

## SUPPLEMENTARY INFORMATION AVAILABLE:

### Supplementary Figure Captions:

#### Supplementary Figure 1

Control IgE immuno-blots of secreted 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.

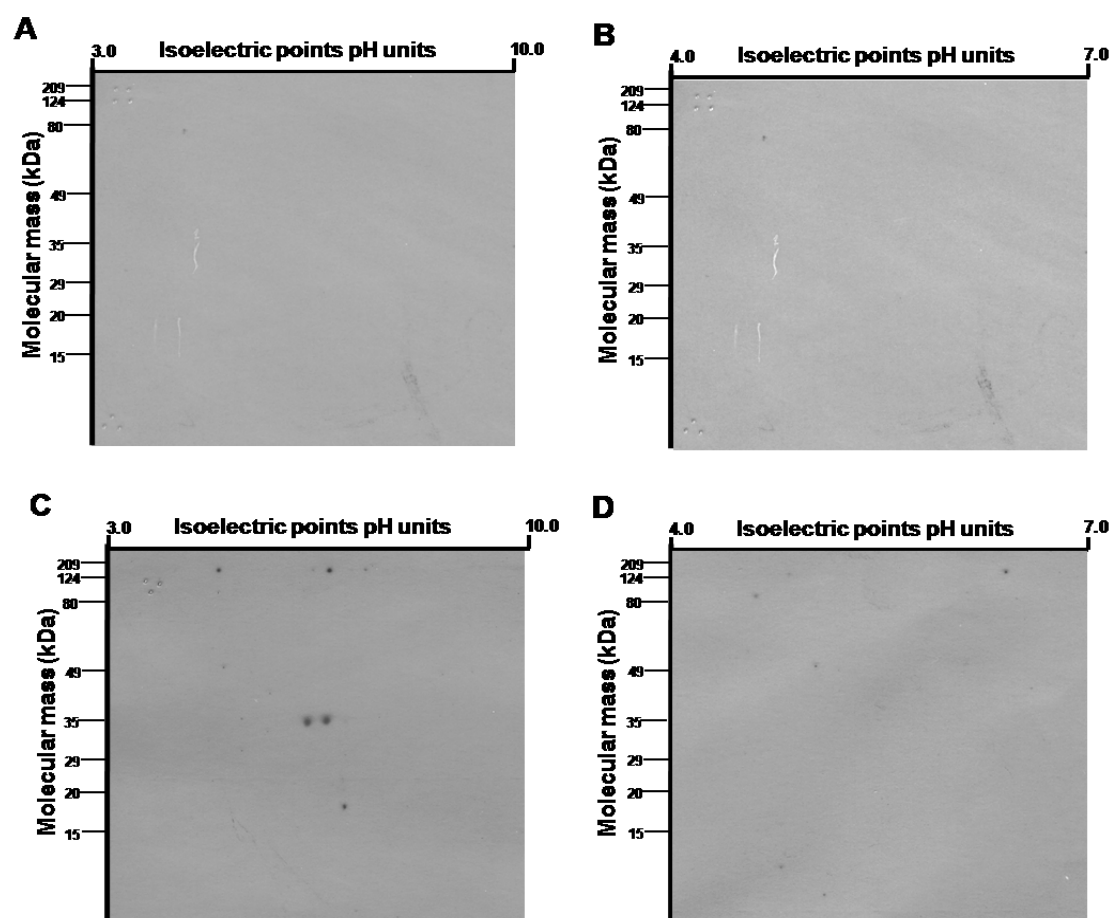
#### Supplementary Figure 3

Functional classification of **(a)** known allergens of *A. fumigatus* (source; [www.aspergillus.org.uk](http://www.aspergillus.org.uk)) Proteins in bold type were also identified in the present study reacting with pooled ABPA patients sera. **(b)** Predicted allergens<sup>31</sup> of *A. fumigatus* (source; [www.aspergillus.org.uk](http://www.aspergillus.org.uk)). Proteins in bold type were also identified in the present study reacting with pooled ABPA patients' sera. **(c)** Identified immunogenic proteins which reacted with IgE and IgG antibodies of ABPA patients' sera. Proteins in bold type specifically reacted with IgE; proteins in bold and underlined only reacted with IgG. The remaining proteins showed reactivity both with IgE and IgG antibodies. Functional annotation to the proteins

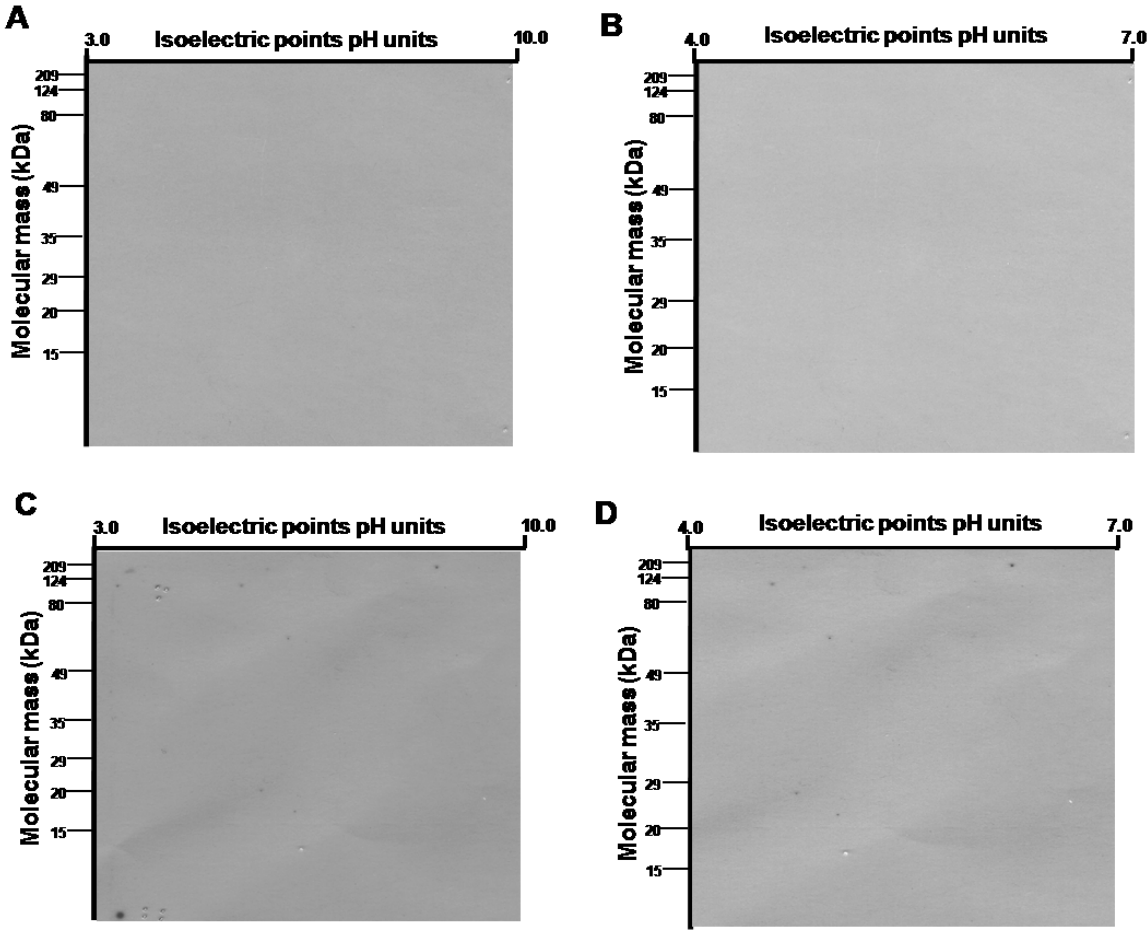
is assigned in accordance with the uniprot database ([www.uniprot.org](http://www.uniprot.org)) and Kognitor<sup>32</sup>.

**Abbreviations (a)** Asp f: *A. fumigatus* allergen, pmp20:putative peroxiredoxin-pmp20, Mep:extracellular elastinolytic metalloproteinase, hsp90:heat shock protein-90, Alp2:autophagic serine proteases-Alp2, TrxA:thioredoxin-TrxA, HP:hypothetical protein, MnsodB:superoxide dismutase [Mn] mitochondrial, rpl3:60S ribosomal protein-rpl3, crf1:probable glycosidase-crf1, AFMP1:antigenic cell wall glactomannoprotein-AFMP1, enoA:enolase. **(b)** GliG: glutathione-S-transferase-GliG, Alp1:alkaline serine protease, Pdi1-protein disulfide isomerase, DppV:dipeptidyl peptidase precursor-V, XylA:beta-xylosidase, NagA:beta-N-acetyl-hexosaminidase-NagA, MSSP2:RNA binding protein-MSSP2, Pst2:NADH-quinone-oxidoreductase-Pst2, Hyp1:conidial hydrophobin, AldA:aldehyde dehydrogenase-AldA, NTF-2:nuclear transport factor-2. **(c)** Asp f: *A. fumigatus* allergen, HP:hypothetical protein, DppV:Dipeptidyl peptidase precursor-V, MsdS:mannosidase, MreA:FAD/FMN containing isoamyl alcohol oxidase, Aci/Fdh:NAD dependent formate dehydrogenase, crf1:probable glycosidase-crf1, Bgt1:1,3-beta-glucanosyl transferase-Bgt1, Gel:1,3-beta-glucanosyl transferase-Gel(1 and 2), Cat-B:catalase-B, Plb:lysophospholipase(3 and 1) NTF-2:nuclear transport factor-2, FleA:fucose specific lectin, EglC:GPI-anchored cell wall beta-1,3-endoglucanase, Chi-B:chitinase, Asp-HS:*A. fumigatus*-hemolysin, pmp-20:putative peroxiredoxin-pmp20, Cat2-bifunctional catalase-peroxidase.

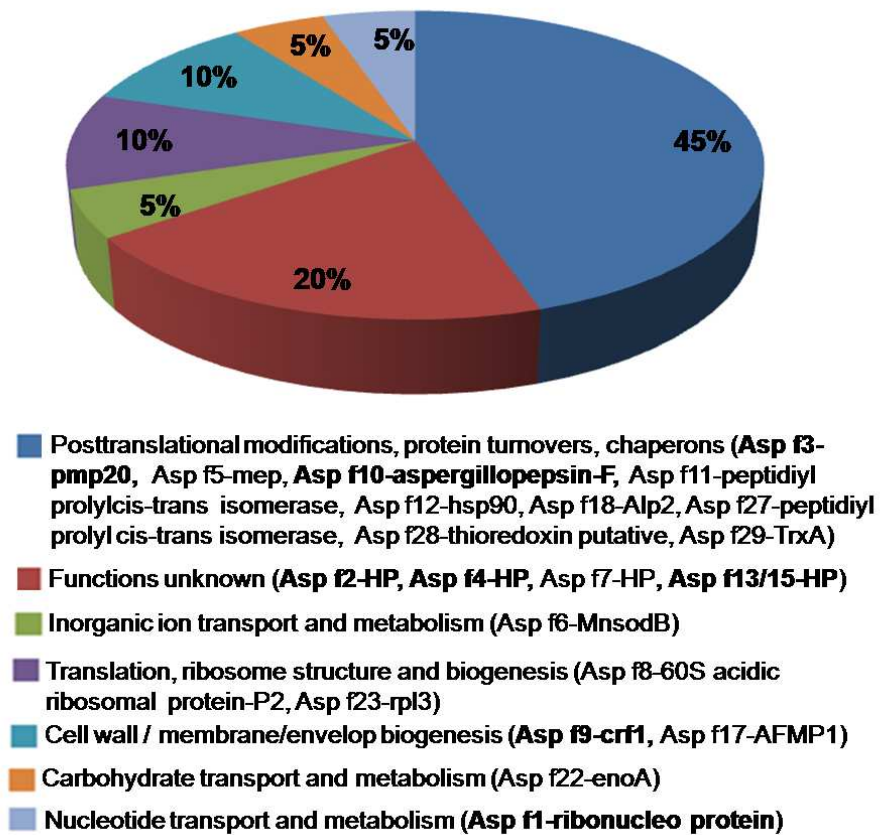
Supplementary Figure 1.



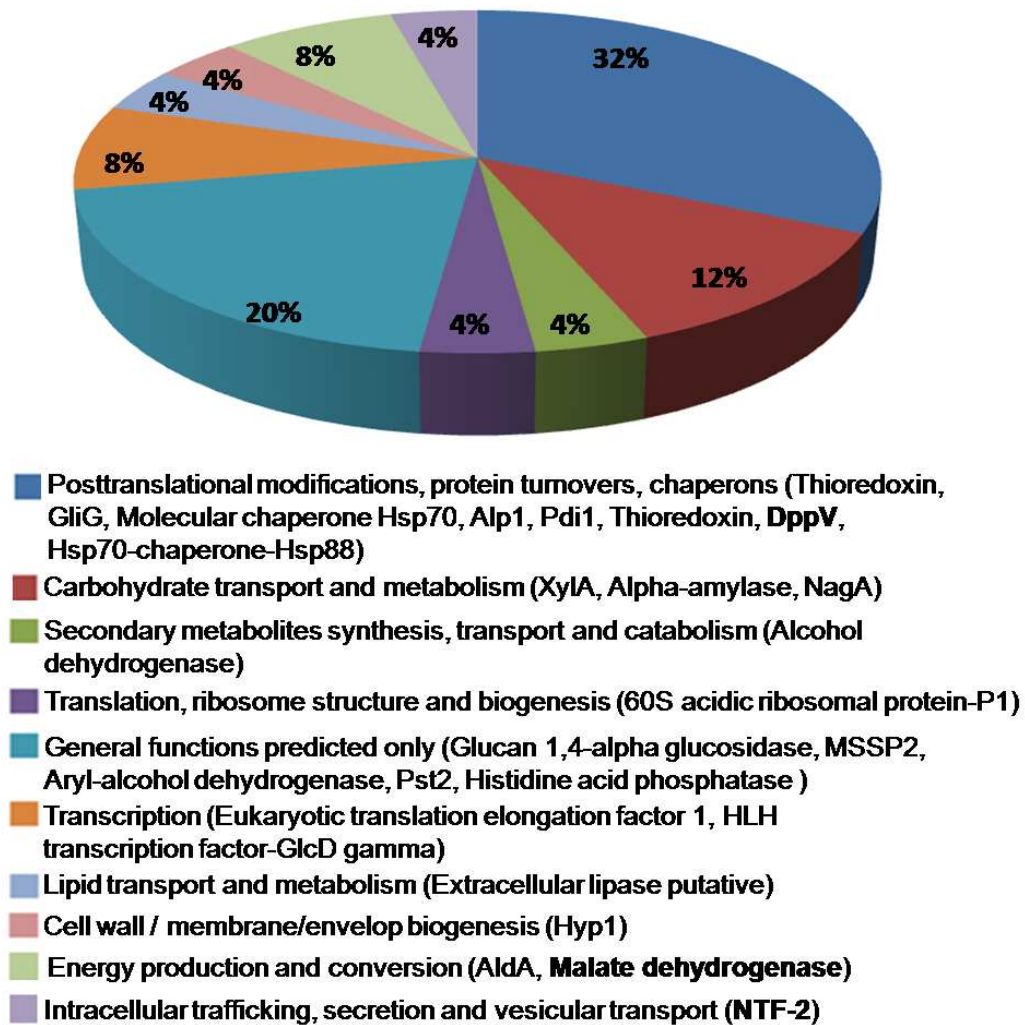
Supplementary Figure 2



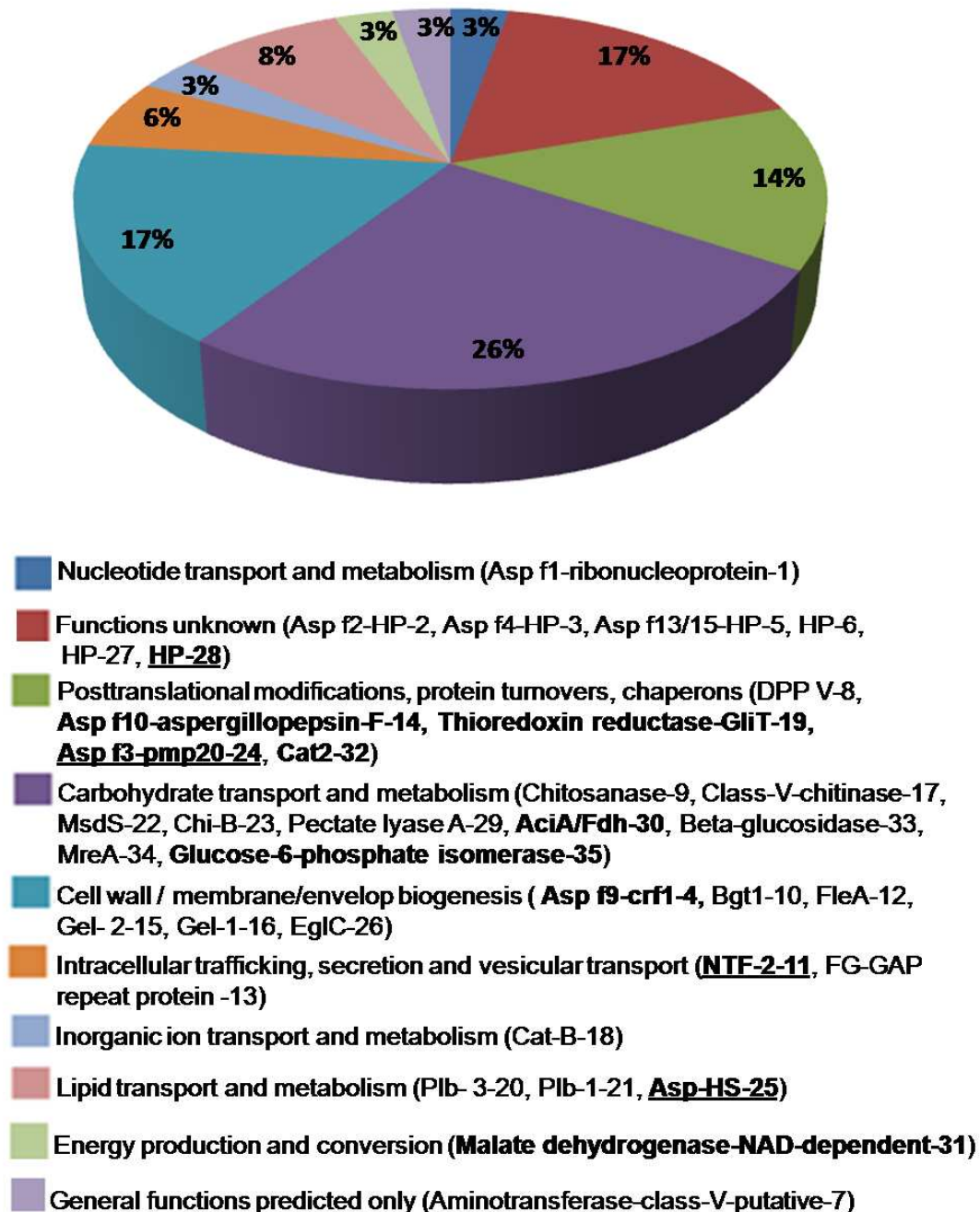
Supplementary Figure 3 (a).



Supplementary Figure 3 (b).



Supplementary Figure 3 (c).



# Supplementary Table:

**Table 1.** MS/MS analysis table of reported proteins

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

| Spot no. | Accession no. | Mass <sup>1</sup> (kDa) | MASCOT Score <sup>2</sup> | Peptide matched <sup>3</sup> | pI <sup>4</sup> | Protein name                 | MS/MS Analysis                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|----------|---------------|-------------------------|---------------------------|------------------------------|-----------------|------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1        | A46497        | 19610                   | 164                       | 8                            | 9.23            | Asp f1-ribonuceoprotein      | <b>Sequence coverage 30%</b><br>1 MVAIKNLFLL AATAVSVLAA PSPLDAR <b>ATW</b><br><b>TCINQQLNPK</b> TNKWEDKRLL<br><b>51 YNQAKAESNS HHAPLSDGKT</b><br>GSSYPHWFTN GYDGNGKLIK GRTPIKFGKA<br><b>101 DCDRPPKHSQ NGMGKDDHYL</b><br>LEFPTFPDGH DYKFDSKKPK EDPGPAR <b>VIY</b><br><b>151 TYPNKVFCGI VAHQRGNQGD LRLCSH</b><br><br><b>28 - 40 787.4089 1572.8032 1572.7719</b><br><b>0.0314 0 R.ATWTCINQQLNPK.T</b><br>Carbamidomethyl (C)<br><b>49 - 55 425.2517 848.4888 848.4756</b><br><b>0.0133 0 R.LLYNQAK.A</b><br><b>56 - 69 483.8826 1448.6260 1448.6644</b><br><b>-0.0384 0 K.AESNSHHAPLSDGK.T</b><br><b>56 - 69 483.9055 1448.6947 1448.6644</b><br><b>0.0303 0 K.AESNSHHAPLSDGK.T</b><br><b>56 - 69 483.9148 1448.7226 1448.6644</b><br><b>0.0582 0 K.AESNSHHAPLSDGK.T</b><br><b>56 - 69 483.9220 1448.7442 1448.6644</b><br><b>0.0798 0 K.AESNSHHAPLSDGK.T</b><br><b>148 - 155 499.2735 996.5324 996.5280</b><br><b>0.0044 0 R.VIYTYPNK.V</b><br><b>166 - 176 419.5544 1255.6414 1255.5728</b><br><b>0.0686 1 R.GNQGD LRLCSH.-</b><br>Carbamidomethyl (C) |
| 2a       | P79017        | 32818                   | 175                       | 6                            | 5.34            | Asp f 2-hypothetical protein | <b>Sequence coverage 20%</b><br>1 MAALLRLAVL LPLAAPLVAT LPTSPVPIAA<br>RATPHEPVFF SWDAGAVTSF<br><b>51 PIHSSCATQ RRQIEAGLNE</b><br><b>AVELARHAKA HILRWGNESE IYRKYFGNRP</b><br><b>101 TMEAVGAYDV IVNGDKANVL</b><br>FR <b>CDNPDGNC ALEGWGGHWR</b> GANATSETVI<br><b>151 CDRSYTTRRW LVSMCSQGYT</b><br>VAGSETNTFW ASDLMHRLYH VPAVGQGWVD<br><b>201 HFADGYDEVI ALAKSNGTES</b><br>THDSEALQYF ALEAYAFDIA APGVGCAGES<br><b>251 HGPDQGHDTG SASAPASTST</b><br>SSSSSGSGSG ATTTPTDPS ATIDVPSNCH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

|    |        |       |     |   |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|----|--------|-------|-----|---|------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |        |       |     |   |      | <b>301</b> THEGGQLHCT<br><b>Start - End Observed Mr(expt) Mr(calc)</b><br><b>Delta Miss Sequence</b><br>62 - 76 556.9632 1667.8678 1667.8954<br>-0.0277 1 R.QIEAGLNEAVELAR.H<br>63 - 76 756.8688 1511.7230 1511.7943<br>-0.0713 0 R.QIEAGLNEAVELAR.H<br>63 - 76 756.8866 1511.7586 1511.7943<br>-0.0357 0 R.QIEAGLNEAVELAR.H<br>85 - 93 577.2723 1152.5300 1152.5200<br>0.0101 0 R.WGNESEIYR.K<br>95 - 116 811.3719 2431.0939 2431.1478<br>-0.0539 0<br><b>K.YFGNRPTMEAVGAYDIVVNGDK.A</b><br>Oxidation (M)<br>123 - 140 700.9316 2099.7730 2099.8327<br>-0.0597 0 R.CDNPDGNCALGWGGHWR.G<br>2 Carbamidomethyl (C)                                                                                                                                                                                                                                                                                                                                                                                          |
| 2b | P79017 | 32818 | 162 | 6 | 5.34 | Asp f 2-<br>hypothetical<br>protein<br><br>Sequence Coverage: <b>4%</b><br><br>1 MAALLRLAVL LPLAAPLVAT LPTSPVPIAA<br>RATPHEPVFF SWDAGAVTSF<br><b>51</b> PIHSSCNATQ <b>RQIEAGLNE</b><br><b>AVELAR</b> HAKA HILRWGNESE IYRKYFGNRP<br><b>101</b> TMEAVGAYDV IVNGDKANVL<br>FRCDNPDGNC ALEGWGGHWR GANATSETVI<br><b>151</b> CDRSYTTRRW LVSMCSQGYT<br>VAGSETNTFW ASDLMHRLYH VPAVGQGWVD<br><b>201</b> HFADGYDEVI ALAKSNGTES<br>THDSEALQYF ALEAYAFDIA APGVGCAGES<br><b>251</b> HGPDQGHDTG SASAPASTST<br>SSSSSGSGSG ATTTPTDSPS ATIDVPSNCH<br><b>301</b> THEGGQLHCT<br><br>62 - 76 556.9737 1667.8993 1667.8954<br>0.0038 1 R.QIEAGLNEAVELAR.H<br>62 - 76 556.9737 1667.8993 1667.8954<br>0.0038 1 R.QIEAGLNEAVELAR.H<br>62 - 76 834.9613 1667.9080 1667.8954<br>0.0126 1 R.QIEAGLNEAVELAR.H<br>63 - 76 756.8671 1511.7196 1511.7943<br>-0.0747 0 R.QIEAGLNEAVELAR.H 63 -<br>76 756.8781 1511.7416 1511.7943 -<br>0.0527 0 R.QIEAGLNEAVELAR.H<br>63 - 76 756.9092 1511.8038 1511.7943<br>0.0095 0 R.QIEAGLNEAVELAR.H |
| 2c | P79017 | 32818 | 76  | 6 | 5.34 | Asp f 2-<br>hypothetical<br>protein<br><br>Sequence Coverage: <b>4%</b><br><br>1 MAALLRLAVL LPLAAPLVAT LPTSPVPIAA<br>RATPHEPVFF SWDAGAVTSF<br><b>51</b> PIHSSCNATQ <b>RQIEAGLNE</b><br><b>AVELAR</b> HAKA HILRWGNESE IYRKYFGNRP<br><b>101</b> TMEAVGAYDV IVNGDKANVL<br>FRCDNPDGNC ALEGWGGHWR GANATSETVI<br><b>151</b> CDRSYTTRRW LVSMCSQGYT<br>VAGSETNTFW ASDLMHRLYH VPAVGQGWVD<br><b>201</b> HFADGYDEVI ALAKSNGTES<br>THDSEALQYF ALEAYAFDIA APGVGCAGES<br><b>251</b> HGPDQGHDTG SASAPASTST<br>SSSSSGSGSG ATTTPTDSPS ATIDVPSNCH<br><b>301</b> THEGGQLHCT<br><br>62 - 76 556.9737 1667.8993 1667.8954<br>0.0038 1 R.QIEAGLNEAVELAR.H 62 -<br>76 556.9737 1667.8993 1667.8954<br>0.0038 1 R.QIEAGLNEAVELAR.H<br>62 - 76 834.9613 1667.9080 1667.8954<br>0.0126 1 R.QIEAGLNEAVELAR.H                                                                                                                                                                                                                         |

|    |          |       |     |   |      |                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|----|----------|-------|-----|---|------|-------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |          |       |     |   |      |                                     | 63 - 76 756.8671 1511.7196 1511.7943<br>-0.0747 0 R.QIEAGLNEAVELAR.H<br>63 - 76 756.8781 1511.7416 1511.7943<br>-0.0527 0 R.QIEAGLNEAVELAR.H<br>63 - 76 756.9092 1511.8038 1511.7943<br>0.0095 0 R.QIEAGLNEAVELAR.H                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 3  | Q4WV60   | 32572 | 153 | 6 | 6.64 | Asp f 4-hypothetical protein        | Sequence Coverage: <b>12%</b><br><br>1 MWSETPMVSS MTIAGETCDS<br>SGFCLRSNRI RQLSHSFKMI KPSILGALAL<br>51 LSCALPSNAT QIFRNTGTLA<br>GWDSVNHEHS GTVQQVSNVV YEGSTALK <b>MT</b><br>101 <b>QVYDASYTGR YHSEVVKNNV</b><br><b>YKRGDTGFYGF</b> AFRLQEDWQ FSPAQSYNIA<br>151 QFIADFSNTG CDDYMPSSMV<br>WLVGNQLYSR VKQGSVCAQK TKTFSNLATV<br>201 TAGVWHKVII QASWK <b>SDGTG</b><br><b>FYK</b> MWFDGVK VLDQHDIATT VDDNRPFQFR<br>251 VGLYANGWHD DKGMKGTQGT<br>RQIWYDEIAA GTTFADADPA QW<br>Start - End Observed Mr(expt) Mr(calc)<br>Delta Miss Sequence<br>99 - 110 704.3072 1406.5998 1406.6136<br>-0.0138 0 K.MTQVYDASYTGR.Y Oxidation (M)<br>99 - 110 704.3232 1406.6318 1406.6136<br>0.0182 0 K.MTQVYDASYTGR.Y Oxidation (M)<br>111 - 122 493.9350 1478.7832 1478.7518<br>0.0314 1 R.YHSEVVKNNVYK.R<br>124 - 134 619.2792 1236.5438 1236.5564<br>-0.0125 0 R.GDTGFYGF <b>AFR.L</b><br>124 - 134 619.2929 1236.5712 1236.5564<br>0.0149 0 R.GDTGFYGF <b>AFR.L</b><br>216 - 223 437.6962 873.3778 873.3869<br>-0.0090 0 K.SDGTGFYK.M |
| 4a | CAA11266 | 32298 | 193 | 4 | 4.63 | rAsp f 9-probable glycosidase, crf1 | Sequence Coverage: <b>12%</b><br><br>1 KRSFILRSAD MYFKYTAAAL<br>AAVLPLCSAQ TWSKCNPLEK TCPPNKGALAA<br>51 STYTADFTSA SALDQWEVTA<br>GK <b>VPVGPQGA EFTVAK</b> QGDA PTIDTDFYFF<br>101 FGKAEVVMKA APGTGVVSSI<br>VLESDDLDEV DWEVLGGDTT QVQTNFYFG <b>K</b><br>151 <b>DTTTYDR</b> GTY VPVATPQETF<br>HTYTIDWTKD AVTWSIDGAV VRT <b>LTYNDAK</b><br>201 GGTR <b>FPQTPM RL</b> RLGSWAGG<br>DPSNPKGTIE WAGGLTDYSA GPYTMVYKSV<br>251 RIENANPAES YTYSDNSGSW<br>QSIKFDGSVD ISSSSSVTSS TTSTASSASS<br>301 TS<br><br>73 - 86 700.4063 1398.7980 1398.7507<br>0.0473 0 K.VPVGPQGA <b>EFTVAK.Q</b><br>150 - 157 464.7145 927.4144 927.3934<br>0.0210 0 K.GDTTTYDR.G<br>193 - 200 463.2510 924.4874 924.4552<br>0.0322 0 R.TLTYNDAK.G<br>205 - 211 446.7318 891.4490 891.4273<br>0.0218 0 R.FPQTPMR.L Oxidation (M)                                                                                                                                                                                                                       |
| 4b | CAA11266 | 32298 | 68  | 2 | 4.63 | rAsp f 9-probable glycosidase, crf1 | Sequence Coverage: <b>7%</b><br><br>1 KRSFILRSAD MYFKYTAAAL<br>AAVLPLCSAQ TWSKCNPLEK TCPPNKGALAA<br>51 STYTADFTSA SALDQWEVTA<br>GK <b>VPVGPQGA EFTVAK</b> QGDA PTIDTDFYFF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |

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|----|----------|-------|-----|---|------|----------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |          |       |     |   |      |                                  | <div><div><div>101FGKAEVVMKAAPGTGVVSSI</div><div>VLESDDLDEV DWEVLGGDTT QVQTNFYFGKG</div><div>151DTTTYDRGTYVPVATPQETF</div><div>HTYTIDWTKD AVTWSIDGAV VR</div><div>201GGTRFPQTPMLRLRGSWAGG</div><div>DPSNPKGTIE WAGGLTDYSA GPYTMVYKSV</div><div>251RIENANPAESYTYSNDSGSW</div><div>QSIKFDGSVD ISSSSSVTSS TTSTASSASS</div><div>301TS</div></div><div><div>73 - 86700.40021398.78581398.7507</div><div>0.03510K.VPVGPPQGAFTVAK.Q</div><div>193 - 200463.2462924.4778924.4552</div><div>0.02260R.TLTYNDAK.G</div></div></div>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 5a | AJ002026 | 15934 | 111 | 4 | 4.61 | Asp f 13/15-hypothetical protein | <div>Sequence Coverage: 19%</div> <div><div>1MKFTTPISLISLFVSSALAAPTPENEAR</div><div>IPVSVSYDPRYDNAGTSMND</div><div>51VSCSNGVNLVTKWPTFGSV</div><div>PGFARIGGAPTIPGWNSPNC GKCYKLQYEQ</div><div>101NTIYVTAIDAAPGGFNIATS</div><div>AMDQLTNGMA VELGR</div><div>VQATYEEADPSHCAS</div><div>151GV</div><div>Start - EndObservedMr(expt)Mr(calc)</div><div>DeltaMiss Sequence</div><div>29 - 40659.82171317.62881317.6565</div><div>-0.02760R.DAIPVSVSYDPR.Y</div><div>29 - 40659.83691317.65921317.6565</div><div>0.00280R.DAIPVSVSYDPR.Y</div><div>136 - 152910.87621819.73781819.7683</div><div>-0.03040R.VQATYEEADPSHCASGV.-</div><div>Carbamidomethyl (C)</div><div>136 - 152910.87811819.74161819.7683</div><div>-0.02660R.VQATYEEADPSHCASGV.-</div><div>Carbamidomethyl (C)</div></div>                                                                                                                                                                                                                                          |
| 5b | AJ002026 | 15934 | 218 | 7 | 4.61 | Asp f 13/15-hypothetical protein | <div>Sequence Coverage: 38%</div> <div><div>1MKFTTPISLISLFVSSALAA</div><div>PTPENEAR</div><div>IPVSVSYDPRYDNAGTSMND</div><div>51VSCSNGVNLVTK</div><div>WPTFGSV</div><div>PGFARIGGAPTIPGWNSPNC GKCYKLQYEQ</div><div>101NTIYVTAIDAAPGGFNIATS</div><div>AMDQLTNGMA VELGR</div><div>VQATYEEADPSHCAS</div><div>151GV</div><div>29 - 40659.84391317.67321317.6565</div><div>0.01680R.DAIPVSVSYDPR.Y</div><div>29 - 40659.84991317.68521317.6565</div><div>0.02880R.DAIPVSVSYDPR.Y</div><div>64 - 75661.35461320.69461320.6615</div><div>0.03310K.WPTFGSVPGFAR.I</div><div>64 - 75661.35631320.69801320.6615</div><div>0.03650K.WPTFGSVPGFAR.I</div><div>76 - 92863.44231724.87001724.8304</div><div>0.03960R.IGGAPTIPGWNSPNC</div><div>GK.C</div><div>Carbamidomethyl (C)</div><div>76 - 92863.44501724.87541724.8304</div><div>0.04500R.IGGAPTIPGWNSPNC</div><div>GK.C</div><div>Carbamidomethyl (C)</div><div>136 - 152910.90811819.80161819.7683</div><div>0.03340R.VQATYEEADPSHCASGV.-</div><div>Carbamidomethyl (C)</div></div> |
| 6  | Q4WEM3   | 35496 | 41  | 3 | 6.00 | Hypothetical protein             | <div>Sequence Coverage: 12%</div> <div><div>1MASIRIGYVEHYLAPHLALRSPAASSLP</div><div>EKTTLVPEPSGTGHMITSRLR</div></div>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |

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|----|--------|-------|-----|---|------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |        |       |     |   |      | <p> <b>51</b> EKEIDVAIGL TEGWIAGLAG<br/> KQQAQKDAAS GGYKVVGHV DTPLRWAIVT<br/> <b>101</b> GR<b>EREELHTV</b> <b>ADLK</b>DKRVGM<br/> TDVSHSGSHI MSFVLAQKQG WKPDSLTPAV<br/> <b>151</b> LGPFQALRNG VTGYNASHPD<br/> QATPAAEFFM WEHFTTKPYF HADADKPHPP<br/> <b>201</b> LKKIGEFTP WPSWLIVAST<br/> SVFPDPEHDE KLKQLFQVLD QGIKDFQADH<br/> <b>251</b> DNVVRLGTG ELGCTYVEED<br/> AKEWLKDVRF TSSTRGVDRK <b>VVDGVVDVLK</b><br/> <b>301</b> <b>VAGVIDPGMS NDEAAER</b>VIG IPR<br/> Start - End Observed Mr(expt) Mr(calc)<br/> Delta Miss Sequence<br/> <b>103 - 114 480.6071 1438.7995 1438.7416</b><br/> <b>0.0579 1 R.EREELHTVADLK.D</b><br/> <b>291 - 300 521.8356 1041.6566 1041.6070</b><br/> <b>0.0496 0 K.VVDGVVDVLK.V</b><br/> <b>301 - 317 873.9219 1745.8292 1745.7890</b><br/> <b>0.0402 0 K.VAGVIDPGMSNDEAAER.V</b><br/> Oxidation (M) </p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| 7a | Q4WTF6 | 41824 | 196 | 8 | 6.46 | <p>Aminotransferas<br/>e- class V,<br/>putative</p> <p>Sequence Coverage: <b>21%</b></p> <p> <b>1</b> MSSQAPHSTL LIPGPIEFDD AVLQSMASHYA<br/> ESHVSPAFVK <b>VFGETLTLVR</b><br/> <b>51</b> KLFQSTKPSA QPFVISGSGT<br/> LGWDVVASNL IEKGENALVL HTGYFADSFA<br/> <b>101</b> ACLETYGAHA TQLKAPIGDR<br/> PSFEQIEQAL KEKPYKIITI THVDTSTGVL<br/> <b>151</b> SDIK<b>RVTEIV</b> <b>RRVSPDTLVV</b><br/> VDGVCSVGCE EIAFDEWDLD VVLTASQK<b>AI</b><br/> <b>201</b> <b>GCPPGLSILM</b> <b>LSGR</b>AIDRFK<br/> SRKTPSSYF ASIANWMPIM QNYENNKPSY<br/> <b>251</b> FATPPTQLVH ALHTSLSQIT<br/> ARPMAR<b>FAI</b> <b>HAQTSDRVKA</b> <b>AIADLGLR</b>QL<br/> <b>301</b> ASQPESQAHA MTAIYLPDGL<br/> TPADVLPSSL KR<b>GVIFAAGL</b> <b>HKEIATR</b>YIR<br/> <b>351</b> <b>FGHMGVSVTD</b> <b>PARNDIDKAI</b><br/> VALKEALTEA KQAKGL </p> <p> Start - End Observed Mr(expt) Mr(calc)<br/> Delta Miss Sequence<br/> <b>41 - 50 567.8623 1133.7100 1133.6445</b><br/> <b>0.0656 0 K.VFGETLTLVR.K</b><br/> <b>155 - 161 436.7982 871.5818 871.5239</b><br/> <b>0.0579 1 K.RVTEIVR.R</b><br/> <b>199 - 214 829.4871 1656.9596 1656.8691</b><br/> <b>0.0905 0 K.AIGCPPGLSILMLSGR.A</b><br/> Carbamidomethyl (C); Oxidation (M)<br/> <b>278 - 287 573.3184 1144.6222 1144.5625</b><br/> <b>0.0597 0 R.FAIHAQTSDR.V</b><br/> <b>278 - 289 458.2789 1371.8149 1371.7259</b><br/> <b>0.0890 1 R.FAIHAQTSDRVK.A</b><br/> <b>290 - 298 450.3003 898.5860 898.5236</b><br/> <b>0.0625 0 K.AAIADLGLR.Q</b><br/> <b>333 - 347 528.3434 1582.0084 1581.8991</b><br/> <b>0.1093 1 R.GVIFAAGLHKEIATR.Y</b> <b>351 -</b><br/> <b>363 463.9276 1388.7610 1388.6507</b><br/> <b>0.1103 0 R.FGHMGVSVTDPAR.N</b> Oxidation<br/> (M) </p> |
| 7b | Q4WTF6 | 41824 | 66  | 3 | 6.46 | <p>Aminotransferas<br/>e- class V,<br/>putative</p> <p>Sequence Coverage: <b>9%</b></p> <p> <b>1</b> MSSQAPHSTL LIPGPIEFDD AVLQSMASHYA<br/> ESHVSPAFVK <b>VFGETLTLVR</b><br/> <b>51</b> KLFQSTKPSA QPFVISGSGT<br/> LGWDVVASNL IEKGENALVL HTGYFADSFA<br/> <b>101</b> ACLETYGAHA TQLKAPIGDR<br/> PSFEQIEQAL KEKPYKIITI THVDTSTGVL<br/> <b>151</b> SDIKRVTEIV <b>RRVSPDTLVV</b> </p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

|    |        |       |     |    |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|----|--------|-------|-----|----|------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |        |       |     |    |      | <p>VDGVCSVGCE EIAFDEWDL D VVLTSQKAI<br/> <b>201</b> GCPPGLSILM LSGRAIDRFK<br/> SRKTPSSYF ASIANWMPIM QNYENNKPSY<br/> <b>251</b> FATPPTQLVH ALHTSLSQIT<br/> ARPMARFAI HAQTS DRVKA <b>A</b> <b>AIADLGLRQL</b><br/> <b>301</b> ASQPESQAHA MTAIYLPDGL<br/> TPADVLP SLL KR<b>GVIFAAGL HKEIATR</b>YIR<br/> <b>351</b> FGHMGVSVTD PARNDIDKAI<br/> VALKEALTEA KQAKGL<br/> <b>Start - End Observed Mr(expt) Mr(calc)</b><br/> <b>Delta Miss Sequence</b><br/> <b>41 - 50 567.8691 1133.7236 1133.6445</b><br/> <b>0.0792 0 K.VFGETLTLVR.K</b><br/> <b>290 - 298 450.2998 898.5850 898.5236</b><br/> <b>0.0615 0 K.AAIADLGLR.Q</b><br/> <b>333 - 347 528.3448 1582.0126 1581.8991</b><br/> <b>0.1135 1 R.GVIFAAGLHKEIATR.Y</b></p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| 8a | O13479 | 79696 | 414 | 11 | 5.59 | <p>Dipeptidyl-peptidase-V precursor, DppV</p> <p>Sequence Coverage: <b>15%</b></p> <p><b>1</b> MGAFRWLSIA AAALSTALALT<br/> PEQLITAPRR <b>SEAIPDP</b>SGK VAVFSTSQYS<br/> <b>51</b> FETHKRTSWW SLLDLKTGQT<br/> KVL TNDSSVS EIVWLSDDSI LYVNSTNADI<br/> <b>101</b> PGGVELWVTQ ASSFAKGYKA<br/> <b>ASLPASFSGL</b> KTAKTKSGDI RFVAYGQSYP<br/> <b>151</b> NGTAYNEELA TAPLSSARIY<br/> <b>DSIYVR</b>HWDY WLSTTFNAVF SGTLLKKGHGK<br/> <b>201</b> NGYSLDGELK NLVSPVKNAE<br/> SPYPPFGGAS DYDLSPDGKW VAFKSKAPEL<br/> <b>251</b> PKANFTTSYI YLVPHDASET<br/> ARPIGPDSP GTPKGIK <b>GDS SSPVFSPNGD</b><br/> <b>301</b> <b>K</b>LAYFQMRDE <b>TYESDRRVLY</b><br/> <b>VYSLGSK</b>KTI PSVAGDWDRS PDSVKWTPDG<br/> <b>351</b> <b>KT</b>LIVGSEDL <b>GR</b>TRLFSLPA<br/> <b>NAK</b>DDYKPKN FTDGGSASAY YFLPDSSLLV<br/> <b>401</b> TGSALWTNWN VYTAKPEKGV<br/> IKK<b>IASANEI DPEL</b>KGLGPS DISEFYQGN<br/> <b>451</b> FTDIHAWVIY PENFDKSKKY<br/> PLIFFIHGGP QGNWADGWST RWNPKAWADQ<br/> <b>501</b> GYVVVAPNPT GSTGFGQALT<br/> DAIQNNWGGGA PYDDL VKCWE YVHENLDYVD<br/> <b>551</b> TDHGVAAGAS YGGFMINWIQ<br/> GSPLGRKFK <b>A LVSHDGT</b>FVA <b>DAK</b>VSTEELW<br/> <b>601</b> FMQREFNGTF WDARDNYRRW<br/> DPSAPERILQ FATPMLVIHS DKDYRLPVAE<br/> <b>651</b> GLSLFNVLQE RGVPSRFLNF<br/> PDENHWV VNP ENSLVWHQQA LGWINKYSGV<br/> <b>701</b> EKSNPNAVSL EDTVVPV VNY N</p> <p><b>30 - 40 578.8086 1155.6026 1155.5884</b><br/> <b>0.0143 1 R.RSEAIPDP</b>SGK.V<br/> <b>31 - 40 500.7545 999.4944 999.4873</b><br/> <b>0.0072 0 R.SEAIPDP</b>SGK.V<br/> <b>120 - 131 574.8253 1147.6360 1147.6237</b><br/> <b>0.0123 0 K.AASLPASFSGL</b>K.T<br/> <b>169 - 176 514.7824 1027.5502 1027.5338</b><br/> <b>0.0164 0 R.IYDSIYVR</b>.H<br/> <b>288 - 301 697.3243 1392.6340 1392.6158</b><br/> <b>0.0183 0 K.GDSSSPVFSPNGD</b>K.L<br/> <b>309 - 317 585.7585 1169.5024 1169.4949</b><br/> <b>0.0076 1 R.DETYESDRR</b>.V<br/> <b>318 - 327 564.8238 1127.6330 1127.6227</b><br/> <b>0.0104 0 R.VLYVYSLGSK</b>.K<br/> <b>352 - 362 580.3250 1158.6354 1158.6245</b><br/> <b>0.0110 0 K.TLIVGSEDLGR</b>.T<br/> <b>365 - 373 480.7827 959.5508 959.5440</b><br/> <b>0.0069 0 R.LFSLPANAK</b>.D<br/> <b>424 - 435 650.3501 1298.6856 1298.6718</b><br/> <b>0.0139 0 K.IASANEIDPEL</b>K.G</p> |

|    |          |       |     |    |      |                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|----|----------|-------|-----|----|------|----------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |          |       |     |    |      |                                        | 580 - 593 477.5842 1429.7308 1429.7202<br>0.0106 0 K.ALVSHDGTFFVADAK.V                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 8b | O13479   | 79696 | 194 | 16 | 5.59 | Dipeptidyl-peptidase-V precursor, DppV | <p>Sequence Coverage: 19%</p> <p>1 MGAFRWLSIA AAATALALT<br/>PEQLITAPRR <b>SEAIPDPSGK</b> VAVFSTSQYS<br/>51 FETHKRTSWW SLLDLKTGQT<br/>KVLTDNDSSVS EIVWLSDDSI LYVNSTNADI<br/>101 PGGVELWVTQ ASSFAKGYKA<br/><b>ASLPASFSGL</b> KTAKTKSGDI RFVAYGQSYP<br/>151 NGTAYNEELA TAPLSSARIY<br/><b>DSIYVR</b>HW DY WLSTTFNAVF SGTLLKKGHGK<br/>201 <b>NGYSLDGELK</b> NLVSPVKNAE<br/>SPYPPFGGAS DYDLSPDGKW VAFKSKAPEL<br/>251 PKANFTTSYI YLVPHDASET<br/>ARPIGPDSP GTPKGIK <b>GDS SSPVFSPNGD</b><br/>301 <b>KLAYFQMRDE</b> <b>TYESDRRVLY</b><br/><b>VYSLGSK</b>TI <b>PSVAGDWDRS</b> PDSVKWTPDG<br/>351 <b>KTIVGSEDL</b> <b>GRTRLFSLPA</b><br/><b>NAK</b>DDYKPKN FTDGGSASAY YFLPDSSLLV<br/>401 TGSALWTNWN VYTAKPEKGV<br/>IKKI<b>ASANEI</b> <b>DPELK</b>GLGPS DISEFYFQGN<br/>451 FTDIHAWVIY PENFDKSKKY<br/>PLIFFIHGGP QGNWADGWST RWNPKAWADQ<br/>501 GYVVVAPNPT GSTGFGQALT<br/>DAIQNNWGA PYDDLKVCWE YVHENLDYVD<br/>551 TDHGVAAGAS YGGFMINWIK<br/>GSPLGRKFK<b>A</b> <b>LVSHDGTFFVA</b> <b>DAK</b>VSTEELW<br/>601 FMQREFNGTF WDARDNYRRW<br/><b>DPSAPER</b>ILQ FATPMLVIHS DKDYRLPVAE<br/>651 GLSLFNVLQE RGVPSRFLNF<br/>PDENHWVVNP ENSLVWHQQA LGWINKYSGV<br/>701 EKSNPNAVSL EDTVVPVYNY N</p> <p>30 - 40 578.8094 1155.6042 1155.5884<br/>0.0159 1 R.RSEAIPDPSGK.V<br/>31 - 40 500.7616 999.5086 999.4873<br/>0.0214 0 R.RSEAIPDPSGK.V<br/>120 - 131 574.8310 1147.6474 1147.6237<br/>0.0237 0 K.AASLPASFSGLK.T<br/>169 - 176 514.7838 1027.5530 1027.5338<br/>0.0192 0 R.IYDSIYVR.H<br/>201 - 210 548.2815 1094.5484 1094.5244<br/>0.0241 0 K.NGYSLDGELK.N<br/>288 - 301 697.3328 1392.6510 1392.6158<br/>0.0353 0 K.GDSSSPVFSPNGDK.L<br/>309 - 317 585.7639 1169.5132 1169.4949<br/>0.0184 1 R.DETYESDRR.V<br/>318 - 327 564.8301 1127.6456 1127.6227<br/>0.0230 0 R.VLYVYSLGSK.K<br/>318 - 327 564.8467 1127.6788 1127.6227<br/>0.0562 0 R.VLYVYSLGSK.K<br/>329 - 339 608.8175 1215.6204 1215.5884<br/>0.0320 0 K.TIPSVAGDWDR.S<br/>352 - 362 580.3299 1158.6452 1158.6245<br/>0.0208 0 K.TLIVGSEDLGR.T<br/>365 - 373 480.7879 959.5612 959.5440<br/>0.0173 0 R.LFSLPANAK.D<br/>424 - 435 650.3600 1298.7054 1298.6718<br/>0.0337 0 K.IASANEIDPELK.G<br/>580 - 593 477.5895 1429.7467 1429.7202<br/>0.0265 0 K.ALVSHDGTFFVADAK.V<br/>580 - 593 715.8877 1429.7608 1429.7202<br/>0.0407 0 K.ALVSHDGTFFVADAK.V<br/>620 - 627 479.2334 956.4522 956.4352<br/>0.0171 0 R.WDPSAPER.I</p> |
| 9a | AAD26111 | 21522 | 184 | 4  | 5.76 | Chitosanase                            | Sequence Coverage: 29%                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

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|-----|----------|-------|-----|----|------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |          |       |     |    |      | <p>1 KCSKVLAKGF TNGDASQGKS<br/> <b>FSYCGDIPGA IFISSSKGYT NMDIDCDGAN</b><br/> 51 <b>NSAGKCANDP SGQGETAFKS</b><br/> DVKKFGISDL DANIHPYVVF GNEDHSPKFK<br/> 101 PQSHGMQPLS VMAVVCNGQL<br/> HYGIWGD TNG GVSTGEASIS LADLCFPNEH<br/> 151 LDGNHGHDPN DVLFIGFTSK<br/> DAVPGATAKW KAK<b>NAKEFED SIK</b>SIGDKLV<br/> 201 AGLKA</p> <p>20 - 37 968.4805 1934.9464 1934.9084<br/> 0.0380 0 K.SFSYCGDIPGAIFISSSK.G<br/> Carbamidomethyl (C)<br/> 38 - 55 959.8876 1917.7606 1917.7469<br/> 0.0137 0 K.GYTNDIDCDGANNSAGK.C<br/> Carbamidomethyl (C); Oxidation (M)<br/> 56 - 69 741.3326 1480.6506 1480.6253<br/> 0.0254 0 K.CANDPSGQGETAFK.S<br/> Carbamidomethyl (C)<br/> 184 - 193 590.8002 1179.5858 1179.5771<br/> 0.0087 1 K.NAKEFEDSIK.S</p>                                                                                                                                                                          |
| 9b  | AAD26111 | 21522 | 122 | 4  | 5.76 | Chitosanase <p>Sequence Coverage: <b>29%</b></p> <p>1 KCSKVLAKGF TNGDASQGKS<br/> <b>FSYCGDIPGA IFISSSKGYT NMDIDCDGAN</b><br/> 51 <b>NSAGKCANDP SGQGETAFKS</b><br/> DVKKFGISDL DANIHPYVVF GNEDHSPKFK<br/> 101 PQSHGMQPLS VMAVVCNGQL<br/> HYGIWGD TNG GVSTGEASIS LADLCFPNEH<br/> 151 LDGNHGHDPN DVLFIGFTSK<br/> DAVPGATAKW KAK<b>NAKEFED SIK</b>SIGDKLV<br/> 201 AGLKA</p> <p>20 - 37 968.4849 1934.9552 1934.9084<br/> 0.0468 0 K.SFSYCGDIPGAIFISSSK.G<br/> Carbamidomethyl (C)<br/> 38 - 55 959.9023 1917.7900 1917.7469<br/> 0.0431 0 K.GYTNDIDCDGANNSAGK.C<br/> Carbamidomethyl (C); Oxidation (M)<br/> 56 - 69 741.3394 1480.6642 1480.6253<br/> 0.0390 0 K.CANDPSGQGETAFK.S<br/> Carbamidomethyl (C)<br/> 184 - 193 590.8033 1179.5920 1179.5771<br/> 0.0149 1 K.NAKEFEDSIK.S</p>                                                                                                                         |
| 10a | Q4WSV9   | 33063 | 343 | 15 | 5.02 | 1,3-beta-glucanosyltransferase Bgt1 <p>Sequence Coverage: <b>29%</b></p> <p>1 MRVSTLLPLA LAAGTAAASK NGTLGFALGN<br/> KNEGKCK<b>VQ SDYETDFDTL</b><br/> 51 <b>KEVTSLVRIY SASDCDTAKH</b><br/> IIPAAKAKNF K<b>VVLGVWPDY DKSFTDDFNA</b><br/> 101 <b>LKEAVPGNEE</b> VIDAITVGSE<br/> VLYR<b>KSLTPQ ALLARIQQVQ KEFPKITVGM</b><br/> 151 <b>VDSWNK</b>FADG TADPIQGGV<br/> TYFLANGFAY WQGQELSNAT NTYFDDMAQA<br/> 201 LGHIEQVAGS NADKIRFGNG<br/> ETGWPTTGGT NYGPAVASTA NAADYYKSAV<br/> 251 CGMLAWGVDV FYFEAFDESW<br/> KPKTKGDNGE MQDETHWGAF TADRKAK<b>FDL</b><br/> 301 <b>TCPKH</b><br/> Start - End Observed Mr(expt) Mr(calc)<br/> Delta Miss Sequence<br/> 39 - 51 780.8468 1559.6790 1559.6991<br/> -0.0201 0 K.VQSDYETDFDTLK.E<br/> 39 - 58 782.3757 2344.1053 2344.1434<br/> -0.0382 1 K.VQSDYETDFDTLKEVTSLVRI<br/> 59 - 69 615.7523 1229.4900 1229.5234<br/> -0.0334 0 R.IYSASDCDTAK.H<br/> Carbamidomethyl (C)</p> |

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|     |           |       |     |   |      | <p>82 - 92 645.8239 1289.6332 1289.6656<br/> -0.0324 0 K.VVLGVWPDYDK.S<br/> 82 - 92 645.8319 1289.6492 1289.6656<br/> -0.0164 0 K.VVLGVWPDYDK.S<br/> 82 - 92 645.8323 1289.6500 1289.6656<br/> -0.0156 0 K.VVLGVWPDYDK.S<br/> 93 - 102 579.2645 1156.5144 1156.5401<br/> -0.0256 0 K.SFTDDFNALK.E<br/> 125 - 135 599.3566 1196.6986 1196.7241<br/> -0.0254 1 R.KSLTPQALLAR.I<br/> 125 - 135 599.3740 1196.7334 1196.7241<br/> 0.0094 1 R.KSLTPQALLAR.I<br/> 126 - 135 535.3019 1068.5892 1068.6291<br/> -0.0399 0 K.SLTPQALLAR.I<br/> 126 - 135 535.3159 1068.6172 1068.6291<br/> -0.0119 0 K.SLTPQALLAR.I<br/> 136 - 145 415.5504 1243.6294 1243.6925<br/> -0.0631 1 R.IQQVQKEFPK.I<br/> 146 - 156 633.2993 1264.5840 1264.6122<br/> -0.0281 0 K.ITVGMVDSWNK.F Oxidation (M)<br/> 298 - 304 440.7141 879.4136 879.4160<br/> -0.0024 0 K.FDLTCPK.H Carbamidomethyl (C)<br/> 298 - 305 509.2375 1016.4604 1016.4750<br/> -0.0145 1 K.FDLTCPKH.- Carbamidomethyl (C)</p>                                                                                                                                                                  |
| 10b | XP_752511 | 33063 | 157 | 6 | 5.02 | <p>1,3-beta-glucanosyltransferase Bgt1</p> <p>Sequence Coverage: <b>27%</b></p> <p>1 MRVSTLLPLA LAAGTAAASK<br/> NGTLGFALGN KNEGGKCK<b>VQ SDYETDFDTL</b><br/> 51 <b>KEVTSLVRIY SASDCDTAKH</b><br/> IIPAAKAKNF K<b>VVLGVWPDY DKSFTDDFN</b>A<br/> 101 <b>LKEAVPGNEE VIDAIVGSE</b><br/> <b>VLYRKSLTPQ ALLAR</b>IQQVQ KEFPKITVGM<br/> 151 VDSWNKFADG TADPIIQGGV<br/> TYFLANGFAY WQGQELSNAT NTYFDDMAQA<br/> 201 LGHIEQVAGS NADKIRFGNG<br/> ETGWPTTGGT NYGPAVASTA NAADYYKSAV<br/> 251 CGMLAWGVDV FYFEAFDESW<br/> KPKTKGDNGE MQDETHWGAF TADRKAKFDL<br/> 301 TCPKH</p> <p>39 - 51 780.8803 1559.7460 1559.6991<br/> 0.0469 0 K.VQSDYETDFDTLK.E<br/> 39 - 58 782.4119 2344.2139 2344.1434<br/> 0.0704 1 K.VQSDYETDFDTLKEVTSLVR.I<br/> 59 - 69 615.7861 1229.5576 1229.5234<br/> 0.0342 0 R.IYSASDCDTAK.H<br/> Carbamidomethyl (C)<br/> 82 - 92 645.8563 1289.6980 1289.6656<br/> 0.0324 0 K.VVLGVWPDYDK. 93 - 102<br/> 579.2878 1156.5610 1156.5401 0.0210 0<br/> K.SFTDDFNALK.E 103 - 124 1180.6356<br/> 2359.2566 2359.1907 0.0659 0<br/> K.EAVPGNEEVIDAIVGSEVLYR.K<br/> 126 - 135 535.3295 1068.6444 1068.6291<br/> 0.0153 0 K.SLTPQALLAR.</p> |
| 11  | Q4WXR8    | 14194 | 117 | 4 | 4.63 | <p>Nuclear transport factor 2, NTF-2</p> <p>Sequence Coverage: <b>23%</b></p> <p>1 MADFQNIQQ FVQFYYQTFD<br/> TNR<b>QALASLY</b> RDHSMILTFET SSVQGVSGIV<br/> 51 EK<b>LTSLPFQK</b> VQHQIATFDA<br/> QPSNTEGGIM VMVTGGLLVD EEQKPMSYSQ<br/> 101 TFQLLR<b>EGES YYVFNDMFRL</b> IYPA<br/> Start - End Observed Mr(expt) Mr(calc)<br/> Delta Miss Sequence<br/> 24 - 31 461.2686 920.5226 920.5079</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |

|     |           |       |     |    |      |                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|-----|-----------|-------|-----|----|------|------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |           |       |     |    |      |                              | <b>0.0147</b> 0 <b>R.QALASLYR.D</b><br>53 - 60 467.2826 932.5506 932.5331<br><b>0.0175</b> 0 <b>K.LTSLPFQK.V</b><br>107 - 119 836.8615 1671.7084 1671.6875<br><b>0.0209</b> 0 <b>R.EGESYYVFNDMFR.L</b> Oxidation (M)<br>107 - 119 836.8632 1671.7118 1671.6875<br><b>0.0243</b> 0 <b>R.EGESYYVFNDMFR.L</b> Oxidation (M)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| 12a | Q4WW81    | 34639 | 117 | 5  | 7.79 | Fucose-specific lectin, FleA | Sequence Coverage: <b>14%</b><br><br>1 MSTPGAQQVL FRTGIAAVNL<br>TNHLRVYFQD VYGSIRESLY EGSWANGTEK<br><b>51</b> NVIGNAK <b>LGS</b> <b>PVAATSK</b> ELK<br>HIRVYTLTEG NTLQEFAYDS GTGWYNGGLG<br><b>101</b> GAK <b>FQVAPYS</b> <b>RIAAVFLAGT</b><br><b>DALQLRI</b> YAK KPDNTIQEYM WNGDGWKEGT<br><b>151</b> NLGGALPGTG IGATSFRTD<br><b>YNGPSIR</b> IWF QTDDLKLVR AYDPHKGWYP<br><b>201</b> DLVTIFDRAP PRTAIAATSF<br>GAGNSSIYMR IYFVNSDNTI WQVCWDHGKG<br><b>251</b> YHDKGTITPV IQGSEVAIS<br>WGSFANNGPD LRLYFQNGTY ISAVSEWVWN<br><b>301</b> RAHGSQGLRS ALPPA<br>Start - End Observed Mr(expt) Mr(calc)<br>Delta Miss Sequence<br>58 - 67 465.7780 929.5414 929.5182<br><b>0.0233</b> 0 <b>K.LGSPVAATSK.E</b><br>104 - 111 484.2622 966.5098 966.4923<br><b>0.0175</b> 0 <b>K.FQVAPYSR.I</b><br>112 - 126 779.9742 1557.9338 1557.8879<br><b>0.0460</b> 0 <b>R.IAAVFLAGTDALQLR.I</b><br>168 - 177 593.2953 1184.5760 1184.5462<br><b>0.0299</b> 0 <b>R.YTDYNGPSIR.I</b><br>168 - 177 593.3042 1184.5938 1184.5462<br><b>0.0477</b> 0 <b>R.YTDYNGPSIR.I</b>                                    |
| 12b | Q4WW81    | 34639 | 156 | 5  | 7.79 | Fucose-specific lectin, FleA | Sequence Coverage: <b>20%</b><br><br>1 MSTPGAQQVL FRTGIAAVNL<br>TNHLRVYFQD VYGSIRESLY EGSWANGTEK<br><b>51</b> NVIGNAK <b>LGS</b> <b>PVAATSK</b> ELK<br>HIRVYTLTEG NTLQEFAYDS GTGWYNGGLG<br><b>101</b> GAK <b>FQVAPYS</b> <b>RIAAVFLAGT</b><br><b>DALQLRI</b> YAK KPDNTIQEYM WNGDGWKEGT<br><b>151</b> NLGGALPGTG IGATSFRTD<br><b>YNGPSIR</b> IWF QTDDLKLVR AYDPHKGWYP<br><b>201</b> DLVTIFDRAP PRTAIAATSF<br><b>GAGNSSIYMR</b> IYFVNSDNTI WQVCWDHGKG<br><b>251</b> YHDKGTITPV IQGSEVAIS<br>WGSFANNGPD LRLYFQNGTY ISAVSEWVWN<br><b>301</b> RAHGSQGLRS ALPPA<br>Start - End Observed Mr(expt) Mr(calc)<br>Delta Miss Sequence<br>58 - 67 465.7765 929.5384 929.5182<br><b>0.0203</b> 0 <b>K.LGSPVAATSK.E</b><br>104 - 111 484.2449 966.4752 966.4923<br><b>-0.0171</b> 0 <b>K.FQVAPYSR.I</b><br>112 - 126 779.9538 1557.8930 1557.8879<br><b>0.0052</b> 0 <b>R.IAAVFLAGTDALQLR.I</b><br>168 - 177 593.2745 1184.5344 1184.5462<br><b>-0.0117</b> 0 <b>R.YTDYNGPSIR.I</b><br>213 - 230 917.4475 1832.8804 1832.8727<br><b>0.0078</b> 0 <b>R.TAIAATSFAGAGNSSIYMR.I</b><br>Oxidation (M) |
| 13a | XP_750162 | 33739 | 408 | 16 | 5.53 | FG-GAP repeat protein        | Sequence Coverage: <b>28%</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

|     |           |       |     |   |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|-----|-----------|-------|-----|---|------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |           |       |     |   |      | <p> <b>1</b> MQTRPLSINA IWHLVPLLA<br/> TSATAAPYQT RILATGTTFN APDPYGPWSL<br/> <b>51</b> TPSANKPGPD LAYIK<b>TSNTG</b><br/> <b>TGKVEVHLAS</b> RASNYQTRTL EVGTTFFPED<br/> <b>101</b> NGVWQLIDAD GDGRDDLVI<br/> KTRNTGTGRV <b>EVHIATAASN FQTRI</b>KDVG<br/> <b>151</b> TFLPEDNGTW QMAFDGDGI<br/> LDLIYIKTRN TGTGR<b>VEVHV ASGASNYQTR</b><br/> <b>201</b> IQEVGTTFFYP EDNGVWQMID<br/> FNR<b>DGKLDLV YIK</b>TRNTGTG R<b>VEVHVASGA</b><br/> <b>251</b> <b>STYK</b>TRVQEV GTTFYPEDNG<br/> FWQLIDFNK<b>D GVLDLAYVK</b>T QNTGTGRIEV<br/> <b>301</b> <b>HVANGRN</b> </p> <p> 66 - 81 552.9844 1655.9314 1655.8591<br/> 0.0723 1 K.TSNTGTGKVEVHLASR.A<br/> 74 - 81 455.7697 909.5248 909.5032<br/> 0.0216 0 K.VEVHLASR.A<br/> 74 - 81 455.7852 909.5558 909.5032<br/> 0.0526 0 K.VEVHLASR.A<br/> 130 - 144 548.6440 1642.9102 1642.8427<br/> 0.0675 0 R.VEVHIATAASN<b>FQTR</b>.I<br/> 130 - 144 822.4778 1642.9410 1642.8427<br/> 0.0983 0 R.VEVHIATAASN<b>FQTR</b>.I<br/> 186 - 200 539.9586 1616.8540 1616.7907<br/> 0.0633 0 R.VEVHVASGASNYQTR.I<br/> 186 - 200 539.9623 1616.8651 1616.7907<br/> 0.0744 0 R.VEVHVASGASNYQTR.I<br/> 224 - 233 582.3722 1162.7298 1162.6598<br/> 0.0701 1 R.DGKLDLVYIK.T<br/> 227 - 233 432.2903 862.5660 862.5164<br/> 0.0497 0 K.LDLVYIK.T<br/> 242 - 254 449.9189 1346.7349 1346.6830<br/> 0.0518 0 R.VEVHVASGASTYK.T<br/> 242 - 254 449.9239 1346.7499 1346.6830<br/> 0.0668 0 R.VEVHVASGASTYK.T<br/> 242 - 254 674.3848 1346.7550 1346.6830<br/> 0.0720 0 R.VEVHVASGASTYK.T<br/> 280 - 289 546.8270 1091.6394 1091.5863<br/> 0.0532 0 K.DGVLDLAYVK.T<br/> 298 - 306 497.7976 993.5806 993.5356<br/> 0.0451 0 R.IEVHVANGR.N<br/> 298 - 306 497.8090 993.6034 993.5356<br/> 0.0679 0 R.IEVHVANGR.N<br/> 298 - 307 554.8250 1107.6354 1107.5785<br/> 0.0570 1 R.IEVHVANGRN. </p> |
| 13b | XP_750162 | 33739 | 240 | 4 | 5.53 | <p>FG-GAP repeat protein</p> <p>Sequence Coverage: <b>20%</b></p> <p> <b>1</b> MQTRPLSINA IWHLVPLLA<br/> TSATAAPYQT RILATGTTFN APDPYGPWSL<br/> <b>51</b> TPSANKPGPD LAYIK<b>TSNTG</b><br/> TGKVEVHLAS RASNYQTRTL EVGTTFFPED<br/> <b>101</b> NGVWQLIDAD GDGRDDLVI<br/> KTRNTGTGRV <b>EVHIATAASN FQTRI</b>KDVG<br/> <b>151</b> TFLPEDNGTW QMAFDGDGI<br/> LDLIYIKTRN TGTGR<b>VEVHV ASGASNYQTR</b><br/> <b>201</b> IQEVGTTFFYP EDNGVWQMID<br/> FNR<b>DGKLDLV YIK</b>TRNTGTG R<b>VEVHVASGA</b><br/> <b>251</b> <b>STYK</b>TRVQEV GTTFYPEDNG<br/> FWQLIDFNK<b>D GVLDLAYVK</b>T QNTGTGRIEV<br/> <b>301</b> HVANGRN </p> <p> 130 - 144 548.6489 1642.9249 1642.8427<br/> 0.0822 0 R.VEVHIATAASN<b>FQTR</b>.I<br/> 186 - 200 539.9636 1616.8690 1616.7907<br/> 0.0783 0 R.VEVHVASGASNYQTR.I<br/> 224 - 233 582.3683 1162.7220 1162.6598<br/> 0.0623 1 R.DGKLDLVYIK.T </p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

|     |        |       |     |   |      |                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|-----|--------|-------|-----|---|------|----------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |        |       |     |   |      |                                              | <p>242 - 254 449.9192 1346.7358 1346.6830<br/>0.0527 0 R.VEVHVASGASTYK.T</p> <p>242 - 254 449.9234 1346.7484 1346.6830<br/>0.0653 0 R.VEVHVASGASTYK.T</p> <p>242 - 254 674.3839 1346.7532 1346.6830<br/>0.0702 0 R.VEVHVASGASTYK.T</p> <p>280 - 289 546.8331 1091.6516 1091.5863<br/>0.0654 0 K.DGVLDLAYVK.T</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 14a | P41748 | 41588 | 200 | 5 | 4.85 | Asp f 10-<br>aspergillopepsin-<br>F          | <p>Sequence Coverage: <b>17%</b></p> <p>1 MVVFSKVTAV VVGLSTIVSA<br/>VPVVQPRKGF TINQVARPVT NKKTVNLPVAV</p> <p>51 YANALTKYGG TVPDSVKAAA<br/>SSGSAVTTPE QYDSEYLTPV KVG GTTLNLD</p> <p>101 FDTGSADLWV FSSELSASQS<br/>SGHAIYKPSA NAQKLNGYTW KIQYGDGSSA</p> <p>151 <b>SGDVYK</b>DTVT VGGVTAQSQA<br/>VEAASHISSQ FVQDKDNDGL LGLAFSSINT</p> <p>201 VSPRPQTTF DTVK<b>SQLDSP</b><br/><b>LFAVTLKYHA PGTYDFGYID NSK</b>FQGELTY</p> <p>251 TDVDSSQGFW MFTADGYGVG<br/>NGAPNSNSIS GIADTGTTLL LLDDSVVADY</p> <p>301 YRQVSGAKNS <b>NQYGGYVFPC</b><br/><b>STKLPSFTTV</b> IGGYNAVVPV EYINYAPVTD</p> <p>351 GSSTCYGGIQ SNSGLGFSIF<br/>GDIFLK<b>SQYV VFDSQGPR</b>LG FAPQA</p> <p>142 - 156 773.8713 1545.7280 1545.6947<br/>0.0333 0 K.IQYGDGSSASGDVYK.D</p> <p>215 - 227 709.9139 1417.8132 1417.7817<br/>0.0316 0 K.SQLDSP<b>LFAVTLK.Y</b></p> <p>228 - 243 616.6185 1846.8337 1846.8162<br/>0.0174 0 K.YHAPGTYDFGYIDNSK.F</p> <p>309 - 323 861.3995 1720.7844 1720.7515<br/>0.0329 0 K.NSNQYGGYVFPC<b>STK.L</b></p> <p>Carbamidomethyl (C)<br/>377 - 388 691.8487 1381.6828 1381.6626<br/>0.0202 0 K.SQYVVFDSQGPR.L</p> |
| 14b | P41748 | 41588 | 163 | 3 | 4.85 | Asp f 10-<br>aspergillopepsin-<br>F          | <p>Sequence Coverage: <b>10%</b></p> <p>1 MVVFSKVTAV VVGLSTIVSA<br/>VPVVQPRKGF TINQVARPVT NKKTVNLPVAV</p> <p>51 YANALTKYGG TVPDSVKAAA<br/>SSGSAVTTPE QYDSEYLTPV KVG GTTLNLD</p> <p>101 FDTGSADLWV FSSELSASQS<br/>SGHAIYKPSA NAQKLNGYTW KIQYGDGSSA</p> <p>151 <b>SGDVYK</b>DTVT VGGVTAQSQA<br/>VEAASHISSQ FVQDKDNDGL LGLAFSSINT</p> <p>201 VSPRPQTTF DTVK<b>SQLDSP</b><br/><b>LFAVTLKYHA PGTYDFGYID NSK</b>FQGELTY</p> <p>251 TDVDSSQGFW MFTADGYGVG<br/>NGAPNSNSIS GIADTGTTLL LLDDSVVADY</p> <p>301 YRQVSGAKNS <b>NQYGGYVFPC</b><br/><b>STKLPSFTTV</b> IGGYNAVVPV EYINYAPVTD</p> <p>351 GSSTCYGGIQ SNSGLGFSIF<br/>GDIFLK<b>SQYV VFDSQGPR</b>LG FAPQA</p> <p>215 - 227 709.9030 1417.7914 1417.7817<br/>0.0098 0 K.SQLDSP<b>LFAVTLK.Y</b></p> <p>228 - 243 616.6133 1846.8181 1846.8162<br/>0.0018 0 K.YHAPGTYDFGYIDNSK.F</p> <p>377 - 388 691.8413 1381.6680 1381.6626<br/>0.0054 0 K.SQYVVFDSQGPR.L</p>                                                                                                                                                                                              |
| 15a | B0XT72 | 48091 | 114 | 3 | 4.94 | 1,3-beta-<br>glucanosyltransf<br>erase, gel1 | <p>Sequence Coverage: <b>7%</b></p> <p>1 MKASAVTAAL AVGASTVLAA</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |

|     |        |       |     |   |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|-----|--------|-------|-----|---|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |        |       |     |   |      | <p>PSIKAR<b>DDVT</b> <b>PITVK</b>GNAFF KGDERFYIRG<br/> <b>51</b> VDYQPGGSSD LADPIADADG<br/> CKRDIK<b>FKE</b> LGLN<b>TIR</b>VYS VDNSKNHDEC<br/> <b>101</b> MNALADAGIY LVLDVNTPKY<br/> SINRAKPKES YNDVYLQYIF ATVDAFAGYK<br/> <b>151</b> NTLAFFSGNE VINDGPSSSA<br/> APYVKAVTRD LRQYIRSRKY <b>REIPVGYSAA</b><br/> <b>201</b> <b>DIDTNRLQMA</b> QYMNCGSDDDE<br/> RSDFFAFNDY SWCDPSSFKT SGWDQKVKNF<br/> <b>251</b> TGYGLPLFLS EYGCNTNKRO<br/> FQEVSSLYST DMTGVYSGGL VYEYSQEASN<br/> <b>301</b> YGLVEISGNN VK<b>ELPDFDAL</b><br/> <b>K</b>TAFEKTSNP SGDGNYNKTG GANPCPAKDA<br/> <b>351</b> PNWDVDNDAL PAIPEPAKKY<br/> MTEGAGK<b>GPG</b> FAGPGSQDRG TQSTATAEPG<br/> <b>401</b> SGSATGSSSS GTSTSSKGAA<br/> AGLTVPSLTM APVVVGAVTL LSTVFGAGLV<br/> <b>451</b> LL</p> <p><b>27 - 35 494.2572 986.4998 986.5284 -</b><br/> <b>0.0286 0 R.DDVTPIVK.G</b><br/> <b>192 - 206 810.8940 1619.7734 1619.7791</b><br/> <b>-0.0057 0 R.EIPVGYSAADIDTNR.L</b><br/> <b>313 - 321 524.2626 1046.5106 1046.5284</b><br/> <b>-0.0178 0 K.ELPDFDALK.T</b></p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 15b | B0XT72 | 48091 | 311 | 8 | 4.94 | <p>1,3-beta-glucanosyltransf<br/>erases, gel1</p> <p>Sequence Coverage: <b>15%</b></p> <p><b>1</b> MKASAVTAAL AVGASTVLAA<br/> PSIKAR<b>DDVT</b> <b>PITVK</b>GNAFF KGDERFYIRG<br/> <b>51</b> VDYQPGGSSD LADPIADADG<br/> CKRDIK<b>FKE</b> LGLN<b>TIR</b>VYS VDNSKNHDEC<br/> <b>101</b> MNALADAGIY LVLDVNTPKY<br/> SINRAKPKES YNDVYLQYIF ATVDAFAGYK<br/> <b>151</b> NTLAFFSGNE VINDGPSSSA<br/> APYVKAVTRD LRQYIRSRKY <b>REIPVGYSAA</b><br/> <b>201</b> <b>DIDTNRLQMA</b> <b>QYMNCGSDDDE</b><br/> <b>RSDFFAFNDY SWCDPSSFKT SGWDQKVKNF</b><br/> <b>251</b> TGYGLPLFLS EYGCNTNKRO<br/> FQEVSSLYST DMTGVYSGGL VYEYSQEASN<br/> <b>301</b> YGLVEISGNN VK<b>ELPDFDAL</b><br/> <b>K</b>TAFEKTSNP SGDGNYNKTG GANPCPAKDA<br/> <b>351</b> PNWDVDNDAL PAIPEPAKKY<br/> MTEGAGK<b>GPG</b> <b>FAGPGSQDRG</b><br/> TQSTATAEPG<br/> <b>401</b> SGSATGSSSS GTSTSSKGAA<br/> AGLTVPSLTM APVVVGAVTL LSTVFGAGLV<br/> <b>451</b> LL</p> <p><b>27 - 35 494.2610 986.5074 986.5284 -</b><br/> <b>0.0210 0 R.DDVTPIVK.G</b><br/> <b>78 - 87 595.8361 1189.6576 1189.6819</b><br/> <b>-0.0242 1 K.FKELGLNTIR.V</b><br/> <b>78 - 87 595.8450 1189.6754 1189.6819</b><br/> <b>-0.0064 1 K.FKELGLNTIR.V</b><br/> <b>80 - 87 458.2576 914.5006 914.5185 -</b><br/> <b>0.0179 0 K.ELGLNTIR.V</b><br/> <b>192 - 206 810.8860 1619.7574 1619.7791</b><br/> <b>-0.0217 0 R.EIPVGYSAADIDTNR.L</b><br/> <b>207 - 221 925.3530 1848.6914 1848.7077</b><br/> <b>-0.0162 0 R.LQMAQYMNCGSDDER.S</b><br/> Carbamidomethyl (C); 2 Oxidation (M)<br/> <b>313 - 321 524.2612 1046.5078 1046.5284</b><br/> <b>-0.0206 0 K.ELPDFDALK.T</b><br/> <b>378 - 389 573.2564 1144.4982 1144.5262</b><br/> <b>-0.0279 0 K.GPGFAGPGSQDR.G</b></p> |
| 16  | Q9P8U4 | 51685 | 179 | 5 | 4.62 | <p>1,3-beta-glucanosyltransf<br/>erases, gel2</p> <p>Sequence Coverage: <b>12%</b></p> <p><b>1</b> MLPTYVRLFT AVCALATTAS</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

|    |              |       |     |    |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|----|--------------|-------|-----|----|------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |              |       |     |    |      | <p>AVVPIEVK GK DFNSTK GDR <b>FQILGVDYQP</b><br/> <b>51</b> <b>GGSSGFTK</b>DK DPLSDPDACL<br/> RDAALMQRLG VNTIRIYNLS PSLNHDECAS<br/> <b>101</b> IFNAAGIYMI LDVNSPLYGG<br/> YLDR<b>TDPEST YNDVYFKQVF GVIEAFKNFP</b><br/> <b>151</b> NTLAFFAGNE VINEQSVK<b>NV</b><br/> <b>PTYVR</b>AIQRD MKDYIAKNLD RSIPVGYSAA<br/> <b>201</b> DIRPILMDTL NYFMCADDAN<br/> SQSDFGLNS YSWCGNSSYT KSGYDVLTKD<br/> <b>251</b> FADASIPVFF SEYGCNEVQP<br/> RYFSEVQALY QEEMTQSFSG GLVYEYEQEE<br/> <b>301</b> NDYGLVQIND NGTVTLVDY<br/> DNLMAQYSKL DMSRIQASNT TQTSAPPKC<br/> <b>351</b> ESSLITNSTF TDSFDLPKRP<br/> SKVQTMIDKG LSDANTGKLV EVKNTDIKQK<br/> <b>401</b> <b>IYNANGEEIT</b> <b>GIKLSILASG</b><br/> ESNTPGAHSS GSTSGSSSSG GSSSSSSDKE<br/> <b>451</b> SAAGTISVPF VGLLSAASFM AFFML</p> <p><b>41 - 58</b> <b>950.9658 1899.9170 1899.9367</b><br/> <b>-0.0197 0 R.FQILGVDYQPGSSGFTK.D</b><br/> <b>125 - 137</b> <b>789.8466 1577.6786 1577.6886</b><br/> <b>-0.0099 0 R.TDPESTYNDVYFK.Q</b><br/> <b>138 - 147</b> <b>569.3162 1136.6178 1136.6230</b><br/> <b>-0.0052 0 K.QVFGVIEAFK.N</b><br/> <b>169 - 175</b> <b>424.7297 847.4448 847.4552</b><br/> <b>-0.0104 0 K.NVPTYVR.A</b><br/> <b>401 - 413</b> <b>711.3635 1420.7124 1420.7198</b><br/> <b>-0.0073 0 K.IYNANGEEITGIK.L</b></p>                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 17 | XP_001481609 | 46464 | 525 | 15 | 5.21 | <p>class V chitinase</p> <p>Sequence Coverage: <b>27%</b></p> <p><b>1</b> MLKSLVFSLM AVQAAMGSRF<br/> AMYIDQYHTV DLPGSDQTQG VTHAIMAFAP<br/> <b>51</b> SK<b>QFNSDSSF</b> <b>TPFDTVNNMR</b><br/> KRFAPDTK<b>VM IAIGGWGDTA GFSEGAKEA</b><br/> <b>101</b> <b>SRT</b>KYAKNVA TMINNLGFDG<br/> VDIDWEYPPG NGDDYKKVPN SQK<b>TSEIETY</b><br/> <b>151</b> <b>PLFVQAIRDA</b> IGKDKILSVA<br/> <b>VPGKRGMIA FTK</b>EQGPKIW SAVDMVNVMS<br/> <b>201</b> YDLMNRRDNV TNHHSVAGS<br/> LDTIKAYKE<b>I GLDTAKMNLG FAYYAKW</b>FM<br/> <b>251</b> DPNSDCAQQP IGCVVPLEN<br/> PDGSDPGK<b>SG TLTFEK</b>STMA APPDNLRTST<br/> <b>301</b> DGTCGYSGKT KCPSGSCCSQ<br/> YGNCGTGDDF CQAGCLSDYG ECK<b>GISVTDS</b><br/> <b>351</b> <b>WRR</b>ALKDGKT DEEAGGQYYW<br/> DSTVNLFWTW DTPAIIDRK<b>F KDIVNAEKL</b>G<br/> <b>401</b> GIMAWSLGED TLNWEHLKAM QKGLGK</p> <p><b>53 - 70</b> <b>1061.9353 2121.8560 2121.9062</b><br/> <b>-0.0502 0 K.QFNSDSSFTPFDTVNNMR.K</b><br/> Oxidation (M)<br/> <b>53 - 70</b> <b>1061.9429 2121.8712 2121.9062</b><br/> <b>-0.0350 0 K.QFNSDSSFTPFDTVNNMR.K</b><br/> Oxidation (M)<br/> <b>79 - 97</b> <b>941.9405 1881.8664 1881.8931</b><br/> <b>-0.0267 0 K.VMIAIGGWGDTAGFSEGAKEA.D</b><br/> Oxidation (M)<br/> <b>79 - 102</b> <b>814.3697 2440.0873 2440.1329</b><br/> <b>-0.0456 1</b><br/> <b>K.VMIAIGGWGDTAGFSEGAKEASR.T</b><br/> Oxidation (M)<br/> <b>144 - 158</b> <b>883.9601 1765.9056 1765.9250</b><br/> <b>-0.0194 0 K.TSEIETYPLFVQAIR.D</b><br/> <b>166 - 174</b> <b>442.2652 882.5158 882.5538</b><br/> <b>-0.0380 0 K.ILSVAVPGK.R</b><br/> <b>175 - 183</b> <b>527.7552 1053.4958 1053.5277</b><br/> <b>-0.0319 1 K.RGDMIAFTK.E</b> Oxidation (M)<br/> <b>176 - 183</b> <b>449.7061 897.3976 897.4266</b></p> |

|     |        |       |     |    |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|-----|--------|-------|-----|----|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |        |       |     |    |      | <p>-0.0290 0 R.GDMIAFTK.E Oxidation (M)<br/>229 - 236 423.7140 845.4134 845.4494</p> <p>-0.0360 0 K.EIGLDTAK.M<br/>237 - 246 589.2762 1176.5378 1176.5637</p> <p>-0.0259 0 K.MNLGFAYYAK.W<br/>237 - 246 597.2717 1192.5288 1192.5587</p> <p>-0.0298 0 K.MNLGFAYYAK.W Oxidation (M)<br/>237 - 246 597.2727 1192.5308 1192.5587</p> <p>-0.0278 0 K.MNLGFAYYAK.W Oxidation (M)<br/>279 - 286 441.7117 881.4088 881.4494</p> <p>-0.0406 0 K.SGTLTFEK.S<br/>344 - 352 510.7444 1019.4742 1019.5036</p> <p>-0.0294 0 K.GISVTDWR.R<br/>390 - 398 532.2772 1062.5398 1062.5709</p> <p>-0.0311 1 K.FKDIVNAEK.L</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| 18a | Q92405 | 79861 | 640 | 26 | 5.50 | <p>Catalase-B, Cat-B</p> <p>Sequence Coverage: <b>22%</b></p> <p>1 MRLTFIPSLI GVANAVCPYM<br/>TGELNRRDEI SDGDAAAATE EFLSQYYLND<br/>51 NDAFMTSDVG GPIEDQNSLS<br/>AGERGPTLLE DFIFRQKIQR FDHERVPERA<br/>101 VHARGAGAHG VFTSYGDFSN<br/>ITAASFLAKE GK<b>QTPVFVR</b> <b>STVAGSR</b>GSS<br/>151 DLAR<b>DVHGFA</b> <b>TRFYTDEGNF</b><br/>DIVGNNIPVF FIQDAILFPD LIHAVKPRGD<br/>201 NEIPQAATAH DSAWDDFFSQQ<br/>PSTMHTLLWA MSGHGIPRSF RHVDGFGVHT<br/>251 FR<b>FVTDDGAS</b> <b>KLVKFHWKSL</b><br/>QKGASMVWEE AQQTSGKNPD FMRQDLHDAI<br/>301 EAGRYPEWEL GVQIMDEEDQ<br/>LR<b>FGFDLLDP TKIVPEEFVP</b> <b>ITKL</b>GKMQLN<br/>351 RNPRNYFAET EQVMFQPGHI<br/>VR<b>GVDFTEDP LLQGR</b><b>LFSYL DTQLNR</b>HGGP<br/>401 NFEQLPINQP <b>RVPVHNNNRD</b><br/>GAGQMFIPLN PHAYSPKTSV NGSPKQANQT<br/>451 VGDGFFTAPG RTTSGKLVRA<br/>VSSSFEDVWS QPR<b>LFYNSLV PAEKQFVIDA</b><br/>501 <b>IRFENANVKS</b> PVVK<b>NNVIIQ</b><br/><b>LNRI</b><b>DNDLAR</b> RVARAIGVAE PEPDPTFYHN<br/>551 NK<b>TADVGTFG</b> <b>TKLKKLDGLK</b><br/><b>VGV</b><b>LGSVQHP GSVEGASTLR</b> DRLKDDGVDV<br/>601 VLVAERLADG VDQTYSTSDA<br/>IQFDAVVVAA GAESLFAASS FTGGSANSAS<br/>651 GASSLYPTGR PLQILIDGFR<br/>FGK<b>TVGALGS GTAALR</b>NAGI ATSRDGVYVA<br/>701 QSVTDDFAND LKEGLRTFKF<br/>LDRFPVDH</p> <p>133 - 139 423.7503 845.4860 845.4760<br/>0.0101 0 K.QTPVFVR.F<br/>133 - 139 423.7525 845.4904 845.4760<br/>0.0145 0 K.QTPVFVR.F<br/>140 - 147 412.7185 823.4224 823.4188<br/>0.0036 0 R.FSTVAGSR.G<br/>155 - 162 451.7334 901.4522 901.4406<br/>0.0116 0 R.DVHGFATR.F<br/>155 - 162 451.7350 901.4554 901.4406<br/>0.0148 0 R.DVHGFATR.F<br/>253 - 261 470.2284 938.4422 938.4345<br/>0.0077 0 R.FVTDDGASK.L<br/>323 - 332 576.8137 1151.6128 1151.5863<br/>0.0266 0 R.FGFDLLDPTK.I<br/>323 - 332 576.8148 1151.6150 1151.5863<br/>0.0288 0 R.FGFDLLDPTK.I<br/>333 - 343 636.3770 1270.7394 1270.7173<br/>0.0222 0 K.IVPEEFVPITK.L<br/>333 - 343 636.3792 1270.7438 1270.7173</p> |

|     |          |       |    |   |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|-----|----------|-------|----|---|------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |          |       |    |   |      | <p>0.0266 0 K.IVPEEFVPITK.L<br/>373 - 385 723.8771 1445.7396 1445.7151<br/>0.0246 0 R.GVDFTEDPLLQGR.L<br/>373 - 385 723.8857 1445.7568 1445.7151<br/>0.0418 0 R.GVDFTEDPLLQGR.L<br/>386 - 396 685.3797 1368.7448 1368.7038<br/>0.0411 0 R.LFSYLDTQLNR.H<br/>412 - 419 475.2592 948.5038 948.4890<br/>0.0149 0 R.VPVHNNNR.D<br/>412 - 419 475.2594 948.5042 948.4890<br/>0.0153 0 R.VPVHNNNR.D<br/>484 - 494 640.8600 1279.7054 1279.6812<br/>0.0242 0 R.LFYNSLVP AEK.Q<br/>484 - 494 640.8623 1279.7100 1279.6812<br/>0.0288 0 R.LFYNSLVP AEK.Q<br/>495 - 502 481.2856 960.5566 960.5393<br/>0.0174 0 K.QFVIDAIR.F<br/>515 - 523 542.3269 1082.6392 1082.6196<br/>0.0196 0 K.NNVIIQLNR.I<br/>515 - 523 542.3337 1082.6528 1082.6196<br/>0.0332 0 K.NNVIIQLNR.I<br/>524 - 530 408.7149 815.4152 815.4137<br/>0.0015 0 R.IDNDLAR.R<br/>553 - 562 498.7574 995.5002 995.4924<br/>0.0078 0 K.TADVGTFGTK.L<br/>553 - 562 498.7629 995.5112 995.4924<br/>0.0188 0 K.TADVGTFGTK.L<br/>571 - 590 650.6984 1949.0734 1949.0331<br/>0.0403 0 K.VGVLGSVQHPSVEGASTLR.D<br/>674 - 686 587.3414 1172.6682 1172.6513<br/>0.0169 0 K.TVGALGSGTAALR.N<br/>674 - 686 587.3438 1172.6730 1172.6513<br/>0.0217 0 K.TVGALGSGTAALR.N</p> |
| 18b | AAB48485 | 79867 | 63 | 5 | 5.50 | <p>Catalase-B, Cat-B</p> <p>Sequence Coverage: 5%</p> <p>1 MRLTFIPSLI GVANAVCPYM<br/>TGELNRRDEI SDGDAAAATE EFLSQYYLND<br/>51 NDAFMTSDVG GPIEDQNSLS<br/>AGERGPTLLE DFIFRQKIQR FDHERVPERA<br/>101 VHARGAGAHG VFTSYGDFSN<br/>ITAASFLAKE GKQTPVFVRF STVAGSRGSS<br/>151 DLARDVHGFA TRFYTDEGNF<br/>DIVGNNIPVF FIQDAILFPD LIHAVKPRGD<br/>201 NEIPQAATAH DSAWDDFFSQQ<br/>PSTMHTLLWA MSGHGIPRSF RHVDGFGVHT<br/>251 FRFVTDDGAS KLVKFHWKSL<br/>QGKASMVWEE AQQTSGKNPDFMRQDLHDAI<br/>301 EAGRYPEWEL GVQIMDEEDQ<br/>LRFQFDLLDP TKIVPEEFVP ITKLGKMQLN<br/>351 RNPRNYFAET EQVMFQPGHI<br/>VRGVDFTEDP LLQGRFLSYL DTQLNRHGGP<br/>401 NFEQLPINQP RVPVHNNNRD<br/>GAGQMFIPLN PHAYSPKTSV NGSPKQANQT<br/>451 VGDGFFTAG RTTSGKLVRA<br/>VSSSFEDVWS QPRLFYNSLV PAEKQFVIDA<br/>501 IRFENANVKS PVVKNNVIIQ<br/>LNRIIDNDLAR RVARAIGVAE PEPDPTFYHN<br/>551 NKADVGTFG TKLKKLDGLK<br/>VGVLGSVQHP GSVEGASTLR DRLKDDGVDV<br/>601 VLVAERLADG VDQTYSTSDA<br/>IQFDAVVAA GAESLFAASS FTGGSANSAS<br/>651 GASSLYPTGR PLQILIDGFR<br/>FGKTVGALGS GTAALRNAGI ATSRDGVYVA<br/>701 QSVTDDFAND LKEGLRTFKF<br/>LDRFPVDH</p> <p>333 - 343 636.3799 1270.7452 1270.7173<br/>0.0280 0 K.IVPEEFVPITK.L<br/>484 - 494 640.8576 1279.7006 1279.6812</p>                     |

|    |           |       |     |   |      |                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|----|-----------|-------|-----|---|------|-----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |           |       |     |   |      |                             | <b>0.0194 0 R.LFYNSLVPAEK.Q</b><br><b>515 - 523 542.3253 1082.6360 1082.6196</b><br><b>0.0164 0 K.NNVIIQLNR.I</b><br><b>553 - 562 498.7596 995.5046 995.4924</b><br><b>0.0122 0 K.TADVGTGFTK.L</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 19 | XP_750863 | 35981 | 103 | 3 | 5.44 | Thioredoxin reductase, GliT | Sequence Coverage: <b>11%</b><br><br><b>1</b> MSIGKLLSNG ALLVDVLIIG AGPAGLSTAT<br>GLAR <b>QLHTAV VFDSGVYR</b> NA<br><b>51</b> KTQHMHNVLG WDHRNPAELR<br>AAGRDLTTR YSTIQFQNST IEAIR <b>QVETN</b><br><b>101</b> <b>QLFEAR</b> DNEG HSWYGRKVV<br>ATGVRDIPLD IEGYSECWAN GIYHCLFCDG<br><b>151</b> YEERGQETVG VLALGPIANP<br>ARALHLARMA LRLSESVTIY TNGNEQLAKE<br><b>201</b> IQQAAEESPV GASGLKFEAR<br>PIRRFEGKDV AK <b>TVIVHLGE SESK</b> TEGFLV<br><b>251</b> YNPQTEVNGP FAKQLALNMT<br>EGGDILTTPP FYETSVPGVF AVGDCATPLK<br><b>301</b> AVTPAVSMGS LAAGGLVAQL<br>QAQALPEFRL DQEL<br><br><b>35 - 48 531.2654 1590.7744 1590.8155</b><br><b>-0.0411 0 R.QLHTAVVFDSGVYR.N</b><br><b>96 - 106 667.8260 1333.6374 1333.6626</b><br><b>-0.0252 0 R.QVETNQLFEAR.D</b><br><b>233 - 244 433.5525 1297.6357 1297.6878</b><br><b>-0.0521 0 K.TVIVHLGESESK.T</b>                                                                                                                                                                                                                                                                                                                                      |
| 20 | Q6U819    | 67374 | 76  | 2 | 5.39 | Lysophospholipase-3, Plb3   | Sequence Coverage: <b>3%</b><br><br><b>1</b> MKALLSLLTA VAVATATPLD<br>LSLRALPNAP DGYTPAKVSC PATRPSIRGA<br><b>51</b> GSLSPNETSW LEIRRKNTVQ<br>PMTDLLGRLN LGFDAAGYID RVSSNASNLP<br><b>101</b> NIAIAVSGGG YRALTNAGAGA<br>IKAFDSRTQG STQSGHLGGL LQSATYVSGL<br><b>151</b> SGGGWLVGSV YLNNFTTIAD<br>LQSGDHGNVW QFSTSILEGP KAKHLQFLST<br><b>201</b> ADYWKDLLKA VDGKSDAGFN<br>TSLTDYWGR <b>A LSYQFINDR</b> T GNGGLSYTWS<br><b>251</b> SIALTDPFRR GEMPLPILVA<br>DGRNPGELLI GSNSTVYEFN PWEFGSFDPS<br><b>301</b> IFGFAPLEYL GSR <b>FDNGQLP</b><br><b>R</b> GEPCVRGFD NAGFVMGTSS SLFNQFILRL<br><b>351</b> NKTDLPDLAK DVFSKILTAI<br>GRDGDIAVY GPNPFYGYRN STAAYSRSRE<br><b>401</b> LDVVDGGEDG QNIPLHPLIQ<br>PVRHVDVIFA VDSSADGPYS WPNGSALVAT<br><b>451</b> YERSLNSSGI GNGTVFPAVP<br>DVNTFVNLGL NTRPTFFGCD PANLSAPAPL<br><b>501</b> VVYLPNAPYS THSNTSTFQL<br>AYSDSERDEI ITNGYNVVTR GNATVDKSWP<br><b>551</b> SCVGCAILQR SMYRTNTSMP<br>AVCNSCFKEY CWNGTVDSKT PRTYEPTLLL<br><b>601</b> GSTSTNAAYT QGVTWLVGIL<br>AVGVAMGMTA<br><br><b>230 - 239 613.8239 1225.6332 1225.6091</b><br><b>0.0241 0 R.ALSYQFINDR.T</b><br><b>314 - 321 473.7449 945.4752 945.4668</b><br><b>0.0084 0 R.FDNGQLPR.G</b> |
| 21 | Q6U820    | 68101 | 73  | 2 | 4.59 | Lysophospholipase-1, Plb1   | Sequence Coverage: <b>3%</b><br><br><b>1</b> MKTTTTVACAV AGLLFSCVSG<br>APDPVHVEIQ QRALPNAPDG YTPSTVGC<br><b>51</b> SRPTIRSAAS LSPNETSWLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |

|     |           |       |     |   |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
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|     |           |       |     |   |      | <p>TRRGKTTSAM KDFFNHVKIQ DFDAAGYIDR<br/> <b>101</b> HSSNSSDLPN IGIADVSGGGY<br/> RALMNGAGAI KAFDSRTPNS TSAGQLGGLL<br/> <b>151</b> QSATYLSGLS GGSWLVGSIY<br/> INNFTTISAL QTHQKGTWVQ FQNSIFEGPD<br/> <b>201</b> GGSIQILDSA TYYR<b>DISNAV</b><br/> <b>SGK</b>SDAGYPT SITDYWGRAL SYQMINATNG<br/> <b>251</b> GPSYTWSSIA LTDAFQKAEM<br/> PMPLVVADGR YPGELLISSN ATVVEFNPWE<br/> <b>301</b> FGTFDPTVFG FAPLEYLGTK<br/> FNGGSVPSNE SCVRGFDNVG FVMGTSSTLF<br/> <b>351</b> NQFLQINST ALPDWLKSVF<br/> TDILKDIGEN DEDIAQYAPN PFYHFSNTTN<br/> <b>401</b> PSAAELELDL VDGGEDLQNI<br/> PLHPLIQPER HVDVIFAVDS SADTTYSWPN<br/> <b>451</b> GTALVATYER SLNSSGIANG<br/> TSFPAIPDQN TFFVKNGLNTR PTFFGCNSSN<br/> <b>501</b> TTGPSPLIVY LPNYPYTAYS<br/> NFSTFQPDYT EQERDSTILN GYDVVTMGNS<br/> <b>551</b> TRDGNWSTCV GCALSRSL<br/> <b>R</b><b>TNTNVPEIC</b> KQCFQRYCWD GSLNSTTPAG<br/> <b>601</b> YEPVTILDSA ASGIIPSIST<br/> VAMAVVFAAW TIF</p> <p><b>215 - 223 445.7285 889.4424 889.4505</b><br/> <b>-0.0081 0 R.DISNAVSGK.S</b><br/> <b>572 - 581 588.2859 1174.5572 1174.5652</b><br/> <b>-0.0080 0 R.TNTNVPEICK.Q</b></p>                                                                                                                                                                                                                                                                                                                                                                                             |
| 22a | XP_752825 | 53807 | 349 | 6 | 5.09 | <p>Mannosidase<br/>MsdS</p> <p>Sequence Coverage: <b>12%</b></p> <p><b>1</b> MHLPSLSVAL ALVSSSLALP<br/> QAVLPENDVS SRAAAVKEAF SHAWDGYMKY<br/> <b>51</b> AFPHDELLPV SNSYGDSRNG<br/> WGASAVDALS TAIVMRNATI VSQILDHIAK<br/> <b>101</b> IDYSK<b>TSDMV</b> <b>SLFETTIRYL</b><br/> GGMLSGYDLL <b>KGPAADLVED</b> <b>RTKVDMLLQQ</b><br/> <b>151</b> SKNLGDVLKF AFDTPSGVPY<br/> NNINITSHGN DGATTNGLAV TGTLVLEWTR<br/> <b>201</b> <b>LSDLTGQEQY</b> <b>AKLSQRAESY</b><br/> LLAPQPSSGE PFPGLVGSAL SIQTGQFTNG<br/> <b>251</b> FVSWNGGSDS FYEYLMKMYV<br/> YDPKRFATYK DRWVAAAESS IDHLASNPAS<br/> <b>301</b> RPDLTFLATY NKGSLGLSSQ<br/> HLACFDGGSY LLGGTVLDRA <b>DLIDFGLKLV</b><br/> <b>351</b> DGCAETYHQT LTGIGPESFG<br/> WDEKSVPADQ KELYERAGFY VQSGAYILRP<br/> <b>401</b> EVIESFYAY RVTGKKQYRD<br/> WVWNAFENIN KYCRT<b>TESGFA</b> <b>GLTNVNAVNG</b><br/> <b>451</b> <b>GGR</b>YDNQESF LFAEVMKYAY<br/> LTHAPGMSSM PAAAEKANK SRG</p> <p><b>106 - 118 758.3962 1514.7778 1514.7287</b><br/> <b>0.0492 0 K.TSDMVSLFETTIR.Y</b> Oxidation<br/> (M)<br/> <b>132 - 141 521.7758 1041.5370 1041.5091</b><br/> <b>0.0280 0 K.GPAADLVEDR.T</b><br/> <b>132 - 141 521.7758 1041.5370 1041.5091</b><br/> <b>0.0280 0 K.GPAADLVEDR.T</b><br/> <b>201 - 212 670.3401 1338.6656 1338.6303</b><br/> <b>0.0353 0 R.LSDLTGQEQYAK.L</b><br/> <b>340 - 348 496.2909 990.5672 990.5386</b><br/> <b>0.0287 0 R.ADLIDFGLK.L</b><br/> <b>435 - 453 910.9742 1819.9338 1819.8813</b><br/> <b>0.0525 0 R.TESGFAGLTNVNAVNGGGR.Y</b></p> |
| 5   | XP_752825 | 53807 | 475 | 9 | 5.09 | <p>Mannosidase<br/>MsdS</p> <p>Sequence Coverage: <b>19%</b></p> <p><b>1</b> MHLPSLSVAL ALVSSSLALP QAVLPENDVS<br/> SRAAAVKEAF SHAWDGYMKY<br/> <b>51</b> AFPHDELLPV SNSYGDSRNG</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |

|    |          |       |     |   |      |                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|----|----------|-------|-----|---|------|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |          |       |     |   |      |                  | <div>WGASAVDALS TAIVMRNATI VSQILDHIAK</div> <div><div>101</div><div>IDYSK<b>TSDMV</b></div><div><b>SLFETTIRYL</b></div></div> <div>GGMLSGYDLL <b>KGPAADLVED</b> <b>RTKVDMLLQQ</b></div> <div><div>151</div><div><b>SK</b>NLGDVLKF</div><div>AFDTPSGVPY</div></div> <div>NNINITSHGN DGATTNGLAV TGTLVLEWTR</div> <div><div>201</div><div><b>LSDLTGQDEY</b></div><div><b>AKLSQRAESY</b></div></div> <div>LLAPQPSSGE PFPGLVGSAL SIQTGQFTNG</div> <div><div>251</div><div>FVSWNGGSDS</div><div>FYEYLMKMYV</div></div> <div>YDPKRFATYK DRWVAAAESS IDHLASNPAS</div> <div><div>301</div><div>RPDLTFLATY</div><div>NKGSLGLSSQ</div></div> <div>HLACFDGGSY LLGGTVLDRA <b>DLIDFGLKLV</b></div> <div><div>351</div><div>DGCAETYHQT</div><div>LTGIGPESFG</div></div> <div>WDEK<b>SVPADQ KELYER</b>AGFY VQSGAYILRP</div> <div><div>401</div><div>EVIESFYYAY</div><div>RVTGKKQYRD</div></div> <div>WVWNAFENIN KYCRT<b>ESGFA GLTNVNAVNG</b></div> <div><div>451</div><div><b>GGRYDNQESF</b></div><div><b>LFAEVMKYAY</b></div></div> <div>LTHAPGMSSM PAAAEDKANK SRG</div>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|    |          |       |     |   |      |                  | <div><div>106 - 118</div><div>758.3821</div><div>1514.7496</div><div>1514.7287</div></div> <div><div>0.0210</div><div>0</div><div>K.TSDMVSLFETTIR.Y</div><div>Oxidation</div></div> <div>(M)</div> <div><div>132 - 141</div><div>521.7680</div><div>1041.5214</div><div>1041.5091</div></div> <div><div>0.0124</div><div>0</div><div>K.GPAADLVEDR.T</div></div> <div><div>142 - 152</div><div>653.8657</div><div>1305.7168</div><div>1305.6962</div></div> <div><div>0.0206</div><div>1</div><div>R.TKVDMLLQQSK.N</div><div>Oxidation</div></div> <div>(M)</div> <div><div>201 - 212</div><div>670.3260</div><div>1338.6374</div><div>1338.6303</div></div> <div><div>0.0071</div><div>0</div><div>R.LSDLTGQDEYAK.L</div></div> <div><div>201 - 212</div><div>670.3290</div><div>1338.6434</div><div>1338.6303</div></div> <div><div>0.0131</div><div>0</div><div>R.LSDLTGQDEYAK.L</div></div> <div><div>340 - 348</div><div>496.2797</div><div>990.5448</div><div>990.5386</div></div> <div><div>0.0063</div><div>0</div><div>R.ADLIDFGLK.L</div></div> <div><div>375 - 386</div><div>478.9163</div><div>1433.7271</div><div>1433.7150</div></div> <div><div>0.0120</div><div>1</div><div>K.SVPADQKELYER.A</div></div> <div><div>435 - 453</div><div>910.9607</div><div>1819.9068</div><div>1819.8813</div></div> <div><div>0.0255</div><div>0</div><div>R.TESGFAGLTNVNAVNGGGR.Y</div></div> <div><div>454 - 467</div><div>868.9119</div><div>1735.8092</div><div>1735.7763</div></div> <div><div>0.0329</div><div>0</div><div>R.YDNQESFLFAEVMK.Y</div><div>Oxidation (M)</div></div>                                                                                                                                                                                                                                                                                                                 |
| 23 | AAP23218 | 47594 | 123 | 5 | 5.10 | Chitinase, Chi-B | <div>Sequence Coverage: <b>8%</b></div> <div><div>1</div><div>MRFATSTIVK VALLLSSLCV DAAVMWNRDT</div><div>SSTDLEARAS SGYRSVVYFV</div></div> <div><div>51</div><div>NWAIYGR<b>NHN</b></div><div><b>PQDLPVERLT</b></div></div> <div>HVLYAFANVR PETGEVHMTD SWADIEKHYP</div> <div><div>101</div><div>GDSWSDTGNN</div><div>VYGCIKQLYL</div></div> <div>LKKQNRNLKV LLSIGGWYYS PNFAPAASD</div> <div><div>151</div><div>AGRKNFAKTA</div><div>VKLLQDLGFD</div></div> <div>GLDIDWEYPE NDQQANDFVL LLREVRTALD</div> <div><div>201</div><div>SYSAANAGGQ</div><div>HFLTVASPA</div></div> <div>GPDKIKVLHL KDMDQQLDFW NLMAVDYAGS</div> <div><div>251</div><div>FSSLSGHQAN</div><div>VYNDTSNPLS</div></div> <div>TPFNTQTALD LYRAGGV PAN <b>KIVLGMPLYG</b></div> <div><div>301</div><div><b>RSFANTD</b>GPG</div><div>KPYNGVGQGS</div></div> <div>WENGWVDYKA LPQAGATEHV LPDIMASYSY</div> <div><div>351</div><div>DATNK<b>FLISY</b></div><div><b>DNPQVANLKS</b></div></div> <div>GYIKSLGLGG AMWWDSSSDK TGSDSLITTV</div> <div><div>401</div><div>VNALGGTGVF</div><div>EQSQNELDYP</div></div> <div>VSQYDNLNRNG MQT</div> <div><div>58 - 68</div><div>440.2397</div><div>1317.6973</div><div>1317.6425</div></div> <div><div>0.0547</div><div>0</div><div>R.NHNPPQDLPVER.L</div></div> <div><div>292 - 301</div><div>567.8453</div><div>1133.6760</div><div>1133.6267</div></div> <div><div>0.0494</div><div>0</div><div>K.IVLGMPLYGR.S</div><div>Oxidation (M))</div></div> <div><div>292 - 301</div><div>567.8479</div><div>1133.6812</div><div>1133.6267</div></div> <div><div>0.0546</div><div>0</div><div>K.IVLGMPLYGR.S</div><div>Oxidation (M))</div></div> <div><div>356 - 369</div><div>811.4740</div><div>1620.9334</div><div>1620.8511</div></div> <div><div>0.0823</div><div>0</div><div>K.FLISYDNPQVANLK.S</div></div> <div><div>356 - 369</div><div>811.4794</div><div>1620.9442</div><div>1620.8511</div></div> |

|    |          |       |     |    |      |                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|----|----------|-------|-----|----|------|---------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |          |       |     |    |      |                                                         | <b>0.0931 0 K.FLISYDNPQVANLK.S</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 24 | CAA12162 | 19413 | 156 | 2  | 4.43 | IgE binding protein/Asp f3/putative peroxiredoxin-pmp20 | Sequence Coverage: <b>12%</b><br><br>1 PTLVSREAPA VGVISDISAQ<br>TSALASAVSS YNGGDPSAVK SASEK <b>LVSTI</b><br>51 <b>NSGVDTVK</b> SG PALSTADALA<br>LTSPVQDLTK QVEGVDDLI SKKDKFVAAN<br>101 AGGTVYEDLK <b>AQYTAADSLA</b><br><b>K</b> AISAKVPES LSDIAAQLSA GITAAIQKGI<br>151 DAYKDAASST GTASSAPAT<br>ETATATETST ATGTVTETAT STPVIPT<br><br>46 - 58 666.9047 1331.7948 1331.7297<br><b>0.0652 0 K.LVSTINSGVDTVK.S</b><br>111 - 121 569.8227 1137.6308 1137.5666<br><b>0.0643 0 K.AQYTAADSLAK.A</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 25 | Q00050   | 15189 | 489 | 18 | 5.29 | Asp-hemolysin, Asp-HS                                   | Sequence Coverage: <b>67%</b><br><br>1 MASVQAYAQW VTVHLINSMS<br>SETLSIQNAS LSWGKWKY <b>DK D</b> KDAEIT <b>SED</b><br>51 <b>VQ</b> QKT <b>AP</b> PGG <b>SVNVNS</b> CGRS<br><b>DASSGTTGGF DLYDGNTK</b> IG RVHWDCPWGS<br>101 <b>KT</b> NDFDVGER NK <b>NYW</b> VEIGT<br><b>W</b> NKYGGAIGT VDVEVGRKR<br><br>39 - 54 593.2791 1776.8155 1776.8014<br><b>0.0141 1 K.DGDKDAEITSEDVQQK.T</b><br>43 - 54 681.8328 1361.6510 1361.6310<br><b>0.0200 0 K.DAEITSEDVQQK.T</b><br>55 - 69 736.8536 1471.6926 1471.6838<br><b>0.0089 0 K.TAPPGGSVNVNSCGR.S</b><br>Carbamidomethyl (C)<br>55 - 69 736.8586 1471.7026 1471.6838<br><b>0.0189 0 K.TAPPGGSVNVNSCGR.S</b><br>Carbamidomethyl (C)<br>70 - 88 946.9325 1891.8504 1891.8072<br><b>0.0432 0 R.SDASSGTTGGFDLYDGNTK.I</b><br>70 - 88 946.9469 1891.8792 1891.8072<br><b>0.0720 0 R.SDASSGTTGGFDLYDGNTK.I</b><br>92 - 101 424.5295 1270.5667 1270.5553<br><b>0.0113 0 R.VHWDCPWGSK.T</b><br>Carbamidomethyl (C)<br>92 - 101 636.2943 1270.5740 1270.5553<br><b>0.0187 0 R.VHWDCPWGSK.T</b><br>Carbamidomethyl (C)<br>102 - 110 526.7186 1051.4226 1051.4571<br><b>-0.0344 0 K.TNDFDVGER.N</b><br>102 - 110 526.7438 1051.4730 1051.4571<br><b>0.0160 0 K.TNDFDVGER.N</b><br>102 - 110 526.7441 1051.4736 1051.4571<br><b>0.0166 0 K.TNDFDVGER.N</b><br>102 - 110 526.7451 1051.4756 1051.4571<br><b>0.0186 0 K.TNDFDVGER.N</b><br>113 - 123 705.3583 1408.7020 1408.6775<br><b>0.0245 0 K.NYWVEIGTWNK.Y</b><br>124 - 137 696.8456 1391.6766 1391.7045<br><b>-0.0279 0 K.YGGAIGTVDVEVGR.K</b><br>124 - 137 696.8497 1391.6848 1391.7045<br><b>-0.0197 0 K.YGGAIGTVDVEVGR.K</b><br>124 - 137 696.8713 1391.7280 1391.7045<br><b>0.0235 0 K.YGGAIGTVDVEVGR.K</b><br>124 - 137 696.8713 1391.7280 1391.7045<br><b>0.0235 0 K.YGGAIGTVDVEVGR.K</b><br>124 - 137 696.8731 1391.7316 1391.7045<br><b>0.0271 0 K.YGGAIGTVDVEVGR.K</b> |

|    |           |       |     |   |      |                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|----|-----------|-------|-----|---|------|-----------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 26 | XP_748349 | 44624 | 146 | 3 | 4.90 | GPI-anchored cell wall beta-1,3-endoglucanase, EglC | <p>Sequence Coverage: <b>8%</b></p> <p> <b>1</b> MQFTHLVALA LALATSEAAH<br/> QGFNYGNTKS DGSAK<b>SQADFQAEFSTAKNL</b><br/> <b>51</b> <b>VGTSGFTSAR</b> LYTMIIQGGTA<br/> NTPISAIPAA ITEQTSLLL GWASGGNFAN<br/> <b>101</b> EIAALCAAIA QYGDDLAKLV<br/> VGISVGSEDL YRNSVDGVKA NAGIGTNPDE<br/> <b>151</b> IVSYINEVRS TIAGTKLSGA<br/> PIGHVDTWTA WVNGSNSAVI DACDWLGFDG<br/> <b>201</b> YPYFQNTMAN SISDAKALFD<br/> ESVAKTQAVA KGKEVWITET GWPVSGK<b>TEN</b><br/> <b>251</b> <b>LAVANLANAK</b> TYWDEVGCPL<br/> FGKTNTWWYI LQDADPVTN PSFGIVGSTL<br/> <b>301</b> STTPLFDLSC SASSSSSAAA<br/> AASSTAGPSA SSVIGGKASG FTAAANSAK<br/> <b>351</b> PTFTVGKPG GSYNGTGFWN<br/> STSSARPSS AISGSSSGSA AGSSGAGASG<br/> <b>401</b> ASGQSSSSTG SSSAPSTSN<br/> LSNAASGLSG SIFGAVVAVC LALAAL </p> <p> <b>36 - 48</b> <b>715.3380 1428.6614 1428.6521</b><br/> <b>0.0093 0 K.SQADFQAEFSTAK.N</b><br/> <b>49 - 60</b> <b>605.3139 1208.6132 1208.6150</b><br/> <b>-0.0017 0 K.NLVGTSGFTSAR.L</b><br/> <b>248 - 260</b> <b>664.8668 1327.7190 1327.7095</b><br/> <b>0.0095 0 K.TENLAVANLANAK.T</b> </p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 27 | XP_748380 | 67923 | 452 | 7 | 6.32 | Hypothetical protein AFUA_3G00600                   | <p>Sequence Coverage: <b>12%</b></p> <p> <b>1</b> MNIFFRIWFY RKCLIVPCM<br/> QVRCVEYHYA IAFLTIPC VK PSVGS DYDES<br/> <b>51</b> DCLTGRDRSL SCDYYVHIRA<br/> TLKECHHEFN VPLPFRFTFI SITLYSFSSH<br/> <b>101</b> RPKKMVAELV PYVDGMQR<b>GQ</b><br/> <b>GYDTYLQELR VANA VTITSK SPPSETYDLT</b><br/> <b>151</b> <b>YKSVQIEEYT ELAKS</b>LEITA<br/> GAAISGWGQS AQIDTSYLN R SKFESATTTY<br/> <b>201</b> QVEVSSQQQA TIDNTYSFNK<br/> <b>ISTTDPNASY GDRFVADFIK</b> GGKFLAR<b>VSI</b><br/> <b>251</b> <b>SSISKS</b>STEE VKEAAKVAFT<br/> MYGVTGEVTE EVKHAVSSIQ KNSRITIIH<br/> <b>301</b> ISGGGTKLGE TKRIDSGPDD<br/> EDSPLFKIKK EADNFYQELK DGKHKYRRFG<br/> <b>351</b> VLWKYTNVPD FNNAFDPFDY<br/> SAANKKVRPS LVMRSIMEFD ELCQSWNFFE<br/> <b>401</b> DFTQYGVYID NVKKMPVDKF<br/> LGGRQQQADL YDEGTRVNVA ISNKIAIDK<br/> <b>451</b> DPTDVKPLP YPKPYEFQRK<br/> VLRALKVTY IAQERSVDGG RLTDIALPTL<br/> <b>501</b> QGGAEKLFEF KAFDFDAVVG<br/> TSVVSFGKRD SSYICLNGQR ASDFGYKEES<br/> <b>551</b> VFWTFPPVD QVAEQKINVS<br/> KLKSADLIRL SRTETGPSFL FDVYTEKSS </p> <p> <b>119 - 130</b> <b>721.8594 1441.7042 1441.6837</b><br/> <b>0.0205 0 R.GQGYDTYLQELR.V</b><br/> <b>131 - 140</b> <b>502.2920 1002.5694 1002.5710</b><br/> <b>-0.0015 0 R.VANA VTITSK.S</b><br/> <b>141 - 152</b> <b>700.8380 1399.6614 1399.6507</b><br/> <b>0.0107 0 K.SPPSETYDLTYK.S</b><br/> <b>153 - 164</b> <b>705.3729 1408.7312 1408.7085</b><br/> <b>0.0227 0 K.SVQIEEYTELAK.S</b><br/> <b>221 - 233</b> <b>698.8264 1395.6382 1395.6266</b><br/> <b>0.0116 0 K.ISTTDPNASYGDR.F</b><br/> <b>234 - 240</b> <b>420.2397 838.4648 838.4589</b><br/> <b>0.0060 0 R.FVADFIK.G</b><br/> <b>248 - 255</b> <b>410.7463 819.4780 819.4702</b><br/> <b>0.0079 0 R.VSISISK.S</b> </p> |

|     |           |       |     |    |      |                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|-----|-----------|-------|-----|----|------|--------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 28  | EDP51083  | 30458 | 122 | 2  | 4.82 | Conserved hypothetical protein | Sequence Coverage: <b>8%</b><br><br>1 MSSLHLEKLD DDPWIIIEVKI FKILRDYLQD<br>PAASPAVAAQ ALDRLFPANR<br><b>51 SDEDQPTDEP REDPGSFLWH</b><br>FWGVVHNVAQ QIPYTAPEQD RLAEIKALK<br><b>101 GLSSQTKTVY LASWDHTFDL</b><br>WGDLPPLGPT FREMYDCMVS LNDKEEREHW<br><b>151 QSLNAYAARL TRDDSANLIL</b><br><b>FAKYSIEGMV</b> EEVLELRLVD DGPRSILESR<br><b>201 MVVAAEWVIQ CGERLVAKED</b><br>EGLSIESWQR CKERFSSLLD NASMSPQTRE<br><b>251 RVQKAKQVME ALRLR</b><br><br><b>51 - 61 644.7736 1287.5326 1287.5215</b><br><b>0.0111 0 R.SDEDQPTDEPR.E</b><br><b>163 - 173 603.8249 1205.6352 1205.6292</b><br><b>0.0061 0 R.DDSANLILFAK.Y</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 29a | XP_749213 | 33801 | 421 | 9  | 6.23 | pectate lyase A                | Sequence Coverage: <b>37%</b><br><br>1 MKFVATLIAC GLSGLALAAP<br>TATVNSLGKR AADDAAFGYA SLNGGTTGGA<br><b>51 GGTTTTVSSY AFTAAVSSD</b><br>AK <b>KVVVYSGP IKQSAKQVKV GSNTSIIGKD</b><br><b>101 STAVLEGFGL LVKEKSNVII</b><br>RNLGVKKVLA ENGDAIGIQY SNNVWVDHVD<br><b>151 VSSDRDHDKD YYDGLIDVTH</b><br>AADYVTISNS YIHDHWKASL VGHSDNNGDE<br><b>201 DKGHLRVTYA NNYWSNINSR</b><br>APSLR <b>FGTGH IYNSYFENVSDGINTRDGAQ</b><br><b>251 VLVESNQFVG SSKALYSTDD</b><br><b>GYAVERDNDG</b> GGAKNTALQG TLTTVPYSYS<br><b>301 LLGSSKVKSA VVGAGQTLK F</b><br><br><b>73 - 82 545.3346 1088.6546 1088.6594</b><br><b>-0.0047 1 K.KVVVYSGPIK.Q</b><br><b>90 - 99 488.2748 974.5350 974.5397 -</b><br><b>0.0046 0 K.VGSNTSIIGK.D</b><br><b>100 - 113 724.8958 1447.7770 1447.7923</b><br><b>-0.0152 0 K.DSTAVLEGFGLLVK.E</b><br><b>226 - 246 797.6946 2390.0620 2390.0927</b><br><b>-0.0308 0 R.FGTGHIYNSYFENVSDGINTR.D</b><br><b>247 - 263 882.9330 1763.8514 1763.8690</b><br><b>-0.0176 0 R.DGAQVLVESNQFVGSSK.A</b><br><b>264 - 276 730.3331 1458.6516 1458.6627</b><br><b>-0.0110 0 K.ALYSTDDGYAVER.D</b><br><b>285 - 306 1151.0945 2300.1744 2300.1900</b><br><b>-0.0155 0</b><br><b>K.NTALQGTLTTVPYSYSLLGSSK.V</b><br><b>309 - 320 565.3287 1128.6428 1128.6503</b><br><b>-0.0074 0 K.SAVVGAGQTLK.F</b><br><b>309 - 321 638.8667 1275.7188 1275.7187</b><br><b>0.0001 1 K.SAVVGAGQTLKF.-</b> |
| 29b | XP_749213 | 33801 | 465 | 11 | 6.23 | pectate lyase A                | Sequence Coverage: <b>37%</b><br><br>1 MKFVATLIAC GLSGLALAAP<br>TATVNSLGKR AADDAAFGYA SLNGGTTGGA<br><b>51 GGTTTTVSSY AFTAAVSSD</b><br>AK <b>KVVVYSGP IKQSAKQVKV GSNTSIIGKD</b><br><b>101 STAVLEGFGL LVKEKSNVII</b><br>RNLGVKKVLA ENGDAIGIQY SNNVWVDHVD<br><b>151 VSSDRDHDKD YYDGLIDVTH</b><br>AADYVTISNS YIHDHWKASL VGHSDNNGDE<br><b>201 DKGHLRVTYA NNYWSNINSR</b><br>APSLR <b>FGTGH IYNSYFENVSDGINTRDGAQ</b><br><b>251 VLVESNQFVG SSKALYSTDD</b><br><b>GYAVERDNDG</b> GGAKNTALQG TLTTVPYSYS<br><b>301 LLGSSKVKSA VVGAGQTLK F</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

|    |           |       |     |    |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|----|-----------|-------|-----|----|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |           |       |     |    |      | <p>73 - 82 545.3358 1088.6570 1088.6594<br/> -0.0023 1 K.KVVYVSGPIK.Q<br/> 74 - 82 481.2851 960.5556 960.5644 -<br/> 0.0088 0 K.VVYVSGPIK.Q<br/> 90 - 99 488.2709 974.5272 974.5397 -<br/> 0.0124 0 K.VGSNTSIIK.D<br/> 100 - 113 724.8900 1447.7654 1447.7923<br/> -0.0268 0 K.DSTAVLEGFGLLVK.E<br/> 100 - 113 724.9009 1447.7872 1447.7923<br/> -0.0050 0 K.DSTAVLEGFGLLVK.E<br/> 226 - 246 797.7007 2390.0803 2390.0927<br/> -0.0125 0 R.FGTGHIYNSYFENVSDGINTR.D<br/> 247 - 263 882.9348 1763.8550 1763.8690<br/> -0.0140 0 R.DGAQVLVESNQFVGSSK.A<br/> 264 - 276 730.3389 1458.6632 1458.6627<br/> 0.0006 0 K.ALYSTDDGYAVER.D<br/> 285 - 306 1151.0940 2300.1734 2300.1900<br/> -0.0165 0<br/> K.NTALQGTLTTPYSYSLGSSK.V<br/> 309 - 320 565.3293 1128.6440 1128.6503<br/> -0.0062 0 K.SAVVGVAGQTLK.F<br/> 309 - 321 638.8622 1275.7098 1275.7187<br/> -0.0089 1 K.SAVVGVAGQTLKF.-</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 30 | XP_747586 | 45718 | 213 | 10 | 8.42 | <p>NAD-dependent<br/>formate<br/>dehydrogenase,<br/>AciA/Fdh</p> <p>Sequence Coverage: 22%</p> <p>1 MVLIRLSLRH LRRPATSFSL<br/> TKGTLSPTSS SPFRAASLGG SISGARTLTA<br/> 51 SANLQGK<b>VLM</b> <b>VLYDGGEHAK</b><br/> <b>QQPGLLGTT</b> <b>NELGLRK</b>WIE EQGHTLVTT<br/> 101 DKDGENSTFD KELVDAEVII<br/> TTPFHPGYLT AERLAKAKKL KLAVTAGVGS<br/> 151 DHVDLNAANK TNGGITVAEV<br/> TGCNVVSAE HVVMTILALV <b>RNFVPAHEQI</b><br/> 201 <b>RNGEWDVA</b>AV AK<b>NEFDLENK</b><br/> <b>VVGTVAVGR</b>I GERVLRRLLKP FDCK<b>ELLYYD</b><br/> 251 <b>YQPLRPEVEK</b> EIGCRRVENL<br/> EEMLAQCDVV TINCPLEST RGLFNKELIS<br/> 301 KMKKGSWLVN TARGAIVVKE<br/> DVAEAVKSGH LRGYGGDVWF PQPAPKDHL<br/> 351 RYVQGPWGGG NAMVPHMSGT<br/> SIDAQIRYAG GTK<b>AILES</b>YF <b>SGRHDYKPED</b><br/> 401 <b>LIVK</b>DGDYVT KAYGQRQK</p> <p>58 - 70 483.2418 1446.7036 1446.7177<br/> -0.0141 0 K.VLMVLYDGGEHAK.Q<br/> Oxidation (M)<br/> 71 - 86 863.4518 1724.8890 1724.9057<br/> -0.0167 0 K.QQPGLLGTTENELGLR.K<br/> 71 - 87 618.6638 1852.9696 1853.0007<br/> -0.0311 1 K.QQPGLLGTTENELGLRK.W<br/> 192 - 201 404.2111 1209.6115 1209.6254<br/> -0.0140 0 R.NFVPAHEQIR.N<br/> 192 - 201 404.2119 1209.6139 1209.6254<br/> -0.0116 0 R.NFVPAHEQIR.N<br/> 213 - 229 616.3165 1845.9277 1845.9585<br/> -0.0308 1 K.NEFDLENKVVGTVAVGR.I<br/> 221 - 229 429.2592 856.5038 856.5131<br/> -0.0092 0 K.VVGTVAVGR.I<br/> 245 - 260 685.6782 2054.0128 2054.0360<br/> -0.0232 0 K.ELLYDYQPLRPEVEK.E<br/> 384 - 393 571.7875 1141.5604 1141.5768<br/> -0.0163 0 K.AILES</p> |
| 31 | XP_748936 | 35876 | 269 | 8  | 9.08 | <p>Malate<br/>dehydrogenase,<br/>NAD-dependent</p> <p>Sequence Coverage: 27%</p> <p>1 MFAARQSFLN LQKRAFSASA</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

|    |           |       |     |   |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|----|-----------|-------|-----|---|------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |           |       |     |   |      | <p>SQASKVAVLG AAGGIGQPLS LLLKLNPR<b>VS</b><br/> <b>51</b> <b>ELALYDIR</b>GG PGVAADLSHI<br/> NTNSTVTGYD PTPSGLRDAL <b>KGSEIVLIPA</b><br/> <b>101</b> <b>GVPR</b>KPGMTR <b>DDL</b>FNT<b>NASI</b><br/> <b>VR</b>DLAKAAAE ASPEANILVI SNPVNSTVPI<br/> <b>151</b> VAEVFKSKGV YNPKR<b>LFGVT</b><br/> <b>TLDVVR</b>ASRF ISQIKKTDPA KEAVPVVGGH<br/> <b>201</b> SGVTIVPLLS QSNHPDIEGE<br/> TRDTLVNRIQ FGGDEVVKAK DGAGSATLSM<br/> <b>251</b> AMAGARFAES LLKAAQGE<b>K</b><br/> <b>VIEPTFVESP LYK</b>DQGV<b>DF</b> <b>ASR</b>VELGPNG<br/> <b>301</b> VEK<b>I</b>LEV<b>GKV</b> <b>NAYEEK</b>LIQA<br/> ALTDLKKNIQ <b>KGRDFVAQNP</b></p> <p><b>49 - 58</b> <b>589.8213 1177.6280 1177.6343</b><br/> <b>-0.0062 0 R.VSELALYDIR.G</b><br/> <b>92 - 104</b> <b>654.3876 1306.7606 1306.7609</b><br/> <b>-0.0002 0 K.GSEIVLIPAGVPR.K</b><br/> <b>111 - 122</b> <b>682.8461 1363.6776 1363.6732</b><br/> <b>0.0045 0 R.DDLFNTNASIVR.D</b><br/> <b>166 - 176</b> <b>610.3493 1218.6840 1218.6972</b><br/> <b>-0.0132 0 R.LFGVTTLDVVR.A</b><br/> <b>270 - 283</b> <b>789.9210 1577.8274 1577.8341</b><br/> <b>-0.0067 0 K.GVIEPTFVESPLYK.D</b><br/> <b>284 - 293</b> <b>571.2679 1140.5212 1140.5200</b><br/> <b>0.0012 0 K.DQGVDFASR.V</b><br/> <b>304 - 316</b> <b>497.9394 1490.7964 1490.7980</b><br/> <b>-0.0016 1 K.ILEVGVNAYEEK.L</b><br/> <b>332 - 340</b> <b>502.2473 1002.4800 1002.4883</b><br/> <b>-0.0082 1 K.GRDFVAQNP.-</b></p>                                                                                                                                                         |
| 32 | XP_747039 | 83710 | 361 | 9 | 6.12 | <p>Bifunctional<br/>catalase-<br/>peroxidase, Cat2</p> <p>Sequence Coverage: <b>12%</b></p> <p><b>1</b> MTQDKCPFKE QSSQPNFAGG<br/> GTSNKDWWPD RLKLNILRQH TAVSNPLDAD<br/> <b>51</b> FDYAAAFNSL DYEGKKDLR<br/> ALMTDSQDWW PADFGHYGGL<br/> FIRMAWHSAG<br/> <b>101</b> TYRVFDGR<b>GG</b> <b>AGQQQQR</b>FAP<br/> LNSWPDNVSL DKARRLLWPI KQKYGNKISW<br/> <b>151</b> ADLLILTGNV ALESMGFKTF<br/> GFAGGRPDTW EADEATYWGR<br/> <b>ETT</b>W<b>L</b>G<b>N</b>D<b>A</b>R<br/> <b>201</b> YAKGFSGSDK RGSLIADEES<br/> HKTTHSRELE TPLAAAHMGL IYVNPEGPDG<br/> <b>251</b> NPDPVAAAH DIRTDFGRMAM<br/> NDEETVALIA GGHTFGKTHG AAPADNVGKE<br/> <b>301</b> PEAGLEAQQ LGWANKHGS<br/> KGPHTITSGLEVTWTKPTQ WNNNFLEYLF<br/> <b>351</b> KFEWELTKSP AGAHQWVAK<b>N</b><br/> <b>ADEIIPDAYD ASKK</b>HKPTML TTDLSLR<b>FDP</b><br/> <b>401</b> <b>AYEK</b>IARRFL EHPDQFADAF<br/> ARAWFKLTHR DMGPRARYLG PEVPSEVLW<br/> <b>451</b> QDPIAVNHP LVDASDIAAL<br/> KDEILASGVP PRSFISTAWA AASTFRGSDK<br/> <b>501</b> RGGANGARIR LAPQRDWEVN<br/> NQPWLR<b>EALS ALEAVQSR</b>FN ARGDSKKVSL<br/> <b>551</b> ADLIVLAGCA AVEKAAQDAG<br/> HPIKVPFVPG RMDASQEETD VQSFNHMEPF<br/> <b>601</b> ADGFRNFAKG PARPRAEHYL<br/> VDKAQLLNLS APEMTVLVGG LRVLNTNYDG<br/> <b>651</b> STHGVFTSRP GALTNDFFVH<br/> LLDMNTAWK<b>D VNGELFE</b>GS <b>DR</b>KTGGKKWT<br/> <b>701</b> ATR<b>ADLVFGS</b> <b>NALRAIAEV</b><br/> <b>YASNDGDMKF</b> VKDFVAAWN VMNLDRFDLK<br/> <b>751</b> GKQTIPARL</p> <p><b>109 - 117</b> <b>429.7133 857.4120 857.4104</b><br/> <b>0.0017 0 R.GGAGQQQQR.F</b><br/> <b>191 - 200</b> <b>581.7803 1161.5460 1161.5414</b></p> |

|    |           |       |     |   |      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|----|-----------|-------|-----|---|------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |           |       |     |   |      | <p>0.0046 0 R.ETTWLGNDAR.Y<br/>370 - 383 761.3643 1520.7140 1520.6994<br/>0.0146 0 K.NADEIIPDAYDASK.K<br/>370 - 384 550.6052 1648.7938 1648.7944<br/>-0.0006 1 K.NADEIIPDAYDASKK.H<br/>398 - 404 435.2072 868.3998 868.3967<br/>0.0032 0 R.FDPAYEK.I<br/>527 - 538 637.3452 1272.6758 1272.6673<br/>0.0085 0 R.EALSALEAVQSR.F<br/>680 - 692 697.8180 1393.6214 1393.6110<br/>0.0105 0 K.DVGNGELFEGSDR.K<br/>704 - 715 646.3384 1290.6622 1290.6568<br/>0.0054 0 R.ADLVFGSNAELR.A<br/>716 - 729 750.3413 1498.6680 1498.6609<br/>0.0071 0 R.AIAEVYASNDGDMK.F<br/>Oxidation (M)</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 33 | XP_750327 | 94694 | 249 | 7 | 5.01 | <p>Beta-glucosidase</p> <p>Sequence Coverage: 8%</p> <p>1 MRFGWLEVAA LTAASVANAQ<br/>VFDNSHGNNQ ELAFSPPFYP<br/>SPWADGQGEW</p> <p>51 ADAHRRAVEI VSQMTLAEKV<br/>NLTTGTGWEM DRCVGTGTSV PRLGINWGLC<br/>101 GQDSPLGIRF SDLNSAFPAG<br/>TNVAATWDKT LAYLRGKAMG EEFNDKGVDI<br/>151 LLGPAAGPLG KYPDGGRIWE<br/>GFSPDPALTG VLFKETIKGI QDAGVIATAK<br/>201 HYILNEQEHF RQVGEAQGYG<br/>YNITETISSN VDDKTMHELY LWPFADEVRA<br/>251 GVGAVMCSYN QINNSYGCQN<br/>SQTNLKLLKA ELGFQGFVMS DWSAHHSVG<br/>301 AALAGLDMSM PGDISFDDGL<br/>SFWGTNLTVS VLNGTVPAPWR VDDMAVRIMT<br/>351 AYYKVGRDRL RIPPNFSSWT<br/>RDEYGWEHSA VSEGAWTKVN<br/>DFVNVQRSHS<br/>401 QIIREIGAAS TVLLKNTGAL<br/>PLTGKEVKVG VLGEDAGSNP<br/>WGANGCPDRG</p> <p>451 CDNGTLAMAW GSGTANFPYL<br/>VTPEQAIQRE VISNGGNVFA VTDNGALSQM<br/>501 ADVASQSSVS LVFVNADSGE<br/>GFISVDGNEG DRKNLTWKN GEVIDTVVS<br/>551 HCNNTIVVIH SVGPVLIDRW<br/>YDNPNTAI WAGLPGQESG NSLVDVLYGR<br/>601 VNPSAKTPFT WGKTRESYGA<br/>PLLTEPNNGN GAPQDDFNEG VFIDYRHFDK<br/>651 RNETPIYEFH HGLSYTTFGY<br/>SHLRVQALNS SSSAYVPTSG ETKPAPTYGE<br/>701 IGSAADYLYP EGLKRITKFI<br/>YPWLNSTDLE DSSDDPNYGW QDSEYIPEGA<br/>751 RDGSPQPLLK AGGAPGGNPT<br/>LYQDLVRVSA TITNTGNVAG YEVPQLYVSL<br/>801 GGPNEPRVVL RKFDRIFLAP<br/>GEQKVWTTTL NRRDLANWDV EAQDWVITKY<br/>851 PKKVHVGSSS RKLPLRAPLP RVY</p> <p>189 - 200 572.3352 1142.6558 1142.6295<br/>0.0263 0 K.GIQDAGVIATAK.H<br/>341 - 347 411.2032 820.3918 820.3749<br/>0.0169 0 R.VDDMAVR.I Oxidation (M)<br/>389 - 397 545.7963 1089.5780 1089.5567<br/>0.0213 0 K.VNDFVNVQR.S<br/>405 - 415 551.3423 1100.6700 1100.6441<br/>0.0259 0 R.EIGAAS TVLLK.N<br/>416 - 425 486.2898 970.5650 970.5447<br/>0.0203 0 K.NTGALPLTGK.E<br/>761 - 777 843.4639 1684.9132 1684.8533<br/>0.0600 0 K.AGGAPGGNPTLYQDLVR.V</p> |

|    |           |       |     |   |      |                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|----|-----------|-------|-----|---|------|--------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|    |           |       |     |   |      |                                                  | <b>816 - 824 501.7950 1001.5754 1001.5546</b><br><b>0.0209 0 R.IFLAPGEQK.V</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 34 | XP_747715 | 61327 | 135 | 2 | 5.55 | FAD/FMN-containing isoamyl alcohol oxidase, MreA | Sequence Coverage: <b>4%</b><br><br><b>1</b> MFPSTNRSWS ILAGLLALAS<br>TASASNASQT ACRCFPGAC WSPSPQVWSAF<br><b>51</b> NQSIDGRLVA TVPLGTPCHA<br>PNYDAATCEA LKAQWQLPEI HYESSSSIMA<br><b>101</b> PFFTNGTCDP FHPVSKPCTL<br>GNYVVYAVNV SRPEHIRTAM QFATKHNIRV<br><b>151</b> VVRNTGHDYN GKSTGAGALA<br>IWTHHLKDIE IKDWSDQHYQ GKAIK <b>VGAGV</b><br><b>201</b> <b>QGIEAYRAAD</b> TNGLEVVGGE<br>CPTVGLAGGY TQGGGHSALA SRHGLAADQV<br><b>251</b> LEWEVIDGQG NFLVANRDNE<br>HADLYWALSG GGGGTYGVVW<br>SMTSKAHAGT<br><b>301</b> PVSGNLNLTFT NAGISQDTFY<br>EAVALYHSTL PAIVDAGAMS VWYFTNTSFS<br><b>351</b> ISPLTGNIP VAKLRELVRP<br>FTDGLTRLGI TYTTYAAQFD SYLAEFEAMQ<br><b>401</b> SPIEVGIAQY GGWLIPR <b>SVV</b><br><b>QTNNAELTAA YRAITSDGAT</b> FIGVGLNVST<br><b>451</b> AVTGDVSNV LPAWRDTLID<br>TVITTPWNWT APTADMIALQ HKMTDEYIPR<br><b>501</b> LEALAPQSGA YLNEADFRQP<br>NFQTAFYGAN YQKLRAIKAK YDPNSLFYGT<br><b>551</b> TAVGSDEWTV TSDGHLCKAT P<br><br><b>196 - 207 610.3396 1218.6646 1218.6357</b><br><b>0.0290 0 K.VGAGVQGIEAYR.A</b><br><b>418 - 432 818.9418 1635.8690 1635.8216</b><br><b>0.0474 0 R.SVVQTNNAELTAAAYR.A</b>                                                                                                                                                                                                                                 |
| 35 | EDP54506  | 61335 | 215 | 6 | 5.85 | Glucose-6-phosphate isomerase                    | Sequence Coverage: <b>14%</b><br><br><b>1</b> MPGFSQATEL GAWKELQEH<br>NSLGRNIVLK EYFEKDPQRF EKFSR <b>TFANP</b><br><b>51</b> <b>VDNTEILFDF</b> <b>SKNFLTEETL</b><br>ALLVKLAREA GVEELRDAMF K <b>GDPINFTE</b><br><b>101</b> <b>RAVYHVALRN</b> <b>VTNEPMQVNG</b><br><b>KSVVEDVNSV</b> LEHMKEFTEQ VRSGEWKGYT<br><b>151</b> GKKITTIINI GIGGSDLGPV<br>MVTEALKPYG AEDMTLHFVS NIDGSHIAEA<br><b>201</b> LK <b>HSDPETTL</b> <b>FLIASKTFTT</b><br><b>AETTTNANSA KKWFLESA</b> KD EAHIAK <b>HFVA</b><br><b>251</b> <b>LSTNEEEVTK</b> FGIDKKNMFG<br>FASWVGGRYS VWSAIGLSVA LYIGFDNFHQ<br><b>301</b> FLAGAHAMDK HFRETPLEQN<br>IPVLGGLLSV WYSDFFGAQT HLVAPFDQYL<br><b>351</b> HRFPAYLQQL SMESNGKAIT<br>RTGEYVKYTT GPILFGEPAT NAQHSFFQLL<br><b>401</b> HQGTKLIPSD FIMAAESHNP<br>VEGGKHQRML ASNFLAQSEA LMVGKTPEQV<br><b>451</b> KTEGAPDNLV PHKTFNGNRP<br>TTSILAQKIT PSTLGALIAI YEHLTFTEGA<br><b>501</b> VWNINSFDQW GVELGKVLAK<br>KIQKELETPG AGGDHDASTS GLLAFKKKA<br><b>551</b> NLA<br><br><b>46 - 62 979.4716 1956.9286 1956.9469</b><br><b>-0.0183 0 R.TFANPVDNTEILFDFSK.N</b><br><b>92 - 101 582.2633 1162.5120 1162.5255</b><br><b>-0.0134 0 K.GDPINFTEDR.A</b><br><b>110 - 121 673.8157 1345.6168 1345.6296</b><br><b>-0.0128 0 R.NVTNEPMQVNGK.S</b> Oxidation<br>(M)<br><b>203 - 216 779.9022 1557.7898 1557.8039</b><br><b>-0.0140 0 K.HSDPETTLFLIASK.T</b> |

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|--|--|--|--|--|--|--|--------------------------------------------------------------------------------------------------------------------------------------------------|
|  |  |  |  |  |  |  | 217 - 231 779.3685 1556.7224 1556.7318<br>-0.0094 0 K.TFTTAETTTNANSK.K<br>247 - 260 535.2649 1602.7729 1602.7889<br>-0.0161 0 K.HFVALSTNEEEVTK.F |
|--|--|--|--|--|--|--|--------------------------------------------------------------------------------------------------------------------------------------------------|