

SUPPLEMENTARY INFORMATION AVAILABLE:

Supplementary Figure Captions:

Supplementary Figure 1.

Control IgE immuno-blots of GC proteome of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3-10 (A and C) and pH 4-7 (B and D) probed with anti-human IgE conjugated with HRP showing no reactivity with sera of apparently healthy controls individuals.

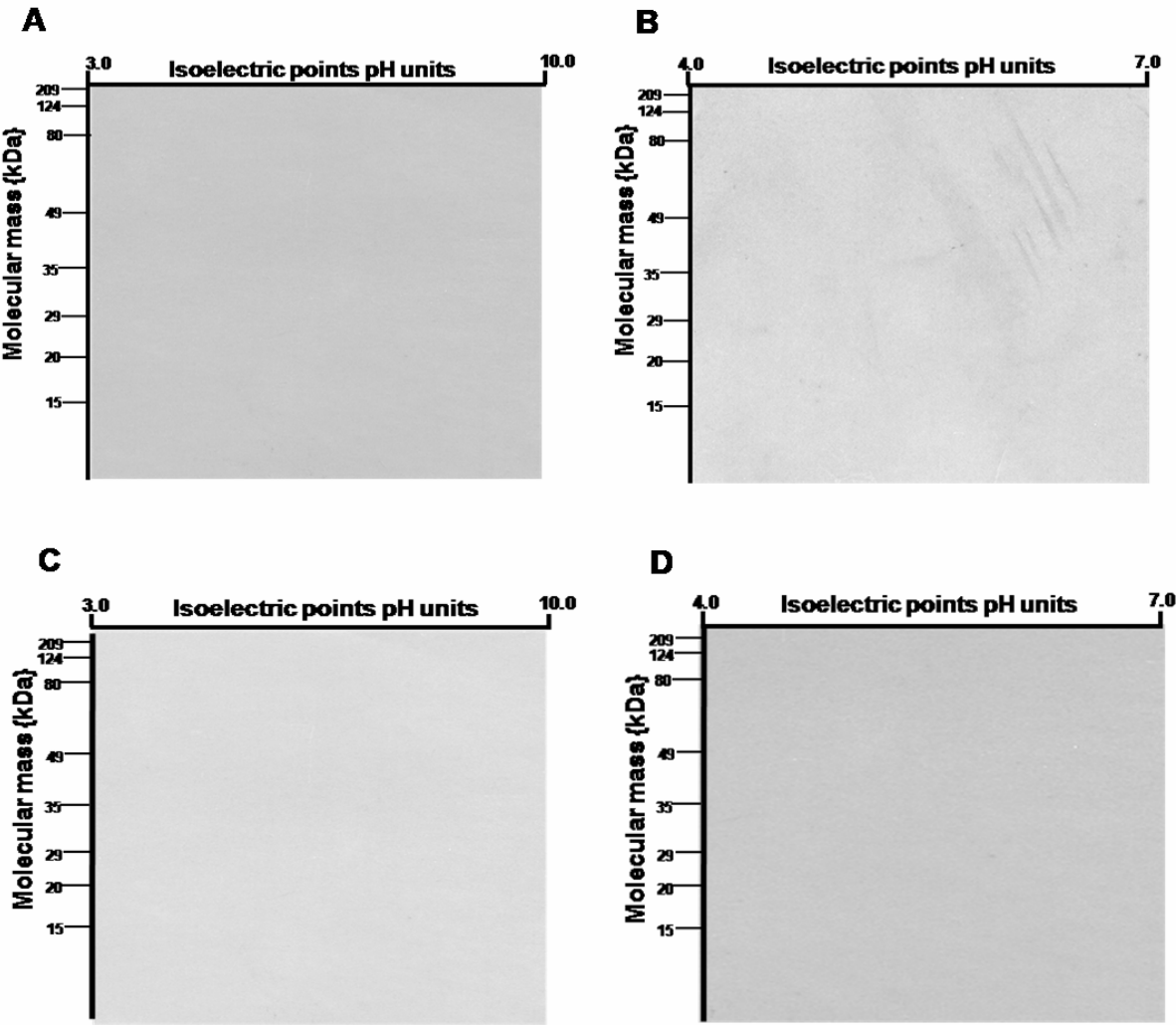
Supplementary Figure 2.

Control IgG immuno-blots of GC proteome of *A. fumigatus* strains 190/96 (A and B) and DAYA (C and D), in pH ranges 3-10 (A and C) and pH 4-7 (B and D) probed with anti-human IgE conjugated with HRP showing no reactivity with sera of apparently healthy controls individuals.

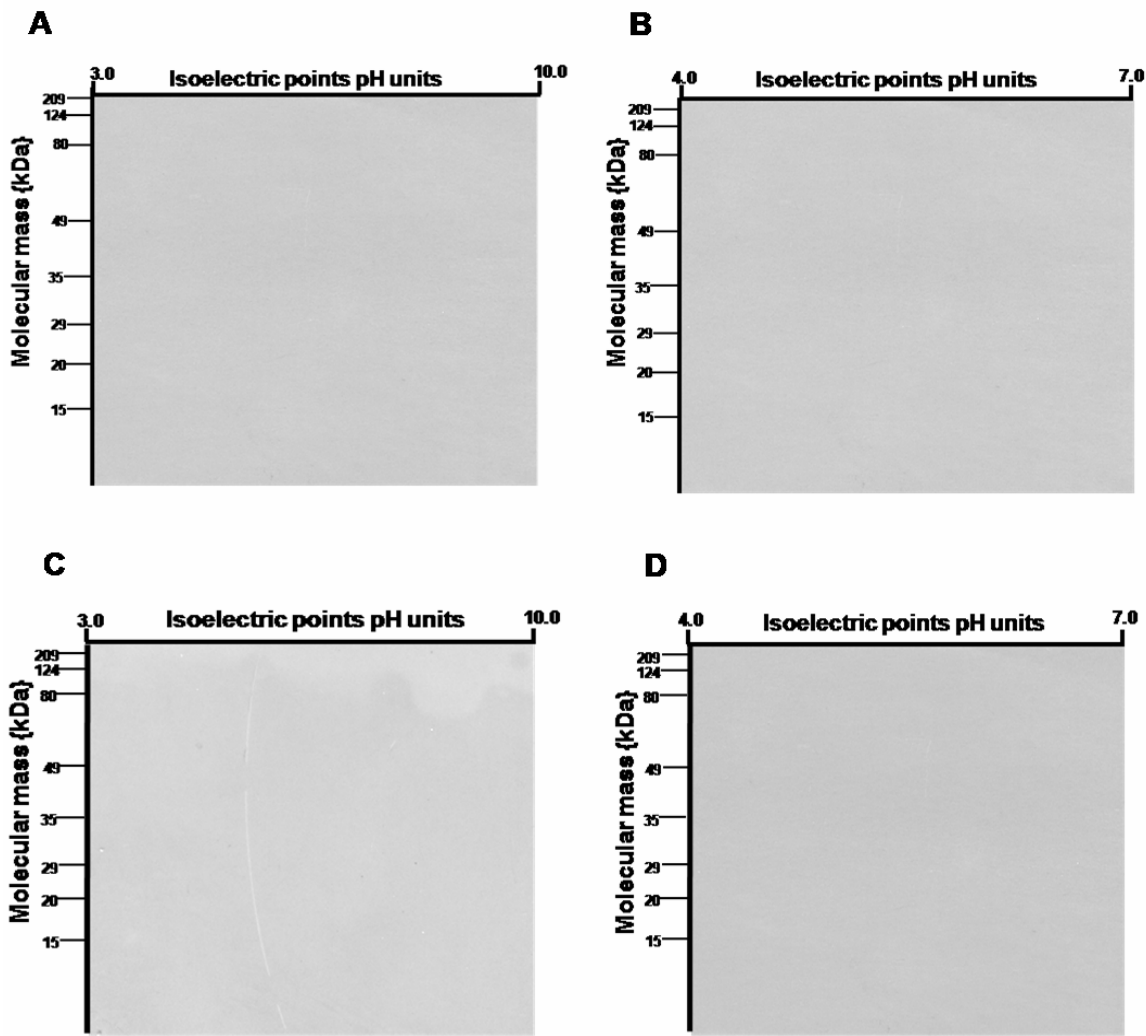
Supplementary Figure 3.

Pie chart showing functional categorization of 66 identified *A. fumigatus* cytosolic proteins with in Kognitor; a function annotation tool of NCBI database; (www.ncbi.nlm.nih.gov/COG/grace/kognitor).

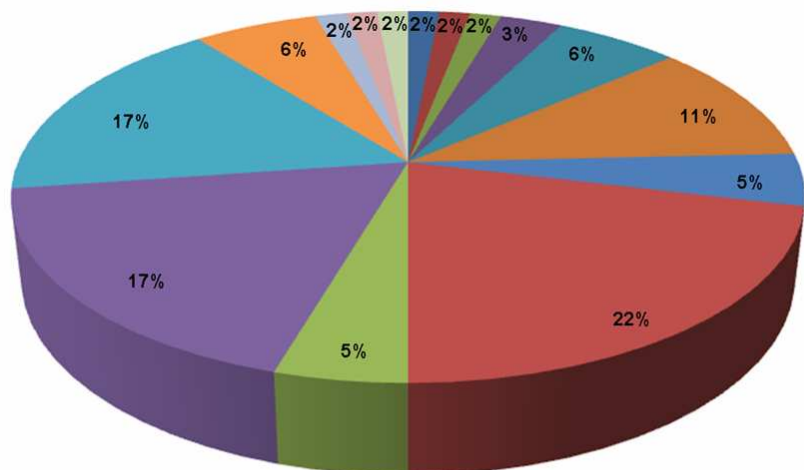
Supplementary Figure 1.



Supplementary Figure 2.



Supplementary Figure 3.



- Q (Secondary metabolites biosynthesis, transport and catabolism) 1
- I (Lipid transport and metabolism) 1
- Z (Cytoskeleton) 1
- S (Function unknown) 2
- J (Translation, ribosomal structure and biogenesis) 4
- C (Energy production and conversion) 7
- F (Nucleotide transport and metabolism) 3
- E (Amino acid transport and metabolism) 14
- H (Coenzyme transport and metabolism) 3
- G (Carbohydrate transport and metabolism) 12
- O (Posttranslational modification, protein turnover, chaperones) 11
- R (General function prediction only) 4
- CR (Energy production and conversion + General function prediction only) 1
- BD (Chromatin structure and dynamics + Cell cycle control, cell division, chromosome partitioning) 1
- AYT (RNA processing and modification + Nuclear structure + Signal transduction mechanisms) 1

Supplementary Table:

Table 1. MS/MS analysis table for reported proteins

Footnotes: ¹Mass 1 = Molecular mass of the protein observed in MASCOT search. ²MASCOT score 2 = >40 indicate identification or extensive homology (p<0.05). ³Peptide matched 3 = Number of peptides matched with protein in MS/MS query. ⁴pI 4 = Isoelectric point of the protein observed in MASCOT search.

Spot No.	Accession no.	Mass ¹ (kDa)	MASCOT Score ²	Peptide matched ³	pI ⁴	Protein name	MS/MS Analysis
1	XP_755878	28202	278	10	5.96	Sorbitol/xylulose reductase Sou1-like	Sequence Coverage: 33% 1 MPIPVPAAASS LLDLLSLK GK TVVVTGASGP RGMGIEAARG CAEMGANIAL 51 TYASRPEGGE KNAAEIAKTY GVKAKAYKCN VGDWESVQKL VADVIAEFGQ 101 IDAFIANAGR TASAGILDGS VNDWAEVIQT DLTGTFYCAK AVGPHFKERG 151 KGSFVITSSM SGHIANYPQE QTSYNVAKAG CIHFAKSLAN EWRDFARVNS 201 ISPGYIDTGL SDFVDKKTQD LWLSMIPMGR NGDAKELKGA YVYLCS DASS 251 YMTGTDLLID GGYCIR 2 - 18 867.5678 1733.1210 1733.0338 0.0872 0 M.PIPVPAAASSLLDLLSLK.G 21 - 31 522.3088 1042.6030 1042.5771 0.0259 0 K.TVVVTGASGPR.G 21 - 31 522.3173 1042.6200 1042.5771 0.0429 0 K.TVVVTGASGPR. 32 - 39 410.7115 819.4084 819.3909 0.0176 0 R.GMGIEAAR.G Oxidation (M) 90 - 110 730.7527 2189.2363 2189.1481 0.0882 0 K.LVADVIAEFGQIDAFIANAGR.T 198 - 216 1014.0510 2026.0874 2025.9895 0.0979 0 R.VNSISPGYIDTGLSDFVDK.K 198 - 216 1014.0542 2026.0938 2025.9895 0.1043 0 R.VNSISPGYIDTGLSDFVDK.K 198 - 217 719.0652 2154.1738 2154.0845 0.0893 1 R.VNSISPGYIDTGLSDFVDK.K.T 198 - 217 719.0670 2154.1792 2154.0845 0.0947 1 R.VNSISPGYIDTGLSDFVDK.K.T 218 - 230 790.4222 1578.8298 1578.7534 0.0764 0 K.TQDLWLSMIPMGR.N 2 Oxidation

							(M)
2	XP_754489	28202	207	4	6.84	Proteasome component Prs2	Sequence Coverage: 17% 1 MTDTLPSFQT RVACTKSFSS ICGLGPHQYA FKAITAANIT SIGVRGKNCA 51 VVLSQKKVAD KLIDPSSVSH IFRLSPSVGC VMTGSIADAR ASVDRARGEA 101 AEFYKYGYE MPCDVLAKRL ANINQVYTQR AYMRPLGVAM TLISVDDEKG 151 PQLYKCDPAG YYVGKATAS GPKQQEALNY LEKKLKNKDY AEGSWEEVVE 201 LGITALSNVL SVDFKKHELE IGIVGGPRAD GREGTDPFR ALTEDEIDER 251 LQAISEKD 33 - 45 643.9045 1285.7944 1285.7354 0.0591 0 K.AITAANITSIGVR. 120 - 130 660.3871 1318.7596 1318.6993 0.0603 0 R.LANINQVYTQR.A 174 - 183 618.3470 1234.6794 1234.6193 0.0601 0 K.QQEALNYLEK. 241 - 250 595.8098 1189.6050 1189.5462 0.0588 0 R.ALTEDEIDER.L
3	XP_750785	28188	171	5	5.80	Proteasome component Pre9	Sequence Coverage: 16% 1 MSRRYDSRTT IFSPEGRLYQ VEYALEAISH AGTALGILAK DGIVLAAEKK 51 VTSKLLEQDT SAEKLYTLND NMICAVAGMT ADANILINYA RQAAQRYLLT 101 YGEEIPCEQL VRRLCDLKQG YTQHGGLRPF GVSFIYAGYD PLREFQLYQS 151 NPSGNYGGWK ATSVGANNAS AQSLKQDYK EDCDLKEACA MAVKVLSKTM 201 DSTKLSSEKI EFATVGKTKE GKIYHHLWNA DEINALLKEH GLAKVDDEPE 251 AGDIK 9 - 17 504.2820 1006.5494 1006.5084 0.0411 0 R.TTIFSPEGR.L 9 - 17 504.2970 1006.5794 1006.5084 0.0711 0 R.TTIFSPEGR.L 55 - 64 567.3104 1132.6062 1132.5612 0.0451 0 K.LLEQDTSAEK.L 205 - 217 470.2768 1407.8086 1407.7609 0.0476 1 K.LSSEKIEFATVGK.T 245 - 255 594.2983 1186.5820 1186.5354 0.0467 0 K.VDDEPEAGDIK.-
4	XP_001481696	28820	309	8	5.84	6-phosphogluconolactonase	Sequence Coverage: 34% 1 MTGTSPNLYS LPNTDALAPH LRAYVLRCQN SAINRHNTFR VAVSGGSLPA 51 VLAKALLAPS NGSPEDTVRF

						DKWDVFFADE RAVPLDHPDS NYRLLKDELL 101 SKIPAEMGTP KVHPIDADHV NDDTQELADL YQEELMRSFA AKDSVKLPVF 151 DLILLGCGPD GHTCSLFPGH KLLREKDAWV AAETNSPKPP PKRITLTLPV 201 VTHAVSIAFV ATGAGKKEIL KQIFDAEEGR ELPSALVNQG AGEKVSFWD 251 HAAVDGVSFP RRGSL 2 - 22 746.7134 2237.1184 2237.1440 - 0.0257 0 M.TGTSPNLYSLPNTDALAPHLR.A 41 - 54 634.8778 1267.7410 1267.7500 - 0.0089 0 R.VAVSGGSLPAVLAK.A 55 - 69 763.8879 1525.7612 1525.7736 - 0.0124 0 K.ALLAPSNGLPEDTVR.F 55 - 69 763.8915 1525.7684 1525.7736 - 0.0052 0 K.ALLAPSNGLPEDTVR.F 94 - 102 529.8221 1057.6296 1057.6383 - 0.0086 1 R.LLKDELLSK.I 103 - 111 480.2419 958.4692 958.4794 - 0.0101 0 K.IPAEMGTPK.V Oxidation (M) 222 - 230 532.7511 1063.4876 1063.4934 - 0.0058 0 K.QIFDAEEGR.E 231 - 244 706.8649 1411.7152 1411.7307 - 0.0154 0 R.ELPSALVNQGAGEK.V
5	XP_7538 27	32716	171	3	6.04	Pyridoxine biosynthesis protein Sequence Coverage: 15% 1 MASNGTNGAS ASNSFTVKAG LAQMLKGGVI MDVVNAEQAR IAEEAGAAAV 51 MALERVPADI RAQGGVARMS DPSMIKEIMA AVTIPVMAKA RIGHFVECQI 101 LEAIGVDYID ESEVLTPADD VYHVKKHDYK VPFVCGCRNL GEALRRIAEG 151 AAMIRTKGEA GTGDVVEAVK HMRTVNSQIA RARSILQNST DPEIELRAYA 201 RELEVPEYELL RETAEKGRLP VVNFAAGGVA TPADAALMMQ LGCDGVFVGS 251 GIFKSGDAKK RAKAIVQAVT HYKDPKVLAE VSEGLGEAMV GINVSQMPEA 301 DRLAKRGW 156 - 170 487.6082 1459.8028 1459.7518 0.0509 1 R.TKGEAGTGDVVEAVK.H 174 - 181 444.7613 887.5080 887.4825 0.0256 0 R.TVNSQIAR.A) 184 - 197 807.9560 1613.8974 1613.8260 0.0714 0 R.SILQNSTDPEIELR.A
6	XP_7527 19	33424	238	8	5.33	Spermidine synthase Sequence Coverage: 17% 1 MSEITHPTIK DGWFSEQSDM WPGQAMNLKV NQILHHEKSK YQDVLVFEST

						51 DYGTVLVLDN VIQCTERDEF SYQEMITHLA MNSHPNPKV LVIGGGDGGV 101 LREVVKHESV EEAILCDIDE AVIRVSKKYL PGMSIGFQHP NVKVHIGDGF 151 QFLKERKNEF DVIITDSSDP EGPAESLFQK PYFELLRDAL RDGGVITTQG 201 SENQWLHLSL ITDLKKACKE VFPVAEYAYT TIPTYPSGQI GFMVCKDAT 251 RNVREPVRTW SREEEERLCR YYNQDIHRAS FVLPNFARKA LDV 89 - 102 447.2879 1338.8419 1338.7984 0.0435 1 K.KVLVIGGGDGGVLR.E 90 - 102 606.3743 1210.7340 1210.7034 0.0306 0 K.VLVIGGGDGGVLR.E 90 - 102 606.3878 1210.7610 1210.7034 0.0576 0 K.VLVIGGGDGGVLR.E 144 - 154 420.9104 1259.7094 1259.6663 0.0431 0 K.VHIGDGFQFLK.E 144 - 154 630.8677 1259.7208 1259.6663 0.0546 0 K.VHIGDGFQFLK.E 252 - 258 435.2691 868.5236 868.4879 0.0358 1 R.NVREPVR.T 271 - 278 554.7820 1107.5494 1107.5097 0.0397 0 R.YYNQDIHR.A 279 - 288 561.3307 1120.6468 1120.6029 0.0439 0 R.ASFVLPNFAR.K
7	XP_754985	33240	131	6	5.51	Phosphoribosyl- aminoimidazole- succinocarboxami de synthase Sequence Coverage: 17% 1 MAEALTNTDL QGALPLIARG KVRDLYEVDD KTLLFIATDR ISAYDVIMEN 51 GIPNKGVLTT LCTKAWFKIL TDAIPSLRTH FITLDLPPQI PPSLRPALQN 101 RSMQVRKLKI LPIEAIVRGY ITGSAWNEYK KSGTVHGIKV APGLRESEAF 151 PDGPITYPST KAEQGEHDEN IHPDQAAAIL GEHASTVASL AVQLYKVAHA 201 YALSRGVIIA DTKFEFGVDE ETNEVVLADE VLTPDSSRFW PKDDYEVGRG 251 QQSFDKQFLR DWLVKEGLKG KEGVRMTEEV VQKTAEKYKE AWERITGGN 24 - 31 498.7505 995.4864 995.4447 0.0417 0 R.DLYEVDDK.T 32 - 40 525.3250 1048.6354 1048.5917 0.0438 0 K.TLLFIATDR.I 69 - 78 549.8499 1097.6852 1097.6444 0.0408 0 K.ILTDAIPSLR.T 110 - 118 512.3498 1022.6850 1022.6488 0.0363 0 K.ILPIEAIVR.G 110 - 118 512.3550 1022.6954 1022.6488 0.0467 0 K.ILPIEAIVR.G

							146 - 161 869.9517 1737.8888 1737.8097 0.0791 0 R.ESEAFDPGPIYTPSTK.A
8	XP_754776	43596	217	6	7.63	Inorganic diphosphatase	Sequence Coverage: 14% 1 MSPVALRMSS KALLPLSPLL RLSTASPALA RPCSPSPRTS ATLAPPTRQA 51 PPPSSLSSSS FSPSFSPQQA NLSSPSSSRV RSSVSSASTR AALLSRHFSS 101 YTPPQSPNMS YTVRKIGQAN TLEHRVYIEK DGVPISPFHD IPLYANPEQT 151 ILNMVVEIPR WTNAKQEISK EEFLNPIKQD VKKGKLRFRV NCFPHKGYLW 201 NYGAFFQTWE DPNVVHPETK AKGDNDPLDV CEIGELVGYP GQVKQVKVLG 251 VMALLDEEET DWKVIVIDIN DPLAPKLNDI EDVERHPLGL LRATNEWFRI 301 YKIPDGKPEN QFAFSGECKN KKYALDVIRE CADAWEKLIT GKSPRGDISL 351 ANTSVENSSD RADPAQLASI PKGENLPPAP IDGSIDKWFF ISGAAV 115 - 125 422.9172 1265.7298 1265.6840 0.0458 1 R.KIGQANTLEHR.V 264 - 276 703.9444 1405.8742 1405.8181 0.0562 0 K.VIVIDINDPLAPK.L 277 - 285 551.7962 1101.5778 1101.5302 0.0477 0 K.LNDIEDVER.H 286 - 292 403.2687 804.5228 804.4970 0.0259 0 R.HLPGLLR.A 323 - 329 425.2589 848.5032 848.4756 0.0277 0 K.YALDVIR.E 362 - 372 555.8337 1109.6528 1109.6080 0.0448 0 R.ADPAQLASIPK.G
9	XP_750257	33474	299	10	5.11	60S ribosomal protein P0	Sequence Coverage: 24% 1 MGGKSATKAA YFDKLKSLLD EYKTVFIVGV DNVSSQQMHE IRLALRGQAV 51 VLMGKNTMVR RAIKGFVADN PEYERLLPHV KGNVGFIFTN GDLKDVTKI 101 LANRVAAPAR AGAIAPADVW VPAGNTGMEP GKTSFFQALG VPTKIARGTI 151 EITTDLKLVE AGAKVGPSEA TLLNMLNISP FTYGMTITQV YDNGQCFAH 201 VLDIEESQLL DAFSSAIKTI TTVSLALNYP TLPVMHSLI NGYKKVLAVA 251 IETDYSWPEI EELKDRIANP DAYAAAAPVA AAPAAGGAAP AAEEKKEEEA 301 EESDEDMGFG LFD 65 - 75 648.8174 1295.6202 1295.5782 0.0420 0 K.GFVADNPEYER.L 65 - 75 648.8209 1295.6272 1295.5782

							0.0490 0 K.GFVADNPEYER.L 82 - 94 691.3812 1380.7478 1380.7038 0.0441 0 K.GNVGFIFTNGDLK.D 82 - 97 575.3206 1722.9400 1722.8941 0.0459 1 K.GNVGFIFTNGDLKDV.K.T 82 - 97 862.4805 1722.9464 1722.8941 0.0523 1 K.GNVGFIFTNGDLKDV.K.T 82 - 97 575.3236 1722.9490 1722.8941 0.0549 1 K.GNVGFIFTNGDLKDV.K.T 133 - 144 648.3787 1294.7428 1294.6922 0.0507 0 K.TSFFQALGVPTK.I 148 - 157 545.8188 1089.6230 1089.5918 0.0313 0 R.GTIEITDLK.L 267 - 295 859.8014 2576.3824 2576.2870 0.0954 0 R.IANPDYAAAAPVAAAPAAGGAAPAAEEK. K 267 - 295 859.8047 2576.3923 2576.2870 0.1053 0 R.IANPDYAAAAPVAAAPAAGGAAPAAEEK. K
10	XP_7539 94	36835	82	2	5.02	Adenosine kinase	Sequence Coverage: 6% 1 MAATQGY PFL CLENPLLDIQ AVGDAALLEK YGLKDNDAIL AEEKHMG LYD 51 ELLSRDAKLI AGGAAQNTAR GAQYMLPDNS VMYIGCVGKD KYADILKEAC 101 NQAGVHTEYR VDDVQPTGKC GVIITGHNRS MCTHLAAANE YKIDHLKQPH 151 VWSLVEKAQY YYVGGYHLTV CVPAILALAE EAAAKNKVFM LSLSAPFIPQ 201 FFKDQLDSVL PYTDYTCNE TEARAYAESH EWNTDDVVEI AKKLAQLPKK 251 NSSRPRVAIV TQGTLPITTA TVKPDGEVEV KEFPVHEISK SSINDTNGAG 301 DAFAGGFCAG VVQNKSL EES MDMGQWLASL SIQELGPS 59 - 70 571.8359 1141.6572 1141.6203 0.0369 0 K.LIAGGAAQNTAR.G 111 - 119 479.7577 957.5008 957.4767 0.0241 0 R.VDDVQPTGK.C
11a	XP_7480 95	38298	295	8	6.04	Thiamine biosynthesis protein (Nmt1)	Sequence Coverage: 26% 1 MSTDKITFLT NWHATPYHAP LYLAHSGKFF KEEGLK VAIL EPNDPSDVTE 51 IIGSGK VDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLK DSGIT 101 EDFRSLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCFCS 201 ILYIANDAFL AANPDKVOKI

						MRAVKRATDY VLAEPAKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLLGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAAE GGFKRLHVSA SA 37 - 56 1027.5695 2053.1244 2053.0579 0.0665 0 K.VAILEPNDPSPDVTEIIGSGK.V 96 - 104 520.2540 1038.4934 1038.4618 0.0316 0 K.DSGITEDFR.S 111 - 119 485.2659 968.5172 968.4967 0.0205 0 R.IGYVGEFGK.I 120 - 127 480.2874 958.5602 958.5335 0.0268 0 K.IQIDELTK.Y 128 - 140 763.3618 1524.7090 1524.6555 0.0536 0 K.YYGMTADDYTAVR.C 227 - 237 589.3241 1176.6336 1176.6026 0.0310 0 R.ATDYVLAEPK.A 261 - 267 439.2237 876.4328 876.4130 0.0199 0 R.SFAYFSR.D 286 - 300 854.9590 1707.9034 1707.8468 0.0567 0 R.LGILDANFEPNYTNK.Y
11b	XP_7480 95	38298	235	8	6.04	Thiamine biosynthesis protein (Nmt1) Sequence Coverage: 25% 1 MSTDKITFLT NWHATPYHAP LYLAHSGGFF KEEGLKVAIL EPNDPSDVTE 51 IIGSGKVDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLKDSGIT 101 EDFRSLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCCFS 201 ILYIANDAFL AANPDKVQKF MRAVKRATDY VLAEPAKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLLGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAAE GGFKRLHVSA SA 28 - 36 527.7964 1053.5782 1053.5495 0.0288 1 K.GFFKEEGLK.V 37 - 56 1027.5746 2053.1346 2053.0579 0.0767 0 K.VAILEPNDPSPDVTEIIGSGK.V 96 - 104 520.2506 1038.4866 1038.4618 0.0248 0 K.DSGITEDFR.S 111 - 119 485.2672 968.5198 968.4967 0.0231 0 R.IGYVGEFGK.I 120 - 127 480.2850 958.5554 958.5335 0.0220 0 K.IQIDELTK.Y 227 - 237 589.3234 1176.6322 1176.6026 0.0296 0 R.ATDYVLAEPK.A 261 - 267 439.2215 876.4284 876.4130

							0.0155 0 R.SFAYFSR.D 286 - 300 854.9556 1707.8966 1707.8468 0.0499 0 R.LGILDANFEPNYTNK.Y
11c	XP_748095	38298	462	14	6.04	Thiamine biosynthesis protein (Nmt1)]	Sequence Coverage: 26% 1 MSTDKITFLT NWHATPYHAP LYLAHSKGFF KEEGLKVAIL EPNDPSDVT 51 IIGSGKVDMG FKAMIHTLAA KARNFPVTSI GSLLDEPFTG VVYLKDSGIT 101 EDFRSLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII 151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCFC 201 ILYIANDAFL AANPDKVQKF MRAVKRATDY VLAEPKAYE EYIDVKPIMG 251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLGILD ANFEPNYTNK 301 YLSWDLADS TDPLGDQKRM AELQKQVAE GGFKRLHVS SA 28 - 36 527.7914 1053.5682 1053.5495 0.0188 1 K.GFFKEEGLK.V 37 - 56 685.3743 2053.1011 2053.0579 0.0432 0 K.VAILEPNDPSDVTIIGSGK.V 37 - 56 1027.5579 2053.1012 2053.0579 0.0433 0 K.VAILEPNDPSDVTIIGSGK.V 37 - 56 1027.5620 2053.1094 2053.0579 0.0515 0 K.VAILEPNDPSDVTIIGSGK.V 96 - 104 520.2471 1038.4796 1038.4618 0.0178 0 K.DSGITEDFR.S 96 - 104 520.2502 1038.4858 1038.4618 0.0240 0 K.DSGITEDFR.S 111 - 119 485.2477 968.4808 968.4967 - 0.0159 0 R.IGYVGEFGK.I 120 - 127 480.2622 958.5098 958.5335 - 0.0236 0 K.IQIDELTK.Y 226 - 237 445.2539 1332.7399 1332.7037 0.0361 1 K.RATDYVLAEPK.A 227 - 237 589.3192 1176.6238 1176.6026 0.0212 0 R.ATDYVLAEPK.A 227 - 237 589.3210 1176.6274 1176.6026 0.0248 0 R.ATDYVLAEPK.A 261 - 267 439.2151 876.4156 876.4130 0.0027 0 R.SFAYFSR.D 286 - 300 854.9557 1707.8968 1707.8468 0.0501 0 R.LGILDANFEPNYTNK.Y 286 - 300 854.9564 1707.8982 1707.8468 0.0515 0 R.LGILDANFEPNYTNK.Y
12a	XP_7544	39766	220	9	5.55	Fructose-bisphosphate	Sequence Coverage: 16%

	52					aldolase, class II	1 MGILDKLSRK SGVIVGDDVL RLFHEYAQEKN FAIPAVNVTS SSTVVACLEA 51 ARDQNCPIIL QVSQGGAAAYF AGKGVSN DGQ KASIAGSIAA AHYIRSIAPS 101 YGIPVVLHTD HCAKKLLPWL DGMLDEDERY FKQHGEPLFS SHMIDLSEEP 151 VDYNIE TTAK YLKRAAPMKQ WLEMEIGITG GEEDGVNNED VDNNSLYTQP 201 EDILAIYNAL APISPYFSIA AGFGNVHGVY KPGNVRLHPE LLSKHQAYVK 251 EKIGSNKDKP VYFVFHGGSG STKEEYKQAI SYGVVKVNLD TDMQYAYMSG 301 VRDYILNKKD YLMSAVGNPD GEDKPNKKYF DPRVWVREGE KTMSKR VQVA 351 LEDFNTAGQL 10 - 21 419.9170 1256.7292 1256.7089 0.0203 1 R.KSGVIVGDDVLR.L 11 - 21 565.3218 1128.6290 1128.6139 0.0151 0 K.SGVIVGDDVLR.L 22 - 29 514.2676 1026.5206 1026.5022 0.0185 0 R.LFEY AQEKN 82 - 95 467.6007 1399.7803 1399.7572 0.0231 0 K.ASIAGSIAAAHYIR.S 82 - 95 700.9099 1399.8052 1399.7572 0.0481 0 K.ASIAGSIAAAHYIR.S 278 - 286 482.7859 963.5572 963.5389 0.0183 0 K.QAISYGVVK.V 346 - 360 830.9594 1659.9042 1659.8580 0.0462 1 K.RVQVALEDFNTAGQL.- 346 - 360 830.9673 1659.9200 1659.8580 0.0620 1 K.RVQVALEDFNTAGQL.- 347 - 360 752.9063 1503.7980 1503.7569 0.0411 0 R.VQVALEDFNTAGQL.-
12b	XP_7544 52	39766	438	13	5.55	Fructose- biphosphate aldolase, class II	Sequence Coverage: 22% 1 MGILDKLSRK SGVIVGDDVL RLFHEYAQEKN FAIPAVNVTS SSTVVACLEA 51 ARDQNCPIIL QVSQGGAAAYF AGKGVSN DGQ KASIAGSIAA AHYIRSIAPS 101 YGIPVVLHTD HCAKKLLPWL DGMLDEDERY FKQHGEPLFS SHMIDLSEEP 151 VDYNIE TTAK YLKRAAPMKQ WLEMEIGITG GEEDGVNNED VDNNSLYTQP 201 EDILAIYNAL APISPYFSIA AGFGNVHGVY KPGNVRLHPE LLSKHQAYVK 251 EKIGSNKDKP VYFVFHGGSG STKEEYKQAI SYGVVKVNLD TDMQYAYMSG 301 VRDYILNKKD YLMSAVGNPD GEDKPNKKYF DPRVWVREGE

							KTMSKRVQVA 351 LEDFNTAGQL 10 - 21 419.9154 1256.7244 1256.7089 0.0155 1 R.KSGVIVGDDVLR.L 10 - 21 629.3725 1256.7304 1256.7089 0.0216 1 R.KSGVIVGDDVLR.L 11 - 21 565.3157 1128.6168 1128.6139 0.0029 0 K.SGVIVGDDVLR.L 22 - 29 514.2490 1026.4834 1026.5022 - 0.0187 0 R.LFEYAQEK.N 82 - 95 467.5998 1399.7776 1399.7572 0.0204 0 K.ASIAGSIAAAHYIR.S 82 - 95 700.9088 1399.8030 1399.7572 0.0459 0 K.ASIAGSIAAAHYIR.S 258 - 273 575.9697 1724.8873 1724.8522 0.0350 0 K.DKPVYFVFHGGSGSTK.E 278 - 286 482.7821 963.5496 963.5389 0.0107 0 K.QAISYGVVK.V 303 - 309 447.2638 892.5130 892.5018 0.0113 1 R.DYILNKK.D 303 - 309 447.2638 892.5130 892.5018 0.0113 1 R.DYILNKK.D 346 - 360 830.9579 1659.9012 1659.8580 0.0432 1 K.RVQVALEDFNTAGQL.- 346 - 360 830.9579 1659.9012 1659.8580 0.0432 1 K.RVQVALEDFNTAGQL.- 347 - 360 752.9050 1503.7954 1503.7569 0.0385 0 R.VQVALEDFNTAGQL.-
13	XP_7537 16	35426	419	17	6.04	Transaldolase	Sequence Coverage: 38% 1 MSSALEQLKA TGTVVVCDSG DFATIGKYKP QDATTNPSLI LAASKKPEYA 51 SLIDAAVQKG KKEGKTLDEQ VDATLDNLLV EFGKKILEII PGKVSTEVDA 101 RFSFDTQASV DKALHIVKLY EQQGISKDRI LIKIASTWEG IKAAHILQSQ 151 HGINCNLTLM FSLVQAIAAA EAGAFLISPF VGRILDWYKA AHKRDFSPEE 201 DPGVKSVQSI FNYYKKGHGYK TIVMGASFRN TGEITELAGC DYLTISPNLL 251 EELYNSTASV PKKLDAASAA SLDIPKRSYI NDEAAFRFDF NEEAMAVEKL 301 REGISKFAAD AVTLKELLKQ KIQA 28 - 45 640.0280 1917.0622 1917.0207 0.0415 0 K.YKPQDATTNPSLILAASK.K 28 - 45 959.5454 1917.0762 1917.0207 0.0555 0 K.YKPQDATTNPSLILAASK.K 46 - 59 511.6237 1531.8493 1531.8246 0.0247 0 K.KPEYASLIDAAVQK.G

						86 - 101 580.6792 1739.0158 1738.9829 0.0329 1 K.ILEIIPGKVSTEVDAR.F 94 - 101 438.7287 875.4428 875.4349 0.0080 0 K.VSTEVDAR.F 102 - 112 622.8083 1243.6020 1243.5721 0.0300 0 R.FSFDTQASVDK.A 119 - 127 533.2903 1064.5660 1064.5502 0.0158 0 K.LYEQQGISK.D 119 - 129 446.2392 1335.6958 1335.6783 0.0175 1 K.LYEQQGISKDR.I 134 - 142 502.7865 1003.5584 1003.5338 0.0246 0 K.IASTWEGIK.A 195 - 205 610.2894 1218.5642 1218.5405 0.0238 0 R.DFSPEEDPGVK.S 206 - 215 624.8318 1247.6490 1247.6186 0.0304 0 K.SVQSIFNYYK.K 206 - 216 459.5841 1375.7305 1375.7136 0.0169 1 K.SVQSIFNYYKK.H 206 - 216 688.8820 1375.7494 1375.7136 0.0359 1 K.SVQSIFNYYKK.H 278 - 287 593.2908 1184.5670 1184.5462 0.0209 0 R.SYNDEAAFR.F 307 - 315 468.2704 934.5262 934.5124 0.0139 0 K.FAADAUTLK.E 307 - 319 473.6196 1417.8370 1417.8180 0.0189 1 K.FAADAUTLKELLK.Q 307 - 319 709.9361 1417.8576 1417.8180 0.0396 1 K.FAADAUTLKELLK.Q
14a	XP_752429	42170	343	10	5.67	S-adenosylmethionine synthetase Sequence Coverage: 26% 1 MGSVAKSNTF LFTSESVGEG HPDKIADQVS DAVLDACLA E DPLSKVACET 51 ATKTGMIMVF GEITNAKLD YQKIIRGAIK DIGYDDSDKG FDYKTCNVLV 101 AIEQQSPDIA QGLHYDEALE KLGAGDQGIM FGATDETPE LLPLTLLSH 151 KLNSAMTQAR KDGSIPWLRP DTKTQVTVEY AHDGGAVKPL RVDTVVVSQAQ 201 HSDDVSTEEL RTVIKEKIIK KVIPAELLDD RTIYHIQPSG RFVIGGPQGD 251 AGLTGRKIIV DTYGGWGAHG GGAFTSGKDYS KVDRSAAYVG RWIAKSLVHA 301 GLARRVLVQL SYAIGVAEPL SIFVETYGTS EKSSDELVEI IRKNFDLRPG 351 VIVKELDLAK PIYFQTAKNG HFTNQSFPE KPKTLKF 81 - 89 514.2290 1026.4434 1026.4142 0.0293 0 K.DIGYDDSDK.G 81 - 94 546.5837 1636.7293 1636.6893 0.0400 1 K.DIGYDDSDKGFDYK.T

						192 - 211 729.3761 2185.1065 2185.0499 0.0566 0 R.VDTVVVSAQHSDDVSTEELR.T 222 - 231 570.8273 1139.6400 1139.6186 0.0214 0 K.VIPAELLDDR.T 232 - 241 586.3302 1170.6458 1170.6145 0.0313 0 R.TIYHIQPSGR.F 242 - 256 722.8976 1443.7806 1443.7471 0.0336 0 R.FVIGGPQGDAGLTGR.K 296 - 304 462.2853 922.5560 922.5348 0.0212 0 K.SLVHAGLAR.R 333 - 342 580.8231 1159.6316 1159.6084 0.0232 0 K.SSDELVEIIR.K 333 - 343 430.2486 1287.7240 1287.7034 0.0206 1 K.SSDELVEIIRK.N 355 - 368 546.3146 1635.9220 1635.8872 0.0348 0 K.ELDLAKPIYFQTAK.N
14b	XP_752429	42170	151	4	5.67	S-adenosylmethionine synthetase Sequence Coverage: 9% 1 MGSVAKSNTF LFTSESVGEG HPDKIADQVS DAVLDACLA E DPLSKVACET 51 ATKTGMIMVF GEITTNAKLD YQKIIRGAIK DIGYDDSDKG FDYKTCNVLV 101 AIEQQSPDIA QGLHYDEALE KLGAGDQGIM FGYATDETPE LLPLTLLSH 151 KLNSAMTQAR KDGSIPWLRP DTKTQVTVEY AHDGGAVKPL RVDTVVVSAQ 201 HSDDVSTEEL RTVIKEKIIK KVIPAELLDD RTIYHIQPSG RFVIGGPQGD 251 AGLTGRKIIV DTYGGWGAHG GGA FSGKDYS KVDRSAAYVG RWIAKSLVHA 301 GLARRVLVQL SYAIGVAEPL SIFVETYGTS EKSSDELVEIIRKNFDLRPG 351 VIVKELDLAK PIYFQTAKNG HFTNQSFWE KPKTLKF 222 - 231 570.8241 1139.6336 1139.6186 0.0150 0 K.VIPAELLDDR.T 242 - 256 722.8914 1443.7682 1443.7471 0.0212 0 R.FVIGGPQGDAGLTGR.K 333 - 342 580.8209 1159.6272 1159.6084 0.0188 0 K.SSDELVEIIR.K 333 - 343 644.8682 1287.7218 1287.7034 0.0184 1 K.SSDELVEIIRK.N
15	XP_751519	39874	113	4	5.48	Glutamine synthetase Sequence Coverage: 10% 1 MAETSTVVS N TENLMKYMSL DQRGHVQA EY VWIDAVGNCR CKTKTLSPV 51 KSVDELPEWN FDGSSTGQAP GDNSDVYLRP VAIFADPFRR GDNILVLCET 101 WSDSGTPNKF NFRHEANRLM EIHAKKEFWF GLEQEYTLTG TDGWPGWPK 151 GGFPGAQGPY YCGVGTGKVY

						CRDIVEAHYR ACLYAGIKIS GINAEVMPSQ 201 WEYQVGPCQG IEMGDQLWMS RFLLRHVAEE FGVKISFEPK PIKGDWNGAG 251 LHTNVSTAAT RAEGGLKVIE AYMQKLEARH NEHIAVYEGEG NEERLTGRHE 301 TGSIDKFSYG VADRGGGSIRI PRQVAKDGKG YFEDRRPASN ADPYQITGII 351 VETLCGGN 501.7632 1001.5118 1001.4930 0.0188 0 R.DIVEAHYR.A 227 - 234 439.7394 877.4642 877.4545 0.0097 0 R.VAEEFGVK.I 280 - 294 585.2807 1752.8203 1752.7815 0.0387 0 R.HNEHIAVYEGEGNEER.L 307 - 314 457.7331 913.4516 913.4294 0.0223 0 K.FSYGVADR.G
16	YP_0013 37378	43219	459	17	5.29	Elongation factor Tu [Klebsiella pneumoniae] Sequence Coverage: 32% 1 MSKEKFERTK PHVNVGTIGH VDHGKTTLTA AITTVLAKTY GGSARAFDQI 51 DNAPEEKARG ITINTSHVEY DTPTRHYAHV DCPGHADYVK NMITGAAQMD 101 GAILVVAATD GPMPQTREHI LLGRQVGVPY IIVFLNKCDM VDDEELLELV 151 EMEVRELLSQ YDFPGDDTPI VRGSALKALE GDAEWEAKII ELAGHLDTYI 201 PEPERAIDKP FLLPIEDVFS ISGRGT VVTG RVERGIKVG EEVEIVGIKE 251 TAKTTCTGVE MFRKLLDEGR AGENVGVLLR GIKREEIERG QVLAKPGTIN 301 PHTKFESEVY ILSKDEGGRH TPFFKGYRPQ FYFRTTDVTG TIELPEGVEM 351 VMPGDNIKMV VTLIHPIAMD DGLRFAIREG GRTVGAGVVA KVLG 26 - 38 652.4144 1302.8142 1302.7759 0.0384 0 K.TTLTAAITTVLAK.T 46 - 57 688.8384 1375.6622 1375.6255 0.0367 0 R.AFDQIDNAPEEK.A 118 - 124 419.2611 836.5076 836.4868 0.0208 0 R.EHILLGR.Q 125 - 137 745.4637 1488.9128 1488.8704 0.0424 0 R.QVGVPYIIVFLNK.C 156 - 172 983.0156 1964.0166 1963.9527 0.0639 0 R.ELLSQYDFPGDDTPIVR.G 156 - 172 983.0182 1964.0218 1963.9527 0.0691 0 R.ELLSQYDFPGDDTPIVR.G 189 - 205 656.0310 1965.0712 1965.0207 0.0505 0 K.IELAGHLDTYIPEPER.A 189 - 205 656.0335 1965.0787 1965.0207

						0.0580 0 K.IIELAGHLDTYIPEPER.A 239 - 249 586.3455 1170.6764 1170.6496 0.0269 0 K.VGEEVEIVGIK.E 239 - 249 586.3455 1170.6764 1170.6496 0.0269 0 K.VGEEVEIVGIK.E 239 - 253 534.3096 1599.9070 1599.8719 0.0350 1 K.VGEEVEIVGIKETAK.T 271 - 280 514.3099 1026.6052 1026.5822 0.0231 0 R.AGENVGVLRL.G 305 - 314 607.8337 1213.6528 1213.6230 0.0298 0 K.FESEVYILSK.D 305 - 319 576.9673 1727.8801 1727.8366 0.0435 1 K.FESEVYILSKDEGGR.H 326 - 334 411.8837 1232.6293 1232.6091 0.0202 0 K.GYRPQFYFR.T 326 - 334 617.3270 1232.6394 1232.6091 0.0304 0 K.GYRPQFYFR.T
17a	Q96X30	47276	806	20	5.39	Enolase/allergen Asp F 22 Sequence Coverage: 36% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHEL 51 DGDKTQWGGK GVLKAVKNVN ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNL GANA ILGVSLAVAK AGAAEKGVPL YAHISDLAGT KKPYPVLPVF 151 QNVLN GGS HA GGRLAFQEFM IVPDSAPSFS EALRQGA EVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYT GK IKIAMDVASS 251 EFYKADVKKY DLDFKNPESD PSKWLTYEQL ADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSD FQIV GDDLTVTNPG RIKKAIELKS CNALLKVNQ 351 IGTLTESIQA AKDSYADNWG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCRSERLAK LNQILRIEEE LGENAVYAGS KFRTAVNL 16 - 32 608.3249 1821.9529 1821.9221 0.0308 0 R.GNPTVEVDVVTETGLHR.A 16 - 32 911.9942 1821.9738 1821.9221 0.0517 0 R.GNPTVEVDVVTETGLHR.A 68 - 79 634.8787 1267.7428 1267.7136 0.0293 0 K.NVNETIGPALIK.E 68 - 79 634.8792 1267.7438 1267.7136 0.0303 0 K.NVNETIGPALIK.E 80 - 89 588.3108 1174.6070 1174.5830 0.0241 1 K.ENIDVKDQSK.V 90 - 96 432.7287 863.4428 863.4389 0.0040 0 K.VDEFLNK.L 90 - 103 521.9471 1562.8195 1562.7940

						0.0255 1 K.VDEFLNKLDGTANK.S 90 - 103 782.4279 1562.8412 1562.7940 0.0472 1 K.VDEFLNKLDGTANK.S 104 - 120 799.4887 1596.9628 1596.9199 0.0430 0 K.SNLGANAILGVSLAVAK.A 127 - 141 514.6233 1540.8481 1540.8249 0.0231 0 K.GVPLYAHISDLAGTK.K 127 - 141 771.4409 1540.8672 1540.8249 0.0423 0 K.GVPLYAHISDLAGTK.K 185 - 192 461.7368 921.4590 921.4556 0.0035 0 R.QGAENVYQK.L 314 - 331 968.0013 1933.9880 1933.9382 0.0499 0 K.TSDFQIVGDDTLVTNPGR.I 314 - 331 968.0177 1934.0208 1933.9382 0.0827 0 K.TSDFQIVGDDTLVTNPGR.I 348 - 362 786.9552 1571.8958 1571.8519 0.0440 0 K.VNQIGTLTESIQAAK.D 377 - 393 873.4741 1744.9336 1744.8843 0.0493 0 R.SGETEDVTIADIAVGLR.S 377 - 393 873.4761 1744.9376 1744.8843 0.0533 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.8974 1607.7802 1607.7678 0.0124 0 R.IEEELGENAVYAGSK.F 417 - 431 804.9162 1607.8178 1607.7678 0.0500 0 R.IEEELGENAVYAGSK.F
17b	Q96X30	47276	114	3	5.39	Enolase /AspF22 Sequence Coverage: 10% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHELK 51 DGDKTQWGGK GVLKAVKNVN ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNLGANAL ILGVSLAVAK AGAAEKGVPYLAHISDLAGT KKPYPVLPVPF 151 QNVNLGGSHA GGRLAFQEFM IVPDSAPSFS EALRQGAENVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYTGK IKIAMDVASS 251 EFYKADVKKY DLDFKNPESD PSKWLTYEQL ADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSDFQIV GDDTLVTNPG RIKKAIELKS CNALLKVNQ 351 IGTLTESIQA AKDSYADNWG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCRSERLAK LNQILRIEEE LGENAVYAGS KFR TAVNL 348 - 362 786.9449 1571.8752 1571.8519 0.0234 0 K.VNQIGTLTESIQAAK.D 377 - 393 873.4615 1744.9084 1744.8843 0.0241 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.9011 1607.7876 1607.7678

							0.0198 0 R.IEEELGENAVYAGSK.F
17c	Q96X30	47276	772	19	5.39	Enolase/ Asp F22	Sequence Coverage: 40% 1 MPISKIHARS VYDSRGNPTV EVDVVTETGL HRAIVPSGAS TGQHEAHEL R 51 DGDKTQWGGK GVLKAVKNNV ETIGPALIKE NIDVKDQSKV DEFLNKLDGT 101 ANKSNLGGANA ILGVSLAVAK AGAAEKG VPL YAHISDLAGT KKPYPVLPVPF 151 QNVNLNGGSHA GGRLAFQEFM IVPDSAPSF S EALRQGAEVY QKLKALAKKK 201 YGQSAGNVGD EGGVAPDIQT AEEALDLITE AIEQAGYTGK IKIAMDVASS 251 EFYKADVKKY DLD FKNPESD PSKWLTYEQL ADLYKSLAAK YPIVSIEDPF 301 AEDDWEAWSY FYKTSD FQIV GDDLTVTNPG RIKKAIELKS CNALLLVNQ 351 IGTLTESIQA AKDSYADNWG VMVSHRSGET EDVTIADIAV GLRSGQIKTG 401 APCRSERLAK LNQILRIEEE LGENAVYAGS K FRTAVNL 16 - 32 608.3074 1821.9004 1821.9221 - 0.0217 0 R.GNPTVEVDVVTETGLHR.A 16 - 32 608.3075 1821.9007 1821.9221 - 0.0214 0 R.GNPTVEVDVVTETGLHR.A 33 - 50 620.6436 1858.9090 1858.9286 - 0.0196 0 R.AIVPSGASTGQHEAHEL.R.D 68 - 79 634.8556 1267.6966 1267.7136 - 0.0169 0 K.NVNETIGPALIK.E 80 - 89 588.2962 1174.5778 1174.5830 - 0.0051 1 K.ENIDVKDQSK.V 90 - 103 521.9288 1562.7646 1562.7940 - 0.0295 1 K.VDEFLNKLDGTANK.S 90 - 103 782.4031 1562.7916 1562.7940 - 0.0024 1 K.VDEFLNKLDGTANK.S 104 - 120 799.4644 1596.9142 1596.9199 - 0.0056 0 K.SNLGANAILGVSLAVAK.A 104 - 120 799.4797 1596.9448 1596.9199 0.0250 0 K.SNLGANAILGVSLAVAK.A 127 - 141 514.6090 1540.8052 1540.8249 - 0.0198 0 K.GVPLYAHISDLAGTK.K 127 - 141 514.6102 1540.8088 1540.8249 - 0.0162 0 K.GVPLYAHISDLAGTK.K 185 - 192 461.7259 921.4372 921.4556 - 0.0183 0 R.QGAEVYQK.L 314 - 331 967.9717 1933.9288 1933.9382 - 0.0093 0 K.TSDFQIVGDDLTVTNPGR.I 314 - 331 967.9889 1933.9632 1933.9382 0.0251 0 K.TSDFQIVGDDLTVTNPGR.I 348 - 362 524.9501 1571.8285 1571.8519 -

						0.0234 0 K.VNQIGTLTESIQAAK.D 348 - 362 786.9335 1571.8524 1571.8519 0.0006 0 K.VNQIGTLTESIQAAK.D 377 - 393 873.4526 1744.8906 1744.8843 0.0063 0 R.SGETEDVTIADIAVGLR.S 417 - 431 804.8896 1607.7646 1607.7678 - 0.0032 0 R.IEEELGENAVYAGSK.F 417 - 431 804.8900 1607.7654 1607.7678 - 0.0024 0 R.IEEELGENAVYAGSK.F
18	CAE17673	45546	134	3	5.72	Putative flavohaemoglobin Sequence Coverage: 7% 1 MPLTPEQVQI IKATVPVLAE HGTITITVFY KNMLTAHPEL NNVFNTTHQV 51 TGHQARALAG ALFAYASNID NLGALGPAVE LMCHKHASLY IKPDDYKIVG 101 KFLLEAMGQV LGDALTPEIL DAWATAYWQL ADIMIGREAQ LYEQAEGWTD 151 FRDFVVALKV PESSEITSFY LKPADGKPLP AFQPGQYISV QVHVPELNYL 201 QARQYSLSDM PRSDYYRISV KKESGLNPAE PGAKAHPGHV SNILHASVNE 251 GDTIKVSHPF GDDFLSDAKA AHPVVLLSAG VGLTPMTSIL NTLTSQAPER 301 KVSFIHGARN ARARAFKNHI TSLEQKLPNL KSTFFTSHPT EEDKEGDDYQ 351 FRGRVDLSQL DSNRDLFLDD ATTEYYVCGP DTFMTDMLNV LKSKGVSEDR 401 VKLELFGTGG VPH 2 - 12 633.3890 1264.7634 1264.7391 0.0244 0 M.PLTPEQVQIIK.A 223 - 234 585.3058 1168.5970 1168.5724 0.0247 0 K.ESGLNPAEPGAK.A 355 - 364 573.8049 1145.5952 1145.5677 0.0276 0 R.VDLSQLDSNR.D
19	XP_752401	44734	762	23	6.31	Phosphoglycerate kinase PgkA Sequence Coverage: 57% 1 MSLTNKLAIT DVDLKDKRVL IRVDFNVPLN EKKEVTNPQR IVGALPTIKY 51 AIEQGAKAVV LMSHLGRPDG KKNPKYSLKP VVPELEKLLG KSVIFTEDCV 101 GKEVEETVNK ASGGQVILE NLRFHPEEEG SYKDEEGKKV KADKEKVAEF 151 RKGLTALGDI YINDAFGTAH RAHSSMVGVD LPQKASGFLV KKELEYFAKA 201 LESPSRPFLA ILGGSKVSDK IQLIDNLLPK VNSLIITGGM AFTFKKTLEN 251 VKIGNSLFDE AGSKTVGDII EKAKKNNVKI VLPVDYITAD KFSADAKTGY 301 ATDEEGIPDG YMGLDVGDKS

						VKLYKETIAE AKTILWNGPP GVFEPEPFAN
						351 GTKQTLDAAV DAAKNGAIVI IGGGDTATVA AKYGAEKLS HVSTGGGASL
						401 ELLEGKELPG VAALSSK
						7 - 15 494.3047 986.5948 986.5648 0.0300 0 K.LAITDVDLK.D
						19 - 32 552.6723 1654.9951 1654.9406 0.0544 1 R.VLIRVDFNVPLNEK.K
						23 - 32 587.8250 1173.6354 1173.6030 0.0325 0 R.VDFNVPLNEK.K
						41 - 49 456.3173 910.6200 910.5851 0.0349 0 R.IVGALPTIK.Y
						58 - 71 499.2876 1494.8410 1494.7977 0.0433 0 K.AVVLMShLGRPDGK.K Oxidation (M)
						76 - 87 467.9474 1400.8204 1400.7915 0.0289 0 K.YSLKPVVPELEK.L
						76 - 87 701.4288 1400.8430 1400.7915 0.0516 0 K.YSLKPVVPELEK.L
						111 - 123 685.4166 1368.8186 1368.7725 0.0462 0 K.ASGGQVILLENLR.F
						153 - 171 669.0314 2004.0724 2004.0065 0.0659 0 K.GLtALGDIIYINDAFGTAHR.A
						172 - 184 462.2453 1383.7141 1383.6817 0.0324 0 R.AHSSMVGVDLPQK.A Oxidation (M)
						172 - 184 692.8756 1383.7366 1383.6817 0.0550 0 R.AHSSMVGVDLPQK.A Oxidation (M)
						193 - 199 450.2427 898.4708 898.4436 0.0272 0 K.ELEYFAK.A
						217 - 230 532.6635 1594.9687 1594.9294 0.0393 1 K.VSDKIQLIDNLLPK.V
						231 - 246 581.6737 1741.9993 1741.9437 0.0556 1 K.VNSLIITGGMAFTFKK.T Oxidation (M)
						253 - 264 619.3207 1236.6268 1236.5986 0.0282 0 K.IGNSLFDEAGSK.T
						265 - 272 437.7579 873.5012 873.4807 0.0205 0 K.TVGDIIK.A
						280 - 291 673.9023 1345.7900 1345.7493 0.0407 0 K.IVLPVDYITADK.F
						280 - 291 673.9078 1345.8010 1345.7493 0.0517 0 K.IVLPVDYITADK.F
						280 - 297 656.0449 1965.1129 1965.0459 0.0670 1 K.IVLPVDYITADKFSADAK.T
						298 - 319 1160.0558 2318.0970 2317.9897 0.1074 0 K.TGYATDEEGIPDGYMGLDVGDK.S Oxidation (M)
						354 - 364 551.8043 1101.5940 1101.5666

						0.0275 0 K.QLDAAVDAAK.N 389 - 406 585.6675 1753.9807 1753.9210 0.0597 0 K.LSHVSTGGGASLELLEGGK.E 407 - 417 536.3262 1070.6378 1070.5972 0.0407 0 K.ELPGVAALSSK.-
20	XP_752379	48459	677	23	5.82	Adenosylhomocysteinase Sequence Coverage: 38% 1 MAAPAQKFKV ADISLAAFGR REIELAEIEM PGLMAIRRKY AEDQPLKGAR 51 IAGCLHMTIQ TAVLIETLTA LGAEVTWTSC NIFSTQDHAA AAIASGVPV 101 FAWKGETEEE YQWCLEQQLN AFKDGQKLN ILDDGGDLTA LVHSKYPEML 151 KGCYGVSEET TTGVHHL YRM LKEGKLLVPA INVNSVTKS KFDNLYGCRE 201 SLIDGIKRAT DVMIAQKVAV VAGYGDVGKG CADALRSMGA RVLVTEIDPI 251 NALQAAVQGY QVVTMEEAAP QGQIFVTTG CRDILVGKHF EVMRNDAIVC 301 NIGHFDIEID VAWLKANAKS VQNIKPQVDR YLMPNGRHII LLAEGRLVNL 351 GCATGHSSFV MSCSFSNQVL AQIALFKAED EAFGK KYVEF GTTGKKPVG 401 YVLPKILDEQ VALLHLEHVN AKLSKLTVPQ AEYLGLDIAG PFKSDM 8 - 20 465.5890 1393.7452 1393.7718 - 0.0266 1 K.FKVADISLAAFGR.R 8 - 20 697.8864 1393.7582 1393.7718 - 0.0135 1 K.FKVADISLAAFGR.R 10 - 20 560.3039 1118.5932 1118.6084 - 0.0152 0 K.VADISLAAFGR.R 10 - 20 560.3195 1118.6244 1118.6084 0.0160 0 K.VADISLAAFGR.R 22 - 37 923.9560 1845.8974 1845.9216 - 0.0241 0 R.EIELAEIEMPGLMAIR.R 2 Oxidation (M) 22 - 37 923.9574 1845.9002 1845.9216 - 0.0213 0 R.EIELAEIEMPGLMAIR.R 2 Oxidation (M) 128 - 145 632.0074 1893.0004 1893.0207 - 0.0204 0 K.LNLILDDGGDLTALVHSK.Y 176 - 189 741.9138 1481.8130 1481.8453 - 0.0323 0 K.LLVPAINVNSVTK.S 176 - 189 741.9387 1481.8628 1481.8453 0.0175 0 K.LLVPAINVNSVTK.S 200 - 208 515.7914 1029.5682 1029.5818 - 0.0136 1 R.ESLIDGIKR.A 208 - 217 539.2856 1076.5566 1076.5648 - 0.0082 1 K.RATDVMIAQK.V Oxidation (M) 209 - 217 461.2349 920.4552 920.4637 -

						0.0085 0 R.ATDVMIA GK.V Oxidation (M) 218 - 229 567.8040 1133.5934 1133.6081 - 0.0146 0 K.VAVVAGYGDVGK.G 289 - 294 417.6919 833.3692 833.3854 - 0.0162 0 K.HFEV MR.N Oxidation (M) 320 - 330 428.5656 1282.6750 1282.6993 - 0.0244 0 K.SVQNIKPQVDR.Y 320 - 330 428.5689 1282.6849 1282.6993 - 0.0145 0 K.SVQNIKPQVDR.Y 338 - 346 511.3010 1020.5874 1020.6080 - 0.0205 0 R.HIILLAEGR.L 386 - 395 565.2932 1128.5718 1128.5815 - 0.0097 1 K.KYVEFGTTGK.K 387 - 395 501.2395 1000.4644 1000.4866 - 0.0221 0 K.YVEFGTTGK.K 396 - 405 550.3407 1098.6668 1098.6801 - 0.0133 0 K.KPVG VYVLPK.I 406 - 422 648.0227 1941.0463 1941.0683 - 0.0221 0 K.ILDEQVALLHLEHVNAK.L 426 - 443 966.5093 1931.0040 1931.0404 - 0.0364 0 K.LTPVQAEYLGLDIAGPFK.S 426 - 443 966.5135 1931.0124 1931.0404 - 0.0280 0 K.LTPVQAEYLGLDIAGPFK.S
21	XP_751658	67070	452	13	6.11	Phosphatidyl synthase Sequence Coverage: 23% 1 MPYMANTRTI PGPTAILPVG PEKGLDAGSA VPGRITMSLV LPIIGNNYSL 51 INTLISFIII LIFAFIHLFS SSPSFLIFSG SRLVNSSSNT DPAHPPPYKS 101 DIIYFSSLIT HSSPSYVSLT LLYVYILSRL SSIATMPRFD DADFGVEPAP 151 AGARSPRDAR GSASGSLPIP NEAGNTVEIP ATRSSISDAA QFMHNL SLSP 201 SMRDRRGSRN SFGTSLPIPR SPRVSRLLSV RKADAASVSR DILASQVQDM 251 SKEKVAAAKN MAFAFDIDGV LAHG NHA IPE AKEALKMLNG DNELGIKIPY 301 ILLTNGGGKT EASRCEQLSE ILEVPISTDQ FIQSHTPMQA LSEYYETVLV 351 LGGEGQKIRE VAENYGFKNV VHPKDILAWD PTISPWR TFT AEDRAEAKPR 401 DFSKIKFDAI LVFADSRDYA TDMQLIIDLL LAEDGKLLTR AKDPVSSRIP 451 IYFSQGDLLM PTDHKGPPRL TQGCFR IAVE AQYKALTGVD LERVVYGKPE 501 RATYTYADEV LKAWMEQIHN ENRLPKNIYM IGDNPQSDIV GGNMYGWNTC 551 LVRTGVFQGG ENDEHN PANF GVFPNVLEAV KAAVRKELGQ EFKFKWNPKV

						601 NPVTHGDGSS AVE 139 - 154 817.8704 1633.7262 1633.7373 - 0.0110 0 R.FDDADFGVEPAPAGAR.S 161 - 183 1119.5671 2237.1196 2237.1288 - 0.0091 0 R.GSASGSLPIPNEAGNTVEIPATR.S 210 - 220 594.8155 1187.6164 1187.6299 - 0.0134 0 R.NSFGTSLPIPR.S 241 - 252 675.8318 1349.6490 1349.6497 - 0.0006 0 R.DILASQVQDMSK.E Oxidation (M) 298 - 309 623.3599 1244.7052 1244.7129 - 0.0076 0 K.IPYILLTNGGGK.T 360 - 368 528.7513 1055.4880 1055.4924 - 0.0043 0 R.EVAENYGFK.N 388 - 394 420.1946 838.3746 838.3821 - 0.0074 0 R.TFTAEDR.A 405 - 417 747.9153 1493.8160 1493.8242 - 0.0082 1 K.IKFDAILVFADSR.D 477 - 484 461.2520 920.4894 920.4967 - 0.0073 0 R.IAVEAQYK.A 485 - 493 487.2698 972.5250 972.5240 0.0010 0 K.ALTGVDLER.V 502 - 512 637.3162 1272.6178 1272.6238 - 0.0059 0 R.ATYTYADEVLK.A 600 - 613 684.8210 1367.6274 1367.6317 - 0.0043 0 K.VNPVTHGDGSSAVE.-
22	EDP5450 6	61335	447	15	5.85	Glucose-6-phosphate isomerase Sequence Coverage: 31% 1 MPGFSQATEL GAWKELQEHH NSLGRNIVLK EYFEKDPQRF EKFSRTFANP 51 VDNTEILFDF SKNFLTEETL ALLVKLAREA GVEELRDAMF KGDPINFTED 101 RAVYHVALRN VTNEPMQVNG KSVVEDVNSV LEHMKEFTEQ VRSGEWWKGYT 151 GKKITTIINI GIGGSDLGPV MVTEALKPYG AEDMTLHFVS NIDGSHIAEA 201 LKHSDPETTL FLIASKTFTT AETTNANSA KKWFLSAKD EAHIAKHFVA 251 LSTNEEEVTK FGIDKKNMFG FASWVGGRYS VWSAIGLSVA LYIGFDNFHQ 301 FLAGAHAMDK HFRETPLEQN IPVLGGLLSV WYSDFFGAQT HLVAPFDQYL 351 HRFPAYLQQL SMESNGKAIT RTGEYVKYTT GPILFGEPAT NAQHSFFQLL 401 HQGTKLIPSD FIMAAESHNP VEGGKHQRML ASNFLAQSEA LMVGKTPEQV 451 KTEGAPDNLV PHKTFLGNRP TTSILAQKIT PSTLGALIA YEHLTFTEGA 501 VWNINSFDQW GVELGKVLAK KIQKELETPG AGGDHDASTS GLLLAFKKKA

						551 NLA 46 - 62 979.5227 1957.0308 1956.9469 0.0839 0 R.TFANPVDNTEILFDFSK.N 46 - 62 979.5259 1957.0372 1956.9469 0.0903 0 R.TFANPVDNTEILFDFSK.N 63 - 75 745.9560 1489.8974 1489.8392 0.0583 0 K.NFLTEETLALLVK.L 79 - 86 451.7460 901.4774 901.4505 0.0270 0 R.EAGVEELR.D 92 - 101 582.3063 1162.5980 1162.5255 0.0726 0 K.GDPINFTEDR.A 110 - 121 673.8437 1345.6728 1345.6296 0.0432 0 R.NVTNEPMQVNGK.S Oxidation (M) 203 - 216 520.2913 1557.8521 1557.8039 0.0482 0 K.HSDPETTLFLIASK.T 217 - 231 779.4053 1556.7960 1556.7318 0.0642 0 K.TFTTAETTTNANSK.K 217 - 231 779.4058 1556.7970 1556.7318 0.0652 0 K.TFTTAETTTNANSK.K 247 - 260 535.2906 1602.8500 1602.7889 0.0610 0 K.HFVALSTNEEEVTK.F 406 - 425 710.0470 2127.1192 2127.0306 0.0885 0 K.LIPSDFIMAAESHNPVEGGK.H Oxidation (M) 406 - 425 710.0478 2127.1216 2127.0306 0.0909 0 K.LIPSDFIMAAESHNPVEGGK.H Oxidation (M) 452 - 463 426.5680 1276.6822 1276.6412 0.0410 0 K.TEGAPDNLVPHK.T 464 - 478 549.6653 1645.9741 1645.9151 0.0589 0 K.TFLGNRPPTSILAQK.I 525 - 547 762.7462 2285.2168 2285.1176 0.0992 0 K.ELETPGAGGDHDASTSGLLLAFK.K
23	XP_750954	52885	474	18	5.88	ATP citrate lyase subunit (Acl), putatibe Sequence Coverage: 29% 1 MSAKSILEAD GKAILNYHLT RAPVIKPTPL PPSSTHNPPP RLASIYPED 51 AAVKDVLDT EVVYPWLLTP GAKFVAKPDQ LIKRRGKSG LALNKTWPEA 101 REWIEARAGK EIKVETVTGV LRQFLVEPFV PHPQETEEYI NINSVREGDW 151 ILFTHEGGVD VGDVDAKAEK LLIPVNLARNY PSNEEIAAAL LSKVPKGVHN 201 VLVD FISRLY AVYVDCQFTY LEINPLVIP NAEGTSAEVH FLDLAAKLDQ 251 TAEFECGTKW AIARSPANLG LATVPQTDGK VNIDAGPPME FPAPFGRELS 301 KEEKFISDMD AKTGASLKLT VLNANGRIWT LVAGGGASVV YADAIASAGF 351 VSELANYGEY SGAPTETQTY

						NYAKTVLDLM LRAPMHPDGK VLFIGGGIAN 401 FTNVASTFKG VIRAIREVAP VLNEHNVQIW VRRAGPNYQE GLKNIKAVGE 451 ELGLKMHVYG PDMHVSIGIVP LALLGKKTDI KEFGSA 13 - 21 550.8359 1099.6572 1099.6138 0.0434 0 K.AILNYHLTR.A 74 - 83 579.8720 1157.7294 1157.6808 0.0486 0 K.FVAKPDQLIK.R 111 - 122 672.4186 1342.8226 1342.7820 0.0406 1 K.EIKVETVTGVLR.Q 114 - 122 487.3033 972.5920 972.5604 0.0316 0 K.VETVTGVLR.Q 171 - 178 469.3264 936.6382 936.6120 0.0262 0 K.LLIPVNL.R 171 - 178 469.3290 936.6434 936.6120 0.0314 0 K.LLIPVNL.R 179 - 193 810.4426 1618.8706 1618.8202 0.0505 0 R.NYPSNEEIAAALLSK.V 179 - 193 810.4478 1618.8810 1618.8202 0.0609 0 R.NYPSNEEIAAALLSK.V 197 - 208 452.6009 1354.7809 1354.7357 0.0451 0 K.GVHNVLVDFISR.L 197 - 208 678.4030 1354.7914 1354.7357 0.0557 0 K.GVHNVLVDFISR.L 197 - 208 678.4041 1354.7936 1354.7357 0.0579 0 K.GVHNVLVDFISR.L 265 - 280 784.9504 1567.8862 1567.8206 0.0657 0 R.SPANLGLATVPQTDGK.V 265 - 280 784.9531 1567.8916 1567.8206 0.0711 0 R.SPANLGLATVPQTDGK.V 281 - 297 915.9880 1829.9614 1829.8771 0.0844 0 K.VNIDAGPPMEFPAPFGR.E Oxidation (M) 305 - 312 471.7370 941.4594 941.4164 0.0430 0 K.FISDMDAK.T Oxidation (M) 319 - 327 479.2922 956.5698 956.5403 0.0295 0 K.LTVLNANGR.I 375 - 382 488.7997 975.5848 975.5423 0.0426 0 K.TVLDLMLR.A Oxidation (M) 391 - 409 978.5823 1955.1500 1955.0517 0.0984 0 K.VLFIGGGIANFTNVASTFK.G
24	Q4WFT3	61393	120	5	5.85	GMP synthase [glutamine- hydrolyzing] Sequence Coverage: 7% 1 MAEEQNPSAT FDTILTLDFG SQYTHLITRR LREIGVYSEM LPCTQKLADL 51 PFKPKGILS GGPYSVYEDG APHADPAVFE LGVPVLGICY GLQEIAAYRLG 101 KDNVVAGTAR EYGHADLNAQ RLDNQGHVDK LFAGLEEHVK

						VWMSHGDKLV 151 KLPEGFHTIA TTANSEYAGI AHETKPVYGI QFHPEVTHTP DGAKLLRNFA 201 VDICGANPNW TMSKFVDQEI LRIRKLVGET DHVLGAVSGG VDSTVAAKLM 251 KEAIGDRFHA VLVNNGCMRL NECETVAETL NKHLGINLTV VDASKRFLDG 301 LKGVTDPEKK RMFIGATFID VFEEEAIEKIE ALAENSGAKV KWFLQGTLYP 351 DVIESISFKG PSATIKTHHN VGALPKRMIE GQGMKLEPL RELFKDEVQR 401 LGRELGIAHE LVMRHPFPGP GIAIRVLGEV TPERVDIARK ADHIFISMIR 451 EAGLYDKISQ AYAALDPSKA VGVMGDKRVY AEIIILRAVE TTDCKLTLGI 501 DGDFVLRYY SVMTARAFPF DNEFLSKCAT RIINEVHGVS RVLYDISSKP 551 PATIEME 215 - 222 510.2953 1018.5760 1018.5447 0.0313 0 K.FVDQEILR.I 426 - 434 500.2962 998.5778 998.5397 0.0382 0 R.VLGEVTPER.V 426 - 439 518.6444 1552.9114 1552.8573 0.0541 1 R.VLGEVTPERVDIAR.K 458 - 469 632.3557 1262.6968 1262.6506 0.0462 0 K.ISQAYAALDPSK.A 479 - 487 545.3557 1088.6968 1088.6593 0.0375 0 R.VYAEIIILR.A
25	XP_7506 96	55764	876	19	5.86	6-phosphogluconate dehydrogenase Gnd1 Sequence Coverage: 31% 1 MSTQAVARLA GINVGAPARP LPSADFGILG LAVMGQNLIL NVADHGFTVC 51 AYNRTTSKVD RFLANEAKGK SIVGAHSVEE FCAKLKPRR IMLVMAGKP 101 VDDFIESLLP HLEEGDIIID GGNSHFPDSN RRTKYLKEKG IRFVGSGVSG 151 GEEGARYGPS LMPGGNEEAW PFIKDIFQSI AAKSDGEACC DWVGDEGAGH 201 FVKMVHNGIE YGDMQLICEA YDIMKRGLGM PVNEIADVFA KWNKGVLDSF 251 LIEITRDVLY FNDNDGTPLV EKILDKAGQK GTGKWTAINA LDLGMPVTLI 301 GEAVFARCLS AIKDERIRAS SLLDGPTPQF TGDQKAFIDD LEQALYASKI 351 ISYAQGFMLI QEAAREYGWK LNKPSIALMW RGGCIIRSVF LKDITNAYRN 401 NPDLENLLFD DFFKAAIQKA QQGWRNVVSK GALWGIPTPA FSTALSFYDG 451 YRTRDLPANL LQAQRDYFGA

						HTFRVKPECA NENYPEGKDI HVNWTGRGGD 501 VSASTYVV 143 - 156 654.8308 1307.6470 1307.6106 0.0364 0 R.FVGSGVSGGEEGAR.Y 175 - 183 496.7874 991.5602 991.5338 0.0264 0 K.DIFQSIAAK.S 227 - 241 788.9334 1575.8522 1575.7967 0.0556 0 R.GLGMPVNEIADVFAK.W Oxidation (M) 245 - 256 681.9071 1361.7996 1361.7555 0.0442 0 K.GVLDSFLIEITR.D 257 - 272 919.9794 1837.9442 1837.8734 0.0708 0 R.DVLYFNDNDGTPLVEK.I 319 - 334 817.4396 1632.8646 1632.7995 0.0651 0 R.ASSLLDGPTPQFTGDK.Q 319 - 334 817.4401 1632.8656 1632.7995 0.0661 0 R.ASSLLDGPTPQFTGDK.Q 335 - 349 856.4639 1710.9132 1710.8464 0.0668 0 K.QAFIDDLEQALYASK.I 350 - 365 609.6726 1825.9960 1825.9396 0.0564 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 350 - 365 914.0105 1826.0064 1825.9396 0.0668 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 350 - 365 914.0181 1826.0216 1825.9396 0.0820 0 K.IISYAQGFMLIQEAAR.E Oxidation (M) 388 - 399 476.2736 1425.7990 1425.7616 0.0374 1 R.SVFLKDITNAYR.N 388 - 399 713.9146 1425.8146 1425.7616 0.0531 1 R.SVFLKDITNAYR.N 393 - 399 426.7232 851.4318 851.4137 0.0181 0 K.DITNAYR.N 400 - 414 920.9688 1839.9230 1839.8679 0.0551 0 R.NNPDLENLLFDDFFK.A 453 - 465 499.2953 1494.8641 1494.8266 0.0374 1 R.TRDLPANLLQAQR.D 455 - 465 619.8625 1237.7104 1237.6779 0.0326 0 R.DLPANLLQAQR.D 455 - 465 619.8661 1237.7176 1237.6779 0.0398 0 R.DLPANLLQAQR.D 466 - 474 557.2783 1112.5420 1112.5040 0.0381 0 R.DYFGAHTFR.V
26	XP_755071	48784	112	6	5.60	Gamma-glutamyl phosphate reductase Sequence Coverage: 14% 1 MSLTDSSAVE IARAASLASR QLATLPTIDR NDALTALHDA LLRNREILD 51 ANAKDVAIAS QAANNGSLSH SVLKRLDLSR PGKYDDMLKG ILSVRDLEDP 101 VGRVTLRTLL DDGLILERVS

						CPIGVLLIIF EARPEVIANI AALSIKSGNA 151 AILKGGKEST ESFIAISKVI SEAISGTRVP VASVQLVKTR DVVSSLLAQD 201 SLIDLVIPRG SNDLVRVKE NTKIPVLGHA DGLCSAYLHA DADPAIAVKV 251 IVDAKTDYPA ACNSLESLLV HEDALGTIFP AVAEALLAKG VRLRCDIQSK 301 SALLKNISSP PADLLEDAVD SDFDTEFLDL VLAVKTIPST SSPISAVEDA 351 ISHINSHSSK HTDLIVTESK EIAEYFMRGV DSAGVFWNAS TRFADGMRFG 401 FGTEVGISTN KIHTRGPVGL DGLTIYKYLL RGQGHRAGDY FEGEGGKKWK 451 HEHLVI 108 - 118 629.3752 1256.7358 1256.6976 0.0382 0 R.TLLDDGLILER.V 169 - 178 516.7999 1031.5852 1031.5611 0.0241 0 K.VISEAISGTR.V 179 - 188 520.3460 1038.6774 1038.6437 0.0337 0 R.VPVASVQLVK.T 361 - 370 571.8203 1141.6260 1141.5979 0.0281 0 K.HTDLIVTESK.E 399 - 411 678.8641 1355.7136 1355.6722 0.0415 0 R.FGFGTEVGISTNK.I 416 - 427 616.8666 1231.7186 1231.6812 0.0374 0 R.GPVGLDGLTIYK.Y
27	XP_7550 56	52982	59	3	5.47	Glutamate carboxypeptidase Sequence Coverage: 9% 1 MAPQLEPFFK QVDELSNSFI DRLRKAVAIP SISAHDENRK DVFRMAHFLA 51 SELEALGAEV EQRPLGKQPG KEHLDLPPVV IARYGNDKNK RTILVYGHYD 101 VQPALKDDGW ATEPFELTID DQGRMFGRGS TDDKGPVLGW LNVIEAHQKA 151 GVLPVNLLC CFEGMEEYGS EGLEEFIKSE SKKFFKDADA VCISDNYWLG 201 TEKPCLTYGL RGCNYYSVSI SGPAQDLHSG VFGGSTHEPM TDMVNILSKL 251 VDPKGNILIP GIMDLVAPLT EEENSLYSKI SYTMDNLHES LGSKTNIHET 301 KERTLMARWR YPSLSIHGIE GAFSAPGAKT VIPAKVIGKF SIRTVPNMES 351 DAVNKLVDY IKAFAKLNS KNTLDVWLQH DGKWWVASPK HWNFTAASKA 401 VKQVFGVEPD MTREGGSIPV TLSFEQATGK NVLLPMGSS TDAAHSVNEK 451 LDKKNYIEGT KLLGAYLHYV AEPPASEV 11 - 22 711.8683 1421.7220 1421.6787

						0.0434 0 K.QVDELSNSFIDR.L 414 - 430 860.9710 1719.9274 1719.8679 0.0595 0 R.EGGSIPVTLSEFQATGK.N 462 - 478 931.0040 1859.9934 1859.9305 0.0630 0 K.LLGAYLHYVAEEPASEV.-
28	XP_755448	52247	349	8	5.33	Secretory pathway gdp dissociation inhibitor Sequence Coverage: 16% 1 MEEIAPEYDV VVLGTGLTEC VLSGVLSVKG NKVLHIDRND HYGGEAASVN 51 IETLFKKYGN VRPGEEPWKK YGRVNDWNID LVPKLLMANG ELTNILVSTD 101 VTRYLEFKQI AGSYVQQGKG PKATVAKVPS DAGEALRSSL MGMFEKRRAK 151 KFLEWVGEFK EDDPATHQGL NVAQCTMKEV YDKFGLEDNT RDFVGHSMAL 201 YPSDDYITTP GMAVETIHRI RLYVNSMARY GKSPYIPLY GLGELPQGFA 251 RLSAIYGGTY MLNTSVDEVL YDESGKVSGI KATMKDRDDN SEAMKFTTKT 301 KKIIADPSYF PGKVRVTGYL LKAICILNHP IEKTDGSDSL QLIPQSQVG 351 RKHDVYIAMV SSAHNVCPKG YYIAIVSTIA ETDANHHLEL EPGFERLGQI 401 EEKFFGPPIP LYEPDLSGEK DNIFISKSYD ATSHFETTTD DVRDLYKRAT 451 GEELVVEGLR EDQRLAED 109 - 119 589.8194 1177.6242 1177.6091 0.0151 0 K.QIAGSYVQQGK.G 128 - 137 507.7666 1013.5186 1013.5142 0.0045 0 K.VPSDAGEALR.S 179 - 191 529.2590 1584.7552 1584.7420 0.0132 1 K.EVYDKFGLEDNTR.D 184 - 191 476.2361 950.4576 950.4458 0.0119 0 K.FGLEDNTR.D 303 - 313 604.3318 1206.6490 1206.6285 0.0206 0 K.IIADPSYFPGK.V 303 - 313 604.3356 1206.6566 1206.6285 0.0282 0 K.IIADPSYFPGK.V 334 - 351 957.5198 1913.0250 1912.9854 0.0396 0 K.TDGSDSLQLIPQSQVGR.K 449 - 460 636.8495 1271.6844 1271.6721 0.0123 0 R.ATGEELVVEGLR.E
29	XP_747854	54420	110	4	5.33	Glucokinase GlkA Sequence Coverage: 11% 1 MSSPLVTEAT RIARQFDFSA EQIQSGVKEY IREMCEGLTK EHTTLSQIPT 51 YVTSVPNGTE KGLYLAVDLG GTNFRVCSID LHGDTTFNLT QSKIMIPREL 101 MASGTSKDLF LFLARQIEAF

						LRIHHNEHFE AHLRRRRREP N SEEELFDLGF 151 TFSFPVRQLG INKGTLRWT KGFNIPDAVG HDVCALLQNA IDELDLPVRV 201 AALVNDTVGT LMARSYTSPG DTSTFIGAIF GTGTNGAYVE KLDRTKLQT 251 IEHADYEKST GEMIINAEWG SFDNHLVLP NTKWDKELDE DSNNGIQMF 301 EKRVS GMFLG EILRRALLDM HKDEAFGLFK PNQSSKVVTP ENSPLYRQWG 351 IDTSFLSLVE ADKTDRMEEV KAALKDHLKI ENPSDAECQA VKVLVHAIGK 401 RAARLSAVPL AAILISTGKL ETDDMVDIGV DGSLVEFYFN FEGYIREALR 451 EVPEVGAAGE KKVIRIGISKD GSGVGAALIA LVASRNETGS GPK 15 - 28 792.3962 1582.7778 1582.7627 0.0151 0 R.QDFSAEQIQSGVK.E 337 - 347 637.8438 1273.6730 1273.6666 0.0064 0 K.VVTPENSPLYR.Q 405 - 419 727.4614 1452.9082 1452.8915 0.0167 0 R.LSAVPLAAILISTGK.L 447 - 461 518.9423 1553.8051 1553.8049 0.0002 1 R.EALREVPEVGAAGEK.K
30	XP_7556 57	78713	376	9	5.66	Bifunctional tryptophan synthase TRPB Sequence Coverage: 14% 1 MEGIKSTFAR CQEQRKRAALV AYITAGYPTV EETVDILLGL ENGGAGSLNA 51 NAIRWISTDI IELGIPFTDP IADGPTIQRA NTQALANGVT VTTVLNMVRQ 101 ARSRGLKAPL LLMGYYNPVL RYGEERMLKD CKEAGVNGFI MVDLPPEEAV 151 RFRDLCASNG MSYVPLIAPA TSEARMKLLC KIADSFYVV SRMGVTGATG 201 KLSSNLPELL KRVHQWSGNV PAALGFGVST REHFLSVQEL AEGVVIGSQI 251 ITVLGQAPAG QAAKHAE EYL SSVTGRKLER DAQGILTNEI NVLEAVEKAQ 301 VPAVSQPTAV VTEADTPDGP GLADQIDALN GTGNPAAQPS RFGEFGGQYV 351 PESLMDCLAE LERGFQEAVN DPTFWEEFRS YYPYMGRPSS LHLANRLTEY 401 VGGANIWLKR EDLNHTGSHK INNALGQILI ARRLGKTRII AETGAGQHGV 451 ATATVCAKFG MKCVVYMGAE DVRRQALNVF RMKLLGASVV AVDAGSRTL R 501 DAVNEALRAW VVDLDTTHYI IGSAIGHPPF PTIVRTFQSV IGEETKQMM 551 EAIGKLPAV VACVGGGSNA VGMFYPPAKD TSVKLVGVEA GGDGIDTNRH 601 SATLTGGSKG VLHGVRTYVL

						QDEHGQISET HSIAGLDYP GVGPELSSWK 651 DSDRARFIAA TDAEALIGFR TLAQTEGIIP ALESSHAVWG AMELAKSMKT 701 GDIVLNLSGR GDKDVQSVAD ELPRLGPKIG WDLRF 108 - 121 818.4405 1634.8664 1634.8854 - 0.0190 0 K.APLLLMGYYNPVLR.Y Oxidation (M) 182 - 192 635.3398 1268.6650 1268.6765 - 0.0114 0 K.IADSFYVVS.R 281 - 298 978.5051 1954.9956 1955.0211 - 0.0255 0 R.DAQGILTNEINVLEAVEK.A 421 - 432 648.3893 1294.7640 1294.7721 - 0.0080 0 K.INNALGQILIAR.R 475 - 481 424.2388 846.4630 846.4712 - 0.0081 0 R.QALNVFR.M 484 - 497 657.8667 1313.7188 1313.7303 - 0.0115 0 K.LLGASVVAVDAGSR.T 501 - 508 444.2325 886.4504 886.4508 - 0.0004 0 R.DAVNEALR.A 657 - 670 747.8901 1493.7656 1493.7878 - 0.0222 0 R.FIAATDAEALIGFR.T 700 - 710 572.8140 1143.6134 1143.6248 -0.0113 0 K.TGDIVLNLSGR.G
31a	XP_7554 59	84023	181	9	5.62	3-isopropylmalate dehydratase Sequence Coverage: 12% 1 MPGVDDKKPKT LYDKVLDHHI VNEQEDGTIL IYIDRHLVHE VTSPQAFEG 51 KNAGRKVRP DCTLATVDHN IPTSSRKNF NVEEFIEETD SRLQCTTLEQ 101 NVKDFGLTYF GMGDKRQGIV HIIGPEQGFT LPGTTVVC GD SHTSTHGAFG 151 ALAFGIGTSE VEHVLATQTL LTRRSKNMRI QVDGELPPGV TSKDVLHII 201 GVIGTAGGTG AVIEFCGSVI RGLSMEARMS MCNMSIEAGA RAGMIAPDET 251 TFEYLKGRPL APKYDSA EWK RAVAFWSSLA SDEGAVYDKT VVLDGKDIIP 301 TVSWGTSPOD VVPITGVVPG PDDFEDENRK VACKRALEYM GLVAGTRI QD 351 IPVDKVFIGS CTNARIEDLR AAAKVVRGKK VAANIKRAMV VPGSGLVKQQ 401 AEAEGLD R VF TDAGFEWREA GCSMCLGMNP DILSPQERCA STSNRNFEGR 451 QGAGGRTHLM SPAMAAAAAI TGHADVREH LTASPLLA QPHLDIQEEH 501 EDPTTEDEFD RIMDM PADNE PHANSSAATA AAGSTAGLPK FTTLRGIAAP 551 MDRSNVD TDA IIPKQFLKTI KRTGLGSALF YELRYNPADG SENKSFVLNQ

						601 EPYRNAKILV VTGPNFGCGS SREHAPWALL DFGIKCIAP SFADIFFNNT 651 FKNGLMPVVI SDPAVLATIA AEASAGREIE VDLVNQEIKD AAGSKLASFE 701 VDAFRKHCLI NGLDDIGLTL QMEDKIRAFE AKRTLETPWL DSGGYLKRGV 751 RGGATMIQAA PVPKTNRGDV KTEPLEW 81 - 92 734.3340 1466.6534 1466.6525 0.0010 0 K.NVEEFIEETDSR.L 180 - 193 720.3961 1438.7776 1438.7668 0.0109 0 R.IQVDGELPPGVTSK.D 399 - 408 558.7718 1115.5290 1115.5207 0.0084 0 K.QQAEAGLDR.V 554 - 564 586.8144 1171.6142 1171.6085 0.0058 0 R.SNVDTDAIPK.Q 573 - 584 663.8622 1325.7098 1325.6979 0.0119 0 R.TGLGSALFYELR.Y 585 - 594 547.7415 1093.4684 1093.4676 0.0009 0 R.YNPADGSENK.S 595 - 604 626.8216 1251.6286 1251.6248 0.0039 0 K.SFVLNQEPYR.N 678 - 689 714.8877 1427.7608 1427.7507 0.0101 0 R.EIEVDLVNQEIK.D 696 - 705 577.7994 1153.5842 1153.5768 0.0075 0 K.LASFEVDAFR.K
31b	XP_7554 59	84023	80	3	5.62	3-isopropylmalate dehydratase Sequence Coverage: 4% 1 MPGVDDKKPKT LYDKVLDHHI VNEQEDGTIL IYDRHLVHE VTSPQAFEG 51 KNAGRKVRPP DCTLATVDHN IPTSSRKNFK NVEEFIEETD SRLQCTTLEQ 101 NVKDFGLTYF GMGDKRQGIV HIIGPEQGFT LPGTTVCCGD SHTSTHGAFG 151 ALAFGIGTSE VEHVLATQTL LTRRSKNMRI QVDGELPPGV TSKDVVLHII 201 GVIGTAGGTG AVIEFCGSVI RGLSMEARMS MCNMSIEAGA RAGMIAPDET 251 TFEYLGKRPL APKYDSAEWK RAVAFWSSLA SDEGAVYDKT VVLDGKDIP 301 TVSWGTSPOD VVPITGVVPG PDDFEDENRK VACKRALEYM GLVAGTRIQQ 351 IPVDDKVFIS CTNARIEDLR AAAKVVRGKK VAANIKRAMV VPGSGLVKQQ 401 AEAEGLDRVF TDAGFEWREA GCSMCLGMNP DILSPQERCA STSNRNFEG 451 QGAGGRTHLM SPAMAAAAAI TGHADVREH LTASPLLAKA QPHLDIQEEH 501 EDPTTEDEFD RIMDMPADNE

						PHANSSAATA AAGSTAGLPK FTTLRGIAAP 551 MDRSNVDTD A IIPKQFLKTI KRTGLGSALF YELRYNPADG SENKSFVLNQ 601 EPYRNAKILV VTGPNFGCGS SREHAPWALL DFGIKCIAP SFADIFFNNT 651 FKNGMLPVVI SDPAVLATIA AEASAGREIE VDLVNQEIKD AAGSKLASFE 701 VDAFRKHCLI NGLDDIGLTL QMEDKIRAFE AKRTLETPWL DSGGYLKRGV 751 RGGATMIQAA PVPKTNRGDV KTEPLEW 399 - 408 558.7700 1115.5254 1115.5207 0.0048 0 K.QQAEAEGLDR.V 573 - 584 663.8600 1325.7054 1325.6979 0.0075 0 R.TGLGSALFYELR.Y 595 - 604 626.8239 1251.6332 1251.6248 0.0085 0 K.SFVLNQEPYR.N
32	XP_7528 26	92824	86	5	5.46	Phosphoribosyl- AMP cyclohydrolase Sequence Coverage: 5% 1 MATPILISYN PTSASSGLSL SQIAYFGRVL IKVSSLSQAE EFLRQNFRL 51 DVYVDATDIT SSGDIVDILN AGAAKAFISL DQLTSLSQEQ SVPSSRLVVY 101 TSSDSQVDAF QSWVGEDAER KEAGICTESA DVKTVADRLG LNLEAQNLVYR 151 TYTTSTVTED AVKETLKQGA VSIVSADALT LDHKNPSGKI AAAALVAARA 201 VADQSNGLYA TSVTDERGVC LGLVWSSDES IAEALRTGTG VYQSRKRGLW 251 YKGQSSGDVQ ELIRLGFDCD SDCLVFVVKQ IGRGFCHLGT ASCFGPYNGL 301 ARLQKTLQAR KADAPAGSYT ARLFNEPKLT QAKIMEEAD LCRATTKEEI 351 AFEAADLLYF ALTRCVAAGV SLEDIERNLD LKSLKVRRK GDAKGPWAEK 401 AGLTASPAET KPAGPAAPAK EAAKKDDSRM EMTRVVTAST PVDKVKEYLK 451 RPSQKSND AI VGLVRPIQD VRDGGDAAVL KYTHKFEKAT SLTSPVIRAP 501 FPPELMKLSP ETQE AIDVSI ANIKKFHSAQ KDSNDVLQVE TMPGVVCSRF 551 SRPIERVGLY VPGGTAVLPS TAMMLGVPAM VAGCQKIVLA SPPRADGSIS 601 PEIVYVAHKV GAESIVLAGG AQAVAAMAYG TESISKVDKI LGPGNQFVTA 651 AKMLVSNDTS AGVSIDMPAG PSEVLVIADK DANPAFVASD LLSQAEHGVD 701 SQVILAIIDL NESQLQAIED EVDAQARALP RMDIVRGLA HSVTFVVRDI 751 DEAMALSNEY APEHLILQVK

						NAESVVEKVV NAGSVFIGQW TPESVGDYSA 801 GVNHSLPTYG YAKQYSGVNL GSFLKHITSS NLTAEGLLGL SRTVEQLAAV 851 EGLDAHKRVA SIRVAAMKKN QA 33 - 44 683.3569 1364.6992 1364.6936 0.0057 0 K.VSSLSQAEEFLR.Q 190 - 199 463.7931 925.5716 925.5709 0.0008 0 K.IAAAALVAAR.A 253 - 264 644.8304 1287.6462 1287.6419 0.0044 0 K.GQSSGDVQELIR.L 489 - 498 522.8088 1043.6030 1043.5975 0.0055 0 K.ATSLTSPVIR.A 587 - 594 426.7669 851.5192 851.5229 - 0.0036 0 K.IVLASPPR.A
33	XP_7538 31	72634	151	4	5.93	Aminopeptidase P Sequence Coverage: 8% 1 MLGFRSPIRL CKLSALGSTR LLPISRPKLF STAVARYAAD METVNTTKRL 51 ARLRQLMQEH KIDVYIVPSE DSHQSEYIAP CDGRREFISG FSGSAGTAIV 101 SMTKAALSTD GRYFNQASKQ LDSNWELLKR GVENVPTWQE WTTEQAQGGK 151 VVGVDPALIT ASGARSLEET LKRNGSSLVG ISQNLVDLVW GKDRPAPPRE 201 KVRVHPDKFS GKTFQEKIAD LRKELEKKKT AGFVISMLDE IAWLFNLRGS 251 DIPYNPVFFA YAIITPTKAE LYIDDDKITP EVVAHLGQDV VIKPYNSIFA 301 DAKALSEARR KEAGETASKF LLSNKASWAL SLSLGEEHV EETRSPiADA 351 KAIKNEVELA GMRACHIRDG AALIEYFAWL ENELVNKKTV LDEVDAADKL 401 EQIRTKHDLF AGLSFDTISS TGPNGAVIHY KPEKGTCsII DPDAIYLCDs 451 GAQYLDGTTD VTRTFHFGKP TELEKKAFTL VLKGLIAIDT AVFPKGTSGF 501 ALDALARQYL WKEGLDYLHG TGHGVGSYLN VHEGPIGIGT RVQYTEVPIA 551 PGNVISDEPG FYEDGKFGIR IENVIMAREV QTTHKFGDKP WLGFHVtMA 601 PIGRNLIEPS LLSDELKwV NDYHAEVWDK THHFFENDEF TRSWLQRETA 651 PITK 151 - 165 713.4113 1424.8080 1424.7987 0.0093 0 K.VVGVDPALITASGAR.S 389 - 404 605.6550 1813.9432 1813.9421 0.0010 1 K.TVLDEVDAADKLEQIR.T 484 - 495 622.8691 1243.7236 1243.7176

						0.0060 0 K.GLIAIDTAVFPK.G 496 - 507 589.8114 1177.6082 1177.6091 - 0.0009 0 K.GTSGFALDALAR.Q
34	XP_7553 28	74420	673	17	6.02	Mitochondrial Hsp70 chaperone (Ssc70) Sequence Coverage: 28% 1 MMPSRLVRV CPSSTGTSSR ARSSGLTLDF LHQLPRTART PAFRVP GASF 51 RRWNSTEGEK VKGQVIGIDL GTTNSAVAVM EGKTPKIIEN AEGARTTPSV 101 VAFAQDGERL VGIAAKRQAV VNPENTLFAT KRLIGRKFTD PEVQRDIKEV 151 PYKIVQHTNG DAWVEARGQK YSPSQIGGFI LQKMKETAEN YLSKPVKNV 201 VTPPAYFNDS QRQATKDAGQ IAGLNVLRV NEPTAAALAY GLEKEADRVV 251 AVYDLGGGTF DISVLEIQKG VFEVKSTNGD THLGGEFDFI HLVRHIVQQF 301 KKDSGLDLSN DRMAIQRIRE AAEKAKIELS SSLQTEINLP FITADASGAK 351 HINLKMTRSQ LESLVEPLIN RTVEPV RKAL KDANLQASDI QDIILVGGMT 401 RMPKVAESVK SMFGRDPAKS VNPDEAVAIG AAIQGAVLAG EVTDVLLLDV 451 TPLSLGIETL GGVFTRLINR NTTIPTKKSQ TFSTAADFQT AVEIKVFQGE 501 RELVKDNKLL GNFQLVGIPP AHRGVPQIEV TFDIDADSIV HVAADKSTG 551 KDQSITIASG SGLSDAEIQS MVEDAKEYGE QDKERKAAIE AANRADSVLN 601 DTEKALKEFE DRLDKAEAEQ IREKIATLRE FVAKNQSGEG TATAEELKQK 651 TDELQTASLT LFDKMHKAQS EQQQSQGQQ GENKP 87 - 95 486.7551 971.4956 971.5036 - 0.0079 0 K.IIENAEGAR.T 96 - 109 739.3746 1476.7346 1476.7209 0.0138 0 R.TTPSVVAFAQDGER.L 118 - 131 766.4130 1530.8114 1530.8042 0.0072 0 R.QAVVNPENTLFATK.R 118 - 132 563.3167 1686.9283 1686.9053 0.0230 1 R.QAVVNPENTLFATKR.L 138 - 145 496.2477 990.4808 990.4771 0.0038 0 K.FTDPEVQR.D 171 - 183 719.3937 1436.7728 1436.7664 0.0065 0 K.YSPSQIGGFILQK.M) 198 - 212 840.9250 1679.8354 1679.8267 0.0087 0 K.NAVVTPPAYFNDSQR.Q 217 - 228 613.8484 1225.6822 1225.6779 0.0044 0 K.DAGQIAGLNVLR.V 229 - 244 823.4462 1644.8778 1644.8723

						0.0056 0 R.VVNEPTAAALAYGLEK.E 295 - 301 450.2551 898.4956 898.5025 - 0.0068 0 R.HIVQQFK.K 303 - 312 546.2505 1090.4864 1090.4891 - 0.0026 0 K.DSGLDLSNDR.M) 359 - 371 749.4215 1496.8284 1496.8198 0.0086 0 R.SQLESLVEPLINR.T 479 - 495 922.4645 1842.9144 1842.9000 0.0145 0 K.SQTFSTAADFQTAVEIK.V 509 - 523 544.6505 1630.9297 1630.9307 - 0.0011 0 K.LLGNFQLVGIPPAHR.G 635 - 648 717.8427 1433.6708 1433.6634 0.0075 0 K.NQSGEGTATAEELK.Q 635 - 650 564.2789 1689.8149 1689.8169 - 0.0021 1 K.NQSGEGTATAEELKQK.T 651 - 664 791.4071 1580.7996 1580.7934 0.0063 0 K.TDELQTASLTFLDK.M
35	XP_746746	64991	102	4	5.83	Heat shock protein (Sti1) Sequence Coverage: 9% 1 MLPRSFQRCG TGFTTRKKTNL FVPRNSEKFTQAIELEPSNHILYSNRSVY 51 AAQSDYQKAL DDANKAIEIK PDWSKGYSRK GAACRGLGDL LGAHDAYEEA 101 LKLDPSNDQA KSGLNAVKRA IDGEARADGV NPAAGLGGIFNDPQMFQKLA 151 SNPKTSHLLA DADFMAKLQR LQQNPNSMSPQEIQDPRFLQVMSVLLGIDM 201 SFGAPPEAAG SSRAAAEAE DVPMPDAKPA AAEKKKEPEPAPQPEPEPED 251 EETIAKKKAQ EAGDAEKKIG NDFYKKKQFD EAIEHYTKAW ELNKDITYLN 301 NIGAAKFEKG DLQGAIEICQ KAVEEGRELRADFKVIKAFARIGTAYEKL 351 GDFTQAIEYY HKSLTEHRT DALTKLRNAEKAKVKAEKEAYIDPVEAEKA 401 RELGQKKFQE ADWPGAVEAF TEMTKRAPHDPRGFSNRAALIKLMAFPQA 451 VQDCDEAIRR DPKFIRAYIR KSQALVAMKEYSKALDACTEAAEQDDGTHT 501 REIDQQQKQC LEAQFSARAG ETEEQTMERIQNDPEIMSILQDPVMSILQ 551 QAKSDPAALQ EHMKNVQVRT KIQKLMAAGVIRLGR 29 - 46 711.3660 2131.0762 2131.0698 0.0064 0 K.FTQAIELEPSNHILYSNR.S 47 - 58 665.8228 1329.6310 1329.6201 0.0110 0 R.SAVYAAQSDYQK.A 295 - 306 646.8488 1291.6830 1291.6772 0.0059 0 K.DITYLNNIGAAK.F

							350 - 362 528.9258 1583.7556 1583.7620 - 0.0064 0 K.LGDFITQAIEYYHK.S
36	XP_747200	66932	478	13	5.30	Hsp70 chaperone (HscA)	Sequence Coverage: 27% 1 MSDEVYEGAI GIDLGTTYSC VANYEGTNVE IIANEQGSYT TPSFVSFTEK 51 ERLIGEAAKN QAAMNPKNTI FDIKRLIGR YEDPIVKDI ESWPFKVVDQ 101 GGNPVVEVEY LGETKTFSPQ EISSMVLMM KEVAETKLGK KVEKAVITVP 151 AYFNDNQRQA TKDAGAIAGL NVLRIINEPT AAAIAYGLGS GKSEKERNVL 201 IYDLGGGTFD VSLNLIQGGV FTVKATAGDT HLGQDFDTN LLEHFKKEFQ 251 KKTGKDLSGD ARALRRLRTA CERAKRTLSN ATQTTVEIDS LFDGEDFNSS 301 ITRARFEDLN AKAFSGTLEP VQQVLKDSGL EKSQVDEIVL VGGSTRIPRI 351 QKLLSDFFDG KKLEKSINPD EAVAYGAAVQ AGILSGKATS AETQDLLLLD 401 VVPLSLGVAM EGNIFAPVVP RGQTVPTIKK RFTTVVDNQ TTVQFPVYQG 451 ERTNCADNTS LGEFTLAPIP PMKAGEAALE VVFEVDVNGI LKVTATEKSS 501 GRSANITISN AVGKLSTTEI EQMINDAAKF KSSDEAFTKK FESRQQLSEY 551 ISRVEEIIISD PTMSLKLKRG NKEKIESALS DAMAQLEIED SAPEDYKKKE 601 LALKRLITKA MATR 80 - 87 510.2887 1018.5628 1018.5447 0.0181 1 R.RYEDPIVK.K 97 - 115 1016.5377 2031.0608 2031.0161 0.0448 0 K.VVDQGGNPVVEVEYLGETK.T 145 - 158 804.4228 1606.8310 1606.8103 0.0207 0 K.AVITVPAYFNDNQR.Q 163 - 174 585.3424 1168.6702 1168.6564 0.0138 0 K.DAGAIAGLNVLR.I 175 - 192 582.6591 1744.9555 1744.9359 0.0196 0 R.IINEPTAAAIAYGLGSGK.S 175 - 192 873.4902 1744.9658 1744.9359 0.0299 0 R.IINEPTAAAIAYGLGSGK.S 313 - 326 758.9335 1515.8524 1515.8297 0.0228 0 K.AFSGTLEPVQQVLK.D 313 - 332 716.0677 2145.1813 2145.1317 0.0495 1 K.AFSGTLEPVQQVLKDSGLEK.S 333 - 346 730.4066 1458.7986 1458.7678 0.0308 0 K.SQVDEIVLVGGSTR.I 353 - 361 521.2710 1040.5274 1040.5179 0.0096 0 K.LLSDFFDGK.K 366 - 387 711.0504 2130.1294 2130.0957

							0.0337 0 K.SINPDEAVAYGAAVQAGILSGK.A 432 - 452 810.7466 2429.2180 2429.1864 0.0316 0 R.TFTTVVDNQTTVQFPVYQGER.T 545 - 553 562.2959 1122.5772 1122.5669 0.0103 0 R.QQLESYISR.V
48	XP_752631	79995	293	10	5.08	Hsp70 chaperone Hsp88	Sequence Coverage: 14% 1 MSVVGIDFGA QSTKVGVARN KGIDIITNEV SNRSTPTLVG FGTR SRHIGE 51 GAKTQEMSNL KNTVGNLKR IGR SFNDPDV EIEQ KYTSAA ICDVNGQAGV 101 EVSYLGKKEK FSATQLAAMY LTKIRDITSK ELKLPVSDVT ISVPAWFTDA 151 QRRAMIDAGE IAGLKVLRLI NDTTATALGY GITKLDLPGP EEKPR RVMFV 201 DIGHSDYTAS VVEFRKGELN VKATAYDRHF GGRDFDIALT EHFADEFKEK 251 FKIDVRSNPK AYARTVAAAE KMKKVLSANP AAPMSIESLM EDVDVRSIVK 301 REELETMVKP LLER VTIPIE EALAEAK LKP EDIDTIEMVG GCTRVPAIKE 351 AISKFFGK TL SFTLNQDEAI ARG CAFSCAI LSPVFRVRDF SVHDIVNYPI 401 EFTWEQSADI PDEDTS�TVF NRGNVMPSTK ILTFYRK QPF DLEAR YAKPD 451 MLPGKINPWI GRFSVKGVKA DANDDFMICK LKARLNLHGI LNVESGYVE 501 DVEVEEPVDE DKMDTDAPEG EQPKKTRKVK KQVRKGDLP STGTNSVDQT 551 VKETWIEREN AMYMEDKLIA ETDEKKNELE STIYELRDKI DGVYAEFASE 601 EEKDKLRAKL TDMEDWLYEE GEDTTKSVYV AKLDEIR FIA GPIVQR YKEK 651 IEAERQAILK AQEEEEAAKKR AEEEEAKRKAEEAKKAEETK PDEEMKDAPA 701 EGEEAAPAEGE EKQQ 22 - 33 665.8676 1329.7206 1329.6888 0.0318 0 K.GIDIITNEVSNR.S 34 - 44 568.3215 1134.6284 1134.6033 0.0251 0 R.STPTLVGFGTR.S 74 - 85 710.8494 1419.6842 1419.6518 0.0325 0 R.SFNDPDVEIEQK.Y 169 - 184 826.4709 1650.9272 1650.8828 0.0444 0 R.LINDTTATALGYGITK.L 185 - 195 417.5722 1249.6948 1249.6666 0.0281 0 K.LDLPGPEEKPR.R 315 - 327 692.4089 1382.8032 1382.7657 0.0376 0 R.VTIPIEEALAEAK.L 315 - 327 692.4202 1382.8258 1382.7657

						0.0602 0 R.VTIPIEEALAEAK.L 359 - 372 789.9308 1577.8470 1577.8049 0.0421 0 K.TLSFTLNQDEAIAR.G 438 - 445 488.2589 974.5032 974.4821 0.0211 0 K.QPFDLEAR.Y 638 - 646 500.8084 999.6022 999.5865 0.0157 0 R.FIAGPIVQR.Y
38	XP_7479 26	80590	613	13	4.95	Asp f12/Heat shock protein P90/Molecular chaperone and allergen Mod- E/Hsp90/Hsp1 Sequence Coverage: 20% 1 MSSETFEFQA EISQLLSLI NTVYSNKEIF LRELISNASD ALDKIRYQSL 51 SDPTKLDTGK DLRIDIIPDK ENKTLTIRD T GIGMTKADLI NNLGTIARSG 101 TKQFMEALSA GADISMIGQF GVGFYSAYLV ADRVTTVVSKN NDDEQYIWES 151 AAGGTFTLTQ DTEGEQLGRG TKIILHLKDE QTDYLNESRI KEVVRKHSEF 201 ISYPIYLHVL KETEKEVPDE EAEETKEED EEKKAKIEEV DDEEEEEKKK 251 KKKTCTVKES KIEEEELNKT KPIWTRNPAD ITQEEYASFY KSLSNDWEDH 301 LAVKHFSVEG QLEFRAILYV PKRAPFDLFE TKTKNNIKL YVRRVFITDD 351 ATDLIPEWLG FIKGVVDS LPLNLSRETL QQNKIMKVIK KNIVKKTLEL 401 FNEIAEDREQ FDKFYSAFSK NIKLGIHEDA QNRQTLAKLL RYQSTKSGDE 451 ATSLADYVTR MPEHQKQIYY ITGESIKAVA KSPFLDSLKQ KNFEVLFLVD 501 PIDEYAFTQL KEFDGKKLVD ITKDFELEET EEEKAEREKE EKEYENLAKS 551 LKNILGDKVE KVVVSHKLVG SPCAIRTGQF GWSANMERIM KAQALRDTSM 601 SSYMSSKKTF EISPKSSIIF ELKKKVEADG ENDRTVKSIT QLLFETSLV 651 SGFTIEEPAS FAERIHKLVS LGLNIDEEAE TTEEKATEEA APAEATTGES 701 AMEEVD 33 - 44 638.3338 1274.6530 1274.6354 0.0177 0 R.ELISNASDALDK.I 33 - 46 515.6200 1543.8382 1543.8205 0.0176 1 R.ELISNASDALDKIR.Y 87 - 98 635.8681 1269.7216 1269.7041 0.0176 0 K.ADLINNLGTIAR.S 173 - 189 696.3751 2086.1035 2086.0694 0.0340 1 K.IILHLKDEQTDYLNESR.I 277 - 291 888.4280 1774.8414 1774.8050 0.0365 0 R.NPADITQEEYASFYK.S 323 - 332 612.3378 1222.6610 1222.6346

						0.0264 1 K.RAPFDLFETK.K 324 - 332 534.2825 1066.5504 1066.5335 0.0169 0 R.APFDLFETK.K 364 - 377 757.4090 1512.8034 1512.7784 0.0251 0 K.GVVDSIEDLPLNLSR.E 397 - 408 725.3771 1448.7396 1448.7147 0.0250 0 K.TLELFNEIAEDR.E 424 - 433 576.8013 1151.5880 1151.5683 0.0197 0 K.LGIHEDAQNR.Q 447 - 460 742.8643 1483.7140 1483.6791 0.0350 0 K.SGDEATSLADYVTR.M 467 - 477 657.8640 1313.7134 1313.6867 0.0268 0 K.QIYYITGESIK.A 668 - 685 995.5217 1989.0288 1988.9790 0.0499 0 K.LVSLGLNIDEEAETTEK.A
39a	XP_750490	69618	336	13	5.09	Molecular chaperone Hsp70 Sequence Coverage: 21% 1 MAPAVGIDLG TTYSCVGVFR DDRIEIIAND QGNRTTPSFV AFTDTERLIG 51 DAAKNQVAMN PHNTVFDAGR LIGRRFQDAE VQSDMKHWPV KVVEKGGKPI 101 IEVEFKGETK QFTPEEISSM VLTKMRETAE AYLGGTVNNA VITVPAYFND 151 SQRQATKDAG LIAGLNVLR INEPTAAAI A YGLDKKAEGE RNVLIFDLGG 201 GTFDVSLITI EEGIFEVKAT AGDTHLGGED FDNRLVNHFV NEFKRKHKKD 251 LTTNARALRR LRTACERAKR TLSSAAQTSI EIDSLFEGID FYTSITRARF 301 EELCQDLFRS TMEPVERVLR DAKLDKSSVH EIVLVGGSTR IPKIQRLVAD 351 FFNKEANKSI NPDEAVAYGA AVQAAILSGD TSSKSTNEIL LLDVAPLSLG 401 IETAGGVMTPLIKRNTTIPT KKSETFSTYS DNQPGVLIQV YEGERARTKD 451 NNLLGKFELTGIPPAPRGVP QIEVTFDQDA NGIMNVSAVE KGTGKTNKIT 501 ITNDKGRLSK EEIERMLADA EKYKEEDEAE AARIQAKNGL ESYAYSLKNT 551 ISEGKLNISD ADKEKVSSKV EEIISWLDNN QTATKDEYES QQKELESVAN 601 PIISAAYGGA AGAAPGGAAP GGATRTADEV EERPEELD 5 - 47 736.3688 1470.7230 1470.6991 0.0240 0 R.TTPSFVAFTDTER.L 158 - 169 606.3643 1210.7140 1210.7034 0.0107 0 K.DAGLIAGLNVLR.I) 219 - 234 559.2525 1674.7357 1674.7234 0.0123 0 K.ATAGDTHLGGEDFDNR.L 219 - 234 838.3826 1674.7506 1674.7234

						0.0272 0 K.ATAGDTHLGGEDFDNR.L 235 - 244 623.8430 1245.6714 1245.6506 0.0208 0 R.LVNHFVNEFK.R 235 - 244 416.2338 1245.6796 1245.6506 0.0290 0 R.LVNHFVNEFK.R 347 - 354 477.2595 952.5044 952.5018 0.0026 0 R.LVADFFNK.E 359 - 384 845.7736 2534.2990 2534.2500 0.0490 0 K.SINPDEAVAYGA AVQAAILSGDTSSK.S 457 - 467 599.3448 1196.6750 1196.6553 0.0197 0 K.FELTGIPPAPR.G 508 - 515 502.2818 1002.5490 1002.5345 0.0145 1 R.LSKEEIER.M 523 - 533 437.5370 1309.5892 1309.5786 0.0106 1 K.YKEEDEAEAAAR.I 538 - 548 622.8206 1243.6266 1243.6084 0.0182 0 K.NGLESYAYSLK.N 626 - 638 766.3547 1530.6948 1530.6685 0.0263 0 R.TADEVEERPEELD.-
39b	XP_750490	69618	5.09	21	693	Molecular chaperone Hsp70 Sequence Coverage: 26% 1 MAPAVGIDLG TTYSCVGVFR DDRIEIIAND QGNRTTPSFV AFTDTERLIG 51 DAAKNQVAMN PHNTVFDAKR LIGRRFQDAE VQSDMKHWPV KVVEKGGKPI 101 IEVEFKGETK QFTPEEISSM VLTKMRETAE AYLGGTVNNA VITVPAYFND 151 SQRQATKDAG LIAGLNLVRI INEPTAAAI YGLDKKAEGE RNVLIFDLGG 201 GTFDVSLITI EEGIFEVKAT AGDTHLGGED FDNRLVNHFV NEFKRKHKKD 251 LTTNARALRR LRTACERAKR TLSSAAQTSI EIDSLFEGID FYTSITRARF 301 EELCQDLFRS TMEPVERVLV DAKLDKSSVH EIVLVGGSTR IPKIQRLVAD 351 FNKEANKSI NPDEAVAYGA AVQAAILSGD TSSKSTNEIL LLDVAPLSLG 401 IETAGGVMTPLIKRNTTIPT KKSETFSTYS DNQPGVLIQV YEGERARTKD 451 NNLLGKFELT GIPPAPRGVP QIEVTFDVDA NGIMNVSAVE KGTGKTNKIT 501 ITNDKGRLSK EEIERMLADA EKYKEEDEAE AARIQAKNGL ESYAYSLKNT 551 ISEGKLNISD ADKEKVSSKV EEIISWLDNN QTATKDEYES QQKELESVAN 601 PIISAAYGGA AGAAPGGAAP GGATRTADEV EERPEELD 24 - 34 621.8320 1241.6494 1241.6364 0.0131 0 R.IEIIANDQGNR.T

							35 - 47736.36621470.71781470.69910.01880 R.TTPSFVAFDTER.L 158 - 169606.36501210.71541210.70340.01210 K.DAGLIAGLNVLR.I 170 - 185553.97491658.90291658.88790.01500 R.IINEPTAAAIAYGLDK.K 170 - 185830.46141658.90821658.88790.02040 R.IINEPTAAAIAYGLDK.K 170 - 186596.67221786.99481786.98280.01191 R.IINEPTAAAIAYGLDKK.A 219 - 234559.25041674.72941674.72340.00600 K.ATAGDTHLGGEDFDNR.L 219 - 234838.38501674.75541674.72340.03200 K.ATAGDTHLGGEDFDNR.L 235 - 244623.84081245.66701245.65060.01640 R.LVNHFVNEFK.R 235 - 244623.84141245.66821245.65060.01760 R.LVNHFVNEFK.R 235 - 244416.23701245.68921245.65060.03860 R.LVNHFVNEFK.R 327 - 340480.93231439.77511439.77330.00180 K.SSVHEIVLVGGSTR.I 327 - 340720.90341439.79221439.77330.01900 K.SSVHEIVLVGGSTR.I 347 - 354477.2532952.4918952.5018-0.01000 R.LVADFFNK.E 347 - 354477.2624952.5102952.50180.00840 R.LVADFFNK.E 359 - 384845.77292534.29692534.25000.04690 K.SINPDEAVAYGAAVQAAILSGDTSSK.S 457 - 467599.33981196.66501196.65530.00970 K.FELTGIPPAPR.G 457 - 467599.36041196.70621196.65530.05090 K.FELTGIPPAPR.G 508 - 515502.27811002.54161002.53450.00711 R.LSKEEIER.M 538 - 548622.82091243.62721243.60840.01880 K.NGLESYAYSLK.N) 626 - 638766.35471530.69481530.66850.02630 R.TADEVEERPEELD.-
40	XP_753589	55586	412	15	5.30	ATP synthase F1, beta subunit	Sequence Coverage: 31% 1MFKSGGLARTFGRAAFARPSP VARRAIQPVR YNGLPSLARF ASSEAGSVGK 51IHQVIGAVVDVKFDGDNLPA ILNAIETENN GQKLVLVLEVSQ HLGENVVRTI 101AMDGTEGLTRGAPARDTGAP IKIPVGPGTL GRIVNVTGDP IDERGPIKAT 151KFAPIHAEAP EFTEOSTSAP

						ILVTGIKVVD LLAPYARGGK IGLFGGAGVG 201 KTVFIQELIN NIAKAHGGYS VFTGVGERTR EGNPLYHEMQ ETGVIQLEGE 251 SKVALVFGQM NEPPGARARV ALTGLTIAEY FRDEEGQDVL LFDNIFRFT 301 QAGSEVSALL GRIPSAVG YQ PTLAVDMGGM QERITTTKKG SITSVQAVYV 351 PADDLTD PAP ATTF AHL DAT TVLSRGISEL GIYP AVD PLD SKSRMLDPRI 401 VGEEHYAVAT RVQQMLQEYK SLQDI IAILG MDELSEADKL TVERARKLQR 451 FLSQPFTVAQ VFTGIEGKLV DLKDTIRSFK AIINGEGDDL PEA AFYMGD 501 FESARAKGEK ILAELEGKA 84 - 98 564.6611 1690.9615 1690.9366 0.0249 0 K.LVLEVSQHLGENVVR.T 116 - 132 550.3268 1647.9586 1647.9308 0.0278 1 R.DTGAPIKIPVGPGLGR.I 133 - 144 664.3539 1326.6932 1326.6779 0.0153 0 R.IVNVTGDPIDER.G 133 - 148 574.9902 1721.9488 1721.9312 0.0176 1 R.IVNVTGDPIDERGPIK.A 178 - 187 558.8283 1115.6420 1115.6339 0.0082 0 K.VVDLLAPYAR.G 191 - 201 488.2902 974.5658 974.5549 0.0109 0 K.IGLFGGAGVGK.T 202 - 214 751.9456 1501.8766 1501.8504 0.0262 0 K.TVFIQELINNIK.A 215 - 228 479.5700 1435.6882 1435.6844 0.0037 0 K.AHGGYSVFTGVGER.T 299 - 312 718.3895 1434.7644 1434.7467 0.0178 0 R.FTQAGSEVSALLGR.I 299 - 312 718.3974 1434.7802 1434.7467 0.0336 0 R.FTQAGSEVSALLGR.I 376 - 392 887.4830 1772.9514 1772.9196 0.0318 0 R.GISELGIYP AVD PLDSK.S 400 - 411 448.9020 1343.6842 1343.6834 0.0008 0 R.IVGEEHYAVATR.V 400 - 411 672.8567 1343.6988 1343.6834 0.0155 0 R.IVGEEHYAVATR.V 451 - 468 985.0487 1968.0828 1968.0357 0.0472 0 R.FLSQPFTVAQVFTGIEGK.L 511 - 519 472.2781 942.5416 942.5386 0.0031 1 K.ILAELEGKA.-
41	XP_750312	29183	615	12	9.18	40S ribosomal protein S3 Sequence Coverage: 56% 1 MAAVQGAISK RRRKFVADGVF YAE LNEFFQR ELAEEGYSGV EVRVTPVT D 51 IIRATHTQE VLGEQGRIR ELTSLIQKRF

						KFPENSVSLEY AAKVQNRGLS
						101 AVAQCESLRY KLLNGLAVRR ACYGVLR FIM ESGAKGCEVV VSGKLRAARA
						151 KSMKFTDGFIM IHSGQPAKEF IDSATRHVLL RQGVLGIVK IMRGSDPEGK
						201 AGPQKTLPDS VTIEPKKEEQ PVLQPM SQDY GAKALAAQQL AEQQRLAEQQ
						251 AAEGQEGAGA EAYAQE
						31 - 43 719.3351 1436.6556 1436.6783 - 0.0227 0 R.ELAEEGYSGVEVR.V
						44 - 54 614.3578 1226.7010 1226.7234 - 0.0224 0 R.VTPTVTDIIR.A
						44 - 54 614.3583 1226.7020 1226.7234 - 0.0214 0 R.VTPTVTDIIR.A
						55 - 67 475.9031 1424.6875 1424.7008 - 0.0133 0 R.ATHTQEV LGEQGR.R
						55 - 68 527.9338 1580.7796 1580.8019 - 0.0223 1 R.ATHTQEV LGEQGR.I
						80 - 93 800.9128 1599.8110 1599.8297 - 0.0186 1 R.FKFPENSVSLEYAAK.V
						98 - 109 645.8162 1289.6178 1289.6398 - 0.0219 0 R.GLSAVAQCESLR.Y Carbamidomethyl (C)
						112 - 119 428.2694 854.5242 854.5338 - 0.0095 0 K.LLNGLA VR.R)
						128 - 135 449.7114 897.4082 897.4266 - 0.0183 0 R.FIMESGAK.G Oxidation (M)
						136 - 144 467.7309 933.4472 933.4590 - 0.0117 0 K.GCEVVVSGK.L Carbamidomethyl (C)
						136 - 144 467.7334 933.4522 933.4590 - 0.0067 0 K.GCEVVVSGK.L Carbamidomethyl (C)
						155 - 168 517.9077 1550.7013 1550.7188 - 0.0175 0 K.FTDGFMIHSGQPAK.E Oxidation (M)
						169 - 176 469.7246 937.4346 937.4505 - 0.0159 0 K.EFIDSATR.H
						169 - 176 469.7295 937.4444 937.4505 - 0.0061 0 K.EFIDSATR.H
						206 - 217 656.8666 1311.7186 1311.7286 - 0.0099 0 K.TLPDSVTIEPK.E
						206 - 217 656.8704 1311.7262 1311.7286 - 0.0023 0 K.TLPDSVTIEPK.E
						218 - 233 918.4173 1834.8200 1834.8407 - 0.0207 0 K.EEQPVLQPM SQDYGAK.A Oxidation (M)
						234 - 245 663.8542 1325.6938 1325.7051 - 0.0113 0 K.ALAAQQLAEQQR.L
						234 - 245 663.8573 1325.7000 1325.7051 -

							0.0051 0 K.ALAAQQLAEQQR.L
42	XP_751171	85475	389	17	6.26	Mitochondrial aconitate hydratase	Sequence Coverage: 21% 1 MISTRRLARAG ALAPKSRLFL GTRAFATVGD SPLDKKVEMA NTEKGNINY 51 KKMSENLDIV RRRLQRPLTY AEKVLVSHLD DPHGQEIERG KSYLKLRPDR 101 VACQDATAQM AILQFMSAGM PSVATPTTVH CDHLIEAQVG GDKDLARANE 151 INKEVYDFLA SATAKYNIGF WKPGSGIIHQ IVLENYAFPG GLMIGTDSHT 201 PNAGGLAMAA IGVGGADAVD VMAGLPWELK APKVIGVKLT GEMSGWTPK 251 DVILKVAGLL TVKGGTGAI EYHGPVTSLSCTGMGTICN MGAEIGATTS 301 MFPFNDRMVD YLKATKRQHI GDFAREYAKE LREDEGAEDY QLEINLSEL 351 EPHINGPFTP DLATPISKFK EAVETNKWPE ELKVGLIGSC TNSSYEDMSR 401 AASIARDALN HGLKAKSLFT VTPGSEQIRA TIERDGLQQT LEEFGGVILA 451 NACGPCIGQW DRRDVKKGEP NSIISSYNRN FTGRNDANPA THAFVASPDL 501 VVAMTIAGTL KFNPLTDKLK DKDGNFLLQ PPTGEGLPK GYDPGRDTYQ 551 APPADRSSVN VAVSPTSDRL QLLAGFEPWD GKDANGIPIL IKCQGKTTTD 601 HISMAGPWLK YRGHLDNISN NMLIGAVNAE NGKANSVKNK FTGEYDAVPA 651 TARDYKARGV KVVVIGDWNV GEGSSREHAA LEPRHLGGLA IITRSFARIH 701 ETNLKKQGML PLTFADPADY DKINPEDTVD LLCTQLEVKG PMTLRVHPKD 751 GSAPFDISLN HTFNESQIEW FKDGSALNTM ARKSGAK 63 - 73 458.9341 1373.7805 1373.7779 0.0026 1 R.RLQRPLTYAEK.V 64 - 73 406.8962 1217.6668 1217.6768 - 0.0100 0 R.LQRPLTYAEK.V 74 - 89 636.6498 1906.9276 1906.9173 0.0102 0 K.VLYSHLDDPHGQEIER.G 148 - 165 662.0120 1983.0142 1982.9949 0.0193 1 R.ANEINKEVYDFLASATAK.Y 154 - 165 657.8387 1313.6628 1313.6503 0.0125 0 K.EVYDFLASATAK.Y 256 - 263 400.7673 799.5200 799.5167 0.0033 0 K.VAGLLTVK.G 417 - 429 717.8925 1433.7704 1433.7514 0.0190 0 K.SLFTVTPGSEQIR.A 512 - 520 538.3137 1074.6128 1074.6073

						0.0055 1 K.FNPLTDKLLK.D 521 - 540 709.3689 2125.0849 2125.0691 0.0157 1 K.DKDGNEFLQPPTGEGLPAAK.G 523 - 540 941.9929 1881.9712 1881.9472 0.0240 0 K.DGNEFLQPPTGEGLPAAK.G 541 - 556 593.6111 1777.8115 1777.8020 0.0095 1 K.GYDPGRDITYQAPPADR.S 557 - 569 659.8389 1317.6632 1317.6525 0.0108 0 R.SSVNVAVSPTSDDR.L 583 - 592 527.3240 1052.6334 1052.6230 0.0105 0 K.DANGIPIILK.C) 639 - 653 547.2748 1638.8026 1638.8002 0.0024 1 K.NKFTGEYDAVPATAR.D 641 - 653 699.3455 1396.6764 1396.6623 0.0142 0 K.FTGEYDAVPATAR.D 677 - 684 461.7411 921.4676 921.4668 0.0009 0 R.EHAALPR.H 685 - 694 525.8295 1049.6444 1049.6346 0.0099 0 R.HLGLAITR.S
43	XP_754479	43328	66	2	4.81	Aspartic endopeptidase Pep2 Sequence Coverage: 8% 1 MKSTSLLTAS VLLGSASAAV HKLKLNVKVL DEQLYTHNID AHVRALGQKY 51 MGIRPNVHQE LLEENSLNDM SRHDLVLDNF LNAQYFSEIS LGTPPQKFKV 101 VLDTGSSNLW VPGSDCSSIA CFLHNKYDSS ASSTYKANGT EFAIKYGSGE 151 LSGFVSQDTL QIGDLKVVKQ DFAEATNEPG LAFAFGRFDG ILGLGYDTIS 201 VNKIVPPFYN MLDQGLLDEP VFAFYLGDTN KEGDNSEASF GGVDKNHYTG 251 ELTKIPLRRK AYWEVDFDAI ALGDNVAELE NTGIILDTGT SLIALPSTLA 301 DLLNKEIGAK KGFTGQYSIE CDKRDSLPLD TFTLAGHNFT IGPYDYTLEV 351 QGSCISSFMG MDFPEPVGPL AILGDAFLRK WYSVYDLGNN AVGLAKAK 170 - 187 970.9763 1939.9380 1939.9064 0.0316 0 K.QDFAEATNEPGLAFAFGR.F 188 - 203 856.4617 1710.9088 1710.8829 0.0260 0 R.FDGILGLGYDTISVKN.I
44	XP_749744	56152	260	7	4.58	Protein disulfide isomerase Pdi1 Sequence Coverage: 16% 1 MRSFAPLVLS LLGASAVASA DATADTTSDV VSLTKDSFKD FMKEHDLVLA 51 EFYAPWCGHC KALAPKYEEA ATELKGNIP LVKVDCTEEE DLCKENGVEG 101 YPTLKIFRGP DSSKPYQGAR QADSIVSYMI QQSLPAVSTV TEENLEEIKT

						151 MDKIVVIGYF ASDDKAANDV FTSFAESQRD NYLFAATSDS AIAKAEGVKQ 201 PSIVLYKDFD EKKAVYDGA EQEAILSWVK TASTPLVGEI GPETYSSYIT 251 AGIPLAYIFA ETKEERDQYA EDFKPVAEKH KGAINIATID AKMFGAHAGN 301 LNLDPQTTPA FAIQDPEKNA KYPYDQSRREF NAKEIGKFIQ DVLDGKVEPS 351 IKSEPIPETQ EGPVTVVVVAH SYQDIVINND KDVLLIFYAP WCGHCKALAP 401 KYEELAALYA GDFKDKVTIA KIDATANDVP DSITGFPTIK LYPAGAKDSP 451 VEYSGSRTVE DLANFIKENG KVKVDALVAA SEKVEEGPDV TASPSATSTE 501 AEAPAATGDE KGDHDEL 67 - 75 527.2641 1052.5136 1052.5026 0.0111 0 K.YEEAATELK.G 154 - 165 663.8634 1325.7122 1325.6867 0.0255 0 K.IVVIGYFASDDK.A 180 - 194 793.9009 1585.7872 1585.7624 0.0249 0 R.DNYLFAATSDSAIAK.A 282 - 292 543.8177 1085.6208 1085.6080 0.0128 0 K.GAINIATIDAK.M 322 - 328 464.7173 927.4200 927.4086 0.0114 0 K.YPYDQSR.E 422 - 440 988.0107 1974.0068 1973.9946 0.0123 0 K.IDATANDVPDSITGFPTIK.L 458 - 467 575.3217 1148.6288 1148.6077 0.0211 0 R.TVEDLANFIK.E
45	XP_7556 86	93139	58	4	6.51	Translation elongation factor EF-2 subunit Sequence Coverage: 5% 1 MVNFTIEIR SLMDRPTNIR NMSVIAHVDH GKSTLTDSMI QRAGIISAAC 51 AGEGRYMDTR PDEQDRGITI KSTAIISLYAK FPDPEDLKEI PQKVDGAEFL 101 VNLIDSPGHV DFSSEVTAAL RVTDGALVVV DCVEGVVCVQT ETVLRQALTE 151 RIKPVLINK VDRALLELQV SKEDLYQSFS RTVESVNVII ATYHDKALGD 201 VQVYPDRGTV AFGSGLHGWA FTVRQFAVKY AKKFGVDRKK MLERLWGDNY 251 FNPQTKKWTk TGEPEQRAFN MFILDPIFKI FAAVNNDKTE EIHKLVEKLE 301 IKLASDEKDL KGKALLKVIM RKFLPAADAM LEMICHLPS PVTAQKYRAE 351 TLYEGPMDDE CAIGIRDCDP KAPLMYLVSK MVPTSDKGRF YAFGRVFSGI 401 VKSGLKVRIQ GPNYIPGKKD DLFVKAIQRT ILMMGFRFVEP IEDVPAGNIV

						451 GLVGVDQFL KSGTLTTSET AHNLKVMKFSPSPVVQRGVE VKNAQDLPLK 501 VEGLKRLSKS DPCVLTMIN SGQHIVAGAG ELHLEICLKD LEEDHAGVPL 551 RISDPVVSYSR ETVGGESSMT ALSKSPNKHNLRYVTAQPLG EEVSLAIESG 601 KINPRDDFKA RARLLADDYG WDVTDARKIW CFGPDTTGAN LLVDQTKAVQ 651 YLNEIKDSFV SGFQWATREG PIAEPMRSIRFNILDVTLH ADAIHRGGGQ 701 IIPARRVLY AATLLAEP SLLEPIFNVEIQVPEQAMGGIY GVLTRRRGHV 751 YSEEQRPGTP LFNVKAYLPV NESFGFNGDL RQATGGQAFP QSVFDHWSIL 801 PGGSPLDPTT KPGQTVAEMR KRKGLKEQVP GYDNYDDKL 2 - 10 560.8113 1119.6080 1119.5924 0.0156 0 M.VNFTIEIR.S 197 - 207 616.8245 1231.6344 1231.6197 0.0147 0 K.ALGDVQVYPDR.G 462 - 475 487.2554 1458.7444 1458.7314 0.0129 0 K.SGTLTTSETAHNLK.V 479 - 487 509.7906 1017.5666 1017.5607 0.0059 0 K.FSVSPVVQR.G
46	XP_752090	86840	89	6	6.33	Cobalamin-independent methionine synthase MetH/D Sequence Coverage: 6% 1 MVQSAVLGFP RMGKLRDLKK ATEAYWGGKI SRDELLSEGG RLRAEHWKIQ 51 KDAGVDIIPS NDAFYDQVL DHIQLFGVVP ERYSKYNLDP LDEYFAMGRG 101 LQKPASEGQP AIDVPSLEMV KWFDSNYHYV KPTLQENQVF KLASNPKPVA 151 QFLEAKEAGI ITRPVILGPV SFLTAKADR GQKIDPIDKI NDLVPVYVDL 201 LAQLKAAGVE DVQIDEPVLV FDLPAKSKAA FKPVEYKIGA LGDKAPRVL 251 ATYFGDIVHN IDVLPALHNL HGIHVDLVRN PEQLDAVIAA LGPKQVLSAG 301 VVDGRNIWKT NFKAIEKVE HAIQKLGKDR VIVSTSSSL HVPHTLESEK 351 NLDPEVREWF SFAVEKTHEV VVIKAVTEGPAAVRDQLEA NAKSVQARAS 401 SARTNDPKVK ERQAAVTEEM HNRKSPFPVR LAEQSKSINL PLFPTTTIGS 451 FPQTKEIRIQ RNKFTKGEIT AEEYEKFIEQELAEVVKIQE ELDLDVLVHG 501 EPERNDMVQY FGERLTGYVF TTHAWVQSYG SRCVRPPIIV GDISRPAPMT 551 VKESKYAVSI SKKPMKGMLT GPITCLRWSF PRDDVHQSVQ AQLALALRD

						601 EVIDLEAAGV KVIQVDEPAL REGLPLRAGK EREDYLTWAV RAFRLATSGV 651 SDGTQIHSHF CYSEFQDFH AIAALDADVL SIENSKSDAK LLKVFVEEAY 701 PRHIGPGVYD IHSPRVPSEQ EIKDRIEEML PYLRPDQLWI NPDCGLKTRQ 751 WPETKAALTN MVNAAKFYRQ KYTK 2 - 11 537.3082 1072.6018 1072.6029 - 0.0011 0 M.VQSAVLGFPR.M 2 - 11 537.3125 1072.6104 1072.6029 0.0075 0 M.VQSAVLGFPR.M 376 - 385 485.7758 969.5370 969.5243 0.0127 0 K.AVTEGPAAVR.D 477 - 487 652.8705 1303.7264 1303.7023 0.0241 0 K.FIEQEIAEVVK.I 612 - 621 570.3284 1138.6422 1138.6346 0.0076 0 K.VIQVDEPALR.E 703 - 715 483.2498 1446.7276 1446.7368 - 0.0092 0 R.HIGPGVYDIHSPR.V
47	XP_7526 50	41701	281	7	8.72	Isocitrate dehydrogenase, NAD-dependent Sequence Coverage: 17% 1 MISARNFVAP ARQCLRTRRV SSGFASHLSQ LRGYASAADD RVAKFKGQKG 51 PDGKYTVTLI EGDGIGPEIA QSVKDIFAAA KAPIKWEPVD VTPILKDGTK 101 TIPEEAIKSV QKNYVALKGP LATPVGKGHV SLNLTLRRTF NLFANLRPCR 151 SVAGYKTPYD NVDTVLIREN TEGEYSGIEH VVVDGVVQSI KLITREASER 201 VLRFAFQYAR SVNKKKVRVV HKATIMKMSD GLFLNTAREI AKEFPDIEFD 251 AELLDNSCLK IVTDPTYND KVLVMPNLYG DILSDMCAGL IGGLGLTPSG 301 NIGDECSIFE AVHGSA PDIA GKGLANPTAL LLSSIMMLQH MGLHEHAARI 351 QKATFDTLAE GKTLTGDLGG KAKTHEYAEA ICKRL 100 - 108 501.2775 1000.5404 1000.5441 - 0.0036 0 K.TTIPEEAIK.S 157 - 168 703.3637 1404.7128 1404.7249 - 0.0121 0 K.TPYDNVDTVLIR.E 204 - 210 451.7187 901.4228 901.4446 - 0.0218 0 R.FAFQYAR.S 228 - 238 620.7956 1239.5766 1239.5918 - 0.0151 0 K.MSDGLFLNTAR.E Oxidation (M) 261 - 271 631.8155 1261.6164 1261.6190 - 0.0026 0 K.IVTDPTYNDK.V 353 - 362 526.7635 1051.5124 1051.5186 - 0.0061 0 K.ATFDTLAEGK.T 363 - 371 431.2336 860.4526 860.4604 -

						0.0077 0 K.TLTGDLGGK.A
48	XP_752056	64987	63	2	6.39	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase Sequence Coverage: 3% 1 MSQQKSAILS VYDKTGLLDL AKGLVKHNVR LLASGGTARM IREAGFPVED 51 VSAITHAPEM LGGRVKTLP AVHGGILARD IESDEKDLAD QNISKVDFVV 101 CNLYPFKETV NKNVNTIAEA VEEIDIGGVT LLRAAAKNHA RVTILSDPQD 151 YPEFLKELEA GEISETSRKQ YALKAFEHTA DYDTAISGFF RKQYAGNGEQ 201 YLPLRYGANP HQKPASAYML HGKLPFKALN GSPGYINLLD ALNAWALVKE 251 LKQALGYPAA ASFKHVSPAG AAVGVPSEK ERKVYMVDDI AGIETSGLAQ 301 AYARARGADR MSSFGDLLAL SDVCDVPTAK IISREVS DGVI AAGYTPEAL 351 EILSKKKGGK YLVLMQMDENY VPASEETR TI YGVQLSQQRN DVVISPKQTF 401 NTIITPKDLK ALPDSALRDL TVATIALKYT QSNSVCYALN GQVIGLGAGQ 451 QSRIHCTRLA GDKADNWWMR FHDRVNLKWK KAGTKRADKS NAIDLLCSGQ 501 TPRNEVEKAE YERVFEVPA PFTQEERDSW LSKMGEVAVS SDAFFPFIDN 551 VFRAARSGAK YIAAPSGSQN DGPVFETAEK LGIVFVEQGT RLFHH 379 - 389 646.8580 1291.7014 1291.6884 0.0130 0 R.TYGVQLSQQR.N 581 - 591 609.8524 1217.6902 1217.6768 0.0134 0 K.LGIVFVEQGT.R
49	XP_754077	48306	94	4	4.43	Nucleosome assembly protein Nap1 Sequence Coverage: 11% 1 MSEPIRNKKA DFPVAPTQPN TPANNAPISS HAQQPGVASI KEESLDHATA 51 ASLFARNPGL VSMIQGKLGS LVGR SSGYIE SLPAPVRRRV AGLKGIQKEH 101 AKLEAQFQEE VLELEKKYFA KFTPLYQRRRA TIVNGAAEPT DDEVQAGKEE 151 EEEEEVDVKA EDERKQEEKD ITTPGIPEFW LSAMKNQISL AEMITDRDEE 201 ALKHLTDVRM EYLD RPPGFRL IFEFAENEFF TNKTISKTTY YKEESGYGGD 251 FIYDHAEGCK IDWKADKDLT VRVESKKQRN KNTKQTRVVK VTPPTESFFN 301 FFSPQPPTD DDDTIATDIE ER LELDYQLG EDIKEKLIPR AIDWFTGEAL 351 QFEELGDDMD ADEFDDDEDDE DEEEDEDDDD DRRSDRDVDD ESEEEVRFSS 401 LYASKYIFAS TPFFTMTAL PQS

						75 - 87 688.3735 1374.7324 1374.7143 0.0181 0 R.SSGYIESLPAPVR.R 103 - 116 852.9508 1703.8870 1703.8617 0.0253 0 K.LEAQFQEEVLELEK.K 122 - 128 462.7514 923.4882 923.4865 0.0018 0 K.FTPLYQR.R 323 - 336 564.9607 1691.8603 1691.8617 - 0.0015 1 R.LELDYQLGEDIKEK.L
50	XP_754843	46200	99	5	4.62	Ran GTPase activating protein 1 (RNA1 protein) Sequence Coverage: 12% 1 MAPPKVFSLE GKGLKLDTAE DIEAHIKPLI ESTDFTEIRL GGNTLGVPAS 51 ERLASVLASQ KSLEVADLAD IFTSRLLSEI PQALTALLNA LLEIKTLHTV 101 NLSDNAFGLN TQAPLVDFLS RHVPLRHLIL NNNGLGPAAG TLIADALTKL 151 AERKEEARKA GEEIPLLDISI VCGRNRLENG SMEAWARAYK VHAAGIRSVK 201 MTQNGIRQEG ISLLKEGLR HASALEVLDL QDNTFTIMGS TALAGVVAGW 251 PSLRELGVGD CLLSARGGVK VAQALAEKGK QNIQTLRLQY NEITAEGVKL 301 FLHATKTALP SLRRIELNGN KFLEEDPNVT ELQEVLEARK EEHGTDDDDPD 351 DMWGVDELDE LEESEEEEE AEEEEEEEEQ EEEERKADKF LKDNVKAEDE 401 KVAQRQDKDV DALAEALGKT AL 40 - 52 635.8472 1269.6798 1269.6677 0.0121 0 R.LGGNTLGVPASER.L 53 - 61 458.7786 915.5426 915.5389 0.0037 0 R.LASVLASQK.S 271 - 279 443.7540 885.4934 885.4920 0.0015 0 K.VAQALAEKGK.N 280 - 287 493.7731 985.5316 985.5305 0.0012 0 K.NQNIQTLR.L 288 - 299 682.8656 1363.7166 1363.6983 0.0183 0 R.LQYNEITAEGVK.L
51	XP_756019	46529	131	4	7.61	Curved DNA-binding protein Sequence Coverage: 11% 1 MEAWYQSHTL ASVRGHNIYF TMAENQAPEV DYTLNPNPTL TKYKTAAQIS 51 HKVLEAVTAL CSEGAKIVEI CQKGDELLEE ELTKVYKGKK ITKGIGHPTT 101 VSPSSYVTPY TPLVSDAQEA ETTLKAGEIV KIQLGAQIDG FGTIVCDMVV 151 VADKESPKDV VTGREADLIH ATHYANELLL RLMVPPGLLA SGTEEEKKKA 201 AAEKPPTQSQ ISALIEKVAK

						AYDCNVVENT TSWLFRNEI EGGKKIILAP 251 GSGVKGEVGP DVGEVWGVEV GLSLGSGKVK TLPHRATLHR RTTTYILKR 301 PSSRQTLSEI VKKFGTFPFS LRQLEDEKSA KVGVEVCVRG GVLRRQYEPAG 351 DADNAPVSRL LTTIAITKNG ITRLAAPNPP DLSKFQTDKK IEDEEILKIL 401 ERPLARNTGN KNKKKKKPTK DSKDEE 74 - 84 638.3303 1274.6460 1274.6241 0.0219 0 K.GDELLEELTK.V 246 - 255 477.8061 953.5976 953.5910 0.0067 0 K.IILAPGSGVK.G 345 - 359 795.3772 1588.7398 1588.7117 0.0281 0 R.QYEPAGDADNAPVSR.L 374 - 384 561.8163 1121.6180 1121.6080 0.0100 0 R.LAAPNPPDLSK.F
52	XP_754690	57418	276	5	5.44	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent Sequence Coverage: 11% 1 MTKVDHKVVL IVIDGWGIPG PDSPKGDGAI AAAETPYMSG FAEENSKTAQ 51 GYTELDASSL AVGLPEGLMG NSEVGHLNIG AGRVWQDSV RIDQTLKKGE 101 LNKVDNVVKS FTRAKEGNR LHLLGLVSDG GVHSNITHLV GLLKVAKEME 151 IPQVFIHFFG DGRDTPKSA IKYMQDLLDH TKEIGIGEIA TVVGRYYAMD 201 RDKRWDRVEV AMKGIVSGEG EESDPVKTI KERYEKGEND EFLKPIIVGG 251 KERRVQDNDT LFFFNYSRDR VREITQLLGD YDRSPKPDFP YPKNIQITTM 301 TQYKTDYTFP VAFPPQHMG VLAEWLSKKD IQQCHVAETE KYAHVTFFFN 351 GGIEKQFPGE VRDMIPSPKV PTYDHEPEMS AEA VGKKMAE RIAEGKFEFV 401 MNNFAPPDMV GHTGVYEAAI KGVAATDKAI GEIYQACKKH GYILFITADH 451 GNAEEMLTEK GTPKTSHTTN KVPFVLANAP EGWSLKKEEG VLGDVAPTVL 501 AAMGIEQPEE MSGKSLLVKA 84 - 91 494.7629 987.5112 987.5138 - 0.0025 0 R.VWQDSVR.I 183 - 195 657.3822 1312.7498 1312.7351 0.0148 0 K.EIGIGEIATVVGR.Y 214 - 228 745.3665 1488.7184 1488.6944 0.0241 0 K.GIVSGEGEESDPVK.T 255 - 267 839.9080 1677.8014 1677.7787 0.0227 0 R.VQDNDTLFFFNYS.S 273 - 283 661.8368 1321.6590 1321.6514 0.0077 0 R.EITQLLDYDR.S

53	XP_748938	51999	101	4	6.25	Pyruvate dehydrogenase complex, dihydrolipoamide acetyltransferase component	Sequence Coverage: 11% 1 MVASAVRMRI PSAMLSKGGL YVRRPHVIHR FKDAVQPQLP ALSALSRFYA 51 SKSFPPHTII SMPALSPTMS AGNIGAWQKK AGDSLSPGDV LVEIETDKAQ 101 MDFEFQEEGV LAKVLKETGE KDVAVGTPIA VLVEEGTDVA PFESFTLEDA 151 GGDKGTAPPK ESKEEPKAEA APAPSTPEPA PAAQEPETST EKLLQPSLDRE 201 PNISPAAKAL ALEKGVPIKA LKGTGRGGQI TKEDVEKYKP SISAAAAAPT 251 YEDIPLTSMR KTIATRLQQS MRENPHFFVS TTLSVTKLLK LRQALNASAE 301 GKYKLSVNDF LVKACAAALM KVPVAVNSSWR EENGQVVIRQ HNTVDISVAV 351 ATPNGLITPV VKNVHSLGLS SISNQIKDLG KRARENKLKP EEYQGGTFTI 401 SNMGMNPAVE RFTAVINPPQ AAILAVGTTR KVAVPVETEE GTSVEWDDQI 451 IVTGSFDHKV VDGAVGAEWI KELKKIVENP LELL 193 - 208 579.3189 1734.9349 1734.9264 0.0085 1 K.LQPSLDREPNISPAAK.A 227 - 237 401.8735 1202.5987 1202.6143 - 0.0156 1 R.GGQITKEDVEK.Y 331 - 339 522.2769 1042.5392 1042.5407 - 0.0015 0 R.EENGQVVIR.Q 412 - 430 970.5660 1939.1174 1939.0891 0.0284 0 R.FTAVINPPQAAILAVGTTR.K
54	XP_664146	41682	64	4	5.54	ACT_BOTCI Actin <i>A. nidulans</i>	Sequence Coverage: 13% 1 MPTEEVAALV IDNGSGMCKA GFAGDDAPRA VFPSIVGRPR HHGIMIGMQ 51 KDSYVGDEAQ SKRGILTTRY PIEHGVVTNW DDMEKIWHHT FYNELRVAP 101 EHPVLLTEAP INPKSNREKM TQIVFETFNA PAFYVSIQAV LSLYASGRIT 151 GIVLDSGDGV THVVPYIEGF ALPHAISRVD MAGRDLTDYL MKILAERGYT 201 FSTTAEREIV RDIKEKLCYV ALDFEQEIQT ASQSSSLEKS YELPDGQVIT 251 IGNERFRAPE ALFQPSVLGL ESGGIHVTTF NSIMKCDVDV RKDLYGNIVM 301 SGGTTMYPGI SDRMQKEITA LAPSSMKVKI IAPPERKYSV WIGGSILASL 351 STFQQMWISK QEYDESGPSI VHRKCF 20 - 29 488.7349 975.4552 975.4410 0.0142 0 K.AGFAGDDAPR.A 240 - 255 895.9830 1789.9514 1789.8846

						0.0668 0 K.SYELPDGQVITIGNER.F 317 - 327 582.3156 1162.6166 1162.5903 0.0263 0 K.EITALAPSSMK.V Oxidation (M) 361 - 373 506.2470 1515.7192 1515.6954 0.0238 0 K.QEYDESGPSIVHR.K
55	XP_7522 65	40002	88	3	5.85	UPF0160 domain protein MYG1 Sequence Coverage: 8% 1 MADETVAKKL KTSPLIGH NGHFHADEAL AVYLLRQLPT YASSPLIRTR 51 DPAQLATCHT VVDVGGEYDP ASNRDHHQR TFSTTFPNHN TRLSAGLVY 101 MHFGRAlIAQ HTSLPLDHED VTLLYEKLYT DFIEAVDAND NGVSVYDPAA 151 LASANIEKRF RDGGITIASV VNDMNNPDPT CPPGEPQDED SLFNRASTFM 201 GHVFTRKLHH AFTSWLPARA TVGAAYQSR EVHPSGRIII LPQGGVPWKE 251 HLYNFEKEAS GAGDINPDEQ VYYVLYPESA TEGSKWRVQC VSVNEGSFES 301 RKPLPESWRG VRDADLDGCL AAEAESGKP KIPEGAVFVH ASGFIGGHKT 351 KEGAFAMAVR SLEL 37 - 48 673.3708 1344.7270 1344.7401 - 0.0131 0 R.QLPTYASSPLIR.T 220 - 229 512.2616 1022.5086 1022.5145 - 0.0058 0 R.ATVGAAAYQSR.R 352 - 360 484.2316 966.4486 966.4593 - 0.0106 0 K.EGAFAMAVR.S Oxidation (M)
56	XP_7517 80	50540	334	10	5.66	Homocitrate synthase Sequence Coverage: 28% 1 MCPGADNEPN GHTNGANGTV PHPGFTAVET RQNPSPASR NPYGHNVGVT 51 DFLSNVSRFK IESTLREGE QFANAFFDTE KKIEIAKALD DFGVDYIELT 101 SPCASEQSRK DCEAICKLGL KAKILTHIRC HMDDARVAVE TGVGDGVDVVI 151 GTSSYLREHS HGKDMTYIKN TAIEVIEFVK SKGIEIRFSS EDSFRSDLVD 201 LLSIYSAVDK VGVNRVGIAD TVGCASPRQV YELVRVLRGV VSCDIETHFH 251 NDTGCAIANA YCALEAGATH IDTSVLGIGE RNgITPLGGL MARMMVADPE 301 YVKSKYKLEK LKDIEDLVAA AVEVNIPFNN YITGFCAFTH KAGIHAKAIL 351 NNPSTYEIIN PADFGMTRYV HFASRLTGWN AIKSRAQQLN IEMTDAQYKE 401 CTAKIKALAD IRPIAVDDAD SIIRAYYRNL KSGENKPLLD LTAEEQAQFA 451 AKEKELAGSG VIA 41 - 58 659.3185 1974.9337 1974.9548 -

						0.0211 0 R.NPYGHNVGVTDFLSNVSR.F 68 - 81 816.8560 1631.6974 1631.7104 - 0.0129 0 R.EGEQFANAFDTEK.K 137 - 157 1068.5507 2135.0868 2135.1111 - 0.0242 0 R.VAVETGVDGVDVVGITSSYLRE 170 - 180 631.8462 1261.6778 1261.6918 - 0.0139 0 K.NTAIEVIEFVK.S 188 - 195 487.7136 973.4126 973.4141 - 0.0015 0 R.FSSEDSFR.S 196 - 210 819.4235 1636.8324 1636.8560 - 0.0235 0 R.SDLVDLLSIYSAVDK.V 229 - 235 453.7491 905.4836 905.4971 - 0.0134 0 R.QVYELVR.V 282 - 293 608.3268 1214.6390 1214.6441 - 0.0051 0 R.NGITPLGGLMAR.M Oxidation (M) 294 - 303 607.7679 1213.5212 1213.5359 - 0.0146 0 R.MMVADPEYK.S 2 Oxidation (M) 407 - 424 642.0159 1923.0259 1923.0425 - 0.0166 0 K.ALADIRPIAVDDADSIHR.A
57	XP_755754	64716	284	10	7.55	Dihydroxy acid dehydratase IIv3 Sequence Coverage: 18% 1 MLLSQTRGRL PSTLRSFSRR ALSTTLPRGK DSEETALNKV SRNVTQPISQ 51 GASQAMLYAT GLTEEDMNKA QVGISVWYN GNPCNMHLLD LSNRVREGVQ 101 KAGLVGFQFN TVGVSDAISM GTKGMRYSLQ SRDLIADSIE TVMGGQWYDA 151 NISIPGCDKN MPGVLMAMGR VNRPSLMVYG GTIKPGCART QNNADIDIVS 201 AFQAYGQFLT GEITENQRFD IIRNACPGGG ACGGMYTANT MATAIEVMGM 251 TLPGSSSNPA ESKAKDLECL AAGEAIKRLL KEDIRPSDIL TRQAFENAMI 301 VVNITGGSTN AVLHLIAIAD SVGIKLDIED FQKVS DRTF LADLKPSGKY 351 VMADLHNIGG TPSLLKFLK EGVIDGSGMT VTGETLAKNL EKVPDFPADQ 401 KIIRPLSNPI KKTGHIQILR GSLAPGGSVG KITGKEGTRF VGKARVFDDE 451 DDFIAALERN EIKKEEKTVV VIRYTGPKGG PGMPEMLKPS SALMGAGLGS 501 SCALITDGRF SGGSHGFLIG HIVPEAAVGG PIGLVKDGDT ITIDAEKRLL 551 DLDVDETELA RRRKEWEALR DAGKLPQTGL TMRGTLGKYA RTVKDASHGC 601 ITDSVE 160 - 170 612.7891 1223.5636 1223.5461 0.0176 0 K.NMPGVLMAMGR.V 3 Oxidation (M)

						279 - 292 556.9983 1667.9731 1667.9570 0.0161 1 R.LLKEDIRPSDILTR.Q 338 - 349 425.2448 1272.7126 1272.7078 0.0048 0 R.TPFLADLKPSGK.Y 371 - 388 890.9545 1779.8944 1779.8561 0.0384 0 K.EGVIDGSGMTVTGETLAK.N Oxidation (M) 421 - 431 465.2571 928.4996 928.4978 0.0018 0 R.GSLAPGGSVGK.I 446 - 459 827.9002 1653.7858 1653.7522 0.0336 0 R.VFDEDDFIAALER.N 537 - 548 445.2258 1332.6556 1332.6521 0.0035 1 K.DGDTITIDAEKR.L 549 - 561 751.4067 1500.7988 1500.7671 0.0317 0 R.LLDLDVDETELAR.R 549 - 562 553.2981 1656.8725 1656.8682 0.0042 1 R.LLDLDVDETELARR.R 575 - 583 516.7834 1031.5522 1031.5434 0.0089 0 K.LPQTGLTMR.G Oxidation (M)
58	XP_749237	58635	204	6	5.82	Myo-inositol-phosphate synthase Sequence Coverage: 11% 1 MAPHATSDAV ANGAVNGSAR TTTAPLFTVN SPNVEYTDNE IKSRYAYHHT 51 DITRTAEGKM VATPKVTNYQ FKVDRKVGKV GMMLVGWGGN NGSTVTAGIL 101 ANRRRLVWET REGERAANY GSLVMSSTVK LGTDSKTGEE INIPFHDMLP 151 MIHPNDLVIG GWDISSMNLA DAMDR AQVLE PTLKQLVRKE MAEMKPLPSI 201 YYPDFIAANQ EDRADNVIEG NKASWAHVER IQQDIRDFKA QNGLDKVIVM 251 WTANTERYAD IIPGVNDTAD NLLNAIKAGH QEVAPSTVFA VACILENVFP 301 INGSPQNTFV PGAIQLAEKH GAFIGGDDFK SGQTKMKSAL VDFLINAGIK 351 LTSIASYNHL GNNDGKNLSS QKQFRSKEIS KSNVDDMV ANHLLYKEGE 401 HPDHTVVIKY MPAVGDNKRA LDEYYAEIFM GGHQTISLFN ICEDSLLASP 451 LIIDLVVIAE MMTRITWKSA DDEEYKGFHS VLSVLSYMLK APLTPPGTPV 501 VNALAKQRSA LTNIFRACVG LQPDSEMTLE HKLF 45 - 54 414.2033 1239.5881 1239.5884 - 0.0003 0 R.YAYHTTDITR.T 176 - 184 499.8025 997.5904 997.5808 0.0097 0 R.AQVLEPTLK.Q 214 - 222 480.2441 958.4736 958.4720 0.0017 0 R.ADNVIEGNK.A 320 - 330 582.2874 1162.5602 1162.5407

						0.0195 0 K.HGAFIGGDDFK.S 491 - 506 773.4732 1544.9318 1544.8926 0.0392 0 K.APLTPPGTPVVNALAK.Q 509 - 516 461.2667 920.5188 920.5080 0.0109 0 R.SALTNIFFR.A
59	XP_752164	49337	481	10	5.79	Glutamate/Leucine/Phenylalanine/V aline dehydrogenase Sequence Coverage: 24% 1 MSNLPHEPEF EQAYKELAST LENSTLFEKN PEYRKALAVV SVPERVVQFR 51 VVWEDDNHQQV QINRGYRVQF NSALGPYKGG LRFHPSVNLS ILKFLGFEQI 101 FKNALTGLNM GGGKGGSDFD PKGKSDNEIR RFCVAFMTEL CKHIGADTDV 151 PAGDIGVTGR EIGFLFGQYR KIRNQWEGVL TGKGGSWGGS LIRPEATGYG 201 LVYYVDHMIK YVTKGAESFA GKRVAISGSG NVAQFAALKV IELGGSVVSL 251 SDSKGSLLVN GEGSFTPAEI DIIAQLKVDR KQLSEVATTE AFATKFKYIE 301 GARPWVHVGGK VDVALPSATQ NEVSGEEAQA LIDAGCKFIA EGSNMGCTQA 351 AIDIFEHRQ ANPGAAAIWY APGKAANAGG VAVSGLEMAQ NSARISWTAE 401 EVDSRLKDIM ESCFRNGLDT AVKYATPAEG VLPSLVGTGSN IAGFTKVAEA 451 MKEQGDWW 35 - 45 584.8536 1167.6926 1167.6975 - 0.0049 1 R.KALAVVSVPER.V 36 - 45 520.8068 1039.5990 1039.6026 - 0.0035 0 K.ALAVVSVPER.V 68 - 78 612.3279 1222.6412 1222.6346 0.0066 0 R.VQFNSALGPYK.G 94 - 102 564.8085 1127.6024 1127.6015 0.0009 0 K.FLGFEQIFK.N 143 - 160 584.2945 1749.8617 1749.8646 - 0.0029 0 K.HIGADTDVPAGDIGVTGR.E 161 - 170 615.3186 1228.6226 1228.6241 - 0.0014 0 R.EIGFLFGQYR.K 215 - 223 461.7382 921.4618 921.4668 - 0.0050 1 K.GAESFAGKR.V 224 - 239 766.9347 1531.8548 1531.8358 0.0190 0 R.VAISGSGNVAQFAALK.V 240 - 254 745.4188 1488.8230 1488.8035 0.0195 0 K.VIELGGSVVSLSDSK.G 282 - 295 748.3948 1494.7750 1494.7566 0.0185 0 K.QLSEVATTEAFATK.F
60	XP_750781	114548	283	9	5.03	Assimilatory sulfite reductase Sequence Coverage: 10% 1 MMGSSSPSLS ALGGPTYVTA QTLIQQVAYI LSDKIFSYSP ESFDLDNALR

						51 EWASRQETNA IGESTVVKAM ETRQGAGNIA LGYLFSQDFD LKKRHVPQGI 101 VASSATLPYM RSALEQLSLL YSVASPVA AH VAAVDYAGEN GLVSDYASAL 151 SLAEELGLGL VSSASVHEAQ HMALLTTLLA SVLPSVHIYD GVRVGRETTR 201 VIDVLDQAGV ARTYEAIKKT LDESRNRHLD TQGVLELFA SLNGELGTDY 251 GLFEYHGHA E PVSVLVAFGT VEASLTAQVA RSLAKDGVRV GVVNVRVYRP 301 FVEEEFLRVL PQSTKTVGVL GQVTDEQDVQ EQGVRSALEY DVLAALTFAS 351 GREHAPTCVD IKYPRSQRWD LINTAAAFQL IFEKPIPAS GESAPLQLID 401 PATVQEYTFW DVDSSVCESA AAVLSEALAA DSASNVTTSK SYDNLIQGGGA 451 LRIDIRKSSK ILDTPYAITA ADTTYVGDIK LLGDIDVAAS IKNKGVVIIN 501 APGVKDDELE KKLPLGFRQA VAQREISLYI VDPSAAGASA PESSVLQSAF 551 LRVALPSQEG VGLKKLSSIT GDSETLETVA KDLDKLLRQV EIPESWRISE 601 EGTEVTQLSK DISINSFVPF DKDEAEAPL LNDWQAAAKG LAFKEAYGTK 651 KALRPETATK TFTVHVKENR RLTPVTYDRN IFHIEFDLGD SGLKYDIGEA 701 LGVHAENDPQ EVSEFITFYG LNPDDVVGVP SREDPAVLEN RTVYQALVQN 751 VDIFGRPPKR FYEALAEFAT DEKEKKDLLT LGGPEGAVEF KRRAEVDTIT 801 FADVLEFPS AHPDFQDLIR IVGPLKRREY SIASCQKVTP NSVALMIVAV 851 NWVDPRGRDR FGLATRYLSR LQPGTPVTVS VKSSVMKLPP KSTQPLIMAG 901 LGTGLAPFRA FVQHRALEKA QGKEIGAVLL YMGRHQREE YCYGEEWEAY 951 QEAGVITLLG RAFSRDQPEK IYIQDRMRET LPEIIQAYIR EEGAFYLCGP 1001 TWPVPDVTAV LEEAIA TEAK NTGKKVDTRK EIEKLKDEER YVLEVY 201 - 212 628.3577 1254.7008 1254.6932 0.0076 0 R.VIDVLDQAGVAR.T 441 - 452 653.8477 1305.6808 1305.6677 0.0132 0 K.SYDNLIQGGALR.I 481 - 492 607.8539 1213.6932 1213.6918 0.0015 0 K.LLGDIDVAASIK.N 497 - 511 547.3056 1638.8950 1638.8828 0.0121 1 K.VIINAPGVKDDELEK.K 553 - 565 442.5987 1324.7743 1324.7714
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						0.0028 1 R.VALPSQEGVGLKK.L 598 - 610 710.8676 1419.7206 1419.7093 0.0114 0 R.ISEEGTEVTQLSK.D 672 - 679 482.7568 963.4990 963.5025 - 0.0035 0 R.LTPVTYDR.N 733 - 741 521.7685 1041.5224 1041.5091 0.0134 0 R.EDPAVLENR.T 871 - 882 613.3641 1224.7136 1224.7078 0.0058 0 R.LQPGTPVTVSVK.S
61	XP_754687	51841	131	4	7.64	Serine hydroxymethyltransferase Sequence Coverage: 8% 1 MATYALSQAH REQMEKSLVD SDPEIAQIME KEIQRQRESI LLIASENVTS 51 RAVFDALGSP MSNKYSEGYP GARYYGGNQH IDAIELTCQA RALKAFNLDP 101 EKWGVNVQCL SGSPANLEVY QALMRPHDRL MGLDLPHGGH LSHGYQTPSR 151 KISAVSTYFE TFPYRVNTET GIIDYDTLEA NAELYRPKCL VAGTSAYCRL 201 IDYGRMRKIA DKVGAYLIVD MAHISGLVAA GVIPSPEYA DVVTTTTHKS 251 LRGPRGAMIF FRKGVRSTDP KTGKEIMYDL EGPINFSVFP GHQGGPHNHT 301 ITALAVALKQ AATPEFRQYQ EQVLKNAKAL EVEFKALGHK LVSDGTDSDH 351 VLLDLRPKGL DGARVEAVLE QINIACNKNS IPGDKSALTP CGIRIGTPAM 401 TSRGMSEEDF KRVARIDQV INLCKSIQAD LPKEANKLKD FKAKVASGSV 451 PEILALRKEV AEWASTYPLP V 52 - 64 676.8318 1351.6490 1351.6442 0.0049 0 R.AVFDALGSPMSNK.Y Oxidation (M) 65 - 73 500.2264 998.4382 998.4457 - 0.0075 0 K.YSEGYPGAR.Y 95 - 102 467.2356 932.4566 932.4603 - 0.0037 0 K.AFNLDPEK.W 395 - 403 475.2436 948.4726 948.4699 0.0028 0 R.IGTPAMTSR.G Oxidation (M)
62	XP_748936	35876	559	13	9.08	Malate dehydrogenase, NAD-dependent Sequence Coverage: 38% 1 MFAARQSFNL LQKRAFSASA SQASKVAVLG AAGGIGQPLS LLLKLNPRVS 51 ELALYDIRGG PGVAADLSHI NTNSTVTGYD PTPSGLRDAL KGSEIVLIPA 101 GVPRKPGMTR DDLFNTNASI VRDLAKAAAE ASPEANILVI SNPVNSTVPI 151 VAEVFKSKGV YNPKRLEFGVT TLDVVRASRF ISQIKKTDPA KEAVPVVGGH 201 SGTIVPLLS QSNHPDIEGE

						TRDTLVNRIQ FGGDEVVKAK DGAGSATLSM 251 AMAGARFAES LLKAAQGEKG VIEPTFVESP LYKDQGVDFD ASRVELGPNG 301 VEKILEVGKV NAYEEKLIQA ALTDLKKNIQ KGRDFVAQNP 49 - 58 589.8170 1177.6194 1177.6343 - 0.0148 0 R.VSELALYDIR.G 88 - 104 579.0051 1733.9935 1734.0040 - 0.0105 1 R.DALKGSEIVLIPAGVPR.K 92 - 104 654.3834 1306.7522 1306.7609 - 0.0086 0 K.GSEIVLIPAGVPR.K 92 - 104 654.3902 1306.7658 1306.7609 0.0050 0 K.GSEIVLIPAGVPR.K 111 - 122 682.8453 1363.6760 1363.6732 0.0029 0 R.DDLFNTNASIVR.D 166 - 176 610.3547 1218.6948 1218.6972 - 0.0024 0 R.LFGVTTLDVVR.A 229 - 238 546.2822 1090.5498 1090.5659 - 0.0160 0 R.IQFGGDEVVK.A 241 - 256 749.8348 1497.6550 1497.6552 - 0.0001 0 K.DGAGSATLSMAMAGAR.F 2 Oxidation (M) 270 - 283 789.9274 1577.8402 1577.8341 0.0061 0 K.GVIEPTFVESPLYK.D 284 - 293 571.2678 1140.5210 1140.5200 0.0010 0 K.DQGVDFFASR.V 294 - 303 521.2324 1040.4502 1040.5502 - 0.1000 0 R.VELGPNGVEK.I 304 - 316 497.9310 1490.7712 1490.7980 - 0.0268 1 K.ILEVGVKNAYEEK.L 332 - 340 502.2418 1002.4690 1002.4883 - 0.0192 1 K.GRDFVAQNP.-
63	XP_754009	37156	381	11	7.55	Alcohol dehydrogenase Sequence Coverage: 31% 1 MTIPDKQWAQ VVLEKGSPPV YKEIPVPKPG PDDILVKLRY SGVCHTDLHA 51 MKGDWPLALK LPLVGGHEGV GVVVAKGELV TGFEIGDHAG IKWLNGSCME 101 CEFCKQSEEP LCPRATMSGY TVDGTFQQYC VAKATHASKI PNGVPLDAAA 151 PILCAGLTVY KGLKESGARP GQTVAIVGAG GGLGSLAQQY AKAMGLRVVA 201 IDGGDEKREM CEKLGAEAYI DFTKSTNVVE DVKAATPGGL GAHAVLLLAV 251 SEKPFQQATD YVRSRGTIVA IGMPAGAYLK APVFNTVVKM ITIKGSYVGN 301 RQDGVEAIDF FARGLINAPF KKAPLKDLPK IFELMEQGVV AGRYVLEIPE 351

						23 - 37 539.6475 1615.9207 1615.9185 0.0022 0 K.EIPVPPKPGDDILVK.L 61 - 76 510.9688 1529.8846 1529.8930 - 0.0084 0 K.LPLVGGHEGVGVVAK.G 77 - 92 548.2800 1641.8182 1641.8362 - 0.0181 0 K.GELVTGFEIGDHAGIK.W 77 - 92 821.9328 1641.8510 1641.8362 0.0148 0 K.GELVTGFEIGDHAGIK.W 198 - 208 579.8058 1157.5970 1157.6040 - 0.0070 1 R.VVAIDGGDEKR.E 214 - 224 614.3152 1226.6158 1226.6183 - 0.0024 0 K.LGAEAYIDFTK.S 266 - 280 739.4138 1476.8130 1476.8010 0.0120 0 R.GTIVAIGMPAGAYLK.A Oxidation (M) 295 - 313 701.0146 2100.0220 2100.0025 0.0195 1 K.GSYVGNRQDGVEAIDFFAR.G 302 - 313 684.3364 1366.6582 1366.6517 0.0065 0 R.QDGVEAIDFFAR.G 314 - 321 430.2508 858.4870 858.4963 - 0.0093 0 R.GLINAPFK.K 331 - 339 555.7706 1109.5266 1109.5427 - 0.0160 0 R.IFELMEQGK.V Oxidation (M)
64a	XP_748145	36292	341	12	6.96	Glyceraldehyde 3-phosphate dehydrogenase GpdA Sequence Coverage: 28% 1 MATPKVGING FGRIGRIIGL NSLSHGLVDV VAVNDPFIEV HYAAYMLKYD 51 TTHGQFKGTI ETYDQGLIVN GKKIRFYAEK DPSQIPWSET GAAYIVESTG 101 VFTTKEKASA HLKGGAKKVI ISAPSADAPM FVMGVNNTTY TSDIQVLSNA 151 SCTTNCLAPL AKVINDKFGE VEGLMTTVHS YTATQKVVD PSNKDWRGGR 201 TAAQNIIPSS TGAAKAVGKV IPSLNGKLTG MAMRVPTSNV SVVDLTCRLE 251 KGASYDEIKQ AIKAASEEGE LKNILGYTED DVVSSDLNGD ERSSIFDAKA 301 GISLNPNFVK LVAWYDNEWG YSRRVVDLIA YIAKVDSQ 6 - 13 410.2177 818.4208 818.4399 - 0.0190 0 K.VGINGFGR.I 58 - 72 804.4276 1606.8406 1606.8203 0.0204 0 K.GTIETYDQGLIVNGK.K 201 - 215 715.3840 1428.7534 1428.7572 - 0.0038 0 R.TAAQNIIPSTGAAK.A 228 - 234 406.1888 810.3630 810.3728 - 0.0097 0 K.LTGMAMR.V 2 Oxidation (M) 228 - 248 780.4000 2338.1782 2338.1443 0.0338 1 K.LTGMAMRVPTSNVSVVDLTCR.L Carbamidomethyl (C); 2 Oxidation (M)

						235 - 248 773.9117 1545.8088 1545.7821 0.0267 0 R.VPTSNVSVVDLTCR.L Carbamidomethyl (C) 264 - 272 467.2303 932.4460 932.4451 0.0010 0 K.AASEEGELK.N 300 - 310 580.3291 1158.6436 1158.6397 0.0040 0 K.AGISLNPNFVK.L 324 - 334 420.9211 1259.7415 1259.7601 - 0.0187 1 R.RVVDLIAIYIAK.V 324 - 334 630.8852 1259.7558 1259.7601 - 0.0043 1 R.RVVDLIAIYIAK.V 325 - 334 552.8303 1103.6460 1103.6590 - 0.0130 0 R.VVDLIAIYIAK.V 325 - 338 767.4362 1532.8578 1532.8450 0.0128 1 R.VVDLIAIYIAKVDSQ.
64b	XP_748145	36292	162	6	6.96	Glyceraldehyde 3-phosphate dehydrogenase GpdA Sequence Coverage: 23% 1 MATPKVGING FGRIGRIIGL NSLSHGLVDV VAVNDPFIEV HYAAYMLKYD 51 TTHGQFKGTI ETYDQGLIVN GKKIRFYAEK DPSQIPWSET GAAYIVESTG 101 VFTTKEKASA HLKGGAKKVI ISAPSADAPM FVMGVNNTTY TSDIQVLSNA 151 SCTTNCLAPL AKVINDKFGI VEGLMTTVHS YTATQKVVDA PSNKDWRGGR 201 TAAQNIIPSS TGAAKAVGKV IPSLNGKLTG MAMRVPTSNV SVVDLTCRLE 251 KGASYDEIKQ AIKAASEEGE LKNILGYTED DVVSSDLNGD ERSSIFDAKA 301 GISLNPNFVK LVAWYDNEWG YSRRVVDLIAIYIAKVDSQ 58 - 72 804.4311 1606.8476 1606.8203 0.0274 0 K.GTIETYDQGLIVNGK.K 187 - 194 415.2221 828.4296 828.4341 - 0.0045 0 K.VVDAPSNK.D 201 - 215 715.3871 1428.7596 1428.7572 0.0024 0 R.TAAQNIIPSSSTGAAK.A 264 - 272 467.2277 932.4408 932.4451 - 0.0042 0 K.AASEEGELK.N 300 - 310 580.3285 1158.6424 1158.6397 0.0028 0 K.AGISLNPNFVK.L 325 - 334 552.8398 1103.6650 1103.6590 0.0060 0 R.VVDLIAIYIAK.V
65	XP_747920	52079	258	10	8.69	Citrate synthase (Cit1) Sequence Coverage: 19% 1 MASTMRLGAF ALRSTSITAK PAVQSAAFNG LRCYSTGKAK SLKETFADKL 51 PGEIEKVKKL RKEHGSKVIG EVTLDQAYGG ARGVKCLVWE GSVLDSEEGI 101 RFRGYTIPEC QKLLPKAPGG

						EEPLPEGLFW LLLTGEIPTE QQVRDLSEAW 151 AARSDLPKFI EELIDRCPST LHPMAQFSLA VTALHEHSAF AKAYAKGINK 201 KDYWNYTYED SMDLIACLPT IAAKIYRNVF KDGGVAPIQK DKDYSFNLN 251 QLGYGDNNDV VELMRLYLTI HSDHEGGNVS AHTTHLVGSA LSSPMLSLAA 301 GLNGLAGPLH GLANQEVNLW LTKMKKSGN DLSDQAIKDY LWSTLNAGQV 351 VPGYGHAVLR KTDPRYVSQR EFALRKLPDD PMFKLVSVQVY KIAPGVLTEH 401 GKTKNPYPNV DAHSGVLLQY YGLTEANYYT VLFQVSRALG VLPQLIIDRA 451 LGAPIERPKS FSTEAYAKLV GAKL 68 - 82 774.9149 1547.8152 1547.7944 0.0209 0 K.VIGEVTLAQYGGAR.G 104 - 112 548.2610 1094.5074 1094.5066 0.0008 0 R.GYTIPECQK.L Carbamidomethyl (C) 159 - 166 517.7797 1033.5448 1033.5444 0.0005 0 K.FIEELIDR.C 159 - 166 517.7823 1033.5500 1033.5444 0.0057 0 K.FIEELIDR.C 228 - 234 404.2158 806.4170 806.4286 - 0.0116 1 R.NVFKDGK.V 376 - 384 553.7829 1105.5512 1105.5478 0.0035 1 R.KLPDDPMFK.L Oxidation (M) 392 - 402 561.3177 1120.6208 1120.6241 - 0.0032 0 K.IAPGVLTEHGK.T 438 - 449 654.4129 1306.8112 1306.7973 0.0140 0 R.ALGVLPQLIIDR.A 450 - 459 526.3135 1050.6124 1050.6185 - 0.0061 0 R.ALGAPIERP.KS 460 - 468 502.2373 1002.4600 1002.4658 - 0.0058 0 K.SFSTEAYAK.L
66	EDP5020 2	36847	286	8	7.01	Zinc-containing alcohol dehydrogenase, putative Sequence Coverage: 20% 1 MKQWVVADKE NGFDSLNFKE GPVPCGENE VLVKLRAASL NYRDLIIPKG 51 MYPPINFPV VPGSDGAGEV VGVGSKVTQF KKGDKVVTLF NQLHQYGPVD 101 TRSTNSGLGG VLDGTLRQYG VFNENGLVRA PRNLNFLESS TLTCALTSW 151 NALYGMNALK PGEIVLVQGT GGVSMFALQF AKAAGATVIA TTSSDTKAKK 201 LKELGADHVI NYKTNPNWGE IARSLTPDNV GVDHIEVGG AGTLSQSLKC 251 IKFEGTISII GFLGGADPKG QPGMLEALNH ICTIRGVYVG SKALMNDMIR 301 AIEVNDIHPV VDEKVFRLDQ

							AKEAYEYMW A QKHLGKLAIE IE 50 - 76 898.4539 2692.3399 2692.3207 0.0191 0 K.GMYPPINFPVVPVPGSDGAGEVVGVGSK.V Oxidation (M) 103 - 117 723.8821 1445.7496 1445.7474 0.0022 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8857 1445.7568 1445.7474 0.0094 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8862 1445.7578 1445.7474 0.0104 0 R.STNSGLGGVLDGTLR.Q 103 - 117 723.8864 1445.7582 1445.7474 0.0108 0 R.STNSGLGGVLDGTLR.Q 118 - 129 698.3651 1394.7156 1394.6943 0.0214 0 R.QYGVFNENGLVR.A 253 - 269 861.4684 1720.9222 1720.9036 0.0187 0 K.FEGTISIIGFLGGADPK.G 293 - 300 498.2244 994.4342 994.4576 - 0.0233 0 K.ALMNDMIR.A 2 Oxidation (M)
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