASGTGNMKFMLNGALTIGTMDGANVEMAEEAGEENFFIFGMRVEDVDRLDQRGYNAQEYY
DRIPELRQIIEQLSSGFFSPKQPDLFKDIVNMLMHHDRFKVFADYEEYVKCQERVSALYKNPREWTRMVIRNIATSGKFSSDR
TIAQYAREIWGVEPSRQRLPAPDEKIP
>cont|000140|  spt|O18751| Glycogen phosphorylase, muscle form (EC 2.4.1.1) (Myophosphorylase) [Ovis aries (contaminant)]
SRPLTDQEKRKQISVRGLAGVENVTELKKNFNRHLHFTLVKDRNVATPRDYYFALAYTVRDHLVGRWIRTQQHYYEKDPK
RIYYLSLEFYIGRTLQNTMVNLALENACDEATYQLGLDMEELEEIEEDAGLGNGGLGRLAACFLDSMATLGLAAYGYGIRY
EFGIFNQKISGGWQMEEADDWLRYGNPWEKARPEFTLPVHFYGRVEHTSQGAKWVDTQVVLAMPYDTPVPGYRNNVVNT
MRLWSAKAPNDFNLKDFNVGGYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVAATLQDIIRRFKSSKFGCLDPV
RTNFDAFPDKVAIQLNDTHPSLAIPELMRILVDQERLEWEKAWEVTVKTCAYTNHTVLPEALERWPVHLIETLLPRHLQIIYEI
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NQRFLNRVAAAFPGDVDRLRRMSLVEEGAVKRINMAHLCIAGSHAVNGVARIHSEILKKTIFKDFYELEPHKFQNKTNGITP
RRWLVMCNPGLAEVIAERIGEEYIADLDQLRKLLSYVDDESFIRDVAKVKQENKLKFSAYLEKEYKVHINPNSLFDIQVKRIH
EYKRQLLNCLHVITLYNRIKKEPNKFFVPRTVMIGGKAAPGYHMAKMIIRLITAIGDVVNHDPVVGDRLRVIFLENYRVSLAE
KVIPAADLSEQISTAGTEASGTGNMKFMLNGALTIGTMDGANVEMAEEAGEENFFIFGMRVEDVERLDQKGYNAQEYYDRI
PELRHIIDQLSSGFFSPKQPDLFKDIVNMLMHHDRFKVFADYEEYVKCQERVSALYKNPREWTRMVIRNIATSGKFSSDRTIA
QYAREIWGVEPTRQRMPAPDEKI
>cont|000141|  spt|P00761| Trypsin precursor (EC 3.4.21.4) [Sus scrofa (contaminant)]
FPTDDDDKIVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNF
NGNTLDNDIMLIKLSSPATLNSRVATVSLPRSCAAAGTECLISGWGNTKSSGSSYPSLLQCLKAPVLSDSSCKSSYPGQITGNM
ICVGFLEGGKDSCQGDSGGPVVCNGQLQGIVSWGYGCAQKNKPGVYTKVCNYVNWIQQTIAAN
>cont|000142|  pdb|1EPT_B| B Chain B, Porcine E-Trypsin (E.C.3.4.21.4) [Sus scrofa (contaminant)]
SRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDNDIMLIKLSSPATLNSRVATVSLPRSCAAAGTECLISGWGNTK
>cont|000143|  pdb|1FNI_A| A Chain A, Crystal Structure Of Porcine Beta Trypsin With 0.01% Polydocanol [Sus scrofa
(contaminant)]
IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDN
DIMLIKLSSPATLNSRVATVSLPRSCAAAGTECLISGWGNTKSSGSSYPSLLQCLKAPVLSNSSCKSSYPGQITGNMICVGFLQ
GGKDSCQGDSGGPVVCNGQLQGIVSWGYGCAQKNKPGVYTKVCNYVNWIQQTIAAN
>cont|000144|  pdb|1AN1_E| E Chain E, Leech-Derived Tryptase InhibitorTRYPSIN COMPLEX [Sus scrofa (contaminant)]
IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDN
DIMLIKLSSPATLXSRVATVSLPRSCAAAGTECLISGWGNTKSSGSSYPSLLQCLKAPVLSDSSCKSSYPGQITGNMICVGFLE
GGKDSCQGDSGGPVVCNGQLQGIVSWGYGCAQKNKPGVYTKVCNYVNWIQQTIAAN
>cont|000146|  spt|P00698| Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) (Allergen Gal d 4) (Gal d IV)
[Gallus gallus (contaminant)]
MRSLLILVLCFLPLAALGKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRW
WCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL
>cont|000147|  prf|630460A| lysozyme [Gallus gallus (contaminant)]
KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPC
SALLSSDITASVNCAKKIVSDGDGMNAWVAWRNRCKGTDVQAWIRGCRL
>cont|000148|  pdb|1IOS_A| A Chain A, Stabilization Of Hen Egg White Lysozyme By A Cavity-Filling Mutation [Gallus gallus
(contaminant)]
KVFGRCELAAAFKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPC
SALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL
>cont|000149|  spt|P04188| Glutamyl endopeptidase precursor (EC 3.4.21.19) (Staphylococcal serine proteinase) (V8 proteinase)
(Endoproteinase Glu-C) [Staphylococcus aureus (contaminant)]
MKGKFLKVSSLFVATLTTATLVSSPAANALSSKAMDNHPQQTQSSKQQTPKIQKGGNLKPLEQREHANVILPNNDRHQITDT
TNGHYAPVTYIQVEAPTGTFIASGVVVGKDTLLTNKHVVDATHGDPHALKAFPSAINQDNYPNGGFTAEQITKYSGEGDLAI
VKFSPNEQNKHIGEVVKPATMSNNAETQVNQNITVTGYPGDKPVATMWESKGKITYLKGEAMQYDLSTTGGNSGSPVFNE
KNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFANDDQPNNPDNPDNPNNPDNPNNPDEPNNPDNPNNPDNPDNGD
NNNSDNPDAA
>cont|000150|  trm|Q04186| Glutamic acid specific protease prepropeptide (EC 3.4.21.19) [Staphylococcus aureus (contaminant)]
MKGKFLKVSSLFVATLTTATLVSSPAANALSSKAMDNHPQQTQTDKQQTPKIQKGGNLKPLEQRERANVILPNNDRHQITDT
TNGHYAPVTYIQVEAPTGTFIASGVVVGKDTLLTNKHVVDATHGDPHALKAFPSAINQDNYPNGGFTAEQITKYSGEGDLAI
VKFSPNEQNKHIGEVVKPATMSNNAETQVNQNITVTGYPGDKPVATMWESKGKITYLKGEAMQYDLSTTGGNSGSPVFNE
KNEVIGIHWGGVPNQFNGAVFINENVRNFLKQNIEDINFANDDHPNNPDNPDNPNNPDNPNNPDNPNNPDNPDNPNNPDNP
NNPDNPNNPDQPNNPNNPDNGDNNNSDNPDAA
>cont|000151|  prf|1814271A| Glu-C endoprotease [Staphylococcus aureus (contaminant)]
MKGKFLKVSSLFVATLTTATLVSSPAANALSSKAMDNHPQQTQTDKQQTPKIQKGGNLKPLEQRERANVILPNNDRHQITDT
TNGHYAPVTYIQVEAPTGTFIASGVVVGKDTLLTNKHVVKATHGDPHALKAFPSAINQDNYPNGGFTAEQITKYSGEGDLAI
VKFSPNEQNKHIGEVVKPATMSNNAETQVNQNITVTGYPGDKPVATMWESKGKITYLKGEAMQYDLSTTGGNSGSPVFNE
KNEVIGIHWGGVPNQFNGAVFINENVRNFLKQNIEDINFANDDHPNNPDNPDNPNNPDNPNNPDNPNNPDNPDNPNNPDNP
NNPDNPNNPDQPNNPNNPDNGDNNNSDNPDAA
>cont|000152| gi|62901704|sp|P68082|MYG_HORSE Myoglobin [Equus caballus (contaminant)]
GLSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHGTVVLTALGGILKKKG
HHEAELKPLAQSHATKHKIPIKYLEFISDAIIHVLHSKHPGDFGADAQGAMTKALELFRNDIAAKYKELGFQG
>cont|000153| gi|117995|sp|P00004|CYC_HORSE Cytochrome c [Equus caballus (contaminant)]
GDVEKGKKIFVQKCAQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGFTYTDANKNKGITWKEETLMEYLENPKKYIPGTKM
IFAGIKKKTEREDLIAYLKKATNE
>cont|000154| gi|67462334|sp|P0A6Y8|DNAK_ECOLI Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein)
(HSP70) [Escherichia coli (contaminant)]
MGKIIGIDLGTTNSCVAIMDGTTPRVLENAEGDRTTPSIIAYTQDGETLVGQPAKRQAVTNPQNTLFAIKRLIGRRFQDEEVQR
DVSIMPFKIIAADNGDAWVEVKGQKMAPPQISAEVLKKMKKTAEDYLGEPVTEAVITVPAYFNDAQRQATKDAGRIAGLEV
KRIINEPTAAALAYGLDKGTGNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATNGDTHLGGEDFDSRLINYLVEEFKKDQG
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IDLRNDPLAMQRLKEAAEKAKIELSSAQQTDVNLPYITADATGPKHMNIKVTRAKLESLVEDLVNRSIEPLKVALQDAGLSV
SDIDDVILVGGQTRMPMVQKKVAEFFGKEPRKDVNPDEAVAIGAAVQGGVLTGDVKDVLLLDVTPLSLGIETMGGVMTTLI
AKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSAKDKNSG
KEQKITIKASSGLNEDEIQKMVRDAEANAEADRKFEELVQTRNQGDHLLHSTRKQVEEAGDKLPADDKTAIESALTALETAL
KGEDKAAIEAKMQELAQVSQKLMEIAQQQHAQQQTAGADASANNAKDDDVVDAEFEEVKDKK
>cont|000155| gi|62288014|sp|P0A6F5|CH60_ECOLI 60 kDa chaperonin (Protein Cpn60) (groEL protein) [Escherichia coli
(contaminant)]
MAAKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVAREIELEDKFENMGAQMVKEVAS
KANDAAGDGTTTATVLAQAIITEGLKAVAAGMNPMDLKRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETVGK
LIAEAMDKVGKEGVITVEDGTGLQDELDVVEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKA
GKPLLIIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVI
NKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHATRAA
VEEGVVAGGGVALIRVASKLADLRGQNEDQNVGIKVALRAMEAPLRQIVLNCGEEPSVVANTVKGGDGNYGYNAATEEY
GNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLPKNDAADLGAAGGMGGMGGMGGMM
>cont|000156| gi|68566311|sp|P0A6N1|EFTU_ECOLI Elongation factor Tu (EF-Tu) (P-43) [Escherichia coli (contaminant)]
MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGITINTSHVEYDTPTRHYAHVDC
PGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDF
PGDDTPIVRGSALKALEGDAEWEAKILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVTGRVERGIIKVGEEVEIVGIK
ETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKPGTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFY
FRTTDVTGTIELPEGVEMVMPGDNIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVLS
>cont|000157| gi|62288018|sp|P0A6F9|CH10_ECOLI 10 kDa chaperonin (Protein Cpn10) (groES protein) [Escherichia coli
(contaminant)]
MNIRPLHDRVIVKRKEVETKSAGGIVLTGSAAAKSTRGEVLAVGNGRILENGEVKPLDVKVGDIVIFNDGYGVKSEKIDNEE
VLIMSESDILAIVEA
>cont|000158| gi|62288080|sp|P0A6M8|EFG_ECOLI Elongation factor G (EF-G) [Escherichia coli (contaminant)]
MARTTPIARYRNIGISAHIDAGKTTTTERILFYTGVNHKIGEVHDGAATMDWMEQEQERGITITSAATTAFWSGMAKQYEPH
RINIIDTPGHVDFTIEVERSMRVLDGAVMVYCAVGGVQPQSETVWRQANKYKVPRIAFVNKMDRMGANFLKVVNQIKTRL
GANPVPLQLAIGAEEHFTGVVDLVKMKAINWNDADQGVTFEYEDIPADMVELANEWHQNLIESAAEASEELMEKYLGGEE
LTEAEIKGALRQRVLNNEIILVTCGSAFKNKGVQAMLDAVIDYLPSPVDVPAINGILDDGKDTPAERHASDDEPFSALAFKIAT
DPFVGNLTFFRVYSGVVNSGDTVLNSVKAARERFGRIVQMHANKREEIKEVRAGDIAAAIGLKDVTTGDTLCDPDAPIILER
MEFPEPVISIAVEPKTKADQEKMGLALGRLAKEDPSFRVWTDEESNQTIIAGMGELHLDIIVDRMKREFNVEANVGKPQVAY
RETIRQKVTDVEGKHAKQSGGRGQYGHVVIDMYPLEPGSNPKGYEFINDIKGGVIPGEYIPAVDKGIQEQLKAGPLAGYPVV
DMGIRLHFGSYHDVDSSELAFKLAASIAFKEGFKKAKPVLLEPIMKVEVETPEENTGDVIGDLSRRRGMLKGQESEVTGVKI
HAEVPLSEMFGYATQLRSLTKGRASYTMEFLKYDEAPSNVAQAVIEARGK
>cont|000159| gi|71162378|sp|P0A9K9|SLYD_ECOLI FKBP-type peptidyl-prolyl cis-trans isomerase slyD (PPIase) (Rotamase)
(Histidine-rich protein) (WHP) [Escherichia coli (contaminant)]
MKVAKDLVVSLAYQVRTEDGVLVDESPVSAPLDYLHGHGSLISGLETALEGHEVGDKFDVAVGANDAYGQYDENLVQRV
PKDVFMGVDELQVGMRFLAETDQGPVPVEITAVEDDHVVVDGNHMLAGQNLKFNVEVVAIREATEEELAHGHVHGAHDH
HHDHDHDGCCGGHGHDHGHEHGGEGCCGGKGNGGCGCH
>cont|000160| gi|114939|sp|P00722|BGAL_ECOLI Beta-galactosidase (Lactase) [Escherichia coli (contaminant)]
MTMITDSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQLRSLNGEWRFAWFPAPEAVPESWLECDLP
EADTVVVPSNWQMHGYDAPIYTNVTYPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRWVG
YGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSGIFRDVSLLHKPTTQISDFHVATRFNDDFSRAVLE
AEVQMCGELRDYLRVTVSLWQGETQVASGTAPFGGEIIDERGGYADRVTLRLNVENPKLWSAEIPNLYRAVVELHTADGTL
IEAEACDVGFREVRIENGLLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHYPNHPLWYTLCD
RYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQRDRNHPSVIIWSLGNESGHGANHDALYRWIKSVDPSRP
VQYEGGGADTTATDIICPMYARVDEDQPFPAVPKWSIKKWLSLPGETRPLILCEYAHAMGNSLGGFAKYWQAFRQYPRLQG
GFVWDWVDQSLIKYDENGNPWSAYGGDFGDTPNDRQFCMNGLVFADRTPHPALTEAKHQQQFFQFRLSGQTIEVTSEYLF
RHSDNELLHWMVALDGKPLASGEVPLDVAPQGKQLIELPELPQPESAGQLWLTVRVVQPNATAWSEAGHISAWQQWRLAE
NLSVTLPAASHAIPHLTTSEMDFCIELGNKRWQFNRQSGFLSQMWIGDKKQLLTPLRDQFTRAPLDNDIGVSEATRIDPNAW
VERWKAAGHYQAEAALLQCTADTLADAVLITTAHAWQHQGKTLFISRKTYRIDGSGQMAITVDVEVASDTPHPARIGLNCQ
LAQVAERVNWLGLGPQENYPDRLTAACFDRWDLPLSDMYTPYVFPSENGLRCGTRELNYGPHQWRGDFQFNISRYSQQQL
METSHRHLLHAEEGTWLNIDGFHMGIGGDDSWSPSVSAEFQLSAGRYHYQLVWCQK
>cont|000161| gi|84027873|sp|P0AEX9|MALE_ECOLI Maltose-binding periplasmic protein precursor (Maltodextrin-binding protein)
(MMBP) [Escherichia coli (contaminant)]
MKIKTGARILALSALTTMMFSASALAKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDG
PDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKEL
KAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNK
GETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLG
AVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITK
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Table S2: Mouse tubulin isoforms which were included in the custom database

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>sp|P68369|TBA1A_MOUSE Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1
MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGK
HVPRAVFVDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLD
RIRKLADQCTGLQGFLVFHSFGGGTGSGFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTA
VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLIGQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPP
TVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSE
AREDMAALEKDYEEVGVDSVEGEGEEEGEEY
>sp|P05213|TBA1B_MOUSE Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2
MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGK
HVPRAVFVDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLD
RIRKLADQCTGLQGFLVFHSFGGGTGSGFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTA
VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLISQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIATIKTKRSIQFVDWCPTGFKVGINYQPP
TVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSE
AREDMAALEKDYEEVGVDSVEGEGEEEGEEY
>sp|P68373|TBA1C_MOUSE Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1
MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGK
HVPRAVFVDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLD
RIRKLADQCTGLQGFLVFHSFGGGTGSGFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTA
VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLISQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLTVAEITNACFEPAN
QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPP
TVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSE
AREDMAALEKDYEEVGADSAEGDDEGEEY
>sp|P68368|TBA4A_MOUSE Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1
MRECISVHVGQAGVQMGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFTTFFCETGAGK
HVPRAVFVDLEPTVIDEIRNGPYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDPVLD
RIRKLSDQCTGLQGFLVFHSFGGGTGSGFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTA
VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLISQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIAAIKTKRSIQFVDWCPTGFKVGINYQPP
TVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSE
AREDMAALEKDYEEVGIDSYEDEDEGEE
>sp|Q9JJZ2|TBA8_MOUSE Tubulin alpha-8 chain OS=Mus musculus GN=Tuba8 PE=1 SV=1
MRECISVHVGQAGVQIGNACWELFCLEHGIQADGTFGTQASKINDDDSFTTFFSETGNGK
HVPRAVMVDLEPTVVDEVRAGTYRQLFHPEQLITGKEDAANNYARGHYTVGKESIDLVLD
RIRKLTDACSGLQGFLIFHSFGGGTGSGFTSLLMERLSLDYGKKSKLEFAIYPAPQVSTA
VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLISQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLVTYAPIISAEKAYHEQLSVAEITSSCFEPNS
QMVKCDPRHGKYMACCMLYRGDVVPKDVNVAIAAIKTKRTIQFVDWCPTGFKVGINYQPP
TVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSE
AREDLAALEKDYEEVGTDSFEEENEGEEF
>sp|Q7TMM9|TBB2A_MOUSE Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1
MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGSYHGDSDLQLERINVYYNEAAGNKYV
PRAILVDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVV
RKESESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVV
EPYNATLSVHQLVENTDETYSIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTCL
RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDSKNMM
AACDPRHGRYLTVAAIFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPPRG
LKMSATFIGNSTAIQELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVS
EYQQYQDATADEQGEFEEEEGEDEA
>sp|Q9CWF2|TBB2B_MOUSE Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1
MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGSYHGDSDLQLERINVYYNEATGNKYV
PRAILVDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVV
RKESESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVV
EPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTCL
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RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDSKNMM
AACDPRHGRYLTVAAIFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPPRG
LKMSATFIGNSTAIQELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVS
EYQQYQDATADEQGEFEEEEGEDEA
>sp|P68372|TBB2C_MOUSE Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1
MREIVHLQAGQCGNQIGAKFWEVISDEHGIDPTGTYHGDSDLQLERINVYYNEATGGKYV
PRAVLVDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVV
RKEAESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVSDTVV
EPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTCL
RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDAKNMM
AACDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPPRG
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EYQQYQDATAEEEGEFEEEAEEEVA
>sp|Q9ERD7|TBB3_MOUSE Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1
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PRAILVDLEPGTMDSVRSGAFGHLFRPDNFIFGQSGAGNNWAKGHYTEGAELVDSVLDVV
RKECENCDCLQGFQLTHSLGGGTGSGMGTLLISKVREEYPDRIMNTFSVVPSPKVSDTVV
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RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTARGSQQYRALTVPELTQQMFDAKNMM
AACDPRHGRYLTVATVFRGRMSMKEVDEQMLAIQSKNSSYFVEWIPNNVKVAVCDIPPRG
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>sp|Q9D6F9|TBB4_MOUSE Tubulin beta-4 chain OS=Mus musculus GN=Tubb4 PE=1 SV=3
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PRAVLVDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDAVLDVV
RKEAESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEFPDRIMNTFSVVPSPKVSDTVV
EPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTCL
RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDAKNMM
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EYQQYQDATAEEGEFEEEAEEEVA
>sp|P99024|TBB5_MOUSE Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1
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PRAILVDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVV
RKEAESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVSDTVV
EPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTCL
RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQVFDAKNMM
AACDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPPRG
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>sp|Q922F4|TBB6_MOUSE Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1
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RKECEHCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVV
EPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTSL
RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTARGSQQYRALTVPELTQQMFDAKNMM
AACDPRHGRYLTVATVFRGPMSMKEVDEQMLAIQNKNSSYFVEWIPNNVKVAVCDIPPRG
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EYQQYQDATVNDGEEAFEDEDEEEINE
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Table S3. Bovine tubulin isoforms which were included in the custom database

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>sp|P81947|TBA1B_BOVIN Tubulin alpha-1B chain OS=Bos taurus PE=1 SV=2
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HVPRAVFVDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLD
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VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLISQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIATIKTKRSIQFVDWCPTGFKVGINYQPP
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VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLMSQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPP
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VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLIGQIVSSITA
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QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPP
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>sp|Q32KN8|TBA3_BOVIN Tubulin alpha-3 chain OS=Bos taurus GN=TUBA3 PE=2 SV=1
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VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLIGQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPAN
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VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLISQIVSSITA
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QMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIAAIKTKRSIQFVDWCPTGFKVGINYQPP
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RIRKLTDACSGLQGFLIFHSFGGGTGSGFTSLLMERLSLDYGKKSKLEFAIYPAPQVSTA
VVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLISQIVSSITA
SLRFDGALNVDLTEFQTNLVPYPRIHFPLVTYAPIISAEKAYHEQLSVAEITSSCFEPNS
QMVKCDPRHGKYMACCMLYRGDVVPKDVNVAIAAIKTKRTIQFVDWCPTGFKVGINYQPP
TVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSE
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RKESESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVV
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PRAVLVDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVV
RKEAESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVSDTVV
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RKEAESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVSDTVV
EPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTCL
RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQVFDAKNMM
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EYQQYQDATAEEEEDFGEEAEEEA
>sp|Q2HJ81|TBB6_BOVIN Tubulin beta-6 chain OS=Bos taurus GN=TUBB6 PE=2 SV=1
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PRAALVDLEPGTMDSVRSGPFGQLFRPDNFIFGQTGAGNNWAKGHYTEGAELVDSVLDVV
RKECEHCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVV
EPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTSL
RFPGQLNADLRKLAVNMVPFPRLHFFMPGFAPLTARGSQQYRALTVPELTQQMFDAKNMM
AACDPRHGRYLTVAAVFRGPMSMKEVDEQMLAIQNKNSSYFVEWIPNNVKVAVCDIPPRG
LKMSATFIGNSTAIQELFKRISEQFSAMFRRKAFLHWFTGEGMDEMEFTEAESNMNDLVS
EYQQYQDATADEGEEAFEDDEEEVNE
```

Table S4. List of trypsin generated tubulinα1A/1B sequences that were identified by Paragon

Protein ID /%Coverage	Accession #	Peptides	Modifications	∆Mass	Prec MW	z
Tubulin α-1B chain Tubulin α-1A chain/ 24.6%	P05213 P68369	AVFVDLEPTVIDEVR		-0.0119	1700.8867	2
		QLFHPEQLITGKEDAANNYAR	Gln->pyro-Glu@N-term; Deamidated(N)@17	0.0016	2398.1567	3
		TIGGGDDSFNTFFSETGAGK		0.0081	2006.8934	2
		DIER		0.0015	531.2668	1
		EDMAALEK		0.0442	905.4607	2
		IHFPLATYAPVISAEK	Phospho(T)@7; Phospho(S)@13	0.1378	1916.0265	2
		ITGK	Phospho(T)@2	0.0118	497.2369	1
		TGTYR		0.0013	596.2932	1
		TIGK	Phospho(T)@1	0.0118	497.2369	1
		YTIGKEIIDLVLDR	Phospho(T)@2	0.0263	1726.9171	2
Tubulin α-1B chain Tubulin α-1A chain/ 20.6%	P05213 P68369	AVFVDLEPTVIDEVR	Delta:H(2)C(2)@N-term	0.0025	1726.9166	2
		QLFHPEQLITGKEDAANNYAR		0.0096	2414.2073	4
		TIGGGDDSFNTFFSETGAGK		0.0059	2006.8915	2
		IHFPLATYAPVISAEK		-0.0027	1755.9532	3
		DIER		0.002	531.2673	1
		EDMAALEK		0.0446	905.4611	2
		GTYR		0.0368	495.281	1
		LDIER		-0.0001	644.3494	1
Tubulin α-1B chain Tubulin α-1A chain/ 32.4%	P05213 P68369	AVFVDLEPTVIDEVR		-0.0009	1700.8977	2
		QLFHPEQLITGKEDAANNYAR		-0.0082	2414.1897	4
		TIGGGDDSFNTFFSETGAGK		0.0017	2006.8875	2
		DVNAAIATIK		-0.0033	1014.5677	2
		IHFPLATYAPVISAEK		-0.0061	1755.95	3
		AVCMLSNTTAIAEAWAR	Carbamidomethyl(C)@3; Phospho(S)@6	0.0868	1943.9503	3
		DIER		0.0013	531.2667	1
		EDAANNYARGHYTIGK	Phospho(T)@13	0.1648	1858.9648	2
		EDMAALEK		0.0452	905.4617	2
		EIIDLVLDRIR		-0.0494	1353.7487	2
		GTYR		0.0327	495.2768	1

Table S5 . List of trypsin generated tubulinα1A/1B sequences that were identified by MASCOT

```
TBA1B_BOVIN    Mass: 50804    Score: 495    Queries matched: 34   emPAI: 1.44

 P81947|TBA1B_BOVIN Tubulin alpha-1B chain OS=Bos taurus PE=1 SV=2

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

 1011   307.6794   613.3442   613.3435   0.0007  0   30   0.24  1    R.GDVVPK.D 1010

 1264   388.2103   774.4060   774.4024   0.0035  0   19   4.5  1    R.GHYTIGK.E 1265

 300   391.2100   780.4055   780.4018   0.0038  0   9   1.3e+002  2    R.LSVDYGK.K

 454   444.2199   886.4253   886.4259   -0.0006  0   42   0.074  1    K.FDLMYAK.R

 1406   452.2186   902.4227   902.4208   0.0019  0   (33)  0.21  1    K.FDLMYAK.R

 1412   453.7155   905.4165   905.4164   0.0001  0   64   0.00014  1    R.EDMAALEK.D

 1436   455.2539   908.4932   908.4967   -0.0036  1   28   0.55  1    R.LSVDYGKK.S

 1448   461.7185   921.4225   921.4113   0.0112  0   (39)  0.045  1    R.EDMAALEK.D 1449

 1519   508.2937   1014.5729   1014.5709   0.0020  0   52   0.0023  1    K.DVNAAIATIK.T

 1528   512.2319   1022.4492   1022.4417   0.0075  0   10   33  1    K.EDAANNYAR.G

 1575   543.3144   1084.6143   1084.6128   0.0015  0   71   2.7e-005  1    K.EIIDLVLDR.I 772 1576

 1856   470.9344   1409.7813   1409.7667   0.0146  0   51   0.0027  1    R.QLFHPEQLITGK.E 1857

 1964   792.8817   1583.7488   1583.7443   0.0045  0   62   0.0003  1    R.SIQFVDWCPTGFK.V

 1986   851.4582   1700.9019   1700.8985   0.0034  0   94   1.6e-007  1    R.AVFVDLEPTVIDEVR.T 1985 1987

 1994   573.6383   1717.8932   1717.8747   0.0185  0   59   0.00057  1    R.NLDIERPTYTNLNR.L

 2008   586.3305   1755.9696   1755.9559   0.0137  0   50   0.0035  1    R.IHFPLATYAPVISAEK.A 2006 2007 2009

 2025   609.0058   1823.9957   1823.9782   0.0175  0   47   0.0073  1    K.VGINYQPPTVVPGGDLAK.V 2026

 1024   622.3103   1863.9092   1863.8971   0.0121  0   (21)  8.9  2    R.AVCMLSNTTAIAEAWAR.L

 2030   627.6420   1879.9042   1879.8920   0.0122  0   64   0.00019  1    R.AVCMLSNTTAIAEAWAR.L

 2042   669.9750   2006.9030   2006.8858   0.0172  0   26   1.4  1    K.TIGGGDDSFNTFFSETGAGK.H

 2178   803.7511   2408.2316   2408.2012   0.0304  0   68   6.8e-005  1    R.FDGALNVDLTEFQTNLVPYPR.I

 2215   922.7771   2765.3095   2765.2789   0.0307  0   76   1.2e-005  1    K.AYHEQLSVAEITNACFEPANQMVK.C
```

Table S6: List of excluded masses that were identified as possible matches to a random tubulin$\alpha_{1A/1B}$ sequence

Observed	Mr(Expt)	Mr(Calc)	Delta	Score	Expect	Peptide
468.1450	934.2754	934.3403	-0.0649	(34)	0.0098	G.EGEEEGEE.Y + 2 Methyl (DE)
468.1475	934.2804	934.3403	-0.0599	(36)	0.0051	G.EGEEEGEE.Y + 2 Methyl (DE)
484.1459	1449.4160	1449.6008	-0.1848	40	0.0068	D.SVEGEGEEEGEE.Y + +1E1Me (E); 3 Edehydro (E); Methyl (C-term); Methyl (DE)
558.1967	1114.3789	1114.4125	-0.0335	(24)	0.0039	W.YVGEGMEEGE.F + Oxidation (M)
558.2015	1114.3884	1114.4125	-0.0240	(24)	0.0041	W.YVGEGMEEGE.F + Oxidation (M)
558.2023	1114.3900	1114.4125	-0.0225	(23)	0.0045	W.YVGEGMEEGE.F + Oxidation (M)
558.2024	1114.3901	1114.4125	-0.0223	24	0.0038	W.YVGEGMEEGE.F + Oxidation (M)
580.7080	1159.4015	1159.5608	-0.1593	28	0.012	H.EQLSVAEI.T + 2 +E (E); Methyl (C-term)
720.2916	1438.5686	1438.6524	-0.0838	29	0.046	E.GEFSEAREDMAAL.E + Edehydro (E); Methyl (DE)
945.7027	3778.7817	3778.6806	0.1011	23	0.0052	L.EHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHV.P + Oxidation (M)
977.1455	2928.4148	2928.2733	0.1416	32	0.39	E.DMAALEKDYEEVGVDSVEGEGEEE.G + +2E2Me (E); 3 Edehydro (E); Methyl (DE)
977.1468	2928.4186	2928.2481	0.1705	41	0.048	E.DMAALEKDYEEVGVDSVEGEGE.E + +1E1Me (E); +2E1Me (E); +E (E); Edehydro (E); Methyl (C-term)
1571.0110	4710.0112	4710.0047	0.0065	53	0.012	G.EGMEEGEFSEAREDMAALEKDYEEVGVDSVEGEGEEEGEE.Y + +2E (E); 8 Edehydro (E); 2 Methyl (DE)