### Supplemental Table 1 Differentially changed proteins in the Wild type, agamotype and telemorph of *Aspergillus cristasus* identified by MALDI-TOF-TOF

| Spot No. | Protein name | Accession | PS* | EV | Experimental/Theoretical Protein spot intensity | SL* | M* (%) |
|----------|--------------|-----------|-----|----|-----------------------------------------------|-----|--------|
|          |              |           |     |    |                                               |     |        |
|          |              |           |     |    | mass (kDa) / pI WT* / Ap* / Tel*              |     |        |
|          |              |           |     |    | SL* / M* (%)                                  |     |        |

#### Amino acid metabolism

| Spot No. | Protein name | Accession | PS* | EV | Experimental/Theoretical Protein spot intensity | SL* | M* (%) |
|----------|--------------|-----------|-----|----|-----------------------------------------------|-----|--------|
| 15       | dihydroxy-acid dehydratase | gi|1060925404 | 108 | 1.60E-07 | 61.32/65.60 | 5.43/5.90 | 16.46±3.21 / 81.34±3.82 / 16.27±2.81 | mito | 3 | 6 |
| 19       | putative alanine aminotransferase | gi|1060922197 | 451 | 8.20E-42 | 52.52/54.54 | 5.77/6.07 | 0 / 50.24±0.74 / 0 | mito | 7 | 15 |
| 22       | argininosuccinate synthase | gi|1060919692 | 350 | 1.00E-31 | 46.17/46.59 | 5.50/5.29 | 35.4±6.54 / 86.30±1.81 / 0 | cyto | 7 | 26 |
| 23       | O-acetyltromosine (thiol)-lyase | gi|1060924611 | 325 | 3.30E-29 | 45.06/47.95 | 6.72/6.11 | 35.82±5.53 / 80.57±5.32 / 0 | cyto | 7 | 22 |
| 24       | Acetylornithine aminotransferase | gi|1060920786 | 191 | 8.20E-16 | 44.30/50.43 | 6.90/6.77 | 0 / 128.99±8.11 / 0 | mito | 10 | 32 |
| 25       | Ornithine aminotransferase | gi|1060927763 | 289 | 1.30E-25 | 43.24/49.12 | 6.07/5.74 | 0 / 80.24±3.49 / 0 | nucl | 15 | 47 |
| 26       | S-adenosyl-L-methionine-dependent methyltransferase | gi|1060920829 | 517 | 2.10E-48 | 43.45/47.88 | 5.44/5.26 | 54.08±3.70 / 96.23±3.93 / 0 | cyto | 12 | 34 |
| 30       | 3(2),5'-bisphosphate nucleotidase | gi|1060922043 | 512 | 6.50E-48 | 38.91/40.01 | 5.07/5.51 | 15.97±4.31 / 44.28±2.52 / 0 | nucl | 9 | 27 |
| 46       | putative dimethylallyl tryptophan synthase | gi|1060919206 | 651 | 8.20E-62 | 39.45/46.34 | 5.43/5.17 | 142.33±4.54 / 0 / 124.20±8.62 | cyto | 13 | 34 |
| 57       | assimilatory sulfite reductase | gi|1060922057 | 132 | 6.50E-10 | 118.32/113.87 | 5.27/5.12 | 0 / 93.96±2.20 / 0 | mito | 11 | 15 |
| 59       | Histidine biosynthesis trifunctional protein | gi|1060923463 | 274 | 4.10E-24 | 102.73/93.40 | 5.30/5.27 | 0 / 52.44±9.66 / 16.28±5.82 | cyto | 13 | 20 |
| 69       | Select seq ODM16719.1 Anthranilate synthase component 2 | gi|1060921415 | 259 | 1.30E-22 | 82.50/82.35 | 6.58/6.03 | 0 / 34.64±9.93 / 0 | cyto | 12 | 20 |
| 73       | 2-isopropylmalate synthase | gi|1060923417 | 106 | 2.60E-07 | 72.68/72.26 | 5.50/5.36 | 0 / 66.36±9.54 / 0 | cyto | 10 | 20 |
| 83       | PLP-dependent transerase | gi|1060927687 | 283 | 5.20E-25 | 61.68/53.48 | 6.49/5.90 | 0 / 37.23±9.88 / 18.30±8.69 | cyto | 13 | 22 |
| 84       | PLP-dependent transerase | gi|1060925685 | 104 | 4.10E-07 | 61.08/57.38 | 6.19/5.81 | 0 / 78.17±6.92 / 12.07±1.97 | cyt | 8 | 23 |
| 121      | peptidyl-arginine deiminase domain protein | gi|1060921378 | 237 | 2.10E-20 | 43.36/43.54 | 4.89/5.06 | 85.15±8.29 / 0 / 96.02±4.20 | cyto | 17 | 46 |
| 159      | spermidine synthase | gi|1060923288 | 266 | 2.60E-23 | 15.22/13.49 | 4.74/5.17 | 0 / 18.0±3.87 / 74.87±4.21 | nucl | 5 | 15 |
| 171      | Arginine biosynthesis bifunctional protein ArgJ | gi|1060920200 | 144 | 4.10E-11 | 24.40/48.48 | 4.49/6.78 | 30.79±1.29 / 29.77±8.78 / 0 | mito | 6 | 21 |

#### Antioxidant associated proteins

| Spot No. | Protein name | Accession | PS* | EV | Experimental/Theoretical Protein spot intensity | SL* | M* (%) |
|----------|--------------|-----------|-----|----|-----------------------------------------------|-----|--------|
|          |              |           |     |    | mass (kDa) / pI WT* / Ap* / Tel*              |     |        |
|          |              |           |     |    | SL* / M* (%)                                  |     |        |
| 42       | Catalase B | gi|1060921769 | 445 | 3.30E-41 | 98.30/80.44 | 5.71/5.48 | 123.53±7.96 / 0 / 104.56±6.79 | extr | 13 | 18 |
| 64       | putative glutathione S-transferase | gi|1060922520 | 232 | 6.50E-20 | 23.84/25.87 | 6.91/6.46 | 0 / 82.28±2.94 / 0 | cyto | 10 | 57 |
| 141      | superoxide dismutase [Cu-Zn] | gi|1060925525 | 292 | 6.50E-26 | 13.21/16.03 | 5.65/6.14 | 54.69±4.20 / 0 / 0 | cyto | 6 | 46 |
| Protein Name                                           | Accession Number | Standard Deviation | Value | Fold Change | p-value | Location |
|--------------------------------------------------------|------------------|--------------------|-------|-------------|---------|----------|
| Enolase                                                | gi|1060921926        | 174               | 4.1E-14     | 5.93/5.84 | cyto     | 7        |
| Isocitrate dehydrogenase [NAD] subunit 2              | gi|1060921447        | 106               | 2.6E-07     | 6.90/8.43  | mito     | 6        |
| Putative homoisocitrate dehydrogenase                  | gi|1060928428        | 129               | 1.3E-09     | 5.94/5.95  | cyto     | 9        |
| Putative gluatathione S-transferase                    | gi|1060922520        | 238               | 1.6E-20     | 6.63/6.46  | cyto     | 11       |
| Putative succinate dehydrogenase [ubiquinone] flavoprotein subunit | gi|1060919845        | 141               | 8.2E-11     | 5.84/6.16  | mito     | 5        |
| Gluconate dehydrogenase                               | gi|1060922815        | 122               | 6.5E-09     | 5.64/5.44  | cyto     | 10       |
| Glucokinase                                            | gi|1060919070        | 82                | 6.7E-05     | 5.66/5.54  | cyto     | 9        |
| Hexokinase                                             | gi|1060920562        | 98                | 1.5E-06     | 5.03/4.97  | cyto     | 10       |
| Carbohydrate metabolism                                |                  |                    |       |             |         |          |
| Acetyl-CoA hydrolase                                   | gi|106092188         | 157               | 2.1E-12     | 6.91/6.23  | cyto     | 7        |
| UDP-N-acetylglucosamine pyrophosphorylase              | gi|1060928873        | 259               | 1.3E-02     | 5.78/5.75  | cyto     | 9        |
| Aldehyde dehydrogenase domain                         | gi|1060921926        | 174               | 4.1E-14     | 5.93/5.84  | cyto     | 7        |
| Enoylase                                               | gi|1060928234        | 197               | 2.1E-16     | 7.84/4.28  | cyto     | 5        |
| Isocitrate dehydrogenase [NAD] subunit 2              | gi|1060921447        | 106               | 2.6E-07     | 6.90/8.43  | mito     | 6        |
| Putative homoisocitrate dehydrogenase                  | gi|1060928428        | 129               | 1.3E-09     | 5.94/5.95  | cyto     | 9        |
| Putative dioxygenase                                   | gi|1060929032        | 267               | 2.1E-23     | 6.95/6.28  | mito     | 9        |
| Putative exo-beta-1,3-glucanase                        | gi|1060923248        | 293               | 5.2E-26     | 5.06/5.26  | extr     | 11       |
| Geos-like protein                                       | gi|1060928685        | 699               | 1.3E-66     | 5.54/5.45  | extr     | 3        |
| Fructosyltransferase                                   | gi|1060922304        | 198               | 1.6E-16     | 4.44/4.53  | extr     | 5        |
| Phosphoenolpyruvate carboxykinase [ATP]                | gi|1060922203        | 225               | 3.3E-19     | 6.10/5.74  | cyto     | 17       |
| Glucose dehydrogenase                                  | gi|1060922815        | 122               | 6.5E-09     | 5.64/5.44  | cyto     | 10       |
| Glucokinase                                            | gi|1060919070        | 82                | 6.7E-05     | 5.66/5.54  | cyto     | 9        |
| ID   | Description                                                                 | gi|   | Value  | gi|   | Value  | gi|   | Value  | gi|   | Value  | gi|   | Value  | gi|   | Value  | gi|   | Value  | gi|   | Value  |
|------|------------------------------------------------------------------------------|----|---|--------|----|---|--------|----|---|--------|----|---|--------|----|---|--------|----|---|--------|----|---|--------|----|---|--------|----|---|--------|----|---|--------|----|---|--------|
| 98   | putative ATP-citrate synthase subunit 2                                     | 251| 8.20E-22 | 48.1252.96 | 5.785.66 | 0 | 89.963.37 | 83.15a7.50 | cyto | 7 | 21 |
| 104  | malate dehydrogenase                                                         | 430| 1.00E-39 | 32.4234.52 | 6.626.85 | 0 | 86.953.88 | 0 | cyto | 14 | 42 |
| 115  | fructose1,6-bisphosphate-3-kinase                                             | 173| 5.20E-14 | 63.3656.69 | 4.374.53 | 40.174.66 | 0 | 13.02a2.31 | extr | 7 | 15 |
| 123  | GeoES-like protein                                                           | 138| 1.60E-10 | 38.3138.48 | 6.414.94 | 49.92a1.18 | 0 | 31.84a1.19 | cyto | 8 | 35 |
| 124  | Clavaminic synthase-like protein                                              | 292| 6.50E-26 | 37.7538.46 | 4.854.89 | 37.32a5.10 | 0 | 57.16a12.79 | cyto | 12 | 41 |
| 140  | putative ribose 5-phosphate isomerase                                        | 262| 6.50E-23 | 13.5017.43 | 5.566.11 | 66.94a2.46 | 0 | 91.44a2.27 | cyto | 7 | 40 |
| 145  | putative ribose 5-phosphate isomerase                                        | 469| 1.30E-43 | 11.2717.43 | 4.896.11 | 53.85a1.68 | 0 | 46.23a6.17 | cyto | 9 | 51 |
| 147  | putative exo-beta-1,3-glucanase                                               | 225| 3.30E-22 | 74.0290.76 | 5.045.26 | 0 | 40.03a5.52 | 24.98a3.10 | extr | 10 | 11 |
| 149  | succinate dehydrogenase                                                      | 302| 6.50E-27 | 66.8371.38 | 5.786.16 | 3.63a1.48 | 19.58a1.42 | 8.47a0.94 | mito | 16 | 33 |
| 152  | putative glucan 1,3-beta-glucosidase A                                       | 502| 6.50E-47 | 39.9345.92 | 4.624.81 | 0 | 81.33a3.53 | 134.68a11.75 | extr | 13 | 31 |
| 153  | glyceraldehyde dehydrogenase                                                 | 138| 1.60E-10 | 35.0037.04 | 6.656.02 | 0 | 0 | 129.58a8.19 | cyto | 8 | 31 |
| 165  | aryl-alcohol dehydrogenase                                                   | 159| 1.30E-12 | 61.0167.53 | 5.155.19 | 82.12a5.84 | 57.34a1.24 | 0 | cyto | 12 | 28 |
| 168  | putative glucan 1,3-beta-glucosidase A                                       | 330| 1.00E-29 | 40.9145.92 | 4.594.81 | 22.76a6.36 | 25.97a4.84 | 56.42a3.73 | extr | 13 | 27 |
|      | **Cytoskeleton associate**                                                   |    |    |        |    |    |        |    |    |        |    |    |        |    |    |        |    |    |        |    |    |
| 20   | Actin-related protein 4                                                      | 171| 2.70E-05 | 50.1551.17 | 5.425.24 | 0 | 76.04a6.76 | 0 | cyto | 4 | 12 |
| 78   | Fimbrin                                                                      | 291| 8.20E-26 | 65.7172.35 | 5.785.50 | 0 | 93.95a8.80 | 31.17a3.33 | cyto | 14 | 28 |
| 99   | actin depolymerizing protein                                                 | 85 | 3.40E-05 | 38.9736.66 | 5.285.28 | 0 | 66.23a2.67 | 0 | cyto | 7 | 21 |
| 100  | BAR domain protein                                                           | 225| 3.30E-19 | 37.9733.58 | 5.145.11 | 0 | 78.00a5.37 | 0 | nucl | 7 | 25 |
|      | **Energy metabolism**                                                        |    |    |        |    |    |        |    |    |        |    |    |        |    |    |        |    |    |        |    |    |
| 3    | Cell division control protein 48(AAA ATPase)                                 | 272| 6.50E-24 | 100.3490.46 | 5.104.94 | 0 | 114.01a5.11 | 0 | cyto | 15 | 20 |
| 33   | NAD(P)-binding protein                                                       | 251| 8.20E-22 | 38.3239.94 | 6.876.24 | 52.55a4.87 | 107.71a6.50 | 0 | cyto | 10 | 30 |
| 34   | NAD(P)-binding protein                                                       | 221| 8.20E-19 | 38.1639.94 | 6.656.24 | 51.13a1.60 | 52.74a1.01 | 0 | cyto | 10 | 30 |
| 49   | NAD(P)-binding protein                                                       | 280| 1.00E-24 | 27.7034.15 | 6.577.07 | 20.04a0.51 | 0 | 38.06a1.51 | mito | 11 | 28 |
| 51   | NAD(P)-binding protein                                                       | 205| 3.30E-17 | 21.4322.23 | 5.575.69 | 19.15a0.29 | 0 | 45.10a2.21 | cyto | 5 | 23 |
| 52   | NAD(P)-binding protein                                                       | 291| 8.20E-26 | 21.3722.23 | 5.815.69 | 77.06a2.15 | 0 | 112.94a10.74 | cyto | 6 | 31 |
| 60   | NADH-ubiquinone oxireductase 24 kDa subunit, mitochondrial                   | 214| 4.10E-18 | 27.3334.58 | 5.066.44 | 0 | 30.94a1.65 | 93.33a6.29 | mito | 13 | 27 |
| 75   | NADH-ubiquinone oxireductase 78 kDa subunit                                  | 275| 3.30E-24 | 70.6681.46 | 5.956.08 | 0 | 127.62a4.96 | 31.30a2.14 | mito | 16 | 30 |
| Gene ID | Description | Accession | Length (kDa) | Molec. Type | Location |
|---------|-------------|-----------|-------------|-------------|-----------|
| gi|1060924600 | NADH-ubiquinone oxidoreductase 78 kDa subunit | 137 | 2.10E-10 | 67.69±1.46 | 5.67±5.47 | 0 | 55.86±6.86 | 0 | mito | 12 | 26 |
| gi|1060927601 | Mannitol 2-dehydrogenase | 196 | 2.60E-16 | 60.36±56.23 | 5.82±5.56 | 0 | 138.42±3.30 | 121.46±7.30 | cyto | 8 | 18 |
| gi|1060920062 | NAD(P)-binding protein | 151 | 8.20E-12 | 28.27±30.83 | 5.85±5.77 | 0 | 68.82±3.32 | 0 | cyto | 6 | 16 |
| gi|1060925359 | NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial | 128 | 1.60E-09 | 28.22±34.58 | 5.05±6.44 | 0 | 41.63±1.22 | 26.33±5.13 | mito | 8 | 25 |
| gi|1060922090 | NADH-ubiquinone oxidoreductase 30.4 kDa subunit | 317 | 2.10E-28 | 27.77±32.54 | 5.63±6.26 | 0 | 61.29±8.3 | 25.44±1.66 | mito | 16 | 50 |
| gi|1060926712 | FAD-binding domain-containing protein | 124 | 4.10E-09 | 52.59±54.48 | 4.29±4.48 | 59.46±2.67 | 0 | 0 | cyto | 8 | 19 |
| gi|1060928033 | NAD(P)-binding protein | 520 | 1.00E-48 | 29.67±31.29 | 5.42±5.34 | 0 | 155.23±4.94 | 0 | 147.21±5.77 | mito | 17 | 69 |
| gi|1060926709 | NAD(P)-binding protein | 300 | 1.00E-26 | 20.66±22.23 | 5.68±5.69 | 0 | 207.00±9.17 | 0 | 185.83±1.64 | cyto | 6 | 37 |
| gi|1060926709 | NAD(P)-binding protein | 201 | 8.20E-17 | 20.91±22.23 | 5.91±5.69 | 0 | 169.18±1.85 | 33.72±3.49 | 184.80±1.58 | cyto | 7 | 42 |
| gi|1060926709 | NAD(P)-binding protein | 393 | 5.20E-36 | 21.05±22.23 | 5.74±5.69 | 0 | 181.70±4.00 | 0 | 0 | cyto | 9 | 49 |
| gi|1060926709 | NAD(P)-binding protein | 313 | 5.20E-28 | 20.82±22.23 | 5.85±5.69 | 0 | 181.79±3.10 | 0 | 172.08±0.99 | cyto | 8 | 42 |
| gi|1060926710 | NAD(P)-binding protein | 142 | 6.50E-11 | 20.63±22.24 | 5.61±5.70 | 52.43±1.80 | 0 | 175.17±5.77 | mito | 6 | 35 |
| gi|1060926712 | FAD-binding domain-containing protein | 170 | 1.00E-13 | 18.78±22.26 | 5.88±5.72 | 21.78±4.35 | 0 | 42.09±3.33 | cyto | 8 | 43 |
| gi|1060926713 | NAD(P)-binding protein | 257 | 2.10E-22 | 16.50±22.27 | 5.63±5.73 | 38.63±1.85 | 0 | 7.96±3.72 | mito | 9 | 49 |
| gi|1060926713 | NAD(P)-binding protein | 168 | 1.00E-13 | 35.00±36.37 | 4.97±4.94 | 0 | 31.06±1.99 | 60.25±4.61 | cyto | 7 | 31 |
| gi|1060926713 | NAD(P)-binding protein | 576 | 2.60E-54 | 34.75±36.37 | 5.22±4.94 | 0 | 114.18±4.65 | 113.19±8.66 | cyto | 10 | 45 |
| gi|1060926709 | NAD(P)-binding protein | 312 | 6.50E-28 | 17.13±22.23 | 6.62±5.69 | 0 | 0 | 54.77±3.08 | cyto | 8 | 43 |
| gi|1060926709 | NAD(P)-binding protein | 110 | 1.00E-07 | 13.00±22.23 | 4.79±5.69 | 0 | 0 | 55.74±2.03 | cyto | 4 | 26 |
| gi|1060926713 | NAD(P)-binding protein | 154 | 4.10E-12 | 25.66±26.99 | 4.89±5.04 | 105.12±2.44 | 0 | 0 | cyto | 5 | 18 |

**Genetic Information Processing**

| Gene ID | Description | Accession | Length (kDa) | Molec. Type | Location |
|---------|-------------|-----------|-------------|-------------|-----------|
| gi|1060924819 | Elongation factor 3 | 139 | 1.30E-10 | 110.99±17.56 | 6.39±6.02 | 0 | 70.40±2.01 | 0 | nucl | 9 | 10 |
| gi|1060923425 | RNA recognition motif proteins | 96 | 2.60E-06 | 94.08±33.60 | 4.84±4.82 | 18.48±6.19 | 38.70±7.04 | 0 | nucl | 5 | 10 |
| gi|1060928074 | Phenylalanine-γ-aminotransferase subunit | 200 | 2.50E-06 | 73.36±67.92 | 5.43±14.14 | 0 | 49.33±6.65 | 0 | cyto | 11 | 17 |
| gi|1060923655 | KH domain RNA-binding protein | 270 | 5.20E-51 | 38.55±38.80 | 5.90±5.63 | 66.39±1.79 | 69.51±9.78 | 0 | nucl | 9 | 33 |
| gi|1060919757 | Proteasome component Pup1 | 96 | 1.00E-16 | 25.81±29.76 | 6.50±6.70 | 10.86±4.53 | 50.58±1.13 | 0 | cyto | 3 | 5 |
| gi|1060919728 | Putative Hsp70 chaperone Bp/Kar2 | 543 | 1.3e-018 | 76.53±70.04 | 4.84±4.94 | 10.08±4.82 | 29.97±7.29 | 0 | E.R. | 15 | 25 |
| gi|1060923520 | Putative vacuolar carboxypeptidase Cps1 | 219 | 2.6e-016 | 62.05±61.64 | 5.10±5.07 | 64.53±1.55 | 54.02±2.85 | 0 | vacu | 4 | 9 |
| gi|1060927666 | T-complex protein 1 subunit zeta | 196 | 1.3e-011 | 61.56±58.81 | 6.57±6.09 | 16.61±2.48 | 67.77±13.21 | 0 | mito | 7 | 13 |
26S proteasome regulatory subunitρn-8
g|1060928318 366 8.20E-14 38.52/39.40 6.12/5.60 0 77.64±1.82 0 cyto 13 47

Eukaryotic translation initiation factor 3 subunit F
g|1060926450 165 1.00E-23 36.62/37.10 4.79/4.84 0 88.23±1.13 0 mito 4 15

RNA-binding domain-containing protein
g|1060924745 110 2.60E-33 36.69/3.85 5.77/8.42 86.10±3.89 86.22±8.05 0 nucl 6 26

40S ribosomal protein S0
g|5991450708 243 3.30E-13 34.08/32.42 5.30/4.79 39.82±1.97 59.42±2.72 0 cyto 5 24

Elongation factor 2
g|1060920666 98 1.00E-07 30.52/94.01 5.94/6.15 121.76±3.32 116.56±5.48 0 cyto 8 11

Elongation factor 2

Eukaryotic initiation factor 5a

g|1060925479 155 1.60E-06 16.27/51.62 5.91/5.85 60.46±0.41 0 70.48±3.21 nucl 8 21

BCAS2 family protein
g|1060928177 283 1.30E-18 23.92/28.38 5.21/5.09 0 57.54±5.06 0 nucl 12 55

L30e-like protein
g|599155142 120 1.60E-11 12.11/11.77 4.58/4.84 0 55.84±1.43 20.32±3.23 cyto 4 21

Eukaryotic initiation factor 5a

g|1060925479 256 1.60E-18 70.66/51.62 5.47/5.85 0 106.54±7.55 24.03±2.59 nucl 8 21

Eukaryotic initiation factor 5a

g|1060925479 150 2.10E-17 63.92/51.62 6.16/5.85 0 60.03±5.38 28.41±5.37 nucl 6 19

Heat shock protein Hsp88

g|1060921473 148 3.30E-12 93.36/60.86 4.96/4.99 68.09±12 0 72.24±6.98 cyto 6 9

putative metallo-beta-lactamase domain protein
g|1060923853 207 2.60E-11 32.39/34.32 6.49/5.95 30.81±7.40 0 66.66±6.40 nucl 9 26

putative peroxiredoxin pnp20
g|1060925713 146 4.00E-05 12.13/18.63 4.90/5.30 83.96±7.25 0 140.82±6.98 cyto 5 36

Ubiquitin-activating enzyme E1
g|1060924307 120 1.00E-08 112.49/114.86 5.16/5.87 0 114.00±9.47 48.33±7.14 cyto 8 10

N-terminal nucleophile aminohydrolase
g|1060926927 154 0.0011 22.81/28.74 5.51/5.42 0 58.70±7.08 6.49±2.28 cyto 9 29

putative peroxiredoxin pnp20

g|1060925713 136 5.20E-25 14.33/18.63 5.20/5.30 0 74.77±6.62 187.17±1.50 cyto 2 12

Heat shock protein 90

g|1060924622 377 4.10E-12 74.75/80.04 5.04/4.92 0 131.27±9.94 79.35±8.27 cyto 16 26

Carboxypeptidase Y

g|1060927221 81 2.60E-10 61.68/61.77 4.97/4.98 0 33.91±3.31 29.36±4.00 extir 3 7

Heat shock protein 60

g|1060925809 246 2.60E-36 60.00/61.80 5.25/5.61 0 114.83±10.25 0 mito 14 23

26S proteasome regulatory subunit 6A

g|1060928147 359 1.00E-08 59.85/52.60 4.95/4.89 0 119.86±8.10 31.12±4.69 cyto 14 25

Putative T-complex protein 1 subunit eta

g|1060928185 234 2.10E-34 59.86/61.44 6.20/5.84 0 51.59±2.74 0 cyto 13 27

Protein disulfide-isomerase

g|1060920600 55 2.60E-22 56.43/55.69 4.82/4.78 0 40.09±1.17 0 cyto 6 14

Putative t-complex protein 1 beta subunit

g|1060920067 156 1.00E-11 55.99/57.34 6.10/5.83 0 68.98±5.83 0 cyto 10 23

ATP-dependent RNA helicase sub2

g|1060925743 147 8.40E-05 49.06/49.99 5.52/5.50 0 90.25±5.83 38.61±5.54 nucl 6 18

Putative eukaryotic translation initiation factor 3 subunit EifCf

g|1060926450 229 2.60E-21 36.62/37.10 4.88/4.84 0 111.32±4.29 51.14±6.13 mito 4 17

Eukaryotic initiation factor 5a

g|1060925479 205 1.30E-32 79.43/51.62 6.41/5.85 40.56±1.78 0 30.86±0.42 nucl 11 24

60S ribosomal protein L44

g|1060925258 181 4.10E-20 34.51/33.77 6.00/5.62 131.64±11.10 0 29.69±9.90 nucl 9 35
eukaryotic initiation factor 5a
g|1069025479: 324 0.032 15.91±51.62 5.86±5.85 51.03±3.76 0 9.78±3.33 nucl 7 21
RNA-binding domain-containing protein
g|1069026819: 137 2.60E-12 46.90±36.14 6.87±8.85 91.32±9.28 0 19.57±3.16 nucl 8 28
Mitochondrial-processing peptidase subunit beta
g|1069023390: 364 2.10E-11 31.79±3.91 5.64±5.61 0 40.46±2.92 24.33±2.37 mito 11 35
HSP20-like chaperone
g|1069020348: 168 1.30E-19 26.24±23.67 4.40±4.37 25.37±9.00 0 39.32±19.42 nucl 7 25
proteasome subunit alpha type-5
g|131742700: 193 4.10E-16 25.72±27.15 4.55±4.72 185.18±8.29 0 28.27±1.77 cyto 8 45
Translationally-controlled tumor protein
g|1069026606: 86 4.10E-33 12.86±20.09 5.08±4.75 29.57±6.59 0 7.09±4.29 cyto 6 26
putative peroxiredoxin pmp20
g|1069025713: 204 8.20E-14 11.94±18.63 5.12±5.30 72.22±3.79 0 121.35±4.09 cyto 5 46
U-box domain protein
g|1069021250: 236 3.30E-17 27.85±32.08 5.20±5.13 0 19.09±8.60 78.74±11.47 nucl 8 25
putative peroxiredoxin pmp20
g|1069025713: 132 8.20E-15 14.37±18.63 5.03±5.30 0 17.81±8.46 58.96±1.54 cyto 4 17
putative diisulfide isomerase
g|1069028773: 62 1.60E-13 57.01±50.25 6.46±6.15 34.00±1.73 38.56±0.66 0 nucl 8 23
Vacuolar protease A
g|1069023993: 67 5.20E-16 36.51±43.73 4.73±5.00 59.74±1.80 0 0 extr 3 9
GMP synthase
g|1069022805: 149 4.10E-29 55.33±60.28 5.83±5.71 63.59±2.12 28.81±5.46 110.31±13.24 cyto 9 15
putative UV excision repair protein
g|1069026960: 218 4.10E-17 51.56±39.79 4.26±4.40 68.93±2.20 0 173.90±6.47 nucl 3 9
Carbamoyl-phosphate synthase arginine-specific large chain
g|1069022448: 84 2.60E-20 117.52±129.60 5.12±5.35 0 126.05±1.65 30.46±3.22 cyto 9 10
Adenylyl-sulfate kinase
g|1069026671: 70 6.50E-10 24.56±23.79 6.76±6.33 68.72±5.61 29.98±8.23 65.45±2.40 mito 2 9
dUTPase Dut putative
g|666431402: 396 0.0065 12.81±20.74 5.26±5.50 0 131.71±2.69 98.60±8.50 nucl 9 51
putative polyadenylation factor subunit CsdF64
g|1069025361: 194 2.10E-10 35.98±31.11 4.67±4.72 0 33.73±8.13 0 nucl 2 9
Uricase
g|1069021198: 171 0.0022 30.14±34.77 6.10±5.89 0 109.31±13.94 0 nucl 8 25
uracil phosphoribosyltransferase furA
g|1069024256: 336 2.60E-30 23.92±24.83 5.95±5.70 103.99±10.86 0 0 mito 10 34
Lipid metabolism
sterol 24-C-methyltransferase
g|1069024436: 335 3.30E-30 37.50±42.62 6.60±5.98 19.71±4.73 41.56±5.40 0 cyto 12 28
phytanoyl-CoA dioxygenase family protein
g|1069024291: 173 5.20E-14 30.95±33.60 6.65±5.96 104.08±3.05 49.93±1.14 0 mito 4 20
Sec 14 cytosolic factor
g|1069023795: 137 2.10E-10 36.01±35.34 5.48±5.58 0 68.79±2.37 0 cyto 8 20
fatty-acid amide hydrolase
g|1069026321: 100 1.00E-06 57.01±60.11 5.41±5.30 99.33±5.36 0 94.92±6.04 cyto 11 20
CRAL/TRIO domain-containing protein
g|1069025523: 94 4.50E-06 45.56±45.89 5.38±5.37 87.80±6.32 0 27.01±4.36 cyto 6 21
CoA-dependent acyltransferase
g|1069025390: 242 6.50E-21 44.55±49.05 6.18±5.87 136.47±10.41 0 38.71±10.23 cyto 13 44
Signal transduction
putative EF-hand calcium-binding domain protein
g|1069022288: 481 8.20E-45 25.23±29.03 5.89±5.52 38.42±0.62 5.17±1.28 60.66±0.61 cyto 8 38
| Gene ID          | Description                                                                 | Log2 Fold Change (Mean ± SD)                                                                 | Location |
|-----------------|------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|----------|
| gi|1060928075      | protein phosphatase PP2A regulatory subunit A                                        | 1.60E-23 ± 0.32 72.54±1.17 20.30                                  | nucl     |
| gi|1060926446      | protein phosphatase 2C                                                           | 1.60E-34 ± 0.29 70.31±2.17 7.17                                     | nucl     |
| gi|1060921260      | rab GTPase activator                                                            | 5.20E-14 ± 3.30 0.34±1.35 13.35                                  | cyto     |
| gi|1060920414      | Ser-Thr-rich glycosyl-phosphatidyl-inositol-anchored membrane family protein     | 1.60E-34 ± 0.29 70.31±2.17 7.17                                     | nucl     |
| gi|1060921260      | rab GTPase activator                                                            | 3.30E-25 ± 0.29 5.11±5.14 10.36                                  | cyto     |
| gi|1060923594      | 14-3-3 protein                                                                 | 1.60E-21 ± 0.28 4.57±4.72 11.37                                  | cyto     |
| gi|1060924834      | Mitochondrial import receptor subunit tom-20                                     | 2.6e-036 ± 0.28 47.47±1.30 0                                    | nucl     |
| gi|1060925575      | periplasmic binding protein-like II                                               | 1.10E-06 ± 0.12 5.69±5.54 0                                    | extr     |
| gi|1060927417      | hypothetical protein                                                             | 1.60E-15 ± 0.28 17.43±2.83 0                                    | nucl     |
| gi|1060921882      | hypothetical protein                                                             | 6.50E-08 ± 0.24 19.86±5.24 0                                    | nucl     |
| gi|1060925957      | UPF0047 protein C4A8.02c                                                         | 5.20E-18 ± 0.28 3.65±1.58 0                                    | E.R.     |
| gi|1060925958      | Lactobacillus shifted protein                                                    | 1.00E-13 ± 0.12 24.92±3.73 0                                    | nucl     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060919840      | hypothetical protein                                                             | 5.20E-18 ± 0.28 19.03±6.45 0                                    | E.R.     |
| gi|1060929592      | hypothetical protein                                                             | 1.00E-13 ± 0.12 24.92±3.73 0                                    | nucl     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060925957      | hypothetical protein                                                             | 5.20E-18 ± 0.28 19.03±6.45 0                                    | E.R.     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
| gi|1060921067      | hypothetical protein                                                             | 4.10E-11 ± 0.24 9.5a±4.45 0                                    | cyto     |
Ps indicates protein score.
^WT, wild type
^Aga, Agamotype
^Tel, Teleomorph
^SL, subcellular location; cy, cytoplasm; cs, cytoskeleton; m, mitochondria; n: nuclear; ER, Endoplasmic reticulum; va, vacuole.; EM, Extracellular matrix
^M refers to number of peptides matched.
^C indicates coverage rate.

All the proteins are matched to Aspergillus cristatus, with the exception of spots 38, 67, 68 and 129 matched to Aspergillus ruber CBS 135680
### Supplemental Table 2  
Corresponding orthologs of the unknown proteins.

| Spot ID | NCBI accession no \(^a\) | NCBI accession no \(^b\) | Protein name | Organism | Identity \(^c\) | similarity \(^d\) |
|---------|--------------------------|---------------------------|--------------|-----------|-----------------|-----------------|
| 1       | gi|599153441               | XP_001272098.1             | conserved lysine-rich protein, putative | *Aspergillus clavatus* NRRL 1 | 59 | 68 |
| 7       | gi|599153985               | XP_001396216.1             | tropomyosin | *Aspergillus niger* CBS 513.88 | 93 | 98 |
| 8       | gi|599156398               | gb|KKZ65673.1               | RalA-binding protein 1 | *Emmonsia crescens* UAMH 3008 | 86 | 93 |
| 63      | gi|599156399               | KJK65500.1                | Zinc-finger domain protein | *Aspergillus parasiticus* SU-1 | 83 | 88 |
| 97      | gi|599159998               | GAA86756.1                | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase | *Aspergillus kawachii* IFO 4308 | 67 | 79 |
| 113     | gi|599150482               | GAA84457.1                | extracellular serine-rich protein | *Aspergillus kawachii* IFO 4308 | 68 | 80 |
| 116     | gi|599155181               | KFX42599.1                | Maintenance of telomere capping protein 1 | *Talaromyces marneffei* PM1 | 62 | 75 |
| 122     | gi|599159092               | WP_014209346.1            | DNA helicase | *Mycobacterium rhodesiae* | 27 | 43 |
| 127     | gi|584405813               | XP_001393280.2            | hypothetical protein | *Aspergillus niger* CBS 513.88 | 91 | 95 |
| 146     | gi|599160514               | KFY01418.1                | hypothetical protein | *Pseudogymnoascus pannorum* VKM F-3808 | 53 | 74 |
| 150     | gi|599159998               | GAA86756.1                | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase | *Aspergillus kawachii* IFO 4308 | 67 | 79 |
| 161     | gi|599159791               | dbj|GAA86176.1              | conidial hydrophobin Hyp1/RodA | *Aspergillus kawachii* IFO 4308 | 42 | 59 |
| 163     | gi|599159791               | dbj|GAA86176.1              | conidial hydrophobin Hyp2/RodA | *Aspergillus kawachii* IFO 4308 | 42 | 59 |
| 164     | gi|599159791               | dbj|GAA86176.1              | conidial hydrophobin Hyp3/RodA | *Aspergillus kawachii* IFO 4308 | 42 | 59 |

**BLASTP (NCBI)** was applied to the orthologs searching of the unknown proteins in Supplemental Table 1. The orthologs with the highest homology were selected.
a: protein accession number of the unknown proteins listed in Supplemental Table 1

b: The accession number of the orthologs

c: The extent to which two amino acid sequences are invariant

d: The similarities based on the scoring matrix used.