

Table S1 The detail information of each identified protein.

1.	IAAC3_WHEAT Mass: 18893 Score: 74 Queries matched: 9 Sequences: 2 emPAI: 0.93 Alpha-amylase/trypsin inhibitor CM3 OS=Triticum aestivum PE=1 SV=1									
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	2156	563.7512	1125.4878	1125.4913	-3.10	0	46	0.0025	1	R.EMQWDFVR.L 2157 2158
	2173	564.2440	1126.4734	1126.4753	-1.68	0	(31)	0.048	1	R.EMQWDFVR.L
	5398	849.9633	1697.9120	1697.9141	-1.20	0	31	0.22	1	R.YFIALPVPSQPVDPR.S 5399
	5405	850.4565	1698.8984	1698.8981	0.20	0	(26)	0.91	1	R.YFIALPVPSQPVDPR.S 5404 5406
2.	ALBU_BOVIN Mass: 71244 Score: 868 Queries matched: 56 Sequences: 16 emPAI: 0.80 Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4									
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	29	395.2405	788.4664	788.4644	2.63	0	22	0.6	1	K.LVTDLTK.V
	103	424.2555	846.4964	846.4963	0.15	1	27	0.3	1	R.LSQKFPK.A 102
	200	461.7479	921.4812	921.4807	0.55	0	28	0.31	1	K.AEFVEVTK.L 199 201
	207	464.2513	926.4880	926.4861	2.07	0	23	0.79	1	K.YLYEIAR.R 206 208
	315	507.8136	1013.6126	1013.6121	0.56	0	36	0.026	1	K.QTALVELLK.H 314
	521	571.8611	1141.7076	1141.7070	0.54	1	34	0.035	1	K.KQTALVELLK.H 520
	555	582.3188	1162.6230	1162.6234	-0.27	0	37	0.069	1	K.LVNELTEFAK.T 553 554
	608	398.5399	1192.5979	1192.5949	2.52	1	16	9.2	1	R.DTHKSEIAHR.F 606 607
	716	417.2122	1248.6148	1248.6139	0.72	1	25	0.96	1	R.FKDLGEEHFK.G 715
	718	313.1611	1248.6153	1248.6139	1.14	1	(15)	9.7	1	R.FKDLGEEHFK.G 717

	807	653.3638	1304.7130	1304.7088	3.23	0	40	0.03	1	K.HLVDEPQNLIK.Q 805 806
	1143	480.6087	1438.8043	1438.8045	-0.13	1	48	0.0031	1	R.RHPEYAVSVLLR.L 1144 1145
	1156	722.3264	1442.6382	1442.6347	2.42	0	15	3.7	1	K.YICDNQDTISSK.L
	1212	740.4009	1478.7872	1478.7881	-0.61	0	82	1.9e-006	1	K.LGEYGFQNALIVR.Y 1206 1207 1208 1209 1210 1211 1213 1214
	1218	740.9007	1479.7868	1479.7722	9.93	0	(52)	0.002	1	K.LGEYGFQNALIVR.Y
	1279	756.4255	1510.8364	1510.8355	0.61	0	66	6e-005	1	K.VPQVSTPTLVEVSR.S 1277 1278
	1358	784.3748	1566.7350	1566.7354	-0.25	0	58	0.0005	1	K.DAFLGSFLYEYSR.R 1350 1351 1354 1356 1361 1364
	1463	547.3171	1638.9295	1638.9305	-0.62	1	(65)	4.7e-005	1	R.KVPQVSTPTLVEVSR.S 1462 1465
	1464	820.4726	1638.9306	1638.9305	0.10	1	76	3.6e-006	1	R.KVPQVSTPTLVEVSR.S 1466 1467
3.	HBBF_BOVIN Mass: 15963 Score: 148 Queries matched: 5 Sequences: 3 emPAI: 0.78 Hemoglobin fetal subunit beta OS=Bos taurus PE=1 SV=1									
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	755	633.4185	1264.8224	1264.8231	-0.51	0	58	1.2e-005	1	R.LLGNVLVVVLAR.R 756
	764	637.8669	1273.7192	1273.7183	0.75	0	62	0.00015	1	R.LLVVYPWTQR.F 763
	887	664.8629	1327.7112	1327.7096	1.26	1	49	0.0046	1	K.VKVDEVGGEALGR.L
4.	HBB_PIG Mass: 16212 Score: 3489 Queries matched: 220 Sequences: 17 emPAI: 768.64 Hemoglobin subunit beta OS=Sus scrofa GN=HBB PE=1 SV=3									
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	39	370.2085	738.4024	738.4024	0.04	0	19	1	1	K.HLDNLK.G 38
	169	456.7432	911.4718	911.4712	0.69	0	25	0.48	1	M.VHLSAEEK.E 163 165 166 167 171
	170	304.8313	911.4721	911.4712	0.93	0	(18)	2.5	1	M.VHLSAEEK.E 168

215	486.7794	971.5442	971.5440	0.25	0	42	0.027	1	K.EAVLGLWGK.V 216 217
427	547.2972	1092.5798	1092.5815	-1.54	0	68	4.3e-005	1	K.VLQSFSDGLK.H 425 426 428 429 430 431 432 433 434
436	547.7903	1093.5660	1093.5655	0.47	0	(63)	0.00019	1	K.VLQSFSDGLK.H 437 438
555	383.8960	1148.6662	1148.6666	-0.36	0	(61)	0.00011	1	K.VVAGVANALAHK.Y 558 559
557	575.3407	1148.6668	1148.6666	0.23	0	(67)	1.7e-005	1	K.VVAGVANALAHK.Y 554 556
563	575.8323	1149.6500	1149.6506	-0.47	0	71	1.3e-005	1	K.VVAGVANALAHK.Y 564 566
565	384.2243	1149.6511	1149.6506	0.42	0	(42)	0.0093	1	K.VVAGVANALAHK.Y
681	407.9003	1220.6791	1220.6765	2.12	1	(45)	0.0053	1	K.KVLQSFSDGLK.H 674 678 682
683	611.3476	1220.6806	1220.6765	3.41	1	83	1e-006	1	K.KVLQSFSDGLK.H 675 676 677 679 680
701	622.3429	1242.6712	1242.6721	-0.65	1	58	0.00064	1	K.HLDNLKGTFAK.L 704 707 708
703	415.2313	1242.6721	1242.6721	0.01	1	(29)	0.48	1	K.HLDNLKGTFAK.L 702 705 706
709	415.5596	1243.6570	1243.6561	0.73	1	(32)	0.28	1	K.HLDNLKGTFAK.L 710
755	633.4185	1264.8224	1264.8231	-0.51	0	75	2.7e-007	1	R.LLGNVIVVVLAR.R 749 750 751 752 753 754 756 757 758 759 760 761 762 763 764 765 766 767 769 770 771 772 773 774 775 776 778 779 780 781 782 783 784 785 786 787 788
777	422.6151	1264.8235	1264.8231	0.30	0	(48)	0.00012	1	R.LLGNVIVVVLAR.R 748 768
867	637.8660	1273.7174	1273.7183	-0.66	0	62	0.00018	1	R.LLVVYPWTQR.F 862 863 864 865 866 868 869 870 871 872 873 874 876 877 878 880 881 882 883 884 885 886 887 888 889 890 892 893 894 896 897
898	425.5814	1273.7224	1273.7183	3.20	0	(33)	0.099	1	R.LLVVYPWTQR.F 899
901	638.3624	1274.7102	1274.7023	6.23	0	(48)	0.0046	1	R.LLVVYPWTQR.F 900 902
1024	657.8353	1313.6560	1313.6575	-1.14	0	(64)	0.00012	1	K.VNVDEVGGEALGR.L 1025 1026 1027 1028 1029 1030 1031 1034 1036 1037 1038 1039

	1032	438.8932	1313.6578	1313.6575	0.17	0	79	3.4e-006	1	K.VNVDEVGGEALGR.L 1033 1035
	1045	658.3328	1314.6510	1314.6416	7.22	0	(58)	0.00046	1	K.VNVDEVGGEALGR.L
	1336	474.6480	1420.9222	1420.9242	-1.42	1	13	0.26	1	R.LLGNVIVVVLARR.L
	1606	363.2045	1448.7889	1448.7888	0.05	1	(38)	0.05	1	K.VVAGVANALAHKYH.- 1605 1610
	1608	483.9372	1448.7898	1448.7888	0.66	1	54	0.0013	1	K.VVAGVANALAHKYH.- 1607 1609
	1619	363.4509	1449.7745	1449.7728	1.15	1	(17)	6.8	1	K.VVAGVANALAHKYH.-
	1620	484.2655	1449.7747	1449.7728	1.27	1	(42)	0.02	1	K.VVAGVANALAHKYH.-
	2060	562.9451	1685.8135	1685.8162	-1.60	0	(16)	8.1	1	R.LGHDFNPVQAAFQK.V
	2061	562.9458	1685.8156	1685.8162	-0.35	0	(20)	3.3	1	R.LGHDFNPVQAAFQK.V
	2063	562.9466	1685.8180	1685.8162	1.07	0	26	0.84	1	R.LGHDFNPVQAAFQK.V 2065
	2066	843.9177	1685.8208	1685.8162	2.78	0	(26)	0.92	1	R.LGHDFNPVQAAFQK.V 2062 2064
	2068	563.2749	1686.8029	1686.8002	1.60	0	(19)	4	1	R.LGHDFNPVQAAFQK.V 2071 2072
	2069	844.4091	1686.8036	1686.8002	2.06	0	(18)	5.1	1	R.LGHDFNPVQAAFQK.V
	2070	844.4095	1686.8044	1686.8002	2.54	0	(25)	1.1	1	R.LGHDFNPVQAAFQK.V
	2171	605.3324	1812.9754	1812.9734	1.09	1	34	0.15	1	K.VLQSFSDGLKHLNLIK.G 2170
	2195	921.9658	1841.9170	1841.9173	-0.12	1	(27)	0.93	1	R.RLGHDFNPVQAAFQK.V
	2197	461.4866	1841.9173	1841.9173	0.02	1	(28)	0.66	1	R.RLGHDFNPVQAAFQK.V 2196 2201
	2198	614.9798	1841.9176	1841.9173	0.17	1	50	0.0047	1	R.RLGHDFNPVQAAFQK.V 2193 2194
	2200	614.9800	1841.9182	1841.9173	0.49	1	(37)	0.087	1	R.RLGHDFNPVQAAFQK.V
	2202	921.9675	1841.9204	1841.9173	1.73	1	(27)	0.9	1	R.RLGHDFNPVQAAFQK.V 2199
	2203	461.7323	1842.9001	1842.9013	-0.64	1	(30)	0.46	1	R.RLGHDFNPVQAAFQK.V 2204

2205	615.3085	1842.9037	1842.9013	1.30	1	(32)	0.26	1	R.RLGHDENPNVQAAFQK.V
2207	922.4598	1842.9050	1842.9013	2.05	1	(31)	0.37	1	R.RLGHDENPNVQAAFQK.V 2206
2208	615.3098	1842.9076	1842.9013	3.42	1	(26)	1.1	1	R.RLGHDENPNVQAAFQK.V 2210
2209	615.3102	1842.9088	1842.9013	4.07	1	(29)	0.48	1	R.RLGHDENPNVQAAFQK.V
2223	622.6775	1865.0107	1865.0047	3.22	1	53	0.0013	1	M.VHLSAEEKEAVLGLWGK.V 2222 2224
2619	1023.4645	2044.9144	2044.9200	-2.74	0	(14)	7.2	1	R.FFESFGDLSNADAVMGNP.K.V
2631	1031.4642	2060.9138	2060.9150	-0.54	0	(38)	0.027	1	R.FFESFGDLSNADAVMGNP.K.V 2628 2629 2632
2633	687.9789	2060.9149	2060.9150	-0.04	0	(44)	0.0059	1	R.FFESFGDLSNADAVMGNP.K.V 2630 2634
2638	688.3077	2061.9013	2061.8990	1.12	0	(30)	0.12	1	R.FFESFGDLSNADAVMGNP.K.V 2643 2644
2639	1031.9584	2061.9022	2061.8990	1.59	0	47	0.0028	1	R.FFESFGDLSNADAVMGNP.K.V 2636 2637 2640 2641 2642 2645 2646 2647 2648 2649 2650 2651 2652

5. HBA_PIG Mass: 15087 Score: 4934 Queries matched: 271 Sequences: 12 emPAI: 86.10
Hemoglobin subunit alpha OS=Sus scrofa GN=HBA PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
15	352.2029	702.3912	702.3912	0.08	0	42	0.039	1	-VLSAADK.A 16 17 18 19 20
22	359.2110	716.4074	716.4068	0.84	0	42	0.031	1	K.VADALTK.A 21
58	409.7240	817.4334	817.4334	0.05	0	39	0.061	1	R.VDPVNFK.L 59 60
300	521.2755	1040.5364	1040.5365	-0.05	0	(35)	0.054	1	R.MFLGFPTTK.T 297 298 299 301 302
349	529.2732	1056.5318	1056.5314	0.41	0	51	0.0014	1	R.MFLGFPTTK.T 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 350 351 352 353 354 355 356 357 358 359 360 361
402	544.3160	1086.6174	1086.6186	-1.04	1	(27)	0.47	1	K.LRVDPVNFK.L 403 404 408
406	363.2137	1086.6193	1086.6186	0.64	1	(27)	0.61	1	K.LRVDPVNFK.L 405 407

	410	544.8082	1087.6018	1087.6026	-0.68	1	32	0.19	1	K.LRVDPVNF ^u FK.L 412
	413	363.5419	1087.6039	1087.6026	1.18	1	(22)	2	1	K.LRVDPVNF ^u FK.L 411
	472	372.5523	1114.6351	1114.6346	0.43	1	(54)	0.0014	1	-.VLSAADKANVK.A 471 473
	475	558.3254	1114.6362	1114.6346	1.48	1	56	0.00096	1	-.VLSAADKANVK.A 467 468 469 470 474
	476	558.8182	1115.6218	1115.6186	2.91	1	(27)	0.81	1	-.VLSAADKAN ^u VK.A 477 478
	923	640.3666	1278.7186	1278.7184	0.23	0	57	0.00028	1	K.FLANVSTVLT ^u SK.Y 921 922 924 925 926
	1388	711.8579	1421.7012	1421.7011	0.09	0	83	2.1e-006	1	K.VGGQAGAHGAEALER.M 1340 1341 1346 1347 1356 1365 1366 1367 1368 1373 1387 1401 1402 1403 1404 1412 1413 1414 1415 1418 1419 1420 1421 1422 1425 1426 1427 1428 1434 1435 1436 1437 1438 1440 1442 1443 1444 1447 1448 1451 1452 1456 1457 1458
	1417	474.9079	1421.7019	1421.7011	0.52	0	(72)	2.3e-005	1	K.VGGQAGAHGAEALER.M 1337 1338 1339 1342 1343 1344 1345 1348 1349 1350 1351 1352 1353 1354 1355 1357 1358 1359 1360 1361 1362 1363 1364 1369 1370 1371 1372 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1405 1406 1407 1408 1409 1410 1411 1416 1423 1424 1429 1430 1431 1433 1439 1441 1445 1446 1449 1450 1453 1454
	1459	475.2367	1422.6883	1422.6851	2.20	0	(60)	0.00035	1	K.VGGQAGAHGAEALER.M 1462 1464
	1461	712.3531	1422.6916	1422.6851	4.58	0	(72)	2.3e-005	1	K.VGGQAGAHGAEALER.M 1460 1463
	2231	469.9796	1875.8893	1875.8904	-0.59	0	(12)	22	1	K.TYFPHFNL ^u SHGSDQVK.A 2232 2239 2241 2246 2254
	2236	626.3040	1875.8902	1875.8904	-0.13	0	(12)	22	1	K.TYFPHFNL ^u SHGSDQVK.A 2233 2234 2238 2244 2247 2253
	2249	938.9532	1875.8918	1875.8904	0.77	0	(13)	17	1	K.TYFPHFNL ^u SHGSDQVK.A 2242 2243 2248 2255
	2257	470.2263	1876.8761	1876.8744	0.89	0	(25)	1	1	K.TYFPHF ^u N ^u SHGSDQVK.A 2259 2260 2267
	2261	626.6332	1876.8778	1876.8744	1.79	0	(14)	13	1	K.TYFPHF ^u N ^u SHGSDQVK.A 2258 2266 2268

	2263	939.4468	1876.8790	1876.8744	2.47	0	25	0.94	1	K.TYFPHFNL N SHGSDQVK.A 2264
	2265	626.6344	1876.8814	1876.8744	3.70	0	(6)	76	1	K.TYFPHFNL N SHGSDQVK.A
	2394	645.9976	1934.9710	1934.9711	-0.06	1	47	0.009	1	K.AAWGKVGGQAGAHGAEALER.M
	2986	448.2401	2236.1641	2236.1600	1.83	0	(48)	0.0066	1	K.AVGHLDDLPGALSALSDLHAHK.L 2973 2974 2976 2978 2980 2988 2991 2999
	2989	746.3959	2236.1659	2236.1600	2.62	0	(50)	0.004	1	K.AVGHLDDLPGALSALSDLHAHK.L 2971 2977 2985 2987 2992 2993 2997
	2995	560.0491	2236.1673	2236.1600	3.25	0	53	0.0021	1	K.AVGHLDDLPGALSALSDLHAHK.L 2969 2970 2972 2975 2979 2981 2982 2983 2984 2990 2994 2996 2998
	3000	1119.0918	2236.1690	2236.1600	4.04	0	(19)	5.8	1	K.AVGHLDDLPGALSALSDLHAHK.L
	3553	729.6117	2914.4177	2914.4113	2.20	1	25	1.6	1	R. M FLGFPTTKTYFPHFNL N SHGSDQVK.A 3551 3552
6.	ALBU_PIG Mass: 71643 Score: 605 Queries matched: 32 Sequences: 10 emPAI: 0.50 Serum albumin OS=Sus scrofa GN=ALB PE=1 SV=2									
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
	48	388.7375	775.4604	775.4592	1.59	0	31	0.12	1	K.FVIEIR.G 47
	136	438.2590	874.5034	874.5025	1.12	1	22	1	1	R.LSQRFPK.A 135
	182	464.2500	926.4854	926.4861	-0.74	0	25	0.55	1	K.YLYEIAR.R 183 184
	274	507.8133	1013.6120	1013.6121	-0.03	0	41	0.012	1	K.QTALVELLK.H 273
	511	571.8599	1141.7052	1141.7070	-1.56	1	32	0.036	1	K.KQTALVELLK.H 512
	969	647.8614	1293.7082	1293.7081	0.09	0	17	3.7	1	R.TVLGNFAAFVQK.C 968
	1630	485.9409	1454.8009	1454.7994	1.03	1	43	0.013	1	R.RHPDYSVSLLLR.I 1628 1629 1632
	1631	728.4078	1454.8010	1454.7994	1.15	1	(30)	0.28	1	R.RHPDYSVSLLLR.I
	1697	740.4009	1478.7872	1478.7881	-0.61	0	83	1.9e-006	1	K.LGEYGFQNALIVR.Y 1696 1698 1699 1700

	1709	740.8932	1479.7718	1479.7722	-0.21	0	(53)	0.0015	1	K.LGEYGFQNALIVR.Y 1710
	1730	748.4261	1494.8376	1494.8406	-1.98	0	91	1.4e-007	1	K.VPQVSTPTLVEVAR.K 1731 1732 1733
	1935	812.4725	1622.9304	1622.9356	-3.15	1	69	1.3e-005	1	K.KVPQVSTPTLVEVAR.K
	1936	541.9853	1622.9341	1622.9356	-0.92	1	(49)	0.0014	1	K.KVPQVSTPTLVEVAR.K 1937