**Comparative proteomics in rice seedlings to characterize the resistance to cadmium stress by high-performance liquid chromatography-tandem mass spectrometry (HPLC-MS/MS) with isobaric tag for relative and absolute quantitation (iTRAQ)**

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Table S1:

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Accession | Description | 117-1 | 117-2 | 117-3 | 119-1 | 119-2 | 119-3 | 118-1 | 118-2 | 118-3 | 121-1 | 121-2 | 121-3 |
| A0A0P0V312 | Histone H2A OS=Oryza sativa subsp. japonica GN=Os01g0502700 PE=3 SV=1 | 95.6 | 89.2 | 88.2 | 106.3 | 111 | 109 | 96.5 | 96.7 | 91.7 | 101.5 | 103.1 | 111.2 |
| A0A0P0VBK7 | Os01g0896800 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os01g0896800 PE=3 SV=1 | 101.3 | 93.2 | 95.4 | 98.7 | 97.8 | 98.5 | 95.8 | 108.8 | 101.2 | 104.2 | 100.2 | 104.9 |
| A0A0P0VBL9 | Os01g0899425 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os01g0899425 PE=4 SV=1 | 96.6 | 99.1 | 98.6 | 109.5 | 105.9 | 109.3 | 91.9 | 96.8 | 91.9 | 101.9 | 98.2 | 100.1 |
| A0A0P0VHP9 | Os02g0287000 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os02g0287000 PE=3 SV=1 | 94.2 | 101.7 | 92.8 | 100 | 98.3 | 94 | 107.3 | 103.9 | 109.5 | 98.5 | 96.1 | 103.7 |
| A0A0P0VRI0 | Os02g0814700 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os02g0814700 PE=3 SV=1 | 88.5 | 97.7 | 88.9 | 101 | 99.2 | 103.2 | 96.8 | 104.6 | 96 | 113.6 | 98.6 | 111.9 |
| A0A0P0VRK8 | Os02g0818000 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os02g0818000 PE=4 SV=1 | 96.9 | 88.1 | 93.5 | 109 | 120.2 | 108.4 | 92.9 | 87.1 | 95 | 101.1 | 104.6 | 103 |
| A0A0P0VTX8 | Os03g0182600 protein OS=Oryza sativa subsp. japonica GN=Os03g0182600 PE=4 SV=1 | 99 | 96.8 | 95.3 | 102.7 | 103.3 | 98.5 | 98.9 | 93.1 | 105.2 | 99.4 | 106.8 | 100.9 |
| A0A0P0W2S8 | Os03g0704100 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os03g0704100 PE=4 SV=1 | 115.2 | 201.6 | 188.9 | 91.2 | 122.4 | 121.1 | 99.4 | 41.1 | 49.2 | 94.2 | 34.9 | 40.8 |
| A0A0P0W9W2 | Os04g0390000 protein OS=Oryza sativa subsp. japonica GN=Os04g0390000 PE=4 SV=1 | 98 | 100.8 | 110.2 | 98.6 | 87.1 | 75.8 | 99.8 | 112.5 | 124.5 | 103.6 | 99.5 | 89.5 |
| A0A0P0WA64 | Os04g0419600 protein OS=Oryza sativa subsp. japonica GN=Os04g0419600 PE=3 SV=1 | 90.4 | 98.4 | 95.7 | 101.5 | 97.6 | 97.5 | 104.2 | 109 | 104.4 | 104 | 95.1 | 102.4 |
| A0A0P0WAB9 | Acetyl-coenzyme A synthetase OS=Oryza sativa subsp. japonica GN=Os04g0404800 PE=3 SV=1 | 98.8 | 98.5 | 95.7 | 97.9 | 95.4 | 100 | 108.1 | 111.5 | 104.9 | 95.2 | 94.6 | 99.5 |
| A0A0P0WH35 | Os05g0110300 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os05g0110300 PE=4 SV=1 | 105.7 | 111.1 | 111.7 | 95.3 | 98.2 | 98.4 | 98.4 | 100.9 | 97.7 | 100.6 | 89.8 | 92.2 |
| A0A0P0WKD6 | Os05g0291700 protein OS=Oryza sativa subsp. japonica GN=Os05g0291700 PE=4 SV=1 | 88.4 | 82.9 | 85.9 | 110.3 | 120.8 | 112.3 | 90.8 | 79.9 | 90.4 | 110.5 | 116.4 | 111.4 |
| A0A0P0WL76 | Os05g0337400 protein OS=Oryza sativa subsp. japonica GN=Os05g0337400 PE=4 SV=1 | 95.2 | 97.3 | 95.9 | 112.4 | 113 | 108.9 | 82 | 78.4 | 85.1 | 110.4 | 111.3 | 110.1 |
| A0A0P0WP33 | Phosphoglycerate kinase OS=Oryza sativa subsp. japonica GN=Os05g0496200 PE=3 SV=1 | 106.5 | 105.5 | 105.5 | 99.7 | 99.4 | 99.2 | 93 | 96.1 | 94.4 | 100.7 | 99 | 100.9 |
| A0A0P0WWT3 | Os06g0484500 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os06g0484500 PE=4 SV=1 | 102.9 | 82.6 | 134.9 | 109.3 | 96.3 | 168.5 | 95.1 | 97.9 | 52.1 | 92.6 | 123.2 | 44.5 |
| A0A0P0WZL3 | D-3-phosphoglycerate dehydrogenase OS=Oryza sativa subsp. japonica GN=Os06g0655100 PE=3 SV=1 | 105 | 105.2 | 107.2 | 102.7 | 102.4 | 104.1 | 97.8 | 95.4 | 94.3 | 94.5 | 97 | 94.4 |
| A0A0P0X1Z2 | Os07g0123700 protein OS=Oryza sativa subsp. japonica GN=Os07g0123700 PE=4 SV=1 | 99.1 | 93.8 | 90.4 | 94.7 | 88.6 | 104.3 | 106.3 | 112 | 99.7 | 100 | 105.5 | 105.5 |
| A0A0P0XAY7 | Os08g0117200 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os08g0117200 PE=3 SV=1 | 94.8 | 93.3 | 92.5 | 100.5 | 99.8 | 101.1 | 103.3 | 105.8 | 104.7 | 101.4 | 101.1 | 101.8 |
| A0A0P0XEB3 | Os08g0266300 protein OS=Oryza sativa subsp. japonica GN=Os08g0266300 PE=4 SV=1 | 107.7 | 112.3 | 112 | 102.9 | 101.8 | 104.7 | 93.7 | 92.4 | 89.2 | 95.7 | 93.5 | 94.2 |
| A0A0P0XW86 | Os10g0492101 protein OS=Oryza sativa subsp. japonica GN=Os10g0492101 PE=4 SV=1 | 96.3 | 96.5 | 99.7 | 102.6 | 97.1 | 98.2 | 101.3 | 107.2 | 102.9 | 99.9 | 99.2 | 99.2 |
| A0A0P0XZB0 | Os11g0127800 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os11g0127800 PE=4 SV=1 | 110.9 | 110.4 | 109 | 97.1 | 99.7 | 98.6 | 94.8 | 93 | 94.6 | 97.2 | 96.9 | 97.7 |
| A0A0P0Y1Y5 | Adenosylhomocysteinase (Fragment) OS=Oryza sativa subsp. japonica GN=Os11g0455500 PE=3 SV=1 | 99.1 | 97.4 | 95.1 | 94.1 | 95.8 | 94.4 | 115.7 | 115.6 | 115 | 91.2 | 91.3 | 95.5 |
| A0A0P0Y3G3 | Os11g0544800 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os11g0544800 PE=3 SV=1 | 98.2 | 151.2 | 104 | 103.8 | 147.4 | 102.7 | 95.4 | 51.5 | 95.3 | 102.6 | 49.9 | 97.9 |
| A0A0P0YAL3 | Phenylalanine ammonia-lyase OS=Oryza sativa subsp. japonica GN=Os12g0520200 PE=3 SV=1 | 151.4 | 147.4 | 149.5 | 120.8 | 118.3 | 121.1 | 67.1 | 65.9 | 66.7 | 60.8 | 68.4 | 62.7 |
| A0A0P0YB77 | Os12g0541500 protein OS=Oryza sativa subsp. japonica GN=Os12g0541500 PE=4 SV=1 | 100.8 | 98.9 | 94.3 | 129.8 | 127.6 | 135.8 | 67.5 | 73.6 | 75.2 | 102 | 99.9 | 94.7 |
| A0MLU6 | Eukaryotic translation initiation factor 3 subunit E OS=Oryza sativa subsp. indica GN=OsI\_25391 PE=3 SV=1 | 94.9 | 90.8 | 91.2 | 95.2 | 97.1 | 96.2 | 107 | 105.9 | 108.1 | 103 | 106.1 | 104.5 |
| A2WJR2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_00059 PE=3 SV=1 | 98.3 | 97.2 | 98.3 | 105.9 | 98.2 | 102.7 | 93.9 | 103.8 | 94.6 | 101.9 | 100.8 | 104.4 |
| A2WLD9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_00648 PE=4 SV=1 | 101.5 | 101.6 | 102.8 | 108.3 | 104.4 | 111.6 | 91.1 | 98 | 87.4 | 99.1 | 96 | 98.2 |
| A2WLL0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_00725 PE=4 SV=1 | 92.3 | 90.4 | 92.5 | 90.6 | 90.8 | 92.1 | 114.5 | 114.9 | 113.7 | 102.6 | 104 | 101.6 |
| A2WLL2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_00727 PE=4 SV=1 | 99.9 | 103.8 | 97.4 | 93.9 | 89 | 92.4 | 104.4 | 115.4 | 109.1 | 101.8 | 91.8 | 101.1 |
| A2WLX8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_00846 PE=3 SV=1 | 99.4 | 101.3 | 100.2 | 98.6 | 101.3 | 98 | 103.2 | 92.6 | 97.4 | 98.9 | 104.9 | 104.4 |
| A2WML4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01081 PE=4 SV=1 | 80 | 81.1 | 79.1 | 112.2 | 107.2 | 116.1 | 78.1 | 90.5 | 76.5 | 129.7 | 121.3 | 128.3 |
| A2WN87 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01313 PE=4 SV=1 | 98.2 | 97.8 | 94.8 | 90.4 | 92.8 | 90.1 | 115.9 | 117 | 117.5 | 95.5 | 92.4 | 97.6 |
| A2WNR8 | Peroxidase OS=Oryza sativa subsp. indica GN=OsI\_01501 PE=3 SV=1 | 115.4 | 104.1 | 92 | 107.4 | 118.1 | 90.5 | 85.8 | 83.5 | 106.2 | 91.5 | 94.2 | 111.3 |
| A2WNX6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01556 PE=4 SV=1 | 106.2 | 113.8 | 109.9 | 100.5 | 102.2 | 104.5 | 91.8 | 92.5 | 87.4 | 101.5 | 91.5 | 98.2 |
| A2WQ40 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01974 PE=3 SV=1 | 94.3 | 97.7 | 104.3 | 99 | 88.7 | 91.8 | 105.5 | 118.5 | 106.6 | 101.2 | 95.2 | 97.2 |
| A2WQY7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_02273 PE=4 SV=1 | 105.8 | 104.3 | 104.8 | 100.9 | 97.2 | 100.2 | 100.1 | 101.5 | 101.6 | 93.2 | 96.9 | 93.4 |
| A2WRD4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_02420 PE=4 SV=1 | 105 | 97.3 | 104.9 | 93.1 | 88.9 | 86.8 | 112.8 | 113.7 | 122.9 | 89.1 | 100 | 85.3 |
| A2WS81 | Chlorophyll a-b binding protein, chloroplastic OS=Oryza sativa subsp. indica GN=OsI\_02717 PE=3 SV=1 | 85.1 | 78.2 | 73.9 | 107.2 | 105.1 | 109.4 | 79 | 76 | 71 | 128.7 | 140.7 | 145.7 |
| A2WT25 | Carbonic anhydrase OS=Oryza sativa subsp. indica GN=OsI\_03015 PE=3 SV=1 | 100.1 | 101.9 | 101.4 | 99.9 | 99.7 | 96.4 | 96.6 | 99.5 | 102.3 | 103.4 | 98.9 | 99.9 |
| A2WTA6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_03093 PE=4 SV=1 | 91.9 | 85 | 89.1 | 105.7 | 112.1 | 105.1 | 91 | 79.6 | 90.1 | 111.5 | 123.3 | 115.7 |
| A2WTC5 | Isocitrate dehydrogenase [NADP] OS=Oryza sativa subsp. indica GN=OsI\_03110 PE=3 SV=1 | 98.9 | 99.9 | 101.3 | 93.2 | 93.5 | 93.6 | 116.2 | 116 | 111.7 | 91.7 | 90.5 | 93.5 |
| A2WTF3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_03137 PE=3 SV=1 | 106.5 | 109 | 101 | 92.3 | 87.7 | 90.6 | 111.9 | 116.3 | 112.6 | 89.4 | 87 | 95.8 |
| A2WTQ2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_03241 PE=4 SV=1 | 100.7 | 99.5 | 102.6 | 89.9 | 87.6 | 91.6 | 107 | 105.5 | 100.2 | 102.4 | 107.4 | 105.7 |
| A2WTS1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_03263 PE=3 SV=1 | 99.5 | 100.5 | 95.7 | 103.8 | 116.6 | 116.1 | 99.8 | 82.4 | 87.3 | 96.9 | 100.4 | 101 |
| A2WTW6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_03315 PE=4 SV=1 | 93.9 | 92.7 | 90.8 | 97.7 | 100.1 | 99 | 112.7 | 110.5 | 110 | 95.7 | 96.7 | 100.2 |
| A2WUC5 | Glycine cleavage system P protein OS=Oryza sativa subsp. indica GN=OsI\_03474 PE=3 SV=1 | 112.9 | 109.5 | 108.3 | 100.6 | 97.2 | 101.4 | 96.1 | 104.9 | 96.1 | 90.4 | 88.4 | 94.1 |
| A2WUJ5 | Chlorophyll a-b binding protein, chloroplastic OS=Oryza sativa subsp. indica GN=OsI\_03546 PE=3 SV=1 | 89.8 | 109.7 | 96.2 | 101.1 | 97.3 | 99.9 | 98 | 86.2 | 84.7 | 111.1 | 106.7 | 119.2 |
| A2WUY5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_03697 PE=3 SV=1 | 102 | 103 | 104.7 | 98 | 97.4 | 99.7 | 105.3 | 106.3 | 103.3 | 94.7 | 93.3 | 92.3 |
| A2WVT8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04011 PE=3 SV=1 | 89.6 | 94.1 | 88.3 | 74.7 | 81.6 | 75.8 | 137.6 | 127.1 | 140.8 | 98.2 | 97.2 | 95 |
| A2WW27 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04105 PE=3 SV=1 | 98.1 | 99.9 | 102.3 | 98.3 | 102.7 | 98.5 | 104.1 | 101.1 | 99.9 | 99.5 | 96.3 | 99.2 |
| A2WXD9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04589 PE=4 SV=1 | 112.3 | 115.6 | 115.9 | 108.6 | 108.7 | 101.6 | 91.5 | 88.7 | 97.4 | 87.6 | 87.1 | 85.1 |
| A2WXS1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04723 PE=3 SV=1 | 97.2 | 97.1 | 99.4 | 98.9 | 95.6 | 96.9 | 105 | 100.6 | 102.4 | 98.9 | 106.7 | 101.2 |
| A2WYB1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04915 PE=4 SV=1 | 106.7 | 99.4 | 101.2 | 91.6 | 94.8 | 91.8 | 107.6 | 112.3 | 113.4 | 94.1 | 93.6 | 93.5 |
| A2WZV9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05501 PE=4 SV=1 | 92.3 | 96.9 | 91.3 | 97.2 | 98.3 | 88.2 | 103 | 108.1 | 116.5 | 107.5 | 96.7 | 104 |
| A2X0J1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05726 PE=4 SV=1 | 101.7 | 104.5 | 104.7 | 94.6 | 93.3 | 91.6 | 105.6 | 106.2 | 108.4 | 98.2 | 96 | 95.3 |
| A2X0N5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05771 PE=4 SV=1 | 102 | 98 | 96.7 | 98.6 | 104 | 100.3 | 103.9 | 95 | 104.7 | 95.6 | 103.1 | 98.2 |
| A2X1M1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06100 PE=4 SV=1 | 87.7 | 88.9 | 91.6 | 87.8 | 90.9 | 93.5 | 104.1 | 116.3 | 100 | 120.4 | 103.9 | 115 |
| A2X1T8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06165 PE=3 SV=1 | 99.8 | 106.1 | 96.4 | 119.7 | 108 | 108.7 | 74.5 | 86.3 | 92.8 | 106 | 99.6 | 102.1 |
| A2X1X4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06200 PE=4 SV=1 | 104.8 | 100.1 | 103.6 | 100.2 | 102.7 | 101 | 99.2 | 98.6 | 98.4 | 95.7 | 98.6 | 97 |
| A2X2W1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06527 PE=4 SV=1 | 93.8 | 98.8 | 104.7 | 103.2 | 102.2 | 101.4 | 92.8 | 93.3 | 101.6 | 110.2 | 105.7 | 92.4 |
| A2X335 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06619 PE=4 SV=1 | 91.8 | 90.8 | 136.5 | 108.4 | 110.8 | 89.1 | 89.8 | 81.5 | 79.1 | 110 | 117 | 95.3 |
| A2X358 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06639 PE=3 SV=1 | 101.1 | 101 | 93.3 | 110.8 | 108.1 | 119.8 | 84.8 | 90.6 | 83.2 | 103.3 | 100.3 | 103.8 |
| A2X3G6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06754 PE=4 SV=1 | 108.1 | 107.1 | 105.8 | 94.9 | 95.3 | 92.6 | 98.9 | 102.2 | 108.8 | 98 | 95.4 | 92.9 |
| A2X5H4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_07454 PE=4 SV=1 | 99.5 | 97.7 | 89.5 | 96.1 | 88.3 | 87.3 | 106.6 | 126.5 | 118.3 | 97.7 | 87.5 | 104.9 |
| A2X753 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08047 PE=3 SV=1 | 91.6 | 93.5 | 84.1 | 68 | 63.9 | 56.3 | 162.2 | 167.8 | 181.8 | 78.1 | 74.9 | 77.8 |
| A2X7C5 | Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Oryza sativa subsp. indica GN=OsI\_08117 PE=3 SV=1 | 105.1 | 101.9 | 105.7 | 89.3 | 93 | 89.1 | 110.6 | 112.1 | 111.6 | 94.9 | 93 | 93.6 |
| A2X847 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08402 PE=3 SV=1 | 92.2 | 86.5 | 74.5 | 100.9 | 107.6 | 126.5 | 104.6 | 94.8 | 79.9 | 102.3 | 111.2 | 119.1 |
| A2X8M1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08582 PE=3 SV=1 | 102.6 | 99.6 | 111.6 | 102.2 | 99.5 | 96.8 | 102.1 | 104.5 | 109.1 | 93.1 | 96.3 | 82.5 |
| A2X8Q3 | Soluble inorganic pyrophosphatase OS=Oryza sativa subsp. indica GN=IPP PE=2 SV=1 | 96.7 | 101.2 | 100.2 | 98.8 | 101.7 | 95.7 | 99.9 | 99 | 104.4 | 104.6 | 98 | 99.7 |
| A2X967 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08780 PE=4 SV=1 | 97.7 | 101.2 | 100.2 | 93.3 | 90.8 | 96.3 | 106.6 | 105.9 | 105.1 | 102.4 | 102.1 | 98.4 |
| A2X9N1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08949 PE=4 SV=1 | 98.5 | 97.7 | 90.1 | 96.7 | 97.9 | 96.3 | 93.1 | 102.6 | 102.1 | 111.6 | 101.8 | 111.5 |
| A2X9V8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09029 PE=4 SV=1 | 104.1 | 104.3 | 101.9 | 82.5 | 82.3 | 81.6 | 125 | 126.5 | 124.6 | 88.4 | 87 | 91.9 |
| A2XAI5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09267 PE=3 SV=1 | 107.9 | 104.7 | 108.5 | 93.8 | 92.9 | 93.5 | 108.8 | 112 | 110.1 | 89.5 | 90.4 | 88 |
| A2XAR1 | Proliferating cell nuclear antigen OS=Oryza sativa subsp. indica GN=OsI\_09344 PE=3 SV=1 | 98.5 | 92 | 97.4 | 102.4 | 114.6 | 101.6 | 100.7 | 87.5 | 98.7 | 98.5 | 106 | 102.3 |
| A2XAZ3 | Alcohol dehydrogenase class-3 OS=Oryza sativa subsp. indica GN=ADHIII PE=3 SV=1 | 93.6 | 85.2 | 90 | 92.4 | 92.3 | 90.3 | 110.3 | 110.7 | 109.4 | 103.7 | 111.9 | 110.3 |
| A2XB19 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09452 PE=3 SV=1 | 107.1 | 91 | 107.3 | 97.5 | 96.5 | 97 | 109.6 | 109.6 | 110.8 | 85.8 | 102.9 | 84.9 |
| A2XB94 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09539 PE=4 SV=1 | 124.5 | 120.8 | 129.7 | 85.3 | 95.1 | 83.8 | 119.5 | 106.2 | 112.7 | 70.7 | 78 | 73.8 |
| A2XBF5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09605 PE=4 SV=1 | 87.8 | 81.9 | 69.2 | 105.7 | 111.4 | 121.4 | 89.3 | 83.8 | 64.3 | 117.2 | 122.9 | 145.1 |
| A2XBV9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09778 PE=4 SV=1 | 94.9 | 89.6 | 89.3 | 105 | 110.5 | 105.1 | 92.9 | 96.1 | 98.6 | 107.2 | 103.8 | 107 |
| A2XBY3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09799 PE=3 SV=1 | 98.6 | 98 | 90.4 | 109.1 | 108.2 | 109.8 | 90.2 | 94.1 | 84.7 | 102.1 | 99.7 | 115.1 |
| A2XC62 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09885 PE=3 SV=1 | 85.5 | 93 | 96.6 | 115.5 | 113.2 | 105.7 | 84.6 | 92.7 | 94.4 | 114.4 | 101.1 | 103.4 |
| A2XC67 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09891 PE=3 SV=1 | 87.9 | 91.8 | 93.6 | 132.2 | 124 | 115 | 79.6 | 83 | 95.4 | 100.3 | 101.2 | 96.1 |
| A2XCL6 | AAA-ATPase OS=Oryza sativa subsp. indica GN=cdc48 PE=2 SV=1 | 99.8 | 97 | 99.4 | 95.9 | 94.1 | 91.6 | 106 | 116.3 | 118.2 | 98.3 | 92.6 | 90.7 |
| A2XCU8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10133 PE=3 SV=1 | 103.2 | 100.6 | 104.9 | 96.1 | 99.2 | 92.9 | 103.4 | 105.9 | 104.4 | 97.3 | 94.3 | 97.8 |
| A2XD75 | Proteasome subunit alpha type OS=Oryza sativa subsp. indica GN=OsI\_10259 PE=3 SV=1 | 97.2 | 95.2 | 96.9 | 93.7 | 93.4 | 94.4 | 108.9 | 115.3 | 110.2 | 100.2 | 96.1 | 98.5 |
| A2XDW2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10505 PE=3 SV=1 | 81 | 102.8 | 101 | 73.2 | 91.2 | 92.5 | 137.7 | 112.8 | 110.6 | 108.1 | 93.2 | 95.9 |
| A2XE09 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10555 PE=3 SV=1 | 90.2 | 105 | 99.5 | 106 | 112.8 | 104.6 | 93 | 83.2 | 95.8 | 110.8 | 99 | 100.2 |
| A2XET8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10852 PE=4 SV=1 | 108.7 | 110.4 | 110.9 | 105.4 | 124.6 | 106.1 | 92.7 | 93.1 | 92.4 | 93.2 | 71.9 | 90.6 |
| A2XEZ0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10905 PE=4 SV=1 | 80.8 | 87 | 83.4 | 85.3 | 86.9 | 89.7 | 121.7 | 119.2 | 111.6 | 112.2 | 106.9 | 115.3 |
| A2XF36 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10952 PE=4 SV=1 | 90.2 | 104.5 | 91 | 91.7 | 91.4 | 94.2 | 119.9 | 118.8 | 121.7 | 98.3 | 85.4 | 93 |
| A2XF65 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_11006 PE=3 SV=1 | 98.8 | 112 | 99.2 | 88.1 | 94.3 | 89.2 | 71.7 | 83.1 | 81.4 | 141.4 | 110.6 | 130.3 |
| A2XFC7 | L-ascorbate peroxidase 1, cytosolic OS=Oryza sativa subsp. indica GN=APX1 PE=2 SV=1 | 79.6 | 67.6 | 67.8 | 70.1 | 72.1 | 69.6 | 124.2 | 127.6 | 128.8 | 126.2 | 132.7 | 133.8 |
| A2XFI3 | Pyruvate decarboxylase 2 OS=Oryza sativa subsp. indica GN=PDC2 PE=2 SV=2 | 94.7 | 100.3 | 100.2 | 98.7 | 98.9 | 98.6 | 112 | 102.9 | 102.9 | 94.6 | 97.8 | 98.3 |
| A2XFY5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_11285 PE=4 SV=1 | 96.3 | 99.3 | 95.5 | 96.5 | 91.1 | 97.9 | 112.8 | 113.8 | 112.3 | 94.4 | 95.8 | 94.3 |
| A2XFY9 | Adenylosuccinate lyase OS=Oryza sativa subsp. indica GN=OsI\_11289 PE=3 SV=1 | 115.8 | 103.2 | 103.9 | 103.8 | 96.9 | 98.6 | 95.2 | 107.7 | 101 | 85.3 | 92.3 | 96.5 |
| A2XG06 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_11307 PE=4 SV=1 | 98.6 | 99.2 | 100.8 | 114.1 | 110.2 | 116.9 | 79.5 | 85.5 | 74.5 | 107.8 | 105.1 | 107.9 |
| A2XG88 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_11398 PE=4 SV=1 | 95.8 | 93.6 | 88.5 | 108.5 | 109.1 | 110.7 | 90.1 | 90.2 | 92.8 | 105.6 | 107.1 | 108.1 |
| A2XGG9 | Ribosomal protein L19 OS=Oryza sativa subsp. indica GN=OsI\_11477 PE=3 SV=1 | 104.7 | 102.9 | 104.2 | 98.5 | 102.4 | 101.1 | 100.1 | 97.1 | 97.6 | 96.7 | 97.6 | 97.2 |
| A2XHR1 | Sucrose synthase OS=Oryza sativa subsp. indica GN=OsI\_11950 PE=3 SV=1 | 82.2 | 77.8 | 85.8 | 107.1 | 102.1 | 104.8 | 96.4 | 104.5 | 100.6 | 114.2 | 115.6 | 108.8 |
| A2XHR6 | 40S ribosomal protein SA OS=Oryza sativa subsp. indica GN=OsI\_11954 PE=3 SV=1 | 97.5 | 100.4 | 95.6 | 99.8 | 97.4 | 97.9 | 101.9 | 107.5 | 105.5 | 100.8 | 94.7 | 101.1 |
| A2XK95 | Ferredoxin OS=Oryza sativa subsp. indica GN=OsI\_12871 PE=3 SV=1 | 75.4 | 71.4 | 72.5 | 128.8 | 142.1 | 135.9 | 78.3 | 67.6 | 70.5 | 117.5 | 118.9 | 121 |
| A2XL95 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13240 PE=3 SV=1 | 110.6 | 127.3 | 163.6 | 103.7 | 118.5 | 145.5 | 102 | 85.4 | 48.3 | 83.6 | 68.7 | 42.6 |
| A2XLA1 | Coatomer subunit alpha OS=Oryza sativa subsp. indica GN=OsI\_13245 PE=4 SV=1 | 99.4 | 97.3 | 98.3 | 94.5 | 94.4 | 94.5 | 110.9 | 108.7 | 111.5 | 95.3 | 99.7 | 95.7 |
| A2XLS8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13431 PE=4 SV=1 | 97.7 | 98.2 | 97.1 | 100 | 100.2 | 98.6 | 102.1 | 102.1 | 106.3 | 100.2 | 99.4 | 98 |
| A2XLW5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13470 PE=4 SV=1 | 98.7 | 110.4 | 94.6 | 99.4 | 107.1 | 99.3 | 102.2 | 86.8 | 102.2 | 99.8 | 95.7 | 104 |
| A2XM21 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13529 PE=3 SV=1 | 97.1 | 95.5 | 100.3 | 109.1 | 107.1 | 105.7 | 88.2 | 96.5 | 95.2 | 105.7 | 100.9 | 98.8 |
| A2XMP7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13813 PE=3 SV=1 | 102.2 | 105.2 | 96.2 | 85.1 | 93.1 | 91.7 | 127 | 119.4 | 128.1 | 85.6 | 82.3 | 84 |
| A2XMV1 | Glutamate dehydrogenase 1, mitochondrial OS=Oryza sativa subsp. indica GN=GDH1 PE=3 SV=2 | 109.5 | 104.8 | 101.1 | 100.8 | 98 | 100.3 | 102.6 | 106 | 106.2 | 87.1 | 91.2 | 92.3 |
| A2XMY4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13912 PE=3 SV=1 | 90.6 | 98.2 | 95.3 | 102.4 | 100.2 | 102.2 | 104.5 | 102.4 | 100.9 | 102.5 | 99.2 | 101.5 |
| A2XMY6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13914 PE=3 SV=1 | 92.1 | 92.6 | 99 | 101 | 102.6 | 98.6 | 105.8 | 100.5 | 99.5 | 101.1 | 104.2 | 102.9 |
| A2XN63 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13996 PE=3 SV=1 | 95 | 94.8 | 95.6 | 103.3 | 99.9 | 101.4 | 103.5 | 105.7 | 105.5 | 98.2 | 99.6 | 97.5 |
| A2XN99 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14032 PE=3 SV=1 | 103 | 104.4 | 101.3 | 92.7 | 87.7 | 92.6 | 119.2 | 123.4 | 118.7 | 85 | 84.5 | 87.4 |
| A2XNC0 | Methylenetetrahydrofolate reductase OS=Oryza sativa subsp. indica GN=OsI\_14054 PE=3 SV=1 | 98.9 | 95.2 | 103 | 94 | 94.7 | 90.6 | 116.2 | 116.5 | 118.9 | 90.8 | 93.7 | 87.5 |
| A2XP52 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14356 PE=4 SV=1 | 89.8 | 91.3 | 93.6 | 101.5 | 108.2 | 103.2 | 101.6 | 91.7 | 95.4 | 107 | 108.8 | 107.8 |
| A2XPN8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14602 PE=4 SV=1 | 84.5 | 83 | 84.3 | 95.3 | 99.3 | 101.6 | 114.9 | 109.1 | 103.3 | 105.3 | 108.6 | 110.7 |
| A2XQV4 | Electron transfer flavoprotein subunit beta, mitochondrial OS=Oryza sativa subsp. indica GN=ETFB PE=3 SV=1 | 111.3 | 111.6 | 99.5 | 78.6 | 81.5 | 78.9 | 109.1 | 117.8 | 112.3 | 101 | 89.1 | 109.2 |
| A2XRZ0 | Probable aldo-keto reductase 2 OS=Oryza sativa subsp. indica GN=OsI\_15387 PE=3 SV=1 | 124.5 | 80 | 111.2 | 87.2 | 90.6 | 97.3 | 100.6 | 112.8 | 101.7 | 87.8 | 116.6 | 89.9 |
| A2XSY5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_15719 PE=4 SV=1 | 97.5 | 99.5 | 101.6 | 102.4 | 96.3 | 96.5 | 100.6 | 96 | 104.8 | 99.5 | 108.1 | 97.2 |
| A2XTX6 | 3-oxoacyl-[acyl-carrier-protein] synthase OS=Oryza sativa subsp. indica GN=OsI\_16057 PE=3 SV=1 | 101.2 | 94.2 | 99.8 | 101.8 | 111.7 | 102.1 | 102.7 | 111.1 | 103.3 | 94.3 | 82.9 | 94.7 |
| A2XUS0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_16357 PE=4 SV=1 | 110.2 | 116.1 | 105 | 88.7 | 88.3 | 90.7 | 106.5 | 107.5 | 109 | 94.6 | 88.1 | 95.2 |
| A2XUU7 | Glyceraldehyde-3-phosphate dehydrogenase OS=Oryza sativa subsp. indica GN=OsI\_16384 PE=3 SV=1 | 96.3 | 97.1 | 100.6 | 95.6 | 100.8 | 89.5 | 113.3 | 105.2 | 119.4 | 94.8 | 96.9 | 90.5 |
| A2XV50 | 6,7-dimethyl-8-ribityllumazine synthase OS=Oryza sativa subsp. indica GN=OsI\_16488 PE=3 SV=1 | 96.1 | 103 | 104.1 | 94.1 | 90 | 88.3 | 112.7 | 108 | 110.5 | 97.2 | 99 | 97.1 |
| A2XVY3 | Elongation factor G, chloroplastic OS=Oryza sativa subsp. indica GN=OsI\_16800 PE=3 SV=1 | 91.3 | 91.7 | 89.8 | 115.5 | 112.9 | 119.4 | 84.6 | 92.2 | 82.3 | 108.7 | 103.1 | 108.5 |
| A2XXN8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17449 PE=4 SV=1 | 98.1 | 99.6 | 103.1 | 93.5 | 92 | 96.2 | 116.4 | 115.3 | 110 | 92.1 | 93 | 90.7 |
| A2XY00 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17578 PE=4 SV=1 | 101.3 | 105.8 | 99.5 | 105 | 109.9 | 98.8 | 96.3 | 90.3 | 99.7 | 97.5 | 94 | 102 |
| A2XY09 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17588 PE=3 SV=1 | 91.5 | 125.4 | 107.1 | 109.9 | 97.4 | 93.9 | 103.9 | 90.3 | 109.6 | 94.7 | 87 | 89.5 |
| A2XY57 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17640 PE=4 SV=1 | 106.7 | 87.4 | 104.7 | 92.5 | 90.2 | 86.2 | 118.9 | 120.9 | 122.6 | 82 | 101.5 | 86.5 |
| A2XYU1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17872 PE=4 SV=1 | 113.5 | 92 | 101.7 | 88.5 | 104.8 | 91.4 | 108 | 108.9 | 111 | 89.9 | 94.4 | 95.8 |
| A2XYZ3 | Pyruvate kinase OS=Oryza sativa subsp. indica GN=OsI\_17926 PE=3 SV=1 | 102.7 | 93.7 | 105 | 88.4 | 88.8 | 87.6 | 112.6 | 117.5 | 118.9 | 96.3 | 99.9 | 88.5 |
| A2XZE6 | Peptidyl-prolyl cis-trans isomerase OS=Oryza sativa subsp. indica GN=OsI\_18093 PE=3 SV=1 | 106.9 | 114.2 | 100.3 | 99.8 | 105.7 | 109.1 | 103.8 | 95.1 | 98.3 | 89.5 | 85.1 | 92.3 |
| A2XZQ4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_18214 PE=4 SV=1 | 98.7 | 106.5 | 103.9 | 100.4 | 88 | 89.3 | 107.2 | 112.9 | 114.7 | 93.8 | 92.6 | 92.1 |
| A2Y043 | Peroxidase OS=Oryza sativa subsp. indica GN=OsI\_18348 PE=3 SV=1 | 103.2 | 97.9 | 89.1 | 135.2 | 115 | 89.5 | 71.3 | 93.5 | 104.9 | 90.3 | 93.6 | 116.5 |
| A2Y053 | S-adenosylmethionine synthase 1 OS=Oryza sativa subsp. indica GN=SAM1 PE=2 SV=2 | 95.2 | 95.6 | 96.9 | 79.7 | 85.4 | 92.9 | 158.2 | 134.6 | 124.2 | 66.9 | 84.4 | 86 |
| A2Y0P2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_18566 PE=4 SV=1 | 91.8 | 91.2 | 86.6 | 115.5 | 116.1 | 123.6 | 81.5 | 84.8 | 74.6 | 111.2 | 107.8 | 115.3 |
| A2Y0Q1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_18575 PE=3 SV=1 | 94.2 | 92.6 | 97.6 | 102.4 | 97.2 | 102.2 | 100.5 | 107.9 | 100.8 | 102.9 | 102.4 | 99.5 |
| A2Y2C4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_19156 PE=4 SV=1 | 113.3 | 103.3 | 111.8 | 90.7 | 85.6 | 92.6 | 115.3 | 122.3 | 110.6 | 80.7 | 88.8 | 85 |
| A2Y3I6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_19569 PE=4 SV=1 | 98.3 | 102.8 | 96.2 | 96.7 | 95.2 | 99.5 | 107.4 | 106.9 | 107.7 | 97.7 | 95.1 | 96.6 |
| A2Y4Y3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20059 PE=4 SV=1 | 98.8 | 97.3 | 96.6 | 101 | 99.2 | 101.6 | 100.3 | 101.9 | 102.9 | 99.9 | 101.7 | 98.9 |
| A2Y5G2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20232 PE=3 SV=1 | 95.6 | 103 | 94.5 | 100.8 | 106.5 | 102.7 | 102.8 | 94.2 | 103.6 | 100.8 | 96.3 | 99.2 |
| A2Y5W6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20389 PE=4 SV=1 | 79.9 | 82.6 | 84.7 | 116 | 117.1 | 113.7 | 83.8 | 86.4 | 83.5 | 120.3 | 113.9 | 118.1 |
| A2Y727 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20842 PE=4 SV=1 | 84.1 | 97.3 | 107.8 | 100.2 | 104.8 | 91 | 104.4 | 101.5 | 102.5 | 111.3 | 96.4 | 98.8 |
| A2Y746 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20861 PE=4 SV=1 | 99.6 | 75.5 | 111.6 | 88.6 | 75.6 | 93 | 117 | 133 | 103.4 | 94.8 | 115.9 | 92.1 |
| A2Y7J4 | Eukaryotic translation initiation factor 3 subunit D OS=Oryza sativa subsp. indica GN=OsI\_21011 PE=3 SV=1 | 85.6 | 93.6 | 105.2 | 97.4 | 96.5 | 99.5 | 112.6 | 113.5 | 103.2 | 104.4 | 96.4 | 92.1 |
| A2Y7R5 | GTP-binding nuclear protein Ran-2 OS=Oryza sativa subsp. indica GN=RAN2 PE=2 SV=1 | 104.6 | 97.7 | 100.3 | 88.8 | 94.4 | 80.4 | 117.8 | 112.8 | 125.8 | 88.7 | 95.1 | 93.5 |
| A2Y7Y4 | Carboxypeptidase OS=Oryza sativa subsp. indica GN=OsI\_21150 PE=3 SV=1 | 132.5 | 128.6 | 134.9 | 92.7 | 96.3 | 93.8 | 96.2 | 98.2 | 95.8 | 78.7 | 76.9 | 75.6 |
| A2Y886 | Plastocyanin, chloroplastic OS=Oryza sativa subsp. indica GN=PETE PE=2 SV=1 | 107.2 | 108.4 | 101.3 | 104.7 | 100 | 106.1 | 90.8 | 92.9 | 90.6 | 97.4 | 98.8 | 102.1 |
| A2Y8A0 | Acyl-coenzyme A oxidase OS=Oryza sativa subsp. indica GN=OsI\_21277 PE=3 SV=1 | 97.9 | 96.4 | 95.9 | 97.5 | 99.4 | 98.3 | 117.6 | 117.5 | 112.6 | 87 | 86.7 | 93.2 |
| A2Y8K1 | 60S ribosomal protein L13 OS=Oryza sativa subsp. indica GN=OsI\_21382 PE=2 SV=1 | 96 | 96.1 | 96.6 | 99.1 | 104.2 | 98.7 | 102.8 | 96.5 | 102.9 | 102 | 103.2 | 101.8 |
| A2YBK1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_22484 PE=3 SV=1 | 113.7 | 108.3 | 106.1 | 92 | 92 | 90.8 | 107.7 | 112 | 113.9 | 86.6 | 87.6 | 89.1 |
| A2YBW4 | Glycosyltransferase OS=Oryza sativa subsp. indica GN=OsI\_22594 PE=3 SV=1 | 64.8 | 56 | 55.2 | 115 | 101.8 | 124.6 | 93.3 | 98.4 | 91.1 | 126.9 | 143.8 | 129.2 |
| A2YBX1 | Glycosyltransferase OS=Oryza sativa subsp. indica GN=OsI\_22600 PE=3 SV=1 | 77.3 | 80.6 | 92.1 | 91.7 | 97.1 | 93.9 | 112.2 | 104.6 | 102.5 | 118.8 | 117.6 | 111.5 |
| A2YG06 | Phosphoglycerate kinase OS=Oryza sativa subsp. indica GN=OsI\_24050 PE=3 SV=1 | 116.9 | 110.8 | 118.5 | 81.2 | 78.6 | 82.4 | 125.1 | 125 | 120 | 76.9 | 85.6 | 79.1 |
| A2YG12 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_24055 PE=3 SV=1 | 94.4 | 93.5 | 94.9 | 104.4 | 106.4 | 103.5 | 95.7 | 93.9 | 94.5 | 105.5 | 106.2 | 107.1 |
| A2YGS3 | Delta-aminolevulinic acid dehydratase OS=Oryza sativa subsp. indica GN=OsI\_24384 PE=3 SV=1 | 92.8 | 77.5 | 79.5 | 107.1 | 118.5 | 99.4 | 90.5 | 83.9 | 93.4 | 109.6 | 120.2 | 127.7 |
| A2YH08 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_24473 PE=3 SV=1 | 106.2 | 105 | 103.8 | 84.7 | 85.3 | 86.9 | 125.1 | 123.6 | 123.6 | 84 | 86.1 | 85.8 |
| A2YHW8 | Peptidylprolyl isomerase OS=Oryza sativa subsp. indica GN=OsI\_24792 PE=4 SV=1 | 102.3 | 97.5 | 101.3 | 95.8 | 98 | 98.2 | 97.7 | 102.4 | 96.6 | 104.2 | 102.2 | 103.8 |
| A2YIF3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_24995 PE=4 SV=1 | 102.3 | 100 | 102.8 | 99.8 | 98.8 | 100.3 | 103.6 | 108.5 | 107.4 | 94.3 | 92.7 | 89.6 |
| A2YIK9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_25059 PE=4 SV=1 | 107.7 | 100.7 | 103.2 | 99.3 | 99.3 | 101.2 | 88.8 | 102 | 95.4 | 104.3 | 98 | 100.2 |
| A2YIS2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_25124 PE=4 SV=1 | 98.1 | 91.4 | 78.4 | 103.5 | 73.9 | 81.7 | 99.5 | 118.3 | 120.1 | 98.9 | 116.4 | 119.8 |
| A2YJC1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_25335 PE=3 SV=1 | 96.7 | 94.7 | 98.9 | 102.9 | 98.2 | 97.7 | 101.6 | 110.8 | 105.8 | 98.7 | 96.3 | 97.6 |
| A2YMD1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_26387 PE=4 SV=1 | 97.3 | 110.3 | 100.7 | 98.6 | 93.9 | 97.4 | 94.6 | 99.2 | 96 | 109.5 | 96.6 | 105.9 |
| A2YML2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_26464 PE=3 SV=1 | 94.5 | 91.1 | 92.5 | 106.6 | 107.7 | 102.3 | 97.5 | 97.9 | 98.4 | 101.4 | 103.3 | 106.8 |
| A2YND5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_26746 PE=4 SV=1 | 93.9 | 96.3 | 85.8 | 106.8 | 106.2 | 99.8 | 97 | 106.2 | 107.7 | 102.3 | 91.4 | 106.7 |
| A2YP40 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27029 PE=4 SV=1 | 91.8 | 97.5 | 96.9 | 79.1 | 87.2 | 87.7 | 143 | 129.3 | 126.9 | 86.1 | 86 | 88.4 |
| A2YP75 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27068 PE=4 SV=1 | 94.8 | 98.6 | 98.3 | 97.9 | 92.9 | 92.8 | 111.5 | 111.1 | 111.7 | 95.9 | 97.4 | 97.2 |
| A2YP98 | NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Oryza sativa subsp. indica GN=OsI\_27090 PE=3 SV=1 | 95.9 | 96.8 | 94.3 | 91.9 | 92.4 | 97.5 | 112.9 | 108.3 | 105.8 | 99.3 | 102.5 | 102.4 |
| A2YPX2 | Peroxidase OS=Oryza sativa subsp. indica GN=OsI\_27326 PE=3 SV=1 | 113.6 | 124.9 | 120.8 | 85.4 | 80.8 | 75.9 | 109.9 | 114.8 | 113.6 | 91.1 | 79.5 | 89.8 |
| A2YQ40 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27400 PE=4 SV=1 | 92 | 94.4 | 94.2 | 97.2 | 97.6 | 97.6 | 105.2 | 109.2 | 104.8 | 105.7 | 98.9 | 103.4 |
| A2YQD9 | Ferredoxin-1, chloroplastic OS=Oryza sativa subsp. indica GN=ADI1 PE=1 SV=1 | 90.2 | 92.6 | 92.7 | 108.2 | 108.1 | 106.7 | 95.7 | 94.1 | 94.4 | 105.8 | 105.3 | 106.2 |
| A2YQM4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27592 PE=4 SV=1 | 100.9 | 91.1 | 107.1 | 95.1 | 87.9 | 97.5 | 106.7 | 119.9 | 103.4 | 97.3 | 101.2 | 92 |
| A2YS08 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_28106 PE=4 SV=1 | 111.6 | 110.1 | 118.2 | 88.4 | 94.8 | 85.9 | 111.2 | 108.1 | 111 | 88.9 | 87.1 | 84.9 |
| A2YSY8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_28439 PE=3 SV=1 | 109.3 | 110.9 | 115.3 | 89.5 | 92 | 97.9 | 104.1 | 105 | 104.5 | 97.1 | 92 | 82.2 |
| A2YU91 | Glucose-1-phosphate adenylyltransferase OS=Oryza sativa subsp. indica GN=OsI\_28901 PE=3 SV=1 | 95.3 | 98.4 | 100.5 | 97.4 | 98.3 | 92.5 | 106.5 | 105.9 | 106.5 | 100.8 | 97.4 | 100.5 |
| A2YUR3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_29063 PE=4 SV=1 | 82.1 | 84 | 90.3 | 80.9 | 79.9 | 91 | 117.7 | 121.5 | 112.2 | 119.3 | 114.7 | 106.5 |
| A2YUU5 | T-complex protein 1 subunit delta OS=Oryza sativa subsp. indica GN=OsI\_29091 PE=3 SV=1 | 103.6 | 103 | 104.5 | 100.5 | 95.1 | 103.1 | 104.1 | 107.5 | 99.2 | 91.8 | 94.3 | 93.1 |
| A2YVG3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_29320 PE=3 SV=1 | 95.8 | 98.1 | 103.3 | 98.2 | 99 | 97.7 | 107.8 | 106.2 | 106.3 | 98.2 | 96.7 | 92.7 |
| A2YWB4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_29626 PE=3 SV=1 | 103.2 | 111.7 | 103.2 | 99.8 | 90 | 96.2 | 103.2 | 103.4 | 104.6 | 93.9 | 94.8 | 96.1 |
| A2YWS7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_29793 PE=4 SV=1 | 96.6 | 97.2 | 90.3 | 95.3 | 95.4 | 99 | 105.6 | 107 | 105 | 102.5 | 100.4 | 105.6 |
| A2YXJ3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_30061 PE=4 SV=1 | 101 | 100.1 | 92.7 | 93.2 | 96 | 81.3 | 108 | 104 | 136.1 | 97.8 | 99.9 | 89.9 |
| A2YXM1 | Peptidylprolyl isomerase OS=Oryza sativa subsp. indica GN=OsI\_30091 PE=4 SV=1 | 101.1 | 101.8 | 92.5 | 91.3 | 84 | 99.7 | 107.3 | 115.6 | 100 | 100.2 | 98.6 | 107.8 |
| A2YXU4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_30161 PE=3 SV=1 | 100.2 | 102.6 | 103.6 | 99.3 | 95.6 | 100.4 | 97.6 | 105.4 | 97.5 | 103 | 96.4 | 98.5 |
| A2YY14 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_30233 PE=4 SV=1 | 93 | 91.5 | 88.5 | 103.4 | 110.6 | 109.1 | 102.7 | 97 | 101.4 | 101 | 100.9 | 101.1 |
| A2YZA3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_30678 PE=4 SV=1 | 92.5 | 89.7 | 87.5 | 97.5 | 98.4 | 97.8 | 100.1 | 102.2 | 101.6 | 109.9 | 109.7 | 113.1 |
| A2Z0D1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_31052 PE=4 SV=1 | 103.4 | 104.2 | 100.4 | 94.9 | 94.1 | 90.4 | 110.1 | 106.4 | 114.6 | 91.6 | 95.3 | 94.6 |
| A2Z0P4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_31170 PE=4 SV=1 | 91.1 | 96.2 | 89.6 | 80.7 | 82.6 | 86.1 | 120.1 | 117.1 | 122.9 | 108.1 | 104 | 101.4 |
| A2Z1W9 | 1-aminocyclopropane-1-carboxylate oxidase 1 OS=Oryza sativa subsp. indica GN=ACO1 PE=2 SV=1 | 94.5 | 85.8 | 85.1 | 110.9 | 121.5 | 123.2 | 95.3 | 90.4 | 88.9 | 99.3 | 102.3 | 102.8 |
| A2Z263 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_31697 PE=3 SV=1 | 107 | 113.2 | 107.9 | 70 | 67.9 | 70.5 | 145.4 | 147.2 | 148 | 77.6 | 71.7 | 73.6 |
| A2Z2J3 | 60S ribosomal protein l9 OS=Oryza sativa subsp. indica GN=OsI\_31831 PE=2 SV=1 | 95.2 | 95.7 | 94.2 | 98.6 | 95.5 | 97.5 | 108.7 | 111 | 108.3 | 97.4 | 97.7 | 100 |
| A2Z2U1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_31936 PE=4 SV=1 | 100 | 99.1 | 95.2 | 82.9 | 93.2 | 92.7 | 107.9 | 109.8 | 115.2 | 109.3 | 97.9 | 97 |
| A2Z3G7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_32171 PE=3 SV=1 | 102.9 | 102.5 | 101.7 | 104.6 | 104.2 | 105.1 | 90.6 | 93.5 | 89.8 | 101.9 | 99.8 | 103.4 |
| A2Z3H3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_32177 PE=4 SV=1 | 100.2 | 96.2 | 94.2 | 91.3 | 91.3 | 80.3 | 112.9 | 121.6 | 122.6 | 95.6 | 90.9 | 102.9 |
| A2Z3I6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_32190 PE=3 SV=1 | 134.4 | 143.9 | 138.4 | 95.8 | 93.4 | 94.2 | 85.2 | 77.6 | 82.3 | 84.6 | 85.2 | 85 |
| A2Z3W4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_32329 PE=4 SV=1 | 98 | 100.9 | 97 | 110.4 | 107.6 | 104.3 | 87.6 | 90.5 | 95.5 | 103.9 | 101 | 103.3 |
| A2Z468 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_32437 PE=4 SV=1 | 101.6 | 103.5 | 109 | 94.9 | 90.3 | 84.7 | 105.3 | 110.4 | 118.8 | 98.3 | 95.8 | 87.5 |
| A2Z469 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_32438 PE=4 SV=1 | 100.2 | 97.4 | 101.6 | 101.1 | 100.3 | 101.5 | 98.5 | 100.4 | 96.1 | 100.2 | 101.9 | 100.7 |
| A2Z5I0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_32907 PE=4 SV=1 | 92.8 | 98.7 | 97.1 | 96.6 | 97.3 | 98.7 | 102.9 | 103.8 | 104.5 | 107.7 | 100.1 | 99.7 |
| A2Z7B3 | GDP-mannose 3,5-epimerase 1 OS=Oryza sativa subsp. indica GN=OsI\_032456 PE=2 SV=1 | 97 | 95.4 | 95.1 | 102.4 | 101.3 | 104.6 | 100.9 | 102.9 | 99 | 99.6 | 100.4 | 101.4 |
| A2Z8U8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34142 PE=4 SV=1 | 101.3 | 101.5 | 100.4 | 101.6 | 104.5 | 103.5 | 97.3 | 94.1 | 92.7 | 99.8 | 99.9 | 103.3 |
| A2Z925 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34214 PE=4 SV=1 | 105 | 106.1 | 105 | 93.1 | 95 | 98.6 | 99.6 | 103.7 | 100 | 102.3 | 95.2 | 96.4 |
| A2Z942 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34233 PE=4 SV=1 | 106.9 | 108.9 | 104 | 95.8 | 97 | 94.8 | 96.5 | 92.1 | 90.2 | 100.8 | 102 | 111 |
| A2Z9J9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34399 PE=4 SV=1 | 83.7 | 90.1 | 98.3 | 69.4 | 83.5 | 84.1 | 175.7 | 151.7 | 134.8 | 71.3 | 74.8 | 82.9 |
| A2Z9L8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34428 PE=3 SV=1 | 111.3 | 116.6 | 111.1 | 73.1 | 73.9 | 78.7 | 115.1 | 115.3 | 116.5 | 100.5 | 94.2 | 93.8 |
| A2Z9L9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34429 PE=3 SV=1 | 108.5 | 100.7 | 105.3 | 112.2 | 112.2 | 112.1 | 76.8 | 87.9 | 81.9 | 102.6 | 99.3 | 100.8 |
| A2ZAB3 | 60S ribosomal protein L27 OS=Oryza sativa subsp. indica GN=OsI\_34676 PE=2 SV=1 | 89.3 | 90.2 | 89.1 | 98 | 97.8 | 96.7 | 111.1 | 115.8 | 110.6 | 101.7 | 96.2 | 103.6 |
| A2ZAT2 | Non-specific lipid-transfer protein OS=Oryza sativa subsp. indica GN=OsI\_34868 PE=3 SV=1 | 126.3 | 121 | 123.8 | 81.3 | 83.5 | 81.1 | 104.8 | 108.3 | 106.3 | 87.6 | 87.1 | 88.9 |
| A2ZCQ7 | 60S ribosomal protein L10-1 OS=Oryza sativa subsp. indica GN=SC34 PE=2 SV=2 | 90.2 | 88.9 | 92.4 | 99.5 | 99.1 | 103.2 | 105.9 | 109.5 | 104.7 | 104.5 | 102.5 | 99.7 |
| A2ZD01 | Chlorophyll a-b binding protein, chloroplastic OS=Oryza sativa subsp. indica GN=OsI\_35663 PE=3 SV=1 | 104.4 | 104.7 | 101.9 | 90.5 | 89.9 | 92.2 | 81.8 | 79.7 | 83.3 | 123.2 | 125.8 | 122.6 |
| A2ZFY8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_36693 PE=4 SV=1 | 79.1 | 76.1 | 73.4 | 82.3 | 80.5 | 84 | 131.1 | 130.9 | 137.8 | 107.5 | 112.5 | 104.7 |
| A2ZIF8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_37606 PE=3 SV=1 | 103.8 | 95.5 | 93.3 | 99.1 | 99.8 | 102.2 | 102.9 | 105.1 | 104.1 | 94.1 | 99.5 | 100.4 |
| A2ZIS0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_37721 PE=4 SV=1 | 89.4 | 87 | 83.6 | 103 | 108.4 | 104.7 | 90.8 | 84.9 | 86.4 | 116.9 | 119.7 | 125.4 |
| A2ZJH7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_37967 PE=3 SV=1 | 81.8 | 78.2 | 79.6 | 117.9 | 122 | 116.8 | 88.5 | 85.1 | 88 | 111.8 | 114.7 | 115.6 |
| A2ZK43 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_38200 PE=4 SV=1 | 90.2 | 106.3 | 93.4 | 98.1 | 93.8 | 101.1 | 124.2 | 110.6 | 111.3 | 87.5 | 89.3 | 94.3 |
| A2ZLC1 | Elongation factor Ts, mitochondrial OS=Oryza sativa subsp. indica GN=EFTS PE=3 SV=1 | 87.8 | 89.5 | 88.4 | 113.6 | 109.8 | 112.7 | 86.5 | 93.7 | 87.8 | 112.1 | 107 | 111.1 |
| A2ZLS7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_38771 PE=3 SV=1 | 96.4 | 98.8 | 98.2 | 100.3 | 100.4 | 98.4 | 101 | 101.3 | 99.9 | 102.4 | 99.6 | 103.5 |
| A2ZLT9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_38783 PE=4 SV=1 | 97.2 | 99.3 | 105.4 | 106.1 | 100.5 | 98.8 | 103.4 | 106.3 | 103.5 | 93.3 | 93.9 | 92.3 |
| A2ZMY2 | Cysteine synthase OS=Oryza sativa subsp. indica GN=OsI\_39190 PE=3 SV=1 | 89.9 | 96.1 | 96.2 | 83.9 | 88.3 | 85.1 | 121 | 119.8 | 123.8 | 105.1 | 95.8 | 95 |
| A2ZN76 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_39291 PE=4 SV=1 | 105.5 | 107.8 | 98 | 102.2 | 101.6 | 92.6 | 104.5 | 101 | 106.6 | 87.8 | 89.6 | 102.8 |
| A3BLC3 | Ribosome-recycling factor, chloroplastic OS=Oryza sativa subsp. japonica GN=Os07g0570700 PE=2 SV=2 | 107.2 | 104.7 | 112.8 | 103.2 | 99.9 | 103 | 92.1 | 96 | 92.9 | 97.5 | 99.4 | 91.3 |
| A3C6G9 | Glycine cleavage system H protein, mitochondrial OS=Oryza sativa subsp. japonica GN=GDCSH PE=1 SV=1 | 108.4 | 109.8 | 108 | 99.3 | 100.1 | 99.7 | 102.2 | 101.1 | 102 | 90.1 | 88.9 | 90.3 |
| A6N0M9 | Nucleoside diphosphate kinase 1 OS=Oryza sativa subsp. indica GN=NDKR PE=1 SV=1 | 103.4 | 105 | 104.5 | 86 | 86.1 | 86.4 | 114.9 | 115.6 | 115.1 | 95.7 | 93.2 | 94 |
| B6RGY0 | Peptide deformylase 1A, chloroplastic OS=Oryza sativa subsp. japonica GN=PDF1A PE=2 SV=1 | 103.6 | 102.4 | 103 | 100.4 | 109.5 | 101.8 | 102.7 | 104.6 | 101.3 | 93.3 | 83.5 | 93.9 |
| B7EBF9 | Os04g0459900 protein OS=Oryza sativa subsp. japonica GN=Os04g0459900 PE=2 SV=1 | 113.7 | 105.2 | 104.5 | 95.5 | 98.9 | 103.5 | 101.7 | 102.6 | 102 | 89.1 | 93.3 | 90 |
| B8A6U3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_03104 PE=4 SV=1 | 97.9 | 96.1 | 105.3 | 99.6 | 103.8 | 99.2 | 110.3 | 111.1 | 99.3 | 92.2 | 89 | 96.2 |
| B8A750 | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex OS=Oryza sativa subsp. indica GN=OsI\_01602 PE=3 SV=1 | 112.7 | 115.9 | 105.4 | 92.5 | 88.5 | 95.3 | 105.6 | 109.7 | 99 | 89.2 | 85.9 | 100.2 |
| B8A7H0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01750 PE=4 SV=1 | 99.7 | 102.3 | 101.6 | 105.1 | 100.9 | 98.2 | 100 | 100.7 | 109.4 | 95.2 | 96.1 | 90.9 |
| B8A7X3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01883 PE=4 SV=1 | 98.8 | 98.4 | 98.8 | 108.4 | 105.7 | 109.1 | 89.9 | 97.8 | 93 | 103 | 98 | 99.1 |
| B8A8A8 | Peroxidase OS=Oryza sativa subsp. indica GN=OsI\_02005 PE=3 SV=1 | 102.2 | 100.8 | 98.1 | 110.9 | 94.8 | 99.9 | 95 | 108.5 | 103.9 | 91.9 | 95.9 | 98.1 |
| B8A8E2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04951 PE=4 SV=1 | 104.7 | 99.7 | 103.9 | 94 | 95.7 | 96.8 | 102.1 | 100.9 | 99.6 | 99.2 | 103.7 | 99.6 |
| B8A8F0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04962 PE=3 SV=1 | 97.7 | 101.5 | 88.7 | 93.9 | 92.5 | 91.8 | 116.5 | 113.6 | 123.3 | 91.9 | 92.5 | 96.2 |
| B8A8G2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04995 PE=4 SV=1 | 103.5 | 93.6 | 94.2 | 91 | 97.7 | 97.1 | 112.6 | 106.6 | 103.5 | 92.9 | 102.1 | 105.2 |
| B8A8H2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05010 PE=3 SV=1 | 95.3 | 99.6 | 101.5 | 88.6 | 86.3 | 80.3 | 128.4 | 131.4 | 140.4 | 87.7 | 82.6 | 77.8 |
| B8A8L8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_02088 PE=4 SV=1 | 102 | 99.3 | 102.4 | 102.4 | 101.4 | 101.4 | 93.6 | 96.8 | 94.1 | 102.1 | 102.5 | 102.1 |
| B8A940 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05159 PE=4 SV=1 | 101.6 | 98.2 | 105.5 | 96.1 | 96.9 | 96.1 | 108.1 | 109.4 | 106.8 | 94.3 | 95.4 | 91.6 |
| B8AAT9 | V-type proton ATPase subunit OS=Oryza sativa subsp. indica GN=OsI\_02618 PE=3 SV=1 | 107.7 | 103.6 | 108.8 | 99 | 96.4 | 96.9 | 106.5 | 108.8 | 106.8 | 86.7 | 91.2 | 87.6 |
| B8AAX3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04124 PE=4 SV=1 | 98.4 | 100.5 | 99.5 | 94.1 | 94.6 | 97.9 | 107.1 | 107.3 | 105.1 | 100.4 | 97.6 | 97.5 |
| B8AB01 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01001 PE=3 SV=1 | 93.5 | 88.1 | 88.8 | 87.3 | 95.9 | 96.9 | 110 | 107.3 | 107.4 | 109.1 | 108.6 | 106.8 |
| B8AB29 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01055 PE=4 SV=1 | 93.1 | 85.6 | 90.2 | 96.2 | 103.4 | 106.6 | 101.9 | 101 | 94.9 | 108.9 | 110 | 108.3 |
| B8AB88 | Proteasome subunit alpha type OS=Oryza sativa subsp. indica GN=OsI\_04163 PE=3 SV=1 | 99.1 | 101.8 | 100.4 | 110.7 | 91.6 | 98.8 | 104.1 | 113.5 | 103.1 | 86.1 | 93.1 | 97.7 |
| B8ABA7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04213 PE=4 SV=1 | 100.3 | 102.1 | 103.5 | 91.5 | 92.4 | 90.6 | 111.7 | 111.4 | 107.3 | 96.5 | 94.1 | 98.5 |
| B8ABJ9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_02797 PE=4 SV=1 | 98.7 | 106 | 99.2 | 99.1 | 107.8 | 102.1 | 103.4 | 97.2 | 104.1 | 98.8 | 89 | 94.6 |
| B8ABU1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01215 PE=3 SV=1 | 103.8 | 107.3 | 88.2 | 88.8 | 90 | 100.3 | 119.5 | 114.7 | 120.8 | 87.9 | 87.9 | 90.6 |
| B8AC39 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04429 PE=4 SV=1 | 96.5 | 103.1 | 93.4 | 88.6 | 88.1 | 95.9 | 110.9 | 104.5 | 108.6 | 104 | 104.3 | 102 |
| B8ACF1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_04454 PE=4 SV=1 | 111.9 | 115 | 105.7 | 78.2 | 81 | 88.7 | 134.3 | 124.1 | 134.6 | 75.6 | 79.9 | 70.9 |
| B8ACF5 | Alpha-1,4 glucan phosphorylase OS=Oryza sativa subsp. indica GN=OsI\_04460 PE=3 SV=1 | 95.7 | 93.9 | 97.3 | 86 | 80.2 | 88.1 | 120 | 129 | 117.1 | 98.3 | 96.9 | 97.5 |
| B8ACL5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_01428 PE=4 SV=1 | 111.8 | 110.2 | 122.6 | 81.7 | 93.6 | 92.4 | 115.4 | 106.2 | 107.6 | 91 | 90 | 77.4 |
| B8ACR9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_00013 PE=4 SV=1 | 100.9 | 101.3 | 106.5 | 93.1 | 92.9 | 89.4 | 109.4 | 110.3 | 108.8 | 96.5 | 95.6 | 95.3 |
| B8AD25 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_00236 PE=4 SV=1 | 93.6 | 96.7 | 98.4 | 92.6 | 82.4 | 85 | 125 | 147.5 | 125.2 | 88.8 | 73.5 | 91.4 |
| B8AD93 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_00389 PE=3 SV=1 | 99.1 | 99.4 | 100 | 93.5 | 93.9 | 94.5 | 108.4 | 108.4 | 105.9 | 99.1 | 98.3 | 99.6 |
| B8ADH7 | Phospholipase D OS=Oryza sativa subsp. indica GN=OsI\_00588 PE=3 SV=1 | 106.9 | 110.1 | 107.5 | 89.7 | 92.3 | 93.8 | 112.6 | 107.5 | 107.3 | 90.8 | 90.1 | 91.4 |
| B8ADR9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06236 PE=4 SV=1 | 103.7 | 101 | 107.5 | 95.1 | 98.6 | 93.9 | 109 | 107.5 | 101.7 | 92.3 | 92.9 | 96.9 |
| B8ADY7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_07685 PE=4 SV=1 | 98.5 | 98.6 | 96.3 | 96.4 | 97.8 | 94.4 | 100.5 | 99.2 | 102.1 | 104.6 | 104.5 | 107.1 |
| B8AE20 | Eukaryotic translation initiation factor 3 subunit G OS=Oryza sativa subsp. indica GN=OsI\_09223 PE=3 SV=1 | 100.6 | 89.6 | 98.5 | 99.8 | 95.7 | 95.6 | 96 | 112 | 107 | 103.6 | 102.8 | 98.9 |
| B8AED8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09310 PE=4 SV=1 | 88.3 | 90.1 | 86.9 | 104.8 | 105.4 | 109.3 | 88.1 | 91.8 | 92.2 | 118.8 | 112.7 | 111.7 |
| B8AEF1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09347 PE=4 SV=1 | 103.1 | 114.1 | 104.5 | 87.1 | 82.2 | 88.8 | 114.2 | 111.6 | 111.7 | 95.5 | 92 | 95 |
| B8AEK0 | Citrate synthase OS=Oryza sativa subsp. indica GN=OsI\_06467 PE=3 SV=1 | 104.2 | 108 | 106.7 | 101.2 | 89.5 | 97.9 | 115.7 | 95.8 | 116.6 | 78.9 | 106.7 | 78.9 |
| B8AEQ9 | Elongation factor Tu OS=Oryza sativa subsp. indica GN=OsI\_07899 PE=3 SV=1 | 95.6 | 96.5 | 96.2 | 104.1 | 105.4 | 105.8 | 97.8 | 96.1 | 94.6 | 102.5 | 101.9 | 103.5 |
| B8AEU4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09443 PE=4 SV=1 | 97.5 | 100 | 96.6 | 96.4 | 97.2 | 93.6 | 110.5 | 107.9 | 109.1 | 95.6 | 95 | 100.7 |
| B8AEX3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06526 PE=3 SV=1 | 97.4 | 93.1 | 93.1 | 80.2 | 94 | 80.6 | 138 | 116.4 | 142.8 | 84.4 | 96.5 | 83.4 |
| B8AFE0 | GrpE protein homolog OS=Oryza sativa subsp. indica GN=OsI\_08039 PE=3 SV=1 | 97.7 | 96.6 | 96.7 | 100 | 98.2 | 95.8 | 100.9 | 105.3 | 108.4 | 101.5 | 99.8 | 99.1 |
| B8AFN7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06722 PE=3 SV=1 | 96.4 | 99.2 | 91.2 | 85.9 | 86.7 | 94.7 | 136.9 | 127.9 | 125 | 80.8 | 86.2 | 89.1 |
| B8AG23 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08304 PE=4 SV=1 | 99.2 | 101.4 | 100.1 | 117.8 | 122.7 | 120.2 | 72.3 | 66.9 | 66.3 | 110.7 | 109 | 113.4 |
| B8AG27 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08312 PE=4 SV=1 | 102.6 | 105.7 | 102 | 88.1 | 92.4 | 86.3 | 112.5 | 110.4 | 111.6 | 96.8 | 91.4 | 100.1 |
| B8AGH9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05588 PE=4 SV=1 | 99.4 | 94.4 | 95.4 | 100.3 | 107.2 | 105.5 | 96.7 | 95.3 | 95.2 | 103.6 | 103 | 103.9 |
| B8AGN1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_07017 PE=4 SV=1 | 98.2 | 100.3 | 104 | 102.4 | 99.4 | 100.2 | 97.7 | 100.8 | 92.7 | 101.7 | 99.4 | 103 |
| B8AGZ1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05674 PE=4 SV=1 | 80.6 | 83.6 | 77 | 122.1 | 118.2 | 124.3 | 85.4 | 88.2 | 86.1 | 111.8 | 110 | 112.7 |
| B8AH08 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05707 PE=4 SV=1 | 95.1 | 100.2 | 106.2 | 96.1 | 92.6 | 88.3 | 110.2 | 100.9 | 109.1 | 98.6 | 106.2 | 96.4 |
| B8AHF9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_05817 PE=4 SV=1 | 104.6 | 125.9 | 129.3 | 102.1 | 113.3 | 103.1 | 92.4 | 92.7 | 87.1 | 101 | 68.2 | 80.6 |
| B8AHM8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08713 PE=3 SV=1 | 101.8 | 102.7 | 90.4 | 87.6 | 84.4 | 97.4 | 124.2 | 125.8 | 107.4 | 86.4 | 87.2 | 104.8 |
| B8AI07 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08794 PE=4 SV=1 | 98.9 | 100.4 | 100.8 | 107.6 | 108.6 | 107.3 | 94.1 | 92.6 | 91.5 | 99.4 | 98.5 | 100.4 |
| B8AI32 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08851 PE=4 SV=1 | 96 | 97.9 | 105 | 91.8 | 100.8 | 85.6 | 115.2 | 112 | 117.6 | 96.9 | 89.3 | 91.9 |
| B8AI99 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_07299 PE=4 SV=1 | 106.9 | 98 | 91.4 | 101.8 | 94.2 | 91.2 | 95.3 | 103.2 | 105.2 | 96.1 | 104.6 | 112.2 |
| B8AID9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08886 PE=4 SV=1 | 99.3 | 101.7 | 102 | 94.6 | 95.1 | 95.4 | 111.9 | 110.8 | 104.3 | 94.2 | 92.4 | 98.3 |
| B8AIF7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08911 PE=4 SV=1 | 107.1 | 102 | 104 | 100.6 | 109.7 | 102 | 88.8 | 91.3 | 92.8 | 103.5 | 97.1 | 101.3 |
| B8AIG0 | Starch synthase, chloroplastic/amyloplastic OS=Oryza sativa subsp. indica GN=SSII-2 PE=3 SV=1 | 99.8 | 102.5 | 99.5 | 96.4 | 99.5 | 96.5 | 101.2 | 101.8 | 101.2 | 102.6 | 96.2 | 102.8 |
| B8AIG1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_08919 PE=4 SV=1 | 99 | 100.1 | 98.8 | 94 | 100.3 | 92.7 | 104.2 | 105.2 | 106.6 | 102.8 | 94.4 | 101.8 |
| B8AIH2 | Phosphoglycerate kinase OS=Oryza sativa subsp. indica GN=OsI\_06015 PE=3 SV=1 | 100.9 | 100 | 95.2 | 88.6 | 92.9 | 94.4 | 120.4 | 116 | 118.4 | 90 | 91.1 | 92 |
| B8AIH4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_06001 PE=4 SV=1 | 101.1 | 98.9 | 104.3 | 96.3 | 96.8 | 97.3 | 106.3 | 108.3 | 105.2 | 96.3 | 96 | 93.2 |
| B8AJ26 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_07469 PE=4 SV=1 | 95.4 | 100.6 | 109.4 | 95.7 | 88.7 | 92.5 | 108.2 | 104.2 | 107.5 | 100.7 | 106.5 | 90.6 |
| B8AJ36 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_07554 PE=4 SV=1 | 102.2 | 101.4 | 102.3 | 96.9 | 98.9 | 99.1 | 102.2 | 100.4 | 100 | 98.7 | 99.2 | 98.6 |
| B8AJH5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09155 PE=3 SV=1 | 96.6 | 93.7 | 96.7 | 104.3 | 103.1 | 104.5 | 100 | 98.4 | 94.7 | 99.1 | 104.8 | 104 |
| B8AJX7 | Serine hydroxymethyltransferase OS=Oryza sativa subsp. indica GN=OsI\_13440 PE=3 SV=1 | 100.9 | 101.6 | 103.6 | 97.4 | 96 | 96.2 | 102 | 101.5 | 97.3 | 99.7 | 100.9 | 102.9 |
| B8AJZ3 | Translocase of chloroplast OS=Oryza sativa subsp. indica GN=OsI\_10695 PE=3 SV=1 | 97.8 | 93.5 | 92.1 | 100.7 | 98.6 | 99.4 | 103.7 | 103.9 | 102 | 97.8 | 103.9 | 106.5 |
| B8AK27 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10762 PE=3 SV=1 | 98.9 | 86 | 98.4 | 100.9 | 106 | 106.1 | 95.7 | 101.5 | 92.1 | 104.5 | 106.5 | 103.4 |
| B8AKA5 | Chorismate synthase OS=Oryza sativa subsp. indica GN=OsI\_10797 PE=3 SV=1 | 94.2 | 96 | 92.2 | 96.7 | 98.2 | 99.2 | 108.9 | 111.8 | 116.1 | 100.2 | 94.1 | 92.5 |
| B8AKD7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10855 PE=4 SV=1 | 96.5 | 94.3 | 100.1 | 97.7 | 94.6 | 89.1 | 112.9 | 122.3 | 123.4 | 92.9 | 88.8 | 87.4 |
| B8AKQ1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10925 PE=4 SV=1 | 93 | 95.4 | 93.8 | 99.4 | 95.2 | 101.1 | 106.6 | 113.6 | 101.5 | 101 | 95.8 | 103.6 |
| B8AKQ8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10864 PE=3 SV=1 | 99.9 | 98.8 | 97.7 | 112.8 | 110 | 107 | 78.5 | 83.6 | 91 | 108.8 | 107.7 | 104.3 |
| B8AL25 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_10996 PE=4 SV=1 | 99 | 97.7 | 86 | 99.9 | 100.2 | 99.6 | 108.1 | 111.8 | 103 | 93.1 | 90.3 | 111.5 |
| B8ALD1 | Thioredoxin OS=Oryza sativa subsp. indica GN=OsI\_13929 PE=3 SV=1 | 117.4 | 113.1 | 113.1 | 77.7 | 84.6 | 79.5 | 123 | 114.9 | 121 | 81.9 | 87.4 | 86.4 |
| B8ALJ1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_11062 PE=3 SV=1 | 98.3 | 93.8 | 100.3 | 106.1 | 112.3 | 107.4 | 86.2 | 86.4 | 85.4 | 109.3 | 107.5 | 106.8 |
| B8ALV6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09743 PE=4 SV=1 | 92.1 | 92.6 | 96.8 | 113.2 | 109.7 | 108.2 | 81 | 90.6 | 88.2 | 113.7 | 107.2 | 106.9 |
| B8AMC6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14118 PE=3 SV=1 | 100.1 | 105.9 | 105 | 98.8 | 97.7 | 113.7 | 103.3 | 104.5 | 92.3 | 97.8 | 91.9 | 89 |
| B8AMQ6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14162 PE=4 SV=1 | 84 | 93.4 | 88.1 | 117.3 | 109.1 | 115.7 | 90.5 | 96.4 | 92.5 | 108.1 | 101.2 | 103.8 |
| B8AMW5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_09969 PE=3 SV=1 | 100.5 | 88.6 | 94.6 | 98.2 | 87.6 | 97.3 | 107.1 | 115.7 | 111.1 | 94.2 | 108.1 | 97 |
| B8AN00 | Glucose-6-phosphate 1-dehydrogenase OS=Oryza sativa subsp. indica GN=OsI\_11322 PE=3 SV=1 | 105.7 | 103.4 | 104.4 | 106.9 | 109.1 | 109.1 | 93.8 | 88.3 | 91.6 | 93.7 | 99.2 | 94.9 |
| B8AN85 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14295 PE=4 SV=1 | 88.5 | 92.6 | 93 | 106.2 | 95.2 | 118 | 94.1 | 111.9 | 78.8 | 111.2 | 100.3 | 110.1 |
| B8ANL0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_12872 PE=4 SV=1 | 101 | 107.5 | 105.6 | 87.4 | 88.6 | 91 | 125.3 | 113.9 | 116.6 | 86.3 | 90 | 86.8 |
| B8APD5 | Sucrose synthase OS=Oryza sativa subsp. indica GN=OsI\_11498 PE=3 SV=1 | 96.1 | 99.9 | 97.1 | 80.6 | 83.7 | 88 | 138.6 | 131.4 | 128.6 | 84.7 | 84.9 | 86.3 |
| B8APD9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_11506 PE=4 SV=1 | 94.2 | 93 | 87.8 | 91.4 | 96.3 | 88.4 | 112.1 | 112.7 | 108.1 | 102.4 | 98.1 | 115.7 |
| B8AQZ3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_11955 PE=3 SV=1 | 96.5 | 101.4 | 97 | 100.8 | 96.1 | 97.2 | 103.4 | 104.8 | 108.3 | 99.4 | 97.8 | 97.6 |
| B8AR14 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13383 PE=4 SV=1 | 101.6 | 109.3 | 105 | 93.6 | 84.7 | 89.3 | 99.5 | 104.4 | 104 | 105.3 | 101.5 | 101.8 |
| B8AR23 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_13396 PE=3 SV=1 | 92.9 | 96.5 | 94.2 | 98.3 | 97.3 | 104.1 | 104.9 | 103.7 | 92.6 | 103.8 | 102.6 | 109.1 |
| B8ARP4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_16594 PE=4 SV=1 | 102.5 | 97 | 80.2 | 103.2 | 83.9 | 134.1 | 98.8 | 124.8 | 87 | 95.4 | 94.4 | 98.6 |
| B8ARS2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17972 PE=4 SV=1 | 102.4 | 110.1 | 100.2 | 95 | 98.7 | 99.3 | 107.6 | 100.5 | 104.9 | 95.1 | 90.7 | 95.6 |
| B8ART5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17998 PE=3 SV=1 | 103.1 | 98.1 | 104.3 | 100.3 | 95.9 | 99.6 | 97.5 | 105.7 | 98.5 | 99.2 | 100.3 | 97.6 |
| B8ARV5 | Phosphomannomutase OS=Oryza sativa subsp. indica GN=OsI\_17966 PE=3 SV=1 | 95.9 | 98.6 | 96.2 | 97.7 | 93.9 | 91.1 | 109.1 | 111.1 | 114.2 | 97.3 | 96.4 | 98.5 |
| B8ASC1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_16722 PE=4 SV=1 | 81.1 | 88.7 | 92.8 | 101.8 | 103.8 | 103.1 | 97.9 | 98.6 | 91.7 | 119.2 | 108.8 | 112.3 |
| B8ASD9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_16758 PE=3 SV=1 | 89.6 | 86.7 | 91 | 63.9 | 45.9 | 46.3 | 174 | 212.1 | 208.8 | 72.5 | 55.3 | 53.9 |
| B8ATG9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_15758 PE=4 SV=1 | 93.1 | 101.8 | 94.7 | 92.6 | 88 | 90.5 | 117.7 | 125.1 | 111.1 | 96.6 | 85.1 | 103.7 |
| B8ATS0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_15790 PE=4 SV=1 | 101 | 89.5 | 102.3 | 108.2 | 94.8 | 101.6 | 93.5 | 130 | 99.5 | 97.4 | 85.7 | 96.6 |
| B8ATY0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14495 PE=4 SV=1 | 99.7 | 109.7 | 104.1 | 104.8 | 96.5 | 101.4 | 101.1 | 95.3 | 99.8 | 94.4 | 98.6 | 94.7 |
| B8AU34 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_16005 PE=4 SV=1 | 97.4 | 99.3 | 105.4 | 106.4 | 106.7 | 112.1 | 92.9 | 88.4 | 89.5 | 103.4 | 105.5 | 93 |
| B8AU70 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17346 PE=4 SV=1 | 88.5 | 89.7 | 85.2 | 110.8 | 112.6 | 118.6 | 97.9 | 96.1 | 87.5 | 102.8 | 101.6 | 108.6 |
| B8AU81 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14566 PE=4 SV=1 | 81.5 | 92 | 84.9 | 108.5 | 102.7 | 102.1 | 85.3 | 93 | 91.5 | 124.7 | 112.4 | 121.5 |
| B8AUL8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_14695 PE=4 SV=1 | 94.1 | 99.1 | 97.8 | 99.7 | 87.3 | 91.3 | 117.7 | 113.2 | 112.2 | 88.5 | 100.5 | 98.7 |
| B8AV46 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_16244 PE=3 SV=1 | 90.2 | 88.5 | 90.7 | 97.2 | 105.3 | 100.9 | 107.5 | 100.9 | 99.3 | 105.1 | 105.3 | 109.1 |
| B8AVZ8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17824 PE=4 SV=1 | 105.2 | 110.9 | 101.8 | 93.1 | 87.2 | 96.1 | 104.1 | 108.4 | 98.6 | 97.6 | 93.5 | 103.5 |
| B8AW08 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_17769 PE=4 SV=1 | 100.6 | 94.2 | 96.8 | 98.6 | 103.7 | 109.3 | 106.7 | 105.3 | 101.1 | 94.1 | 96.8 | 92.9 |
| B8AW52 | Lactoylglutathione lyase OS=Oryza sativa subsp. indica GN=OsI\_19332 PE=3 SV=1 | 102.5 | 107.3 | 102 | 92.8 | 91.5 | 98.2 | 104.1 | 113.6 | 101.7 | 100.6 | 87.6 | 98.1 |
| B8AW69 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20809 PE=3 SV=1 | 98.3 | 102.4 | 99.9 | 95.8 | 91.1 | 100.2 | 106.7 | 109.5 | 102.2 | 99.2 | 97 | 97.6 |
| B8AW91 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20777 PE=4 SV=1 | 105.9 | 106.8 | 112.3 | 92.6 | 87.8 | 91.6 | 108.7 | 114.2 | 106.3 | 92.7 | 91.2 | 89.8 |
| B8AWA3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20870 PE=4 SV=1 | 112.4 | 100 | 108.6 | 93.1 | 90.9 | 91.1 | 104.7 | 111.4 | 108.1 | 89.8 | 97.7 | 92.2 |
| B8AWB5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_19367 PE=4 SV=1 | 103.7 | 105 | 111.4 | 95.6 | 91.8 | 94.8 | 106 | 108.7 | 102 | 94.7 | 94.5 | 91.8 |
| B8AXG9 | V-type proton ATPase subunit C OS=Oryza sativa subsp. indica GN=OsI\_21221 PE=3 SV=1 | 107.8 | 117.6 | 102.1 | 91.3 | 81.8 | 91.9 | 111.1 | 117.2 | 108.1 | 89.8 | 83.4 | 97.9 |
| B8AXU6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_19812 PE=3 SV=1 | 101.6 | 100.9 | 99.1 | 113.4 | 109.1 | 111.5 | 78 | 84.3 | 84.1 | 107 | 105.7 | 105.4 |
| B8AXY6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_18449 PE=3 SV=1 | 100.7 | 101.4 | 98.6 | 96.1 | 102.6 | 100 | 109.5 | 102.7 | 110.3 | 93.7 | 93.2 | 91.1 |
| B8AY06 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_19859 PE=4 SV=1 | 109.6 | 107.2 | 107.7 | 100.7 | 105.8 | 101.5 | 99.2 | 99.1 | 99.8 | 90.4 | 87.8 | 91.1 |
| B8AY43 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_18469 PE=3 SV=1 | 102.7 | 100.2 | 97 | 97.6 | 95.8 | 97.6 | 105.2 | 110.4 | 111.3 | 94.5 | 93.5 | 94.1 |
| B8AY81 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_19925 PE=4 SV=1 | 94.6 | 103.5 | 99.8 | 95.2 | 96.5 | 95.7 | 106 | 106.7 | 98.5 | 104.1 | 93.3 | 106 |
| B8AYJ5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20075 PE=4 SV=1 | 102.1 | 106 | 98.6 | 87.3 | 102.9 | 99.4 | 118.2 | 110 | 119.6 | 92.4 | 81.1 | 82.3 |
| B8AYT8 | Delta-1-pyrroline-5-carboxylate synthase OS=Oryza sativa subsp. indica GN=OsI\_20190 PE=3 SV=1 | 98 | 92.7 | 98.7 | 95.1 | 99.3 | 93.9 | 112.8 | 111.1 | 110 | 94 | 96.9 | 97.4 |
| B8AZA5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20353 PE=4 SV=1 | 101.7 | 99.9 | 103 | 95.1 | 95.3 | 99.6 | 106.6 | 106.4 | 102.1 | 96.6 | 98.5 | 95.4 |
| B8AZP1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_19058 PE=4 SV=1 | 102.9 | 97.8 | 106.2 | 90.5 | 90.1 | 91.7 | 112.4 | 116.5 | 113.6 | 94.2 | 95.6 | 88.5 |
| B8AZS4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20556 PE=3 SV=1 | 100.8 | 103.4 | 102.4 | 95.9 | 86 | 88.1 | 98.5 | 132.8 | 124.4 | 104.8 | 77.7 | 85.1 |
| B8AZT0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20569 PE=4 SV=1 | 96.4 | 92.4 | 97.8 | 91.4 | 87.5 | 92.4 | 99.3 | 118.5 | 109.3 | 112.9 | 101.6 | 100.5 |
| B8B082 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20751 PE=4 SV=1 | 94.5 | 96.9 | 96.6 | 103 | 99 | 102.8 | 94.5 | 101.5 | 91.7 | 108 | 102.6 | 109 |
| B8B092 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_20689 PE=4 SV=1 | 98.5 | 103 | 104.5 | 103.7 | 105.5 | 103.3 | 96.6 | 92.4 | 93.1 | 101.2 | 99.1 | 99.1 |
| B8B0E2 | Stromal processing peptidase, chloroplastic OS=Oryza sativa subsp. indica GN=OsI\_23765 PE=1 SV=2 | 93.1 | 96.8 | 98.9 | 97.8 | 95 | 92.2 | 101.7 | 107.2 | 112.6 | 107.3 | 101 | 96.3 |
| B8B0N6 | Glycosyltransferase OS=Oryza sativa subsp. indica GN=OsI\_22585 PE=3 SV=1 | 100 | 82 | 90.5 | 154.6 | 89.1 | 137.5 | 73.1 | 110.3 | 90.7 | 72.4 | 118.5 | 81.3 |
| B8B107 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_24004 PE=3 SV=1 | 101.6 | 96.9 | 102.9 | 91.2 | 90.5 | 90.9 | 113.1 | 118.1 | 113.4 | 94.2 | 94.4 | 92.9 |
| B8B198 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_21278 PE=3 SV=1 | 95.6 | 93.4 | 91 | 97.4 | 102.9 | 96.8 | 102.5 | 101.4 | 106 | 104.6 | 102.3 | 106.2 |
| B8B2A2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_21538 PE=3 SV=1 | 97.6 | 98 | 100.1 | 97.1 | 91.9 | 91.2 | 105.1 | 105.5 | 117.2 | 100.1 | 104.6 | 91.5 |
| B8B2F2 | Formate dehydrogenase, mitochondrial OS=Oryza sativa subsp. indica GN=OsI\_23019 PE=3 SV=1 | 98.8 | 100.4 | 101.9 | 92.7 | 91.6 | 88.9 | 113.9 | 119.7 | 117.9 | 94.6 | 88.2 | 91.3 |
| B8B2U7 | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex OS=Oryza sativa subsp. indica GN=OsI\_23094 PE=3 SV=1 | 98.8 | 100.4 | 98.5 | 89.7 | 92.8 | 92 | 117.3 | 109.3 | 114.1 | 94.2 | 97.5 | 95.4 |
| B8B2X2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_24541 PE=4 SV=1 | 94.1 | 99.2 | 97.3 | 99.3 | 100.5 | 97.1 | 103.2 | 100.4 | 106.7 | 103.4 | 99.9 | 98.9 |
| B8B3B1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_23231 PE=4 SV=1 | 110.1 | 114.9 | 107.5 | 107 | 110 | 109.3 | 95.9 | 91.5 | 94.1 | 87 | 83.6 | 89.1 |
| B8B3L5 | Peroxidase OS=Oryza sativa subsp. indica GN=OsI\_23305 PE=3 SV=1 | 89.5 | 88 | 89.9 | 75.9 | 85.5 | 74.1 | 98.6 | 101.7 | 95.2 | 136 | 124.8 | 140.8 |
| B8B3U4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_23436 PE=4 SV=1 | 102.3 | 98.4 | 96.2 | 97.2 | 97.1 | 101 | 106 | 108.2 | 99.8 | 94.5 | 96.4 | 103 |
| B8B402 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_22171 PE=3 SV=1 | 103.5 | 104.7 | 114.1 | 104.8 | 102.2 | 91.9 | 95.7 | 100.4 | 98.7 | 96 | 92.7 | 95.3 |
| B8B4H5 | Alanine--tRNA ligase, chloroplastic/mitochondrial OS=Oryza sativa subsp. indica GN=OsI\_22356 PE=3 SV=1 | 96.8 | 100.4 | 101.2 | 100.2 | 103.4 | 102.6 | 106.9 | 95.4 | 98.7 | 96.1 | 100.8 | 97.5 |
| B8B5K7 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27219 PE=4 SV=1 | 98.1 | 99.2 | 102.2 | 91.9 | 92.7 | 98 | 110.9 | 111.4 | 105.3 | 99 | 96.7 | 94.6 |
| B8B5L9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27174 PE=4 SV=1 | 107.6 | 102.4 | 116.2 | 89.6 | 98.8 | 86.3 | 112 | 111.1 | 108.8 | 90.8 | 87.8 | 88.7 |
| B8B5P9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_25842 PE=4 SV=1 | 109.1 | 116.7 | 106.2 | 91 | 93.4 | 95.9 | 97.3 | 101.5 | 98.5 | 102.6 | 88.5 | 99.3 |
| B8B6A3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27428 PE=4 SV=1 | 96.6 | 99.1 | 93.9 | 103.5 | 99.9 | 103.9 | 96.6 | 100.5 | 94.6 | 103.3 | 100.4 | 107.6 |
| B8B6B4 | Phosphoinositide phospholipase C OS=Oryza sativa subsp. indica GN=OsI\_27447 PE=4 SV=1 | 104.9 | 114 | 108.3 | 95.8 | 96.9 | 102.3 | 100.9 | 100.9 | 95.8 | 98.4 | 88.2 | 93.5 |
| B8B6B6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27453 PE=3 SV=1 | 102.9 | 105.9 | 101.3 | 96.4 | 92.1 | 94.5 | 105.2 | 113.2 | 110.3 | 95.5 | 88.7 | 93.9 |
| B8B6C9 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_26077 PE=4 SV=1 | 102.8 | 111.1 | 103.6 | 94.9 | 98.7 | 97.9 | 112.7 | 98.1 | 104.8 | 89.6 | 92.1 | 93.7 |
| B8B764 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_24866 PE=4 SV=1 | 96.9 | 83.8 | 107.1 | 93.4 | 102.4 | 95.1 | 95.1 | 89.9 | 88 | 114.6 | 123.9 | 109.9 |
| B8B7K0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_25003 PE=3 SV=1 | 91.9 | 96.6 | 92.2 | 103.7 | 97.7 | 105.6 | 94.3 | 104.5 | 89.8 | 110 | 101.2 | 112.3 |
| B8B7P6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_25096 PE=3 SV=1 | 104.8 | 103 | 103.6 | 99.1 | 100.3 | 99.1 | 90.8 | 94.1 | 93.3 | 105.4 | 102.6 | 104 |
| B8B7Z2 | Pyruvate kinase OS=Oryza sativa subsp. indica GN=OsI\_25125 PE=3 SV=1 | 91.8 | 91 | 92.9 | 106.7 | 107.8 | 102.2 | 97.6 | 102.5 | 103.7 | 103.9 | 98.6 | 101.2 |
| B8B833 | Eukaryotic translation initiation factor 5A OS=Oryza sativa subsp. indica GN=OsI\_26733 PE=3 SV=1 | 98 | 103.7 | 104.6 | 98.6 | 93.2 | 101.7 | 105.5 | 103 | 99.3 | 97.9 | 100.2 | 94.4 |
| B8B8E2 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Oryza sativa subsp. indica GN=OsI\_25342 PE=3 SV=1 | 106.6 | 107.9 | 105.3 | 90.3 | 89.5 | 92 | 116 | 118.2 | 113.1 | 87 | 84.4 | 89.6 |
| B8B8K0 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_26859 PE=3 SV=1 | 100.1 | 100.3 | 100.1 | 93.3 | 94.2 | 102.9 | 107.8 | 108.8 | 83.2 | 98.8 | 96.7 | 113.7 |
| B8B982 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_28627 PE=3 SV=1 | 100.6 | 100.1 | 106.8 | 102.6 | 97.2 | 96.6 | 94.1 | 108.9 | 97.7 | 102.7 | 93.8 | 98.9 |
| B8B9C5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_30129 PE=3 SV=1 | 102.5 | 90.4 | 80.9 | 86 | 76.2 | 77.6 | 121.4 | 138.2 | 133.4 | 90.1 | 95.2 | 108 |
| B8B9L3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_30287 PE=4 SV=1 | 97.3 | 112.1 | 104.6 | 102.6 | 100.9 | 103.5 | 97 | 94.4 | 95.5 | 103.1 | 92.6 | 96.3 |
| B8BAB3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_29072 PE=4 SV=1 | 101.3 | 99.8 | 101.7 | 100.4 | 99.6 | 99.2 | 101.8 | 103 | 102.7 | 96.4 | 97.6 | 96.4 |
| B8BAH2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_29109 PE=4 SV=1 | 100.6 | 118.7 | 106.9 | 91.9 | 104.9 | 92.4 | 118.8 | 89.6 | 112.2 | 88.7 | 86.8 | 88.5 |
| B8BAI7 | Aminopeptidase OS=Oryza sativa subsp. indica GN=OsI\_29144 PE=3 SV=1 | 95.5 | 100.7 | 106.6 | 93.7 | 94.3 | 91.7 | 112.7 | 105 | 115.1 | 98.2 | 100 | 86.5 |
| B8BAQ6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_27818 PE=4 SV=1 | 105.1 | 106.3 | 106.5 | 91.6 | 91.6 | 87.6 | 107.9 | 111.3 | 115.1 | 95.5 | 90.8 | 90.8 |
| B8BB05 | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex OS=Oryza sativa subsp. indica GN=OsI\_29326 PE=3 SV=1 | 83.5 | 94.3 | 84.7 | 109.4 | 108.9 | 115.5 | 100.2 | 95.4 | 90.7 | 106.8 | 101.4 | 109.1 |
| B8BB36 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_29378 PE=3 SV=1 | 102 | 102.9 | 106 | 103.4 | 105.4 | 105.2 | 99.2 | 97.2 | 95.3 | 95.3 | 94.6 | 93.5 |
| B8BBN7 | Obg-like ATPase 1 OS=Oryza sativa subsp. indica GN=OsI\_28170 PE=3 SV=1 | 94.5 | 98.6 | 85.6 | 96.3 | 99.6 | 108.2 | 103.7 | 101.1 | 92.9 | 105.5 | 100.7 | 113.2 |
| B8BCQ3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_31743 PE=3 SV=1 | 83.6 | 58.1 | 82.8 | 96.5 | 57.8 | 91.6 | 102.5 | 132 | 103.3 | 117.4 | 152.1 | 122.3 |
| B8BD60 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_30469 PE=4 SV=1 | 107.4 | 108 | 111.8 | 75.9 | 75.3 | 71.5 | 143.3 | 147.9 | 149.2 | 73.3 | 68.8 | 67.5 |
| B8BD97 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_30535 PE=4 SV=1 | 98.3 | 99.3 | 99 | 96.6 | 98.1 | 98.1 | 110.2 | 112.3 | 109.1 | 94.9 | 90.3 | 93.8 |
| B8BDK7 | ATPase ASNA1 homolog OS=Oryza sativa subsp. indica GN=OsI\_32081 PE=3 SV=1 | 100.2 | 101.5 | 97.3 | 92.4 | 95.4 | 95.4 | 112.9 | 104.1 | 116.8 | 94.5 | 99 | 90.5 |
| B8BEE0 | Transmembrane 9 superfamily member OS=Oryza sativa subsp. indica GN=OsI\_32361 PE=3 SV=1 | 106.1 | 110.2 | 98 | 88.5 | 89.7 | 86.9 | 104.2 | 108.9 | 126.9 | 101.3 | 91.2 | 88.2 |
| B8BF46 | Annexin OS=Oryza sativa subsp. indica GN=OsI\_31267 PE=3 SV=1 | 94.5 | 96.8 | 98.7 | 110.8 | 105.7 | 107.1 | 91.3 | 96.6 | 93 | 103.4 | 100.9 | 101.2 |
| B8BF66 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_31321 PE=4 SV=1 | 107.2 | 116.4 | 101.8 | 100.1 | 101.3 | 99.3 | 106.7 | 95.3 | 106 | 86 | 87 | 92.9 |
| B8BHC8 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_33947 PE=4 SV=1 | 98.1 | 101.5 | 103.4 | 96.8 | 101.5 | 103.2 | 107.1 | 97.9 | 94.4 | 98.1 | 99.2 | 98.9 |
| B8BHM5 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34144 PE=4 SV=1 | 41.8 | 86.1 | 22.8 | 42.3 | 80.4 | 24.9 | 138.1 | 113.2 | 148.9 | 177.7 | 120.4 | 203.5 |
| B8BHR1 | Malic enzyme OS=Oryza sativa subsp. indica GN=OsI\_34227 PE=3 SV=1 | 106 | 103.9 | 105.1 | 94 | 95.2 | 88.1 | 113 | 104.9 | 116.7 | 87 | 96 | 90.1 |
| B8BIC2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34713 PE=4 SV=1 | 88.5 | 91.1 | 82.7 | 85.9 | 71.3 | 72.2 | 130.9 | 156 | 165.2 | 94.6 | 81.6 | 79.8 |
| B8BIF4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_34798 PE=4 SV=1 | 95.6 | 95.8 | 100.2 | 90.6 | 96.7 | 89.4 | 115.9 | 108.1 | 111.3 | 97.9 | 99.4 | 99.1 |
| B8BJ39 | Pyruvate kinase 1, cytosolic OS=Oryza sativa subsp. indica GN=OsI\_35105 PE=3 SV=1 | 97.4 | 98.7 | 100.7 | 98.8 | 89.9 | 92.4 | 111.6 | 115.5 | 105.6 | 92.1 | 96 | 101.3 |
| B8BJ56 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_35151 PE=3 SV=1 | 95.9 | 100.1 | 92.9 | 108.7 | 107.9 | 102.7 | 89.6 | 92.9 | 106.5 | 105.8 | 99.1 | 97.8 |
| B8BKA3 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_35959 PE=3 SV=1 | 104.1 | 103.6 | 101 | 94.1 | 93.3 | 93.2 | 103.4 | 105.6 | 105.2 | 98.5 | 97.4 | 100.6 |
| B8BKT7 | Alpha-mannosidase OS=Oryza sativa subsp. indica GN=OsI\_36309 PE=3 SV=1 | 98.9 | 98.9 | 101.8 | 100.1 | 104.3 | 102.4 | 103.3 | 102.9 | 97 | 97.8 | 93.8 | 98.8 |
| B8BM99 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_38581 PE=3 SV=1 | 93 | 97.4 | 90.1 | 105.8 | 103.6 | 107.3 | 100 | 103.3 | 106.1 | 101.2 | 95.7 | 96.6 |
| B8BMH5 | Lipoxygenase OS=Oryza sativa subsp. indica GN=OsI\_38715 PE=3 SV=1 | 68.6 | 51.1 | 76.2 | 55.3 | 53.1 | 52.5 | 159.7 | 168.1 | 142.1 | 116.4 | 127.7 | 129.1 |
| B8BMJ6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_38756 PE=4 SV=1 | 113.2 | 113.9 | 101.6 | 90.8 | 93.8 | 99.2 | 97.5 | 100.1 | 105.9 | 98.6 | 92.2 | 93.2 |
| B8BMN2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_38846 PE=4 SV=1 | 93.4 | 92 | 92.4 | 105.8 | 117.3 | 119.7 | 90.9 | 83 | 78.7 | 109.9 | 107.8 | 109.2 |
| B8BND6 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_37618 PE=4 SV=1 | 100.6 | 105 | 107.1 | 98.8 | 81.7 | 86.2 | 103.4 | 108 | 105.5 | 97.2 | 105.4 | 101.2 |
| B8BNI2 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_37718 PE=4 SV=1 | 101.7 | 107.9 | 87.4 | 97.5 | 97.3 | 87.8 | 95.8 | 95.3 | 94.3 | 105 | 99.4 | 130.6 |
| B8BNJ1 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_37743 PE=3 SV=1 | 99 | 105 | 101.5 | 95.8 | 97 | 103.5 | 111.8 | 102 | 104.5 | 93.4 | 95.9 | 90.5 |
| B8BNQ4 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_37876 PE=3 SV=1 | 95.4 | 97.7 | 97.3 | 100.7 | 97.9 | 99.9 | 101.8 | 106.8 | 102.8 | 102.1 | 97.6 | 100 |
| B8BP25 | Uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI\_37938 PE=3 SV=1 | 107.6 | 83.1 | 93 | 101.7 | 108.4 | 101.3 | 89 | 98.8 | 102.7 | 101.7 | 109.8 | 103 |
| B9EXM2 | Carbamoyl-phosphate synthase large chain, chloroplastic OS=Oryza sativa subsp. japonica GN=CARB PE=2 SV=1 | 99.2 | 96.2 | 94.9 | 104.3 | 104.1 | 105.2 | 96.7 | 99.9 | 97.3 | 99.8 | 99.8 | 102.6 |
| B9FSC3 | Os06g0232200 protein OS=Oryza sativa subsp. japonica GN=Os06g0232200 PE=3 SV=1 | 107.4 | 108.6 | 104.4 | 95.2 | 96.2 | 97.4 | 105.8 | 103.3 | 100.6 | 91.6 | 91.9 | 97.6 |
| B9FSC8 | Putative 12-oxophytodienoate reductase 11 OS=Oryza sativa subsp. japonica GN=OPR11 PE=2 SV=1 | 107.5 | 100.6 | 115.8 | 95.9 | 92 | 85 | 104.8 | 118.2 | 110.1 | 91.8 | 89.2 | 89.2 |
| G2XMV6 | Hypothetical\_protein OS=Oryza glaberrima GN=Ogl11g0082B12\_4 PE=3 SV=1 | 80 | 100.4 | 94.2 | 101.1 | 97.4 | 84.8 | 127.4 | 102.5 | 115.8 | 91.6 | 99.6 | 105.1 |
| I1NJT6 | Eukaryotic translation initiation factor 3 subunit A OS=Oryza glaberrima PE=3 SV=1 | 98.7 | 97.7 | 94.1 | 97 | 96.1 | 97.8 | 105 | 106.5 | 108.4 | 99.3 | 99.7 | 99.7 |
| I1NK53 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 101.5 | 96.8 | 100.5 | 93.9 | 95.5 | 100.9 | 105.1 | 96.1 | 101.7 | 99.5 | 111.7 | 97 |
| I1NKK9 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 124.4 | 127.3 | 108.9 | 73.2 | 75.8 | 88.3 | 116.1 | 106.2 | 117.7 | 86.3 | 90.7 | 85.1 |
| I1NKU8 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 96.6 | 103.8 | 102 | 94.4 | 91.2 | 92.4 | 113.7 | 111.8 | 110.7 | 95.3 | 93.1 | 94.9 |
| I1NLW9 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 87.4 | 92.8 | 95.8 | 112.9 | 110.1 | 112 | 93.4 | 96.7 | 90.7 | 106.3 | 100.4 | 101.5 |
| I1NMM8 | Protein translocase subunit SecA OS=Oryza glaberrima PE=3 SV=1 | 93.8 | 96.6 | 93.7 | 103.2 | 105.2 | 102.6 | 92.6 | 90.8 | 100.1 | 110.4 | 107.5 | 103.5 |
| I1NMP4 | S-adenosylmethionine synthase OS=Oryza glaberrima PE=3 SV=1 | 99.5 | 96.6 | 96.4 | 88.7 | 92.3 | 95.5 | 122.3 | 121.2 | 127 | 89.4 | 89.8 | 81.2 |
| I1NMR3 | Dihydrolipoyl dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 103.1 | 104.5 | 105.2 | 89.9 | 92.2 | 92.7 | 104.1 | 105.3 | 103.8 | 102.8 | 98 | 98.2 |
| I1NMW5 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 96.4 | 94.8 | 103.5 | 99.4 | 103.5 | 113.9 | 102.2 | 115.6 | 93.3 | 102 | 86.1 | 89.3 |
| I1NPS5 | Uroporphyrinogen decarboxylase OS=Oryza glaberrima PE=3 SV=1 | 95.5 | 86.2 | 81.3 | 102.2 | 111.5 | 121.6 | 101 | 90.4 | 86.9 | 101.3 | 112 | 110.2 |
| I1NPZ9 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 101 | 98.3 | 102.6 | 98.5 | 90.7 | 98 | 108 | 117.1 | 105.5 | 92.5 | 93.9 | 94 |
| I1NQ57 | Malate dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 105.6 | 102.6 | 105 | 96.8 | 91.7 | 90.6 | 105 | 112.2 | 111.2 | 92.6 | 93.5 | 93.2 |
| I1NQP6 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 104 | 102.1 | 102.6 | 89.5 | 94.4 | 94.1 | 115.1 | 110.4 | 113.6 | 91.4 | 93.1 | 89.7 |
| I1NQP9 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 110.8 | 117.7 | 104.9 | 102.5 | 100.3 | 99.4 | 98 | 103.3 | 103.4 | 88.6 | 78.7 | 92.3 |
| I1NQW7 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 94.9 | 96.5 | 92.4 | 101 | 103.1 | 104.9 | 97.2 | 104.3 | 97 | 106.9 | 96.1 | 105.7 |
| I1NRA0 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 88.2 | 84.5 | 94.3 | 97.6 | 111.7 | 109.4 | 104.9 | 88.4 | 100.6 | 109.3 | 115.4 | 95.8 |
| I1NRC3 | Malic enzyme OS=Oryza glaberrima PE=3 SV=1 | 108.6 | 111.5 | 109.9 | 87.4 | 86.7 | 87.1 | 124 | 127.4 | 124 | 80 | 74.4 | 79 |
| I1NRI9 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 94.9 | 111.6 | 92.4 | 98 | 99.2 | 104.8 | 103.9 | 106.8 | 99.9 | 103.1 | 82.4 | 102.9 |
| I1NRJ1 | Phosphotransferase OS=Oryza glaberrima PE=3 SV=1 | 106.5 | 108.4 | 113.7 | 96.7 | 99.7 | 96.7 | 103.4 | 101 | 100.3 | 93.5 | 90.9 | 89.2 |
| I1NRT6 | Aspartate aminotransferase OS=Oryza glaberrima PE=4 SV=1 | 95.3 | 98.9 | 98.4 | 85.9 | 79 | 79.4 | 124.3 | 130.7 | 131.1 | 94.5 | 91.4 | 91.1 |
| I1NRW1 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 108.8 | 100.4 | 106.9 | 92.2 | 95 | 94.1 | 112.8 | 115.5 | 113.1 | 86.3 | 89 | 85.8 |
| I1NSE5 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 91.5 | 100.7 | 83.7 | 102.2 | 103 | 109 | 95.1 | 93.7 | 91 | 111.2 | 102.5 | 116.2 |
| I1NSQ0 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 106.4 | 90.8 | 104.1 | 96.4 | 102.8 | 98.9 | 104.1 | 101.1 | 102.7 | 93.1 | 105.4 | 94.4 |
| I1NTN8 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 98.5 | 98.1 | 98.5 | 98.4 | 99 | 100.4 | 99.6 | 100 | 97.5 | 103.5 | 102.9 | 103.6 |
| I1NU82 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 111.9 | 146.1 | 122.1 | 112 | 146.3 | 118 | 88.6 | 57.9 | 81 | 87.5 | 49.7 | 78.9 |
| I1NVD3 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 95.6 | 98.2 | 94.5 | 101.5 | 102.7 | 100.4 | 96.6 | 103.1 | 100.6 | 106.2 | 96 | 104.5 |
| I1NWJ9 | Catalase OS=Oryza glaberrima PE=3 SV=1 | 77.1 | 81 | 85.4 | 133.6 | 132.2 | 120.8 | 85.3 | 83.2 | 92.3 | 104 | 103.6 | 101.4 |
| I1NY12 | Glycosyltransferase OS=Oryza glaberrima PE=3 SV=1 | 115.4 | 113.4 | 167.9 | 102.3 | 97.5 | 116.4 | 101.7 | 105 | 67 | 80.6 | 84 | 48.6 |
| I1NYV8 | Peroxidase OS=Oryza glaberrima PE=3 SV=1 | 92.1 | 104.1 | 88.7 | 83.9 | 91.8 | 83.7 | 108.7 | 103.2 | 107.8 | 115.3 | 100.9 | 119.7 |
| I1NZB5 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 88.4 | 91.9 | 90.4 | 93.1 | 109.1 | 100.4 | 127.8 | 89.7 | 86.4 | 90.7 | 109.3 | 122.9 |
| I1P0T4 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 95.4 | 96.3 | 95.9 | 93.5 | 96.5 | 99.1 | 112.4 | 109.2 | 105.4 | 98.7 | 98 | 99.5 |
| I1P0Y8 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 105.3 | 104 | 97.1 | 88.1 | 90 | 95.7 | 112.5 | 113.2 | 110.8 | 94.1 | 92.8 | 96.4 |
| I1P182 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 105.1 | 103.3 | 104.5 | 115.1 | 105.7 | 112.8 | 89.2 | 99.4 | 93.4 | 90.6 | 91.6 | 89.3 |
| I1P1T4 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 101.4 | 103 | 103 | 93.8 | 111.9 | 93.9 | 110.6 | 101.1 | 113.3 | 94.3 | 84 | 89.8 |
| I1P2D6 | Phenylalanine ammonia-lyase OS=Oryza glaberrima PE=3 SV=1 | 83.4 | 83.5 | 85 | 81.2 | 83.6 | 82.6 | 151.8 | 149.4 | 150.4 | 83.7 | 83.5 | 82 |
| I1P3E5 | V-type proton ATPase subunit G OS=Oryza glaberrima PE=3 SV=1 | 92.1 | 81.5 | 103.6 | 86.2 | 92.7 | 84.3 | 101.5 | 106.7 | 107.3 | 120.2 | 119 | 104.7 |
| I1P3G6 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 102.2 | 102.7 | 101.9 | 93.7 | 97 | 93.3 | 105.9 | 105.6 | 106.8 | 98.2 | 94.7 | 98 |
| I1P3K4 | Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha OS=Oryza glaberrima GN=PFP-ALPHA PE=3 SV=1 | 81.2 | 95 | 87.3 | 108.5 | 105.8 | 110.5 | 117.8 | 99.4 | 87.9 | 92.5 | 99.9 | 114.3 |
| I1P3L4 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 98.7 | 97.4 | 97.5 | 97 | 102.4 | 99.8 | 102.3 | 100.9 | 99.3 | 102 | 99.3 | 103.4 |
| I1P3S8 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 129.1 | 88.3 | 98.5 | 79.3 | 91.3 | 91 | 115.1 | 108.7 | 114.4 | 76.5 | 111.7 | 96.1 |
| I1P4R4 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 106.4 | 104.8 | 103.2 | 93 | 96 | 93.4 | 100 | 104.1 | 96.8 | 100.6 | 95.2 | 106.6 |
| I1P4R6 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 101.9 | 98.7 | 102 | 93.2 | 94.8 | 92.2 | 108.9 | 112.7 | 112.5 | 96 | 93.8 | 93.3 |
| I1P4U6 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 94.5 | 94.7 | 97.5 | 89.1 | 106.9 | 106.2 | 104.6 | 100.8 | 101.2 | 111.9 | 97.5 | 95.1 |
| I1P526 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 90.9 | 100.2 | 92.5 | 91 | 93.6 | 94.5 | 124.3 | 114.9 | 112.5 | 93.8 | 91.3 | 100.4 |
| I1P5G4 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 106.5 | 110.6 | 109.6 | 85.4 | 86.7 | 85.2 | 118 | 113.7 | 119.3 | 90.1 | 89 | 85.8 |
| I1P5P0 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 95.3 | 98.7 | 100.3 | 113.6 | 116.6 | 117.8 | 73.8 | 77.1 | 73.7 | 117.2 | 107.7 | 108.2 |
| I1P5U5 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 99.8 | 94.3 | 97.7 | 89.2 | 91.7 | 90.2 | 113.1 | 113.6 | 113.5 | 97.9 | 100.4 | 98.6 |
| I1P782 | Catalase OS=Oryza glaberrima PE=3 SV=1 | 98.1 | 97.2 | 98.3 | 108.8 | 108 | 111.8 | 90 | 89.6 | 83 | 103.1 | 105.2 | 106.9 |
| I1P7Z7 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 104.7 | 104.2 | 105.2 | 99.2 | 97.5 | 99.9 | 92.2 | 100.1 | 91.1 | 103.9 | 98.3 | 103.8 |
| I1P838 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 110.9 | 98.4 | 96.4 | 92.2 | 97.2 | 99.4 | 102.2 | 107.7 | 97.2 | 94.7 | 96.7 | 107 |
| I1P850 | Elongation factor 1-alpha OS=Oryza glaberrima PE=3 SV=1 | 97.8 | 97.1 | 95.8 | 97.4 | 97.2 | 96.8 | 110.1 | 111.6 | 109.9 | 94.7 | 94.1 | 97.5 |
| I1P8K7 | 40S ribosomal protein S3a OS=Oryza glaberrima PE=3 SV=1 | 96.3 | 97.5 | 96.3 | 100.1 | 101.8 | 101.3 | 101.7 | 99.8 | 99.9 | 101.9 | 101 | 102.6 |
| I1P9L8 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 104.4 | 102.7 | 103.2 | 97.7 | 90.5 | 94.2 | 105.8 | 113.1 | 103.3 | 92.1 | 93.7 | 99.3 |
| I1PA01 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 102.6 | 98.9 | 101 | 86.7 | 90.8 | 90.7 | 121.1 | 119.5 | 118.9 | 89.6 | 90.7 | 89.3 |
| I1PAF1 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 90.3 | 99.2 | 103.1 | 98.6 | 86.4 | 81.3 | 114.3 | 129.6 | 137.4 | 96.8 | 84.7 | 78.2 |
| I1PB13 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 98.2 | 100.2 | 99.7 | 95.8 | 95.4 | 96.7 | 97.3 | 97.4 | 96.4 | 108.6 | 107 | 107.2 |
| I1PB43 | Uroporphyrinogen decarboxylase OS=Oryza glaberrima PE=3 SV=1 | 77.5 | 79.6 | 74.3 | 123.6 | 118.4 | 128.7 | 75.6 | 82.3 | 74.9 | 123.2 | 119.8 | 122.1 |
| I1PBB4 | Superoxide dismutase [Cu-Zn] OS=Oryza glaberrima PE=3 SV=1 | 108.6 | 103.8 | 107.6 | 94.9 | 93.3 | 92 | 110.1 | 114 | 109.9 | 86.4 | 88.9 | 90.5 |
| I1PBU0 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 104.3 | 103.8 | 87.9 | 90.2 | 91 | 73.3 | 112.9 | 111.6 | 146 | 92.6 | 93.6 | 92.7 |
| I1PC51 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 109.7 | 103 | 113.4 | 88.6 | 90.5 | 86.1 | 112.6 | 110.5 | 112.3 | 89 | 95.9 | 88.2 |
| I1PC79 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 102.7 | 105.5 | 104.1 | 99.9 | 98.3 | 98.8 | 102.3 | 99.2 | 103.1 | 95.1 | 97.1 | 93.9 |
| I1PCE5 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 94.2 | 99.4 | 92.5 | 97 | 96.1 | 84.1 | 108.1 | 108.1 | 115.3 | 100.7 | 96.4 | 108.1 |
| I1PCF7 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 102.3 | 95.4 | 92.9 | 99.8 | 99.7 | 97.7 | 101.3 | 102.2 | 104.1 | 96.6 | 102.8 | 105.2 |
| I1PCP0 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 97.7 | 95.6 | 96.3 | 109.1 | 112.5 | 106.3 | 91.1 | 88 | 95.2 | 102.2 | 103.9 | 102.2 |
| I1PDI7 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 104.2 | 96.8 | 99.5 | 94.9 | 95.1 | 94 | 106.6 | 118.5 | 109.9 | 94.3 | 89.6 | 96.6 |
| I1PDU5 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 96.2 | 98.5 | 96.4 | 104.7 | 110.4 | 113.8 | 95.5 | 89.7 | 84.6 | 103.6 | 101.4 | 105.2 |
| I1PE00 | 3-isopropylmalate dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 101.8 | 101.6 | 102.1 | 98.3 | 103.5 | 102.5 | 103.5 | 98.7 | 99.8 | 96.4 | 96.2 | 95.5 |
| I1PET6 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 113.8 | 119.8 | 116.1 | 136.1 | 136.4 | 141.8 | 69.1 | 69.7 | 69 | 81 | 74.1 | 73.1 |
| I1PEZ3 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 98.3 | 98.5 | 95.4 | 94.7 | 96.5 | 103.7 | 107.5 | 105.3 | 97.7 | 99.6 | 99.7 | 103.1 |
| I1PF07 | Tubulin alpha chain OS=Oryza glaberrima PE=3 SV=1 | 88.6 | 92.5 | 88.2 | 114.4 | 106.6 | 112.9 | 97.4 | 101.1 | 97.6 | 99.7 | 99.7 | 101.3 |
| I1PF58 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 89.9 | 94 | 91.7 | 97.8 | 105.6 | 100.7 | 111.2 | 106.3 | 99.3 | 101.1 | 94 | 108.2 |
| I1PF71 | Glucose-1-phosphate adenylyltransferase OS=Oryza glaberrima PE=3 SV=1 | 93.7 | 96.1 | 97.2 | 95.9 | 96.2 | 92.5 | 105.6 | 105.9 | 103.1 | 104.8 | 101.8 | 107.2 |
| I1PFI3 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 85.8 | 79.1 | 86.3 | 113.6 | 122.1 | 116 | 90.5 | 86.8 | 91.4 | 110.1 | 112.1 | 106.3 |
| I1PFN6 | UDP-glucose 6-dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 98.7 | 94.8 | 97.7 | 93.9 | 91 | 94.9 | 115.3 | 126.2 | 111.3 | 92.1 | 88 | 96 |
| I1PFQ5 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 94.7 | 102.6 | 99.6 | 96.3 | 95.5 | 96.5 | 104.1 | 102.4 | 105.4 | 104.9 | 99.5 | 98.5 |
| I1PFY8 | Malate dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 101.3 | 99.7 | 96.3 | 109.6 | 108.9 | 107.2 | 85.3 | 88.8 | 88.1 | 103.7 | 102.6 | 108.3 |
| I1PG16 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 98.5 | 96.7 | 95.9 | 104.5 | 106.7 | 105.2 | 96.5 | 96.5 | 97.6 | 100.5 | 100.2 | 101.2 |
| I1PG29 | Obg-like ATPase 1 OS=Oryza glaberrima PE=3 SV=1 | 102.7 | 104.4 | 104.8 | 99.7 | 102 | 103.8 | 105.3 | 99.8 | 100.9 | 92.2 | 93.7 | 90.5 |
| I1PGJ4 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 100.4 | 95.8 | 107.3 | 97.6 | 101.2 | 100.3 | 100.7 | 108.4 | 94.8 | 101.3 | 94.6 | 97.6 |
| I1PGU1 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 101 | 103.9 | 99.9 | 98.2 | 82.1 | 94.6 | 108.8 | 130.2 | 113.5 | 92 | 83.8 | 92 |
| I1PGY3 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 84.9 | 90.3 | 90.3 | 106.5 | 105.5 | 105 | 104.2 | 80.2 | 96.7 | 104.5 | 124 | 108 |
| I1PHB6 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 110.2 | 108.2 | 105.8 | 98.8 | 99.9 | 103.7 | 105.8 | 107.8 | 100 | 85.2 | 84 | 90.4 |
| I1PHK9 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 109.6 | 109.1 | 107.2 | 89.8 | 95.7 | 92 | 107.6 | 104.7 | 107.7 | 93 | 90.5 | 93.1 |
| I1PHZ3 | Cytochrome f OS=Oryza glaberrima GN=19493583 PE=3 SV=1 | 90.7 | 91.2 | 94.4 | 110.3 | 109.4 | 109.9 | 92.4 | 92.4 | 91 | 106.6 | 107.1 | 104.8 |
| I1PI01 | Cytochrome b6 OS=Oryza glaberrima GN=petB PE=3 SV=1 | 87.8 | 95.7 | 91 | 102.8 | 105.7 | 104.4 | 92.4 | 88.7 | 90.6 | 117 | 109.9 | 114 |
| I1PIA1 | Glutamate decarboxylase OS=Oryza glaberrima PE=3 SV=1 | 93.6 | 91.9 | 98.3 | 93.1 | 97.1 | 103.6 | 119.6 | 112.1 | 103.8 | 93.7 | 98.9 | 94.3 |
| I1PIV8 | CBS domain OS=Oryza glaberrima GN=G10 PE=4 SV=1 | 101.4 | 101 | 98.1 | 79.3 | 73.7 | 100.4 | 117.2 | 134.6 | 97.1 | 102.1 | 90.7 | 104.4 |
| I1PJL5 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 103 | 108.3 | 103.6 | 100.5 | 102 | 102.7 | 96.9 | 93.3 | 92.6 | 99.6 | 96.5 | 101 |
| I1PK08 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 100.1 | 102.3 | 95.9 | 107.4 | 108.8 | 96.7 | 96.2 | 93.5 | 101 | 96.3 | 95.4 | 106.5 |
| I1PK11 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 100.4 | 101.1 | 102.1 | 90.8 | 96.5 | 99.9 | 114.1 | 110.9 | 99.8 | 94.7 | 91.6 | 98.2 |
| I1PKR1 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 101.9 | 101.2 | 98.3 | 93.1 | 98.7 | 99.9 | 109.2 | 110.3 | 108.6 | 95.8 | 89.8 | 93.1 |
| I1PKT8 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 92.5 | 95.9 | 95.6 | 91.5 | 97.8 | 99 | 127.9 | 111.1 | 105 | 88 | 95.2 | 100.4 |
| I1PL30 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 88.2 | 101 | 95.9 | 106.6 | 104.1 | 102.3 | 98.5 | 95.6 | 99.3 | 106.8 | 99.3 | 102.4 |
| I1PLD0 | GrpE protein homolog OS=Oryza glaberrima PE=3 SV=1 | 102.3 | 102.1 | 101.3 | 103.5 | 91.1 | 99.9 | 88.7 | 104.1 | 99.4 | 105.6 | 102.8 | 99.5 |
| I1PLV0 | Chlorophyll a-b binding protein, chloroplastic OS=Oryza glaberrima PE=3 SV=1 | 106 | 104.3 | 106.2 | 99 | 97.2 | 96.9 | 78.4 | 82.5 | 77.6 | 116.5 | 115.9 | 119.2 |
| I1PLW8 | Glyceraldehyde-3-phosphate dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 103.8 | 104.4 | 101.7 | 100 | 101.2 | 100.6 | 95.2 | 92 | 92.7 | 100.9 | 102.5 | 105 |
| I1PM97 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 98.4 | 103.3 | 103.5 | 96.4 | 90.1 | 88.8 | 109.2 | 118 | 112.5 | 96 | 88.6 | 95.2 |
| I1PMT6 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 104.5 | 99.2 | 97.8 | 120.8 | 101.7 | 104.9 | 81.9 | 109.1 | 97.9 | 92.7 | 90 | 99.3 |
| I1PMW4 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 87.8 | 93.2 | 93.3 | 97 | 92.1 | 95 | 113 | 115.5 | 107.3 | 102.2 | 99.2 | 104.4 |
| I1PMX6 | Ammonium transporter OS=Oryza glaberrima PE=3 SV=1 | 108 | 114.1 | 113.6 | 90.9 | 112.8 | 86.9 | 106 | 98.4 | 112 | 95.1 | 74.6 | 87.5 |
| I1PNC2 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 107.7 | 109 | 112.8 | 101.2 | 100.4 | 98.1 | 94.9 | 95.2 | 92.8 | 96.2 | 95.5 | 96.4 |
| I1PP85 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 126 | 95.2 | 106 | 144.4 | 98.8 | 114.2 | 66.5 | 100.6 | 92.5 | 63.1 | 105.4 | 87.3 |
| I1PPF2 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 105.9 | 104.8 | 102.1 | 102.7 | 101.4 | 100.7 | 95.4 | 95.7 | 96.9 | 96.1 | 98.1 | 100.2 |
| I1PPH8 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 95.7 | 96.2 | 97.8 | 97.2 | 98.4 | 98.3 | 106.5 | 106.5 | 101.9 | 100.5 | 98.9 | 102 |
| I1PQ18 | Aminomethyltransferase OS=Oryza glaberrima PE=3 SV=1 | 109.7 | 109.9 | 109.4 | 98.1 | 97.8 | 99.5 | 99.2 | 100.3 | 96.9 | 93 | 92 | 94.2 |
| I1PQ76 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 106.1 | 105.1 | 102.4 | 99.6 | 100.6 | 100.8 | 100.2 | 101.6 | 102.6 | 94 | 92.6 | 94.2 |
| I1PQ78 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 106.2 | 126.6 | 96.3 | 114.3 | 120.9 | 100.9 | 91 | 81.7 | 99.8 | 88.4 | 70.8 | 103 |
| I1PQ98 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 97.7 | 97.3 | 90.7 | 85.7 | 79.1 | 82.5 | 133.1 | 141.3 | 142.2 | 83.5 | 82.3 | 84.6 |
| I1PQC4 | D-3-phosphoglycerate dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 96.6 | 100.1 | 91.9 | 87.6 | 83.8 | 79.1 | 131.1 | 133.4 | 144.8 | 84.7 | 82.7 | 84.2 |
| I1PQF5 | Plasma membrane ATPase OS=Oryza glaberrima PE=3 SV=1 | 97.1 | 97.1 | 95.9 | 100.7 | 100.4 | 100.3 | 107.7 | 108.2 | 107.6 | 94.5 | 94.2 | 96.2 |
| I1PR23 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 97.3 | 95.2 | 103.4 | 117.6 | 124.8 | 114.9 | 92.8 | 89.2 | 92 | 92.3 | 90.7 | 89.7 |
| I1PR82 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 148.7 | 142.3 | 156.1 | 93.8 | 96 | 100.5 | 75.2 | 75.9 | 76.2 | 82.3 | 85.8 | 67.2 |
| I1PR89 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 103.2 | 100 | 99.6 | 117.4 | 117.4 | 120.3 | 77.9 | 77.7 | 72.8 | 101.5 | 104.9 | 107.3 |
| I1PRN9 | Methionine S-methyltransferase OS=Oryza glaberrima PE=3 SV=1 | 100.5 | 103.4 | 105.9 | 95.8 | 92.3 | 82.9 | 122.2 | 124.4 | 137.4 | 81.5 | 79.9 | 73.8 |
| I1PRU0 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 101 | 114.9 | 101.7 | 99 | 94.4 | 95.2 | 103.2 | 99.8 | 107.2 | 96.8 | 90.9 | 96 |
| I1PSI2 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 96.4 | 98.1 | 98.8 | 99.9 | 102.4 | 103.8 | 102.4 | 101.1 | 99.3 | 101.3 | 98.4 | 98.1 |
| I1PSL1 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 103.3 | 90.2 | 94.6 | 97.1 | 98.4 | 99.1 | 98.3 | 104.9 | 104.4 | 101.3 | 106.5 | 101.9 |
| I1PSM1 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 95 | 97.5 | 99.7 | 94.2 | 92 | 92.6 | 114.3 | 118.8 | 114.2 | 96.4 | 91.8 | 93.5 |
| I1PSP2 | Dihydrolipoyl dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 106.2 | 131.8 | 126.5 | 89 | 91.6 | 94.8 | 110.6 | 101.7 | 98.5 | 94.1 | 74.9 | 80.2 |
| I1PT09 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 110.8 | 109.6 | 113 | 113.2 | 110.6 | 120.4 | 73.2 | 76.6 | 60.4 | 102.7 | 103.2 | 106.2 |
| I1PU82 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 104.2 | 107.5 | 105.2 | 90.8 | 91.5 | 91.7 | 112.7 | 113.9 | 111.8 | 92.3 | 87 | 91.3 |
| I1PU83 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 104.4 | 105.4 | 106.4 | 99.7 | 100.3 | 98.1 | 99.6 | 100 | 98.4 | 96.3 | 94.3 | 97.1 |
| I1PU87 | Guanosine nucleotide diphosphate dissociation inhibitor OS=Oryza glaberrima PE=3 SV=1 | 99.5 | 95.1 | 101 | 89.8 | 86.7 | 93.9 | 123.8 | 116.3 | 109.2 | 86.8 | 101.8 | 95.9 |
| I1PV59 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 94.5 | 110.9 | 90.5 | 99.9 | 100 | 106.7 | 101.5 | 95.8 | 94.5 | 104 | 93.3 | 108.3 |
| I1PV82 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 95 | 88.6 | 91.4 | 106.1 | 112.1 | 110.8 | 94.3 | 93.8 | 90.5 | 104.6 | 105.5 | 107.2 |
| I1PVG8 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 101.8 | 102.4 | 104.4 | 91.4 | 89.4 | 87.8 | 104.1 | 104 | 105.3 | 102.7 | 104.3 | 102.5 |
| I1PVJ3 | Pyruvate, phosphate dikinase OS=Oryza glaberrima PE=3 SV=1 | 105.8 | 108.4 | 109.2 | 107.4 | 102 | 103.6 | 94.4 | 97.7 | 94.5 | 92.4 | 91.9 | 92.7 |
| I1PXT3 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 100.4 | 103 | 100.9 | 96.5 | 88.5 | 92.1 | 106.2 | 116.8 | 116.8 | 96.8 | 91.7 | 90.3 |
| I1PY62 | Malate dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 106.4 | 104.5 | 107.8 | 97.6 | 97.1 | 96.9 | 101 | 104.8 | 101.7 | 95 | 93.6 | 93.5 |
| I1PYR8 | Acetyltransferase component of pyruvate dehydrogenase complex OS=Oryza glaberrima PE=3 SV=1 | 97.7 | 98.6 | 103.7 | 91.5 | 90.1 | 97.4 | 113.2 | 109.9 | 107.8 | 97.6 | 101.5 | 91.1 |
| I1PYW0 | 6-phosphogluconate dehydrogenase, decarboxylating OS=Oryza glaberrima PE=3 SV=1 | 98.4 | 102.3 | 98.7 | 88.7 | 85.2 | 89.1 | 120.8 | 125.5 | 117.1 | 92.1 | 86.9 | 95.1 |
| I1PYX1 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 86.9 | 79.2 | 85.2 | 113.6 | 121.8 | 115.1 | 92.7 | 84.7 | 92.2 | 106.8 | 114.4 | 107.4 |
| I1PZA0 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 99.2 | 94.3 | 92.8 | 100.5 | 98.7 | 98.4 | 96.6 | 100.2 | 97.1 | 103.6 | 106.7 | 111.7 |
| I1PZA2 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 102.5 | 97.7 | 99.1 | 95 | 89.7 | 95.2 | 109.6 | 115.5 | 115.3 | 92.9 | 97.1 | 90.5 |
| I1PZV7 | Proteasome subunit alpha type OS=Oryza glaberrima PE=3 SV=1 | 106.2 | 95 | 109.6 | 91.4 | 91.4 | 90.9 | 114.4 | 111.7 | 110.6 | 87.9 | 101.9 | 88.9 |
| I1Q096 | Sucrose synthase OS=Oryza glaberrima PE=3 SV=1 | 101.5 | 107.3 | 105 | 93.3 | 88.2 | 89.5 | 109.7 | 119.5 | 118.1 | 95.5 | 85 | 87.3 |
| I1Q0A3 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 105.7 | 110.2 | 105.6 | 98.5 | 100.6 | 98.4 | 97.2 | 98 | 101 | 98.7 | 91.1 | 94.9 |
| I1Q0A5 | 3-oxoacyl-[acyl-carrier-protein] synthase OS=Oryza glaberrima PE=3 SV=1 | 102.3 | 95.7 | 98.7 | 101.1 | 98 | 107 | 100.7 | 106.4 | 94.3 | 96 | 99.8 | 100.1 |
| I1Q0Z0 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 114.2 | 111.9 | 119.2 | 85.3 | 89.1 | 87.2 | 100.6 | 98.2 | 92.9 | 99.9 | 100.8 | 100.7 |
| I1Q169 | Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta OS=Oryza glaberrima GN=PFP-BETA PE=3 SV=1 | 108.8 | 86.7 | 89.5 | 100.9 | 99.8 | 95.8 | 96.3 | 105.2 | 120.6 | 94 | 108.3 | 94 |
| I1Q1X7 | Ribosomal protein S4 OS=Oryza glaberrima GN=19493568 PE=3 SV=1 | 100.1 | 97 | 99.4 | 113 | 113 | 119.5 | 79.6 | 85.3 | 74.8 | 107.3 | 104.7 | 106.3 |
| I1Q2U7 | T-complex protein 1 subunit gamma OS=Oryza glaberrima PE=3 SV=1 | 97.6 | 97.1 | 101 | 104.2 | 103.2 | 97.3 | 98.4 | 100.4 | 106.1 | 99.9 | 99.2 | 95.5 |
| I1Q3J5 | Fructose-bisphosphate aldolase OS=Oryza glaberrima PE=3 SV=1 | 104.9 | 105 | 106.2 | 98.2 | 98.8 | 97.5 | 97.4 | 96.9 | 97.6 | 99.5 | 99.3 | 98.7 |
| I1Q3R7 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 109.9 | 109.6 | 108.7 | 98.5 | 97.7 | 98.5 | 102.3 | 105.5 | 104.2 | 89.3 | 87.2 | 88.6 |
| I1Q3Y3 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 99.1 | 94.1 | 95.4 | 110.7 | 104.2 | 115 | 90.8 | 99.1 | 89.5 | 99.3 | 102.6 | 100.1 |
| I1Q461 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 112.7 | 124.3 | 106.1 | 66.8 | 75.5 | 76.3 | 148.4 | 128.5 | 130.1 | 72.1 | 71.7 | 87.4 |
| I1Q4P7 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 102.5 | 100.6 | 104.5 | 96.5 | 95.9 | 97.7 | 104.7 | 113.3 | 106.3 | 96.3 | 90.2 | 91.5 |
| I1Q638 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 95.3 | 101.4 | 92 | 94.3 | 110 | 111.1 | 116 | 80.6 | 95.1 | 94.4 | 108 | 101.8 |
| I1Q6C6 | Ribosomal protein L14 OS=Oryza glaberrima GN=19493608 PE=3 SV=1 | 99.8 | 98.6 | 95.6 | 112.6 | 117.9 | 116 | 82.6 | 74.5 | 77.2 | 105 | 109 | 111.2 |
| I1Q6F0 | Photosystem I iron-sulfur center OS=Oryza glaberrima GN=19493635 PE=3 SV=1 | 97.1 | 98.6 | 96.3 | 107.8 | 107 | 107.3 | 90.3 | 93 | 92.7 | 104.8 | 101.3 | 103.7 |
| I1Q7E3 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 96.8 | 97.8 | 96.7 | 97.7 | 106.6 | 109.4 | 102.6 | 85.6 | 92.5 | 102.8 | 109.9 | 101.3 |
| I1Q830 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 115.6 | 97.4 | 101.8 | 92.7 | 95.2 | 96.5 | 92 | 98.5 | 95.3 | 99.7 | 108.9 | 106.4 |
| I1Q848 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 94.5 | 94.7 | 97 | 108.7 | 105.9 | 105 | 89.2 | 92.8 | 92.5 | 107.6 | 106.7 | 105.5 |
| I1Q8B2 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 95.1 | 89.3 | 100.5 | 107.6 | 110.9 | 104.6 | 103 | 100.1 | 98.1 | 94.2 | 99.7 | 96.9 |
| I1Q8I5 | RuvB-like helicase OS=Oryza glaberrima PE=3 SV=1 | 103.4 | 105.4 | 97.3 | 91.1 | 97 | 93.4 | 112.2 | 102.4 | 118.1 | 93.3 | 95.2 | 91.1 |
| I1Q8K2 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 91.9 | 72.9 | 91.5 | 105.6 | 100 | 108 | 109.1 | 122.2 | 105.8 | 93.4 | 104.9 | 94.7 |
| I1Q912 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 105.2 | 103.2 | 101 | 99.6 | 100.8 | 99.1 | 98.2 | 96.5 | 96.4 | 97 | 99.5 | 103.6 |
| I1QA03 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 101.6 | 99.3 | 101 | 106.8 | 98.7 | 108.2 | 96.1 | 104.8 | 95.2 | 95.5 | 97.2 | 95.6 |
| I1QBD2 | Histone H2A OS=Oryza glaberrima PE=3 SV=1 | 102.7 | 105.1 | 98.9 | 98.8 | 101.9 | 104 | 102.9 | 94.6 | 92.4 | 95.6 | 98.4 | 104.7 |
| I1QBJ9 | Chlorophyll a-b binding protein, chloroplastic OS=Oryza glaberrima PE=3 SV=1 | 99.5 | 98.4 | 96.8 | 106.7 | 105.2 | 105.1 | 94.5 | 96.3 | 98.2 | 99.3 | 100.1 | 99.8 |
| I1QBM2 | Chlorophyll a-b binding protein, chloroplastic OS=Oryza glaberrima PE=3 SV=1 | 99.1 | 101 | 102.3 | 100.3 | 105.5 | 104 | 95.3 | 73.9 | 91.4 | 105.3 | 119.5 | 102.3 |
| I1QCH6 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 76.5 | 84.8 | 84.4 | 120.1 | 115.2 | 115 | 88.2 | 88.2 | 88.6 | 115.2 | 111.9 | 112 |
| I1QEI9 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 100.1 | 101.1 | 89.3 | 99.4 | 94.7 | 107.2 | 107.3 | 103.4 | 108.5 | 93.1 | 100.8 | 95 |
| I1QF56 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 87.5 | 93.3 | 93.1 | 100.2 | 100 | 98 | 102.7 | 102.5 | 100.4 | 109.7 | 104.2 | 108.5 |
| I1QF99 | Glyceraldehyde-3-phosphate dehydrogenase OS=Oryza glaberrima PE=3 SV=1 | 101.4 | 102.7 | 104.1 | 85.8 | 86.7 | 82 | 123.6 | 122.3 | 128.9 | 89.2 | 88.2 | 85 |
| I1QGA1 | Aconitate hydratase OS=Oryza glaberrima PE=3 SV=1 | 91.4 | 97.8 | 77.2 | 103.8 | 98.1 | 82.5 | 110.2 | 116.4 | 161.1 | 94.6 | 87.8 | 79.1 |
| I1QGI8 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 88.7 | 95.3 | 85.1 | 93.4 | 95.5 | 95.4 | 100.4 | 105 | 112.8 | 117.4 | 104.1 | 106.6 |
| I1QGR8 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 108.5 | 102.9 | 99.9 | 102.6 | 113.8 | 113.7 | 95.3 | 98.2 | 95.7 | 93.6 | 85.1 | 90.7 |
| I1QHA7 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 108.1 | 100 | 104.6 | 87.5 | 87.6 | 87.9 | 108.3 | 113.4 | 115.1 | 96.1 | 99 | 92.4 |
| I1QHC3 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 95.4 | 98.7 | 96.7 | 92.8 | 90.8 | 94.5 | 115.2 | 110.5 | 107.4 | 96.6 | 99.9 | 101.5 |
| I1QJW3 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 103.4 | 106.4 | 106.1 | 89.7 | 93.4 | 94.7 | 111.7 | 114.9 | 109.2 | 95.2 | 85.3 | 90 |
| I1QJX3 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 95.1 | 95.8 | 96.1 | 108.1 | 110.7 | 109.9 | 90.4 | 87.7 | 87.8 | 106.4 | 105.9 | 106.2 |
| I1QK10 | Lipoxygenase OS=Oryza glaberrima PE=3 SV=1 | 79.5 | 75.5 | 78.8 | 78.9 | 77.9 | 81.5 | 162.9 | 172.1 | 165.4 | 78.7 | 74.5 | 74.3 |
| I1QKG1 | Superoxide dismutase [Cu-Zn] OS=Oryza glaberrima PE=3 SV=1 | 107.9 | 104.4 | 104.8 | 96.2 | 99.5 | 102.4 | 102.1 | 100.2 | 96.6 | 93.8 | 95.9 | 96.3 |
| I1QKG9 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 90.9 | 93.1 | 89.9 | 96.6 | 97.2 | 97.8 | 109.2 | 109.7 | 107.8 | 103.2 | 100 | 104.5 |
| I1QKN4 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 107.9 | 93.9 | 108.5 | 83.6 | 82.4 | 92.1 | 114.7 | 115.3 | 111 | 93.8 | 108.4 | 88.4 |
| I1QKT5 | Photosystem II CP43 reaction center protein OS=Oryza glaberrima PE=3 SV=1 | 102.2 | 101.9 | 99 | 104.7 | 101.3 | 103 | 92.2 | 99.1 | 95 | 100.9 | 97.7 | 103 |
| I1QKT9 | Ribosomal protein S2 OS=Oryza glaberrima GN=19493557 PE=3 SV=1 | 97.9 | 95.3 | 100.3 | 111.4 | 116 | 107.4 | 85.8 | 84.6 | 91.9 | 104.9 | 104.2 | 100.3 |
| I1QKU4 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 99.7 | 94.4 | 94.8 | 104 | 105.6 | 106.3 | 105.1 | 100.4 | 100.5 | 91.2 | 99.6 | 98.4 |
| I1QKV4 | Cytochrome b559 subunit alpha OS=Oryza glaberrima GN=19493587 PE=3 SV=1 | 106.9 | 107.6 | 107.8 | 92.7 | 92.1 | 93.4 | 76.6 | 77.8 | 81.1 | 123.7 | 122.5 | 117.7 |
| I1QKY4 | NADH-quinone oxidoreductase subunit I OS=Oryza glaberrima GN=19493638 PE=3 SV=1 | 98.3 | 99.3 | 93.4 | 109.9 | 117.7 | 123.1 | 88.8 | 81.3 | 85.8 | 103.1 | 101.7 | 97.7 |
| I1QL27 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 99.5 | 96.9 | 98.2 | 105.4 | 104.9 | 104.3 | 97.1 | 99.4 | 97.1 | 98 | 98.9 | 100.5 |
| I1QLJ6 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 94.5 | 84.5 | 83.5 | 108.3 | 112.2 | 114.4 | 94.4 | 93.4 | 89.8 | 102.7 | 109.9 | 112.4 |
| I1QLP7 | Peptidylprolyl isomerase OS=Oryza glaberrima PE=4 SV=1 | 98.8 | 102.6 | 86.7 | 95.9 | 94.1 | 95 | 114.8 | 104.7 | 123.6 | 90.4 | 98.6 | 94.7 |
| I1QLY6 | Polyadenylate-binding protein OS=Oryza glaberrima PE=3 SV=1 | 100.6 | 91.7 | 99 | 104.6 | 95.3 | 106.3 | 90.7 | 101.4 | 89.3 | 104.2 | 111.7 | 105.4 |
| I1QMG3 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 97.8 | 100.4 | 100 | 101.2 | 99.4 | 102.1 | 102.9 | 104.2 | 103.1 | 98.1 | 96 | 94.8 |
| I1QN54 | Chlorophyll a-b binding protein, chloroplastic OS=Oryza glaberrima PE=3 SV=1 | 99 | 99.1 | 103.8 | 98.4 | 98.9 | 98.4 | 86.4 | 82.5 | 87.3 | 116.2 | 119.6 | 110.5 |
| I1QNT1 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 76.7 | 81.5 | 73.8 | 69.6 | 80.2 | 68.4 | 133.3 | 132.9 | 135.7 | 120.4 | 105.4 | 122.1 |
| I1QPH4 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 104.6 | 97.9 | 102.3 | 96 | 94.4 | 94.8 | 104.4 | 112.1 | 110.1 | 95 | 95.6 | 92.9 |
| I1QQ95 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 94.9 | 92.4 | 94.6 | 100.9 | 101.3 | 101.8 | 102.9 | 107.4 | 100.9 | 101.3 | 98.9 | 102.8 |
| I1QQV9 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 106.6 | 104.5 | 103.1 | 97.5 | 98.5 | 101.6 | 106.7 | 109.5 | 100.1 | 89.2 | 87.5 | 95.2 |
| I1QR41 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 102.7 | 105.6 | 104.4 | 92.6 | 92.4 | 94.3 | 110.9 | 109.7 | 107 | 93.8 | 92.3 | 94.3 |
| I1QSV0 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 99.8 | 100.5 | 103.5 | 94 | 91.6 | 92.2 | 110.8 | 112.6 | 110.7 | 95.4 | 95.3 | 93.6 |
| I1QTD1 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 105.2 | 102 | 101.1 | 90 | 91.9 | 97.2 | 113.6 | 116.7 | 106.9 | 91.3 | 89.4 | 94.9 |
| I1QTS0 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 96.2 | 97.3 | 97.3 | 91.8 | 104.4 | 102.9 | 109.7 | 107.9 | 106.2 | 102.3 | 90.4 | 93.6 |
| I1QUH7 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 106.9 | 100.2 | 111.6 | 87.2 | 93.3 | 83.1 | 118.4 | 115.1 | 113.7 | 87.5 | 91.4 | 91.6 |
| I1QUU6 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 96.1 | 94.1 | 94.8 | 92.1 | 89.9 | 85.3 | 109.7 | 113.1 | 109.5 | 102.1 | 102.8 | 110.3 |
| I1QUZ5 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 93.3 | 89.3 | 92.8 | 110.3 | 111.7 | 110 | 95.6 | 94.3 | 90.4 | 100.8 | 104.8 | 106.8 |
| I1QV49 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 108 | 111.3 | 107.1 | 93.5 | 98.2 | 89.5 | 109.7 | 113.2 | 119.4 | 88.8 | 77.3 | 84 |
| I1QVB5 | Cyanate hydratase OS=Oryza glaberrima GN=CYN PE=3 SV=1 | 105.4 | 109.2 | 112.3 | 95.9 | 85.5 | 87.7 | 104.8 | 113.5 | 115 | 93.9 | 91.8 | 85 |
| I1QW04 | Nucleoside diphosphate kinase OS=Oryza glaberrima PE=3 SV=1 | 89.3 | 93.6 | 88.2 | 98.7 | 92 | 89.8 | 93.9 | 112.5 | 121.9 | 118.1 | 102 | 100.1 |
| I1QWC5 | ATP-dependent Clp protease proteolytic subunit OS=Oryza glaberrima PE=3 SV=1 | 86.9 | 90.4 | 89 | 94.6 | 94.6 | 102.8 | 109.1 | 110.9 | 105.6 | 109.4 | 104.1 | 102.6 |
| I1QWE1 | Peroxidase OS=Oryza glaberrima PE=3 SV=1 | 93.5 | 88.7 | 96.8 | 79.3 | 82 | 84 | 115.1 | 128 | 115.6 | 112.1 | 101.2 | 103.6 |
| I1QWF7 | Photosystem II CP47 reaction center protein OS=Oryza glaberrima GN=19493657 PE=3 SV=1 | 100.9 | 102.3 | 101.4 | 104.6 | 102.3 | 102.7 | 94.4 | 97.7 | 96.6 | 100.1 | 97.7 | 99.3 |
| I1QWG3 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 98.1 | 98 | 97.4 | 107.1 | 108.4 | 107.5 | 89.6 | 87 | 89.2 | 105.2 | 106.6 | 105.9 |
| I1QXJ8 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 92.9 | 91.3 | 88.9 | 98.1 | 101.3 | 107.5 | 106.8 | 105.2 | 100.8 | 102.2 | 102.2 | 102.8 |
| I1QXY9 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 102.1 | 98.4 | 94.6 | 96 | 96.8 | 94.7 | 111 | 110.3 | 116.9 | 90.9 | 94.4 | 93.8 |
| I1QY31 | Fructose-bisphosphate aldolase OS=Oryza glaberrima PE=3 SV=1 | 103.9 | 101.5 | 100.3 | 105.9 | 101.1 | 107.8 | 91 | 95.7 | 86.4 | 99.2 | 101.8 | 105.6 |
| I1QZZ4 | Serine hydroxymethyltransferase OS=Oryza glaberrima PE=3 SV=1 | 89.9 | 85.6 | 95.6 | 102.9 | 106.4 | 107.6 | 102 | 103.1 | 96 | 105.1 | 104.9 | 100.8 |
| I1R078 | 6-phosphogluconate dehydrogenase, decarboxylating OS=Oryza glaberrima PE=3 SV=1 | 109.4 | 109.6 | 108.7 | 101.5 | 103.2 | 106.3 | 95.5 | 98.3 | 95 | 93.6 | 88.8 | 90.1 |
| I1R1E2 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 106.5 | 114.3 | 118.7 | 93.7 | 89.3 | 94.6 | 117.4 | 105.4 | 104 | 82.4 | 91 | 82.8 |
| I1R1G3 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 100.4 | 100.1 | 102.4 | 111.6 | 97.3 | 88.7 | 90.4 | 115.3 | 114.6 | 97.7 | 87.3 | 94.3 |
| I1R2E3 | Photosystem I P700 chlorophyll a apoprotein A2 OS=Oryza glaberrima GN=19493564 PE=3 SV=1 | 97.5 | 97.6 | 100.4 | 102.5 | 107.9 | 104.3 | 103.4 | 95.7 | 101.1 | 96.6 | 98.8 | 94.2 |
| I1R2M1 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 110 | 109.1 | 112.6 | 102.9 | 101.5 | 102.2 | 91.9 | 99.8 | 88.8 | 95.2 | 89.6 | 96.4 |
| I1R357 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 98.1 | 109.7 | 78.4 | 96.9 | 95.2 | 89.2 | 95.9 | 98.3 | 89.1 | 109.1 | 96.8 | 143.4 |
| I1R3L2 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 97.5 | 92.7 | 92.5 | 96.3 | 98.3 | 97.2 | 106.3 | 106.8 | 117.2 | 99.9 | 102.1 | 93 |
| I1R408 | Pyruvate kinase OS=Oryza glaberrima PE=3 SV=1 | 91.8 | 95.4 | 94.7 | 84.6 | 89.3 | 92.1 | 127.8 | 118.2 | 114.8 | 95.7 | 97.1 | 98.4 |
| I1R446 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 119 | 116.7 | 115.2 | 92.6 | 93.6 | 92.3 | 105 | 107.3 | 100.3 | 83.4 | 82.4 | 92.2 |
| I1R4D8 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 99.8 | 89.6 | 101.9 | 103.9 | 98.4 | 102.7 | 96.9 | 109 | 98.4 | 99.4 | 103 | 97 |
| I1R4H0 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 95.1 | 100.5 | 111.8 | 99.3 | 104 | 97.7 | 105.2 | 98.2 | 93.3 | 100.4 | 97.3 | 97.2 |
| I1R4P4 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 105.2 | 103.6 | 99.8 | 92.2 | 99 | 98.8 | 105.4 | 99.7 | 102 | 97.2 | 97.7 | 99.4 |
| I1R550 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 100 | 91.8 | 98.8 | 99.7 | 99.3 | 103 | 98 | 111.2 | 97.3 | 102.3 | 97.6 | 100.9 |
| I1R6V3 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 93 | 92.9 | 89.1 | 101.7 | 108.3 | 108.4 | 102.2 | 90 | 90.8 | 103.1 | 108.8 | 111.7 |
| I1R7V2 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 102.6 | 101 | 102.2 | 99.8 | 97.6 | 99.1 | 103 | 106 | 103.2 | 94.5 | 95.3 | 95.5 |
| I1R7Y8 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 106 | 98.5 | 93.4 | 95.3 | 101.3 | 105.5 | 111.4 | 99.7 | 102.7 | 87.2 | 100.5 | 98.4 |
| I1R8I2 | Aconitate hydratase OS=Oryza glaberrima PE=3 SV=1 | 99.5 | 100.3 | 99.4 | 92.3 | 87.9 | 94.4 | 113.8 | 117.5 | 108.5 | 94.4 | 94.3 | 97.7 |
| I1R8Q3 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 96.8 | 95.6 | 98.1 | 99.3 | 101.2 | 100.4 | 106.3 | 103.4 | 104.7 | 97.6 | 99.9 | 96.8 |
| I1R8W6 | Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1 | 87.8 | 83.3 | 81.8 | 99.5 | 95.6 | 109.6 | 103.2 | 99.3 | 95.2 | 109.5 | 121.8 | 113.4 |
| I1R8Z6 | Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1 | 102.2 | 97.6 | 90.7 | 87.9 | 87.2 | 97.7 | 104.4 | 111.7 | 111 | 105.5 | 103.4 | 100.5 |
| O22386 | 50S ribosomal protein L12, chloroplastic OS=Oryza sativa subsp. japonica GN=RPL12-2 PE=2 SV=2 | 101.8 | 98.7 | 101.1 | 98.7 | 105.4 | 100.8 | 88.5 | 75.9 | 79.9 | 111 | 120 | 118.2 |
| O64422 | Fructose-1,6-bisphosphatase, chloroplastic OS=Oryza sativa subsp. japonica GN=Os03g0267300 PE=2 SV=1 | 103.4 | 102 | 102.1 | 103.7 | 104 | 103.3 | 94.4 | 97.8 | 94.7 | 98.5 | 96.3 | 99.9 |
| P0C2Z0 | ATP synthase subunit b, chloroplastic OS=Oryza sativa subsp. japonica GN=atpF PE=3 SV=1 | 95.9 | 94.9 | 95.4 | 99.2 | 98 | 102.8 | 82.9 | 87.6 | 83.6 | 122 | 119.5 | 118.2 |
| P0C2Z2 | ATP synthase epsilon chain, chloroplastic OS=Oryza sativa subsp. indica GN=atpE PE=3 SV=1 | 92.9 | 97.8 | 91.5 | 102.6 | 99.1 | 102.9 | 92 | 101.7 | 91.7 | 112.5 | 101.4 | 113.9 |
| P0C2Z5 | ATP synthase subunit alpha, chloroplastic OS=Oryza sativa subsp. indica GN=atpA PE=3 SV=1 | 91.6 | 92 | 91.6 | 102.4 | 102.8 | 103.3 | 92.5 | 93.3 | 93.9 | 113.6 | 111.9 | 111.2 |
| P0C340 | NAD(P)H-quinone oxidoreductase subunit J, chloroplastic OS=Oryza sativa subsp. japonica GN=ndhJ PE=3 SV=1 | 96.5 | 96.7 | 100.4 | 100.8 | 111.2 | 100.4 | 99.4 | 85.9 | 99.6 | 103.3 | 106.2 | 99.6 |
| P0C433 | Photosystem II protein D1 OS=Oryza sativa subsp. indica GN=psbA PE=3 SV=1 | 103 | 98.5 | 98.6 | 99.6 | 98.5 | 100.4 | 103.7 | 103.3 | 100.1 | 93.7 | 99.8 | 100.9 |
| P0C436 | Photosystem II D2 protein OS=Oryza sativa subsp. indica GN=psbD PE=3 SV=1 | 103 | 102.8 | 102.3 | 101.5 | 103 | 101.3 | 97.1 | 96.6 | 99.6 | 98.3 | 97.6 | 96.8 |
| P0C450 | 50S ribosomal protein L23, chloroplastic OS=Oryza sativa subsp. indica GN=rpl23-A PE=3 SV=1 | 98.1 | 98 | 98.3 | 102.4 | 97.9 | 105 | 106.7 | 106.6 | 98.6 | 92.8 | 97.5 | 98 |
| P0C457 | 50S ribosomal protein L33, chloroplastic OS=Oryza sativa subsp. japonica GN=rpl33 PE=3 SV=1 | 96 | 96.7 | 96.4 | 107 | 109.5 | 105.5 | 87.7 | 87.4 | 85.8 | 109.3 | 106.5 | 112.2 |
| P0C490 | 30S ribosomal protein S7, chloroplastic OS=Oryza sativa subsp. indica GN=rps7-A PE=3 SV=1 | 98.2 | 96.3 | 96.4 | 113.4 | 116.4 | 117.6 | 80 | 81.4 | 76.4 | 108.4 | 106 | 109.6 |
| P0C497 | 50S ribosomal protein L2, chloroplastic OS=Oryza sativa subsp. japonica GN=rpl2-A PE=3 SV=1 | 94.2 | 93 | 98.5 | 111.5 | 113 | 116.1 | 76.6 | 77.4 | 78.4 | 117.6 | 116.6 | 107 |
| P0C522 | ATP synthase subunit alpha, mitochondrial OS=Oryza sativa subsp. japonica GN=ATPA PE=1 SV=1 | 105.5 | 105.3 | 104.4 | 93.3 | 93.8 | 93.1 | 108.4 | 105.7 | 109.2 | 92.8 | 95.2 | 93.2 |
| P0DKK0 | 26S proteasome regulatory subunit 7B OS=Oryza sativa subsp. japonica GN=RPT1B PE=2 SV=1 | 96.6 | 98.1 | 98.1 | 92.1 | 94.9 | 89.2 | 115.7 | 113.1 | 117.5 | 95.6 | 93.9 | 95.2 |
| P12085 | ATP synthase subunit beta, chloroplastic OS=Oryza sativa subsp. japonica GN=atpB PE=1 SV=2 | 93.7 | 92.2 | 91.1 | 100.4 | 101.5 | 101.2 | 98 | 97.3 | 95.6 | 107.9 | 109 | 112 |
| P12153 | 30S ribosomal protein S19, chloroplastic OS=Oryza sativa subsp. japonica GN=rps19-A PE=3 SV=3 | 93.6 | 85.8 | 91.7 | 117.7 | 111.9 | 112.6 | 80.1 | 102.1 | 96.8 | 108.6 | 100.1 | 98.9 |
| P14655 | Glutamine synthetase, chloroplastic OS=Oryza sativa subsp. japonica GN=GLN2 PE=1 SV=1 | 100.5 | 99.3 | 100.6 | 102.5 | 102.8 | 102 | 98.7 | 98.4 | 96.5 | 98.3 | 99.5 | 100.9 |
| P29545 | Elongation factor 1-beta OS=Oryza sativa subsp. japonica GN=Os07g0662500 PE=1 SV=3 | 98.4 | 96.6 | 97.8 | 94 | 93.2 | 95.5 | 107.8 | 112 | 108.1 | 99.8 | 98.2 | 98.7 |
| P40978 | 40S ribosomal protein S19 OS=Oryza sativa subsp. japonica GN=RPS19A PE=2 SV=1 | 92.2 | 94.9 | 95.1 | 98.9 | 99.1 | 97.6 | 105.2 | 102.6 | 105 | 103.7 | 103.4 | 102.3 |
| P52428 | Proteasome subunit alpha type-1 OS=Oryza sativa subsp. japonica GN=PAF1 PE=2 SV=1 | 99.2 | 101.3 | 95.1 | 95.7 | 89.7 | 84.6 | 110 | 118.5 | 102.1 | 95.1 | 90.5 | 118.3 |
| P83646 | Oxygen-evolving enhancer protein 3, chloroplastic OS=Oryza sativa subsp. indica GN=OsI\_025465 PE=1 SV=2 | 109.4 | 108.7 | 104.8 | 91.1 | 91.1 | 92.7 | 84.5 | 91.2 | 95.6 | 115 | 109 | 106.9 |
| P92683 | Cytochrome c oxidase subunit Vb OS=Oryza sativa subsp. japonica GN=coxVb PE=2 SV=1 | 99 | 99.1 | 100.3 | 96.3 | 95 | 91.8 | 108.4 | 108.4 | 107.8 | 96.3 | 97.5 | 100.1 |
| P93431 | Ribulose bisphosphate carboxylase/oxygenase activase, chloroplastic OS=Oryza sativa subsp. japonica GN=RCA PE=1 SV=2 | 92.5 | 93.4 | 93 | 110.2 | 110 | 109.7 | 88.1 | 90.2 | 89.6 | 109.2 | 106.5 | 107.7 |
| Q01859 | ATP synthase subunit beta, mitochondrial OS=Oryza sativa subsp. japonica GN=ATPB PE=1 SV=2 | 103.3 | 103.4 | 102.4 | 93.5 | 92.4 | 92.1 | 108.5 | 110.7 | 109.7 | 94.6 | 93.5 | 95.8 |
| Q07078 | Heat shock protein 81-3 OS=Oryza sativa subsp. japonica GN=HSP81-3 PE=1 SV=2 | 105.8 | 113.3 | 108.5 | 94.1 | 93.2 | 101.7 | 113 | 102.9 | 99.9 | 87.1 | 90.6 | 89.9 |
| Q08480 | Adenylate kinase 4 OS=Oryza sativa subsp. japonica GN=ADK-B PE=2 SV=1 | 103.2 | 107.8 | 103.2 | 91.4 | 90.1 | 96.1 | 106.5 | 108.3 | 105 | 98.9 | 93.8 | 95.8 |
| Q0D5S1 | Os07g0539900 protein OS=Oryza sativa subsp. japonica GN=Os07g0539900 PE=2 SV=1 | 197.2 | 149.9 | 161.7 | 81.1 | 93.3 | 87.4 | 68.3 | 79.2 | 76.9 | 53.3 | 77.5 | 73.9 |
| Q0DEF1 | Os06g0157000 protein OS=Oryza sativa subsp. japonica GN=Os06g0157000 PE=4 SV=1 | 102.8 | 101 | 104.8 | 83.2 | 84.5 | 82.9 | 111.2 | 115.9 | 113.1 | 102.7 | 98.6 | 99.2 |
| Q0DRB3 | Os03g0399800 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os03g0399800 PE=4 SV=2 | 91.6 | 89.6 | 78.3 | 107.4 | 120.4 | 129 | 104.2 | 90.6 | 82.2 | 96.8 | 99.4 | 110.5 |
| Q0DX85 | Os02g0768600 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os02g0768600 PE=4 SV=1 | 108.1 | 106.1 | 105.1 | 100.1 | 103.1 | 100.8 | 96.3 | 95.2 | 97.6 | 95.5 | 95.7 | 96.5 |
| Q0DZE5 | Os02g0625500 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os02g0625500 PE=4 SV=1 | 91.6 | 96 | 86.2 | 89.8 | 77.2 | 93.7 | 119.2 | 143.6 | 118.2 | 99.4 | 83.1 | 102 |
| Q0E2S4 | Serine/threonine-protein phosphatase PP2A-3 catalytic subunit OS=Oryza sativa subsp. japonica GN=PP2A3 PE=2 SV=1 | 97.3 | 91.6 | 96.2 | 96.6 | 95.4 | 99.8 | 110 | 109.9 | 105.8 | 96 | 103.1 | 98.2 |
| Q0E446 | Os02g0137200 protein (Fragment) OS=Oryza sativa subsp. japonica GN=Os02g0137200 PE=3 SV=1 | 100.3 | 96.9 | 89.9 | 112.8 | 114.1 | 109.9 | 81.7 | 84.8 | 90.1 | 105.3 | 104.3 | 110.1 |
| Q0IMS5 | Nucleoside diphosphate kinase OS=Oryza sativa subsp. japonica GN=Os12g0548300 PE=2 SV=1 | 102.8 | 103 | 100 | 97.1 | 96.8 | 96.3 | 99 | 101.1 | 101.5 | 101.1 | 99.1 | 102.1 |
| Q0IWS0 | Os10g0492300 protein OS=Oryza sativa subsp. japonica GN=Os10g0492300 PE=4 SV=1 | 104.9 | 97.3 | 104 | 111.6 | 104.8 | 110.1 | 89 | 92.1 | 89.7 | 94.5 | 105.8 | 96.2 |
| Q0J1E1 | Os09g0446800 protein OS=Oryza sativa subsp. japonica GN=Os09g0446800 PE=3 SV=1 | 94.2 | 98.9 | 98.9 | 101.3 | 98.6 | 98.1 | 99.9 | 102.5 | 101.5 | 104.6 | 99.9 | 101.5 |
| Q0J2H4 | Os09g0343200 protein OS=Oryza sativa subsp. japonica GN=Os09g0343200 PE=4 SV=1 | 115.7 | 118.9 | 118.2 | 102.7 | 100.5 | 101.4 | 100.8 | 99 | 100 | 80.8 | 81.6 | 80.4 |
| Q0J709 | ACT domain-containing protein DS12, chloroplastic OS=Oryza sativa subsp. japonica GN=Os08g0242700 PE=4 SV=2 | 108.5 | 108.6 | 108.2 | 104.2 | 101.8 | 103.4 | 89.2 | 94.9 | 92.2 | 98.1 | 94.7 | 96.3 |
| Q0J8G4 | Fructokinase-2 OS=Oryza sativa subsp. japonica GN=FRK2 PE=1 SV=1 | 90.3 | 94.4 | 91.2 | 114.3 | 113 | 117.1 | 96.4 | 98 | 95.1 | 99 | 94.5 | 96.7 |
| Q0JCX3 | Os04g0445200 protein OS=Oryza sativa subsp. japonica GN=Os04g0445200 PE=2 SV=1 | 112.8 | 150.7 | 141.7 | 117.1 | 160.6 | 139.6 | 80.6 | 51.2 | 66.1 | 89.5 | 37.6 | 52.6 |
| Q0JGY3 | Os01g0896500 protein OS=Oryza sativa subsp. japonica GN=Os01g0896500 PE=4 SV=1 | 97.1 | 98.2 | 95.8 | 108.8 | 105.3 | 109.1 | 93.2 | 96.5 | 90.1 | 100.9 | 99.9 | 105 |
| Q0JGZ6 | Fructokinase-1 OS=Oryza sativa subsp. japonica GN=FRK1 PE=1 SV=2 | 108.1 | 117.6 | 104.6 | 102.9 | 112 | 101.9 | 106.4 | 88.1 | 100.3 | 82.6 | 82.3 | 93.2 |
| Q0JM17 | DEAD-box ATP-dependent RNA helicase 56 OS=Oryza sativa subsp. japonica GN=AIP1 PE=1 SV=2 | 99.3 | 98 | 101.6 | 97.4 | 96.6 | 97.9 | 111.6 | 112 | 110.5 | 91.6 | 93.5 | 90 |
| Q0JPA6 | Salt stress root protein RS1 OS=Oryza sativa subsp. japonica GN=Os01g0233000 PE=2 SV=1 | 95.3 | 97.6 | 97.8 | 89.7 | 90.1 | 91.4 | 113 | 110.9 | 108.5 | 102 | 101.4 | 102.2 |
| Q0JR29 | Os01g0123900 protein OS=Oryza sativa subsp. japonica GN=Os01g0123900 PE=2 SV=1 | 101 | 103.4 | 93.7 | 68.2 | 72.5 | 62.8 | 126 | 123.6 | 134.6 | 104.8 | 100.5 | 109 |
| Q109L0 | Os10g0461100 protein OS=Oryza sativa subsp. japonica GN=LOC\_Os10g32348 PE=4 SV=1 | 93.3 | 91.9 | 93.6 | 86.4 | 106.4 | 104.3 | 110.4 | 110.2 | 103.1 | 109.9 | 91.6 | 99 |
| Q10CE4 | Peroxisomal (S)-2-hydroxy-acid oxidase GLO1 OS=Oryza sativa subsp. japonica GN=GLO1 PE=1 SV=1 | 99.6 | 99.4 | 97.7 | 103.3 | 102.3 | 104.5 | 91.3 | 92.5 | 94.1 | 105.8 | 105.7 | 103.8 |
| Q10CU9 | Glycosyl hydrolase family 3 N terminal domain containing protein, expressed OS=Oryza sativa subsp. japonica GN=OSJNBa0069E14.7 PE=2 SV=1 | 100.4 | 97.8 | 99.7 | 96.7 | 98.4 | 100.7 | 108.2 | 105.1 | 102.5 | 94.7 | 98.8 | 97.1 |
| Q10I42 | HAD-superfamily hydrolase, subfamily IA, variant 3 containing protein, expressed OS=Oryza sativa subsp. japonica GN=Os03g0565200 PE=4 SV=1 | 95.3 | 96.3 | 97.3 | 102.5 | 100.5 | 97.7 | 96.1 | 96 | 98.8 | 106 | 107.3 | 106.2 |
| Q10MQ2 | Probable LL-diaminopimelate aminotransferase, chloroplastic OS=Oryza sativa subsp. japonica GN=AGD2 PE=2 SV=1 | 104.4 | 95.6 | 93.7 | 110.3 | 104.9 | 110.2 | 90.5 | 95.3 | 87.1 | 94.8 | 104.2 | 109.1 |
| Q10N30 | Os03g0284400 protein OS=Oryza sativa subsp. japonica GN=Os03g0284400 PE=2 SV=1 | 113.4 | 110.1 | 111.3 | 135.2 | 124.5 | 116.2 | 79 | 85.4 | 85.3 | 72.4 | 80.1 | 87.2 |
| Q1KL27 | Peptidyl-prolyl cis-trans isomerase OS=Oryza sativa subsp. indica GN=OsI\_05635 PE=2 SV=1 | 105.8 | 105.8 | 106.3 | 87.7 | 88.6 | 85.2 | 116.3 | 116 | 117.6 | 90.2 | 89.6 | 90.8 |
| Q2QLS0 | CbbY protein, putative, expressed OS=Oryza sativa subsp. japonica GN=LOC\_Os12g43520 PE=2 SV=1 | 100.7 | 107.4 | 96.5 | 98.8 | 83.8 | 101.4 | 99.2 | 105.9 | 93.1 | 101.4 | 103 | 109 |
| Q2QNJ8 | Prefoldin subunit 3 OS=Oryza sativa subsp. japonica GN=LOC\_Os12g37590 PE=2 SV=1 | 96 | 99.5 | 109.1 | 97.8 | 92.5 | 101.3 | 107.5 | 115.1 | 100.3 | 98.7 | 92.8 | 89.3 |
| Q2QNN5 | Lipoxygenase OS=Oryza sativa subsp. japonica GN=LOC\_Os12g37260 PE=3 SV=2 | 144.5 | 141.1 | 143.6 | 52.4 | 55.1 | 55.2 | 113 | 114.5 | 112.1 | 90.2 | 89.3 | 89 |
| Q2QSR7 | Os12g0420200 protein OS=Oryza sativa subsp. japonica GN=LOC\_Os12g23180 PE=4 SV=2 | 102.7 | 102.7 | 103.2 | 103.4 | 101.9 | 101.8 | 91.8 | 94.9 | 93.9 | 102 | 100.5 | 101.1 |
| Q2QYW2 | Clathrin heavy chain 2 OS=Oryza sativa subsp. japonica GN=Os12g0104800 PE=3 SV=1 | 99 | 99.7 | 104.4 | 93.1 | 90.5 | 88.5 | 115.3 | 119.8 | 118.8 | 92.6 | 90 | 88.3 |
| Q2QZ86 | ATP-citrate synthase alpha chain protein 2 OS=Oryza sativa subsp. japonica GN=ACLA-2 PE=2 SV=2 | 100.2 | 90.6 | 98.8 | 98.9 | 97.9 | 103.6 | 106.2 | 110 | 92.8 | 94.7 | 101.5 | 104.8 |
| Q2R2W2 | 14-3-3-like protein GF14-D OS=Oryza sativa subsp. japonica GN=GF14D PE=1 SV=1 | 105 | 99.8 | 102.6 | 91.8 | 93.4 | 88.5 | 110.5 | 103.8 | 109 | 92.7 | 102.9 | 99.9 |
| Q33E23 | Glutamate dehydrogenase 2, mitochondrial OS=Oryza sativa subsp. japonica GN=GDH2 PE=2 SV=1 | 93.9 | 94.7 | 94.6 | 84.7 | 91.3 | 87.6 | 132.8 | 122 | 127.3 | 88.6 | 92 | 90.5 |
| Q53RM0 | Magnesium-chelatase subunit ChlI, chloroplastic OS=Oryza sativa subsp. japonica GN=CHLI PE=1 SV=1 | 83.6 | 76.7 | 87.7 | 121 | 132.3 | 116.8 | 86 | 74.5 | 86.8 | 109.4 | 116.5 | 108.7 |
| Q5JMM6 | Os01g0753100 protein OS=Oryza sativa subsp. japonica GN=Os01g0753100 PE=4 SV=1 | 108.1 | 115.4 | 108.8 | 93.6 | 93.5 | 94.1 | 107 | 102.3 | 105 | 91.3 | 88.8 | 92.1 |
| Q5JMS4 | Peroxidase OS=Oryza sativa subsp. japonica GN=Os01g0962700 PE=2 SV=1 | 95 | 99.7 | 100.8 | 91.4 | 92.2 | 90.3 | 125 | 115.9 | 121.3 | 88.6 | 92.2 | 87.6 |
| Q5JNB0 | Cysteine synthase OS=Oryza sativa subsp. japonica GN=Os01g0978100 PE=2 SV=1 | 108.8 | 106.7 | 107.6 | 111.6 | 109.6 | 111.7 | 88.9 | 92.4 | 91 | 90.8 | 91.3 | 89.8 |
| Q5N725 | Fructose-bisphosphate aldolase 3, cytoplasmic OS=Oryza sativa subsp. japonica GN=FBA3 PE=2 SV=1 | 96.4 | 102.9 | 90.2 | 101.2 | 99.2 | 114.3 | 106 | 103.4 | 102.9 | 96.4 | 94.5 | 92.5 |
| Q5QN02 | Os01g0199900 protein OS=Oryza sativa subsp. japonica GN=B1046G12.39 PE=2 SV=1 | 100.6 | 89.8 | 105.5 | 96.4 | 90 | 91 | 107.4 | 118.9 | 113.2 | 95.5 | 101.3 | 90.3 |
| Q5TKJ2 | Os05g0429400 protein OS=Oryza sativa subsp. japonica GN=Os05g0429400 PE=4 SV=1 | 92.9 | 113.1 | 116.6 | 98.1 | 108.7 | 125.5 | 109.8 | 94.4 | 80.9 | 99.2 | 83.7 | 77.1 |
| Q5UJF9 | Cysteine synthase OS=Oryza sativa subsp. indica GN=CAS PE=2 SV=1 | 100.3 | 100.2 | 98.3 | 98.9 | 102.8 | 98.4 | 98.8 | 100.5 | 100.4 | 102 | 96.4 | 102.9 |
| Q5VPR6 | Os06g0118700 protein OS=Oryza sativa subsp. japonica GN=Os06g0118700 PE=2 SV=1 | 90 | 98.3 | 96.5 | 116.1 | 102.3 | 107.7 | 93.1 | 96.3 | 96 | 100.9 | 103.1 | 99.8 |
| Q5Z4M6 | Os06g0308000 protein OS=Oryza sativa subsp. japonica GN=Os06g0308000 PE=2 SV=1 | 78.6 | 81.1 | 78.2 | 112.9 | 111.9 | 111.7 | 90.6 | 92.8 | 91.2 | 117.8 | 114.3 | 118.9 |
| Q5Z5T3 | Os06g0567900 protein OS=Oryza sativa subsp. japonica GN=Os06g0567900 PE=3 SV=1 | 71.5 | 90.1 | 91.6 | 88.3 | 86.8 | 86.4 | 143 | 119.8 | 108.2 | 97.2 | 103.3 | 113.8 |
| Q5Z974 | ATP-dependent zinc metalloprotease FTSH 1, chloroplastic OS=Oryza sativa subsp. japonica GN=FTSH1 PE=2 SV=1 | 95.9 | 95.2 | 95.4 | 103.6 | 101.8 | 104.2 | 95 | 102.8 | 92.7 | 105.6 | 100.2 | 107.7 |
| Q5ZA96 | Os06g0320700 protein OS=Oryza sativa subsp. japonica GN=Os06g0320700 PE=3 SV=1 | 97.2 | 102.9 | 101.7 | 100.7 | 108.4 | 94.3 | 94.8 | 89.8 | 110.6 | 107.3 | 98.9 | 93.4 |
| Q5ZBH8 | Os01g0618100 protein OS=Oryza sativa subsp. japonica GN=Os01g0618100 PE=4 SV=1 | 109.3 | 109 | 125 | 99.9 | 92.7 | 88.8 | 100.9 | 105.6 | 99.6 | 89.9 | 92.8 | 86.6 |
| Q5ZDX8 | Heterogeneous nuclear ribonucleoprotein A2/B1-like OS=Oryza sativa subsp. japonica GN=Os01g0614500 PE=4 SV=1 | 92.9 | 98.3 | 88.2 | 121.1 | 99.8 | 101.3 | 88.8 | 105.2 | 109.6 | 97.2 | 96.7 | 100.9 |
| Q60EF6 | Eukaryotic translation initiation factor 3 subunit I OS=Oryza sativa subsp. japonica GN=Os05g0256000 PE=2 SV=1 | 97.4 | 99.5 | 100.8 | 96.9 | 93.1 | 94.1 | 105.2 | 108.7 | 107.8 | 100.5 | 98.7 | 97.3 |
| Q650W6 | Os09g0565200 protein OS=Oryza sativa subsp. japonica GN=Os09g0565200 PE=2 SV=1 | 95.7 | 96 | 93.7 | 103.5 | 100.9 | 102.4 | 93.6 | 99.5 | 95.8 | 107.2 | 103.6 | 108.1 |
| Q655Y9 | Os06g0664200 protein OS=Oryza sativa subsp. japonica GN=P0473H04.3-1 PE=2 SV=1 | 103.5 | 103.1 | 102 | 107.8 | 105.9 | 108 | 97.9 | 101.6 | 98.2 | 90.8 | 89.5 | 91.9 |
| Q657T1 | Peptidyl-prolyl cis-trans isomerase OS=Oryza sativa subsp. japonica GN=Os01g0111100 PE=3 SV=1 | 98.4 | 100.2 | 99.8 | 97.5 | 94 | 98.1 | 103.1 | 99 | 102.8 | 101.1 | 106.7 | 99.3 |
| Q65XE5 | Os05g0149400 protein OS=Oryza sativa subsp. japonica GN=Os05g0149400 PE=2 SV=1 | 94.5 | 88.4 | 93 | 76.7 | 72.2 | 84.2 | 150.5 | 156.1 | 143 | 78.3 | 83.3 | 79.9 |
| Q67J09 | Os09g0460400 protein OS=Oryza sativa subsp. japonica GN=Os09g0460400 PE=2 SV=1 | 103.4 | 101.9 | 106.6 | 92.7 | 90.8 | 93.8 | 108.2 | 106.8 | 103.7 | 95.6 | 100.4 | 95.8 |
| Q67W57 | Os06g0646500 protein OS=Oryza sativa subsp. japonica GN=Os06g0646500 PE=2 SV=1 | 106.4 | 104.3 | 89.3 | 89.2 | 94.5 | 111.3 | 101.2 | 106.1 | 88.3 | 103.2 | 95.1 | 111.1 |
| Q69LA6 | Probable pyridoxal 5'-phosphate synthase subunit PDX1.1 OS=Oryza sativa subsp. japonica GN=PDX11 PE=2 SV=1 | 95.3 | 93.3 | 93.3 | 107.4 | 105.4 | 106.3 | 88.8 | 94.9 | 94.9 | 108.5 | 106.4 | 105.5 |
| Q69LE7 | Probable polyribonucleotide nucleotidyltransferase 1, chloroplastic OS=Oryza sativa subsp. japonica GN=PNP1 PE=2 SV=1 | 103.4 | 102 | 99.2 | 99.3 | 99.1 | 100.1 | 103.3 | 103.5 | 106.3 | 94 | 95.4 | 94.4 |
| Q69MW7 | DNA binding protein PF1 OS=Oryza sativa subsp. japonica GN=Os09g0402100 PE=2 SV=1 | 97.6 | 102.8 | 96.5 | 101.3 | 104.9 | 105.5 | 99.2 | 99.1 | 112.2 | 101.8 | 93.2 | 85.8 |
| Q69S39 | Cytochrome b6-f complex iron-sulfur subunit, chloroplastic OS=Oryza sativa subsp. japonica GN=petC PE=1 SV=1 | 95.8 | 97.7 | 95.6 | 109.9 | 100.4 | 99.2 | 81.3 | 94.9 | 104.9 | 113 | 107 | 100.3 |
| Q69SX2 | Os06g0360300 protein OS=Oryza sativa subsp. japonica GN=Os06g0360300 PE=2 SV=1 | 101.6 | 109.3 | 105.9 | 102.4 | 97.3 | 99.9 | 106.6 | 102.1 | 105.3 | 89.4 | 91.2 | 89 |
| Q69UU3 | Os07g0108300 protein OS=Oryza sativa subsp. japonica GN=P0585H11.115 PE=2 SV=1 | 99.4 | 97.2 | 97.8 | 104.3 | 104.6 | 104.2 | 89 | 92.6 | 90.2 | 107.3 | 105.6 | 107.9 |
| Q69XG4 | Os06g0610800 protein OS=Oryza sativa subsp. japonica GN=P0490F09.29-1 PE=3 SV=1 | 91.4 | 99.3 | 101.1 | 97.8 | 96.8 | 97.7 | 102.3 | 101.1 | 101.1 | 108.5 | 102.8 | 100.1 |
| Q6ASR0 | Os05g0147500 protein OS=Oryza sativa subsp. japonica GN=Os05g0147500 PE=4 SV=1 | 109.5 | 91.1 | 103.5 | 96.7 | 107.9 | 92.6 | 106.5 | 94.9 | 109.2 | 87.3 | 106.1 | 94.7 |
| Q6AUB0 | Os05g0413400 protein OS=Oryza sativa subsp. japonica GN=Os05g0413400 PE=2 SV=1 | 103.9 | 113.4 | 120.9 | 120.8 | 111.5 | 105.7 | 83.5 | 95.4 | 89.8 | 91.7 | 79.7 | 83.6 |
| Q6AUN5 | Os05g0568900 protein OS=Oryza sativa subsp. japonica GN=Os05g0568900 PE=2 SV=1 | 111.8 | 118.4 | 110.6 | 94.1 | 91.4 | 95 | 103.1 | 93.6 | 107.5 | 91 | 96.6 | 86.9 |
| Q6AVV6 | Nitrate transporter, putative OS=Oryza sativa subsp. japonica GN=OSJNBb0024N19.9 PE=2 SV=1 | 106.6 | 111.1 | 107.9 | 99.3 | 91.7 | 97 | 101.4 | 111.4 | 101.4 | 92.7 | 85.8 | 93.8 |
| Q6EUP4 | 14-3-3-like protein GF14-E OS=Oryza sativa subsp. japonica GN=GF14E PE=2 SV=1 | 91.8 | 94.4 | 96.3 | 105 | 99.4 | 100.3 | 101.1 | 105.1 | 107.1 | 102.2 | 101.1 | 96.4 |
| Q6H667 | Os02g0643500 protein OS=Oryza sativa subsp. japonica GN=Os02g0643500 PE=2 SV=1 | 102.4 | 101.8 | 100.1 | 97.2 | 94.7 | 94.4 | 100.5 | 102.9 | 102.8 | 99.9 | 100.6 | 102.7 |
| Q6H6B9 | Inositol-1-monophosphatase OS=Oryza sativa subsp. japonica GN=Os02g0169900 PE=2 SV=1 | 102.2 | 99.9 | 98.4 | 108.7 | 104.1 | 107.7 | 92.1 | 94.3 | 94.1 | 96.9 | 101.7 | 99.8 |
| Q6H748 | Chlorophyll a-b binding protein, chloroplastic OS=Oryza sativa subsp. japonica GN=P0026H03.3-1 PE=2 SV=1 | 100.9 | 100.6 | 106.9 | 97.9 | 97 | 99.8 | 88 | 89.1 | 88.6 | 113.2 | 113.4 | 104.7 |
| Q6H7Q6 | Lipoxygenase OS=Oryza sativa subsp. japonica GN=Os02g0194700 PE=3 SV=1 | 148.9 | 158 | 142.7 | 98.8 | 98.7 | 97.5 | 75.7 | 72.8 | 78.7 | 76.5 | 70.5 | 81.1 |
| Q6K1X5 | Os02g0608900 protein OS=Oryza sativa subsp. japonica GN=Os02g0608900 PE=2 SV=1 | 100.5 | 100.1 | 100.2 | 104.9 | 99.3 | 104.1 | 90.9 | 105.3 | 92.9 | 103.7 | 95.2 | 102.8 |
| Q6K4S7 | Os02g0285300 protein OS=Oryza sativa subsp. japonica GN=Os02g0285300 PE=2 SV=1 | 85.2 | 89.4 | 86.8 | 113.9 | 102.8 | 112.3 | 94.3 | 104.3 | 85.1 | 106.7 | 103.5 | 115.9 |
| Q6K8J4 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin), chloroplastic OS=Oryza sativa subsp. japonica GN=ISPG PE=2 SV=1 | 99.4 | 96.6 | 96.3 | 95.5 | 97.9 | 98.5 | 100.4 | 100.9 | 99.5 | 104.6 | 104.6 | 105.7 |
| Q6KA61 | Os02g0285800 protein OS=Oryza sativa subsp. japonica GN=Os02g0285800 PE=4 SV=1 | 86.9 | 83.7 | 84.1 | 104.7 | 100.8 | 103.7 | 97.4 | 103.1 | 90.5 | 111 | 112.4 | 121.7 |
| Q6KAJ2 | Aspartate aminotransferase OS=Oryza sativa subsp. japonica GN=Os02g0797500 PE=2 SV=1 | 104.3 | 103.2 | 104.2 | 96 | 93.3 | 96.8 | 103.8 | 106.3 | 105.1 | 95.9 | 97.2 | 94 |
| Q6L4H5 | Os05g0549700 protein OS=Oryza sativa subsp. japonica GN=P0560C03.1 PE=4 SV=1 | 95.8 | 87.8 | 90 | 104.3 | 119 | 109.5 | 102.5 | 93.7 | 95.8 | 97.3 | 99.5 | 104.7 |
| Q6L4S0 | DNA damage-binding protein 1 OS=Oryza sativa subsp. japonica GN=DBB1 PE=1 SV=1 | 85.4 | 90.5 | 97.2 | 84.8 | 93.2 | 75.8 | 127.4 | 128.3 | 131.2 | 102.4 | 88 | 95.9 |
| Q6L5I5 | Mitochondrial outer membrane protein porin 2 OS=Oryza sativa subsp. japonica GN=VDAC2 PE=2 SV=1 | 115.9 | 110.9 | 111.3 | 96.1 | 95.4 | 95.6 | 112.1 | 113 | 111.8 | 75.8 | 80.7 | 81.3 |
| Q6YPF2 | Os08g0120500 protein OS=Oryza sativa subsp. japonica GN=Os08g0120500 PE=4 SV=1 | 101.9 | 104.5 | 101.7 | 99.1 | 93.6 | 106.7 | 100 | 105.2 | 93.9 | 99 | 96.7 | 97.7 |
| Q6YUR8 | Cold shock domain protein 1 OS=Oryza sativa subsp. japonica GN=CSP1 PE=2 SV=1 | 97.4 | 94.4 | 94.4 | 103.6 | 96.9 | 96 | 95 | 98.9 | 95.1 | 104 | 109.9 | 114.6 |
| Q6YW46 | Elongation factor 1-gamma 2 OS=Oryza sativa subsp. japonica GN=Os02g0220500 PE=2 SV=2 | 96 | 96.3 | 101.2 | 95.5 | 93.1 | 93.3 | 103.9 | 109.3 | 112.5 | 104.5 | 101.4 | 93.1 |
| Q6YY41 | Glycosyltransferase OS=Oryza sativa subsp. japonica GN=OSJNBb0046O12.33 PE=3 SV=1 | 92.6 | 89.3 | 97.8 | 103.4 | 95.2 | 106.5 | 108 | 127.5 | 99.6 | 96 | 88 | 96 |
| Q6Z2T6 | Geranylgeranyl diphosphate reductase, chloroplastic OS=Oryza sativa subsp. japonica GN=CHLP PE=2 SV=1 | 78.3 | 71.1 | 70.4 | 121.9 | 135.5 | 134.9 | 86.9 | 72.4 | 78.8 | 112.9 | 121.1 | 115.9 |
| Q6Z3A3 | Glutamate--cysteine ligase B, chloroplastic OS=Oryza sativa subsp. japonica GN=GSH1-2 PE=3 SV=1 | 123.6 | 125.4 | 95.9 | 124 | 131.3 | 103.9 | 77.8 | 74.6 | 99.2 | 74.7 | 68.7 | 101 |
| Q6Z4E4 | Methylmalonate semi-aldehyde dehydrogenase OS=Oryza sativa subsp. japonica GN=Os07g0188800 PE=2 SV=1 | 115.5 | 115.8 | 117.5 | 96.1 | 96.4 | 98 | 102.4 | 102.8 | 100.5 | 86.1 | 85 | 84 |
| Q6Z7B0 | Heat shock 70 kDa protein BIP1 OS=Oryza sativa subsp. japonica GN=BIP1 PE=1 SV=1 | 93 | 92 | 95.8 | 85.4 | 83.1 | 87 | 132.5 | 131.6 | 125.4 | 89.1 | 93.3 | 91.8 |
| Q6ZBX9 | Os08g0562600 protein OS=Oryza sativa subsp. japonica GN=Os08g0562600 PE=2 SV=1 | 109.2 | 110 | 112.2 | 88.1 | 90.6 | 86.6 | 115.7 | 113.7 | 117.5 | 86.9 | 85.8 | 83.8 |
| Q6ZBZ2 | Germin-like protein 8-14 OS=Oryza sativa subsp. japonica GN=GER5 PE=1 SV=1 | 93.4 | 94.9 | 97.5 | 96 | 97.5 | 97.1 | 113.1 | 108.4 | 107.2 | 97.5 | 99.2 | 98.2 |
| Q6ZHC3 | Os02g0686400 protein OS=Oryza sativa subsp. japonica GN=Os02g0686400 PE=2 SV=1 | 88.6 | 107.1 | 110.1 | 90.2 | 101.2 | 106.7 | 143.1 | 105.3 | 97.2 | 78.1 | 86.5 | 86 |
| Q6ZKI0 | Os08g0139200 protein OS=Oryza sativa subsp. japonica GN=Os08g0139200 PE=2 SV=1 | 104.5 | 105.8 | 104.4 | 95.8 | 95.2 | 109.4 | 100.7 | 101.3 | 100.9 | 99.1 | 97.6 | 85.3 |
| Q70G58 | Thioredoxin reductase NTRC OS=Oryza sativa subsp. japonica GN=Os07g0657900 PE=1 SV=2 | 103.9 | 104.8 | 113.8 | 99.5 | 95.9 | 108.8 | 98.8 | 103.5 | 89.8 | 97.8 | 95.7 | 87.6 |
| Q75G91 | 40S ribosomal protein S3, putative, expressed OS=Oryza sativa subsp. japonica GN=Os03g0577000 PE=2 SV=1 | 83.6 | 91.9 | 85.3 | 106.6 | 101.3 | 105.3 | 104.6 | 101.5 | 107.8 | 105.2 | 105.3 | 101.7 |
| Q75GR6 | 50S ribosomal protein L17, putative, expressed OS=Oryza sativa subsp. japonica GN=LOC\_Os03g60100 PE=2 SV=1 | 97.7 | 96.6 | 98.8 | 113.8 | 118.2 | 105.5 | 80.8 | 77.7 | 92.5 | 107.7 | 107.6 | 103.2 |
| Q75H72 | Os03g0611200 protein OS=Oryza sativa subsp. japonica GN=OSJNBb0007E22.16 PE=4 SV=1 | 95.1 | 106 | 100 | 94.1 | 94 | 96.9 | 118.5 | 108.4 | 106.9 | 92.4 | 91.5 | 96.2 |
| Q75HJ3 | Os03g0804800 protein OS=Oryza sativa subsp. japonica GN=Os03g0804800 PE=3 SV=1 | 104.4 | 99.1 | 96.9 | 98.8 | 100.6 | 97.3 | 105.5 | 109.3 | 109.6 | 91.3 | 91 | 96.2 |
| Q75IQ9 | 'putative 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46) OS=Oryza sativa subsp. japonica GN=Os05g0164100 PE=4 SV=1 | 99.2 | 95.5 | 101.7 | 106.6 | 109.1 | 104.2 | 87.7 | 85.9 | 94.3 | 106.5 | 109.5 | 99.9 |
| Q7EYM8 | Os08g0379400 protein OS=Oryza sativa subsp. japonica GN=Os08g0379400 PE=2 SV=1 | 102.4 | 102.6 | 99.8 | 100.5 | 98.5 | 100.5 | 95.6 | 98 | 97 | 101.5 | 100.9 | 102.7 |
| Q7F190 | Malic enzyme OS=Oryza sativa subsp. japonica GN=OJ1457\_D07.117 PE=2 SV=1 | 102.6 | 109.7 | 108.5 | 97.8 | 100.5 | 98.1 | 108.6 | 94.9 | 100.4 | 91 | 94.9 | 93 |
| Q7FAT6 | OSJNBa0010H02.6 protein OS=Oryza sativa subsp. japonica GN=Os04g0551800 PE=2 SV=1 | 102.2 | 105.6 | 119.7 | 96 | 102.2 | 117.5 | 110 | 107.6 | 84 | 91.8 | 84.5 | 78.8 |
| Q7GCH3 | 26S proteasome regulatory particle triple-A ATPase subunit6 OS=Oryza sativa subsp. japonica GN=OsRPT6 PE=2 SV=1 | 99.4 | 92.8 | 99.8 | 89.5 | 93.2 | 93.5 | 119.8 | 119.5 | 111.6 | 91.4 | 94.5 | 95.1 |
| Q7X6F6 | OSJNBb0079B02.3 protein OS=Oryza sativa subsp. japonica GN=Os04g0640700 PE=4 SV=2 | 105.5 | 124.6 | 105.6 | 113.7 | 109.9 | 111 | 88.4 | 81.2 | 84.4 | 92.4 | 84.3 | 99.1 |
| Q7X7H3 | OSJNBa0076N16.12 protein OS=Oryza sativa subsp. japonica GN=Os04g0490800 PE=2 SV=2 | 105.4 | 104.3 | 108 | 104.1 | 106.6 | 108.4 | 93 | 88.5 | 86.3 | 97.5 | 100.6 | 97.3 |
| Q7XBZ9 | Dynamin-related protein 1C, putative, expressed OS=Oryza sativa subsp. japonica GN=OSJNBa0057L21.1 PE=2 SV=1 | 105.5 | 98.1 | 103.8 | 93.4 | 91.6 | 92 | 104.4 | 117.4 | 105.7 | 96.7 | 92.9 | 98.6 |
| Q7XDC8 | Malate dehydrogenase, cytoplasmic OS=Oryza sativa subsp. japonica GN=Os10g0478200 PE=1 SV=3 | 101.6 | 101.9 | 100.6 | 90.1 | 89.3 | 93.8 | 114.3 | 119.5 | 109.5 | 94 | 89.2 | 96 |
| Q7XEQ3 | 40S ribosomal protein S17-4, putative, expressed OS=Oryza sativa subsp. japonica GN=Os10g0411800 PE=3 SV=1 | 91.2 | 98.1 | 98 | 116.1 | 98.9 | 97.4 | 100.2 | 102.6 | 98.9 | 92.5 | 100.4 | 105.7 |
| Q7XR19 | 60S ribosomal protein L6 OS=Oryza sativa subsp. japonica GN=Os04g0473400 PE=2 SV=2 | 110.8 | 119.5 | 128.9 | 116.7 | 127.1 | 140.7 | 89.5 | 76.1 | 65.6 | 83 | 77.2 | 64.7 |
| Q7XUC9 | Histone H4 OS=Oryza sativa subsp. japonica GN=OSJNBb0064P21.1 PE=2 SV=2 | 91.7 | 91.1 | 91.4 | 101.7 | 100.8 | 108.8 | 101.8 | 109.7 | 94.5 | 104.9 | 98.4 | 105.4 |
| Q7XXS4 | Thiamine thiazole synthase, chloroplastic OS=Oryza sativa subsp. japonica GN=Os07g0529600 PE=2 SV=1 | 145.2 | 144.6 | 141.9 | 94 | 93.8 | 94.4 | 77.1 | 73.2 | 76.2 | 83.7 | 88.4 | 87.4 |
| Q84M68 | Os03g0856500 protein OS=Oryza sativa subsp. japonica GN=LOC\_Os03g63950 PE=2 SV=1 | 93.7 | 103.7 | 100 | 120.3 | 115.2 | 111.9 | 81.1 | 78.3 | 86.5 | 104.9 | 102.8 | 101.6 |
| Q84NN4 | Thioredoxin-like protein CDSP32, chloroplastic OS=Oryza sativa subsp. japonica GN=CDSP32 PE=2 SV=1 | 99.4 | 98.2 | 94.2 | 94.5 | 95.5 | 94.7 | 103.1 | 99.1 | 102.1 | 103 | 107.2 | 108.9 |
| Q84PB4 | Chloroplast photosystem I reaction center subunit II-like protein OS=Oryza sativa subsp. japonica GN=Os08g0560900 PE=2 SV=1 | 91 | 98.6 | 96.9 | 113.6 | 111.6 | 110.4 | 83.3 | 87.3 | 85.7 | 112.1 | 102.5 | 107 |
| Q851K1 | Germin-like protein 3-6 OS=Oryza sativa subsp. japonica GN=Os03g0694000 PE=2 SV=1 | 106.6 | 115.5 | 109.8 | 90.6 | 96.8 | 102.3 | 123.6 | 105.5 | 95.1 | 79.2 | 82.2 | 92.9 |
| Q851S8 | Adenylosuccinate synthetase 2, chloroplastic OS=Oryza sativa subsp. japonica GN=PURA2 PE=2 SV=1 | 92.8 | 102.5 | 100.3 | 89.7 | 107.6 | 109.6 | 88.1 | 98.2 | 96.1 | 129.4 | 91.7 | 94 |
| Q851Y8 | Elongation factor Tu OS=Oryza sativa subsp. japonica GN=LOC\_Os03g63410 PE=2 SV=1 | 99.1 | 105.5 | 100.7 | 94.8 | 90.5 | 94.4 | 108.4 | 114 | 103.4 | 97.7 | 90 | 101.6 |
| Q852A3 | Expressed protein OS=Oryza sativa subsp. japonica GN=OSJNBb0081B07.22 PE=2 SV=1 | 100.1 | 94.2 | 98 | 90.3 | 90.8 | 87.6 | 111 | 111.1 | 111.9 | 98.6 | 103.9 | 102.5 |
| Q8GRU9 | Phosphoribulokinase OS=Oryza sativa subsp. indica GN=OsI\_08574 PE=2 SV=1 | 107.4 | 106.5 | 108.4 | 102 | 102.2 | 102.6 | 93.8 | 95.2 | 91.4 | 96.8 | 96.1 | 97.6 |
| Q8GTK4 | Os07g0141400 protein OS=Oryza sativa subsp. japonica GN=OJ1351\_C05.112 PE=2 SV=1 | 100.8 | 99.7 | 100.8 | 103.5 | 103.3 | 103.1 | 93.4 | 92.5 | 93.3 | 102.3 | 104.5 | 102.8 |
| Q8H3M0 | Os08g0428800 protein OS=Oryza sativa subsp. japonica GN=P0479C08.106 PE=4 SV=1 | 102.2 | 95.9 | 98 | 98.5 | 103.3 | 102.4 | 109.2 | 100.6 | 101.5 | 90.1 | 100.3 | 98.2 |
| Q8H3Q7 | Xylose isomerase OS=Oryza sativa subsp. japonica GN=P0625E02.119 PE=2 SV=2 | 97.8 | 99.6 | 98.3 | 94.1 | 103 | 99.5 | 109.1 | 107 | 106.4 | 99 | 90.4 | 95.8 |
| Q8H4V1 | Os08g0366000 protein OS=Oryza sativa subsp. japonica GN=OJ1484\_G09.129-1 PE=2 SV=1 | 102.6 | 103.5 | 104 | 86.3 | 85.9 | 83.8 | 120.2 | 122.4 | 125 | 90.9 | 88.3 | 87.1 |
| Q8H903 | 60 kDa chaperonin OS=Oryza sativa subsp. japonica GN=Os10g0462900 PE=2 SV=1 | 98.8 | 110.5 | 104.4 | 97.5 | 93 | 93.6 | 107.3 | 110.5 | 113.6 | 96.4 | 86.1 | 88.4 |
| Q8HCQ9 | ORFB protein OS=Oryza sativa subsp. japonica GN=orfB PE=4 SV=2 | 106.9 | 100.6 | 111.1 | 92.6 | 96.1 | 93.3 | 103 | 102.5 | 96.6 | 97.6 | 100.8 | 99 |
| Q8HCR5 | Uncharacterized protein OS=Oryza sativa subsp. japonica GN=orf25 PE=4 SV=2 | 96.2 | 104.9 | 98.3 | 93.9 | 92.9 | 89.9 | 111.2 | 108.4 | 113.1 | 98.6 | 93.7 | 98.7 |
| Q8L4V6 | Glutathione S-transferase GSTU6, putative, expressed OS=Oryza sativa subsp. japonica GN=LOC\_Os10g38780 PE=2 SV=1 | 166.1 | 169.1 | 152.3 | 70.3 | 67.2 | 70.7 | 106.3 | 107 | 113.9 | 57.3 | 56.6 | 63.1 |
| Q8L6I1 | Plasma membrane ATPase OS=Oryza sativa subsp. japonica GN=a3 PE=3 SV=1 | 101.8 | 95.8 | 100.7 | 103.8 | 103.6 | 103.7 | 91.5 | 97.8 | 95.7 | 102.9 | 102.7 | 99.8 |
| Q8LH97 | 40S ribosomal protein S6 OS=Oryza sativa subsp. japonica GN=P0594D10.135 PE=2 SV=1 | 92.4 | 98.4 | 92.4 | 107.3 | 106 | 106.6 | 98.9 | 98.3 | 98.7 | 101.4 | 97.3 | 102.2 |
| Q8W317 | NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial, putative, expressed OS=Oryza sativa subsp. japonica GN=LOC\_Os03g50540 PE=2 SV=1 | 98 | 93.9 | 94.1 | 95.7 | 102.9 | 99.9 | 105.3 | 101.7 | 105.3 | 101.1 | 101.5 | 100.8 |
| Q8W3D9 | Protochlorophyllide reductase B, chloroplastic OS=Oryza sativa subsp. japonica GN=PORB PE=2 SV=1 | 82.8 | 83 | 80.3 | 152 | 113.8 | 127.8 | 82.5 | 82.4 | 78 | 82.8 | 120.8 | 113.9 |
| Q93VT8 | ATP-citrate synthase beta chain protein 1 OS=Oryza sativa subsp. japonica GN=ACLB-1 PE=2 SV=1 | 97.3 | 95 | 93.3 | 98.1 | 95.6 | 96.9 | 106.9 | 108.1 | 109 | 97.7 | 101.3 | 100.8 |
| Q942L2 | Protein disulfide isomerase-like 2-2 OS=Oryza sativa subsp. japonica GN=PDIL2-2 PE=2 SV=1 | 104.2 | 96.1 | 104.6 | 81.4 | 93.5 | 86.4 | 128.7 | 125.3 | 121.3 | 85.7 | 85.1 | 87.7 |
| Q94J17 | Os01g0749200 protein OS=Oryza sativa subsp. japonica GN=Os01g0749200 PE=2 SV=1 | 100.8 | 95.4 | 103.2 | 109 | 112.9 | 106.2 | 85.7 | 90.5 | 90.7 | 104.5 | 101.3 | 99.9 |
| Q9AS12 | Peroxidase OS=Oryza sativa subsp. japonica GN=prx16 PE=3 SV=1 | 112.5 | 106.7 | 112.4 | 105.5 | 106.3 | 105.8 | 99.5 | 101.9 | 100.9 | 82.5 | 85 | 80.8 |
| Q9LRE9 | Cytosolic aldehyde dehydrogenase OS=Oryza sativa subsp. japonica GN=ALDH1a PE=2 SV=1 | 76.5 | 51.6 | 74.8 | 84.9 | 78 | 81.5 | 109.2 | 114.8 | 117.7 | 129.4 | 155.6 | 126 |
| Q9LST8 | Proteasome subunit beta type OS=Oryza sativa subsp. japonica GN=OsPBB1 PE=2 SV=1 | 99.2 | 95.6 | 100.1 | 89.6 | 95.2 | 86.7 | 116.8 | 116 | 120.9 | 94.4 | 93.1 | 92.3 |
| Q9LSU1 | Proteasome subunit alpha type-5 OS=Oryza sativa subsp. japonica GN=PAE1 PE=2 SV=1 | 94.8 | 100.2 | 99.1 | 93.9 | 91.6 | 97.5 | 119.9 | 119 | 112.1 | 91.3 | 89.2 | 91.3 |
| Q9SDG5 | Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Oryza sativa subsp. japonica GN=Os01g0276100 PE=2 SV=1 | 102.9 | 103.7 | 98.3 | 91.2 | 90.5 | 95.4 | 113.5 | 120.1 | 111.3 | 92.4 | 85.7 | 95 |
| Q9SDJ2 | Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase OS=Oryza sativa subsp. japonica GN=ZIP1 PE=2 SV=1 | 79 | 67.7 | 79.9 | 122.5 | 132.4 | 116.3 | 76 | 68.7 | 86.8 | 122.6 | 131.2 | 117 |
| Q9XGP7 | Tricin synthase 1 OS=Oryza sativa subsp. japonica GN=ROMT-15 PE=1 SV=1 | 95.7 | 98.6 | 105.9 | 87.8 | 80 | 79.1 | 131.3 | 143.8 | 135.9 | 85.2 | 77.6 | 79.2 |

Table S2:

|  |  |  |
| --- | --- | --- |
| BCGN\_T VS BCGN\_CK | | |
| Accession | P value | FC |
| A0A0P0VRK8 | 0.013 | 0.825 |
| A0A0P0WKD6 | 0.001 | 0.749 |
| A0A0P0YAL3 | 0.000 | 1.245 |
| A0A0P0YB77 | 0.000 | 0.748 |
| A2WML4 | 0.000 | 0.716 |
| A2WS81 | 0.001 | 0.737 |
| A2WTA6 | 0.003 | 0.824 |
| A2X753 | 0.004 | 1.430 |
| A2X847 | 0.042 | 0.756 |
| A2X9V8 | 0.000 | 1.259 |
| A2XB94 | 0.001 | 1.419 |
| A2XBF5 | 0.010 | 0.706 |
| A2XC62 | 0.011 | 0.823 |
| A2XC67 | 0.003 | 0.736 |
| A2XHR1 | 0.001 | 0.783 |
| A2XK95 | 0.000 | 0.539 |
| A2XQV4 | 0.002 | 1.349 |
| A2XUS0 | 0.003 | 1.238 |
| A2XVY3 | 0.000 | 0.784 |
| A2Y0P2 | 0.001 | 0.759 |
| A2Y2C4 | 0.006 | 1.221 |
| A2Y5W6 | 0.000 | 0.713 |
| A2Y7Y4 | 0.000 | 1.400 |
| A2YBW4 | 0.002 | 0.516 |
| A2YG06 | 0.000 | 1.429 |
| A2YGS3 | 0.027 | 0.769 |
| A2YH08 | 0.000 | 1.226 |
| A2YPX2 | 0.001 | 1.484 |
| A2YS08 | 0.003 | 1.263 |
| A2YSY8 | 0.004 | 1.201 |
| A2Z1W9 | 0.004 | 0.746 |
| A2Z263 | 0.000 | 1.574 |
| A2Z3I6 | 0.000 | 1.470 |
| A2Z9L8 | 0.000 | 1.502 |
| A2ZAT2 | 0.000 | 1.509 |
| A2ZIS0 | 0.001 | 0.823 |
| A2ZJH7 | 0.000 | 0.672 |
| A2ZLC1 | 0.000 | 0.791 |
| A6N0M9 | 0.000 | 1.210 |
| B8A750 | 0.006 | 1.209 |
| B8ACF1 | 0.002 | 1.342 |
| B8ACL5 | 0.009 | 1.287 |
| B8AED8 | 0.000 | 0.830 |
| B8AEF1 | 0.006 | 1.246 |
| B8AGZ1 | 0.000 | 0.662 |
| B8ALD1 | 0.000 | 1.421 |
| B8AMQ6 | 0.002 | 0.776 |
| B8ASD9 | 0.004 | 1.712 |
| B8AU70 | 0.001 | 0.770 |
| B8AU81 | 0.008 | 0.825 |
| B8AXG9 | 0.020 | 1.236 |
| B8BB05 | 0.004 | 0.786 |
| B8BD60 | 0.000 | 1.469 |
| B8BMN2 | 0.007 | 0.810 |
| I1NKK9 | 0.005 | 1.520 |
| I1NLW9 | 0.002 | 0.824 |
| I1NPS5 | 0.026 | 0.784 |
| I1NRC3 | 0.000 | 1.263 |
| I1NWJ9 | 0.001 | 0.630 |
| I1P3K4 | 0.008 | 0.811 |
| I1P5G4 | 0.000 | 1.270 |
| I1PB43 | 0.000 | 0.624 |
| I1PC51 | 0.004 | 1.230 |
| I1PF07 | 0.001 | 0.807 |
| I1PFI3 | 0.001 | 0.714 |
| I1PR23 | 0.006 | 0.828 |
| I1PR82 | 0.000 | 1.540 |
| I1PSP2 | 0.020 | 1.324 |
| I1PYX1 | 0.001 | 0.717 |
| I1Q0Z0 | 0.000 | 1.320 |
| I1Q461 | 0.002 | 1.570 |
| I1Q8K2 | 0.046 | 0.817 |
| I1QCH6 | 0.000 | 0.701 |
| I1QF99 | 0.000 | 1.211 |
| I1QKN4 | 0.037 | 1.202 |
| I1QKY4 | 0.009 | 0.830 |
| I1QLJ6 | 0.004 | 0.784 |
| I1QUH7 | 0.014 | 1.209 |
| I1QUZ5 | 0.000 | 0.830 |
| I1QVB5 | 0.007 | 1.215 |
| I1R1E2 | 0.006 | 1.223 |
| I1R446 | 0.000 | 1.260 |
| I1R8W6 | 0.019 | 0.830 |
| P12153 | 0.001 | 0.792 |
| Q0D5S1 | 0.005 | 1.943 |
| Q0DEF1 | 0.000 | 1.231 |
| Q0DRB3 | 0.013 | 0.727 |
| Q0J8G4 | 0.000 | 0.801 |
| Q0JR29 | 0.001 | 1.465 |
| Q1KL27 | 0.000 | 1.216 |
| Q2QNN5 | 0.000 | 2.638 |
| Q53RM0 | 0.002 | 0.670 |
| Q5Z4M6 | 0.000 | 0.707 |
| Q5ZBH8 | 0.029 | 1.220 |
| Q6AUN5 | 0.002 | 1.215 |
| Q6H7Q6 | 0.000 | 1.524 |
| Q6K4S7 | 0.004 | 0.795 |
| Q6KA61 | 0.000 | 0.824 |
| Q6L4H5 | 0.016 | 0.822 |
| Q6Z2T6 | 0.000 | 0.560 |
| Q6Z4E4 | 0.000 | 1.201 |
| Q6ZBX9 | 0.000 | 1.249 |
| Q75G91 | 0.004 | 0.833 |
| Q7XXS4 | 0.000 | 1.530 |
| Q8H4V1 | 0.000 | 1.211 |
| Q8L4V6 | 0.000 | 2.341 |
| Q8W3D9 | 0.012 | 0.625 |
| Q9SDJ2 | 0.001 | 0.610 |
| Q9XGP7 | 0.012 | 1.216 |

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| --- | --- | --- |
| YZX\_T VS YZX\_CK | | |
| Accession | P value | FC |
| A0A0P0WKD6 | 0.003 | 0.772 |
| A0A0P0WL76 | 0.000 | 0.740 |
| A0A0P0Y1Y5 | 0.000 | 1.246 |
| A0A0P0YB77 | 0.001 | 0.729 |
| A2WML4 | 0.001 | 0.646 |
| A2WN87 | 0.000 | 1.227 |
| A2WRD4 | 0.010 | 1.273 |
| A2WS81 | 0.000 | 0.544 |
| A2WTA6 | 0.004 | 0.744 |
| A2WTC5 | 0.000 | 1.247 |
| A2WTF3 | 0.002 | 1.252 |
| A2WUJ5 | 0.015 | 0.798 |
| A2WVT8 | 0.001 | 1.396 |
| A2X1T8 | 0.034 | 0.824 |
| A2X335 | 0.029 | 0.777 |
| A2X753 | 0.000 | 2.218 |
| A2X9V8 | 0.000 | 1.407 |
| A2XAI5 | 0.000 | 1.235 |
| A2XB19 | 0.033 | 1.206 |
| A2XB94 | 0.001 | 1.521 |
| A2XBF5 | 0.012 | 0.616 |
| A2XCL6 | 0.011 | 1.209 |
| A2XF36 | 0.002 | 1.302 |
| A2XF65 | 0.007 | 0.618 |
| A2XG06 | 0.001 | 0.747 |
| A2XK95 | 0.000 | 0.605 |
| A2XMP7 | 0.000 | 1.487 |
| A2XN99 | 0.000 | 1.406 |
| A2XNC0 | 0.000 | 1.293 |
| A2XVY3 | 0.004 | 0.809 |
| A2XXN8 | 0.000 | 1.239 |
| A2XY57 | 0.007 | 1.342 |
| A2XYZ3 | 0.005 | 1.226 |
| A2XZQ4 | 0.001 | 1.202 |
| A2Y053 | 0.007 | 1.757 |
| A2Y0P2 | 0.001 | 0.721 |
| A2Y2C4 | 0.002 | 1.368 |
| A2Y5W6 | 0.000 | 0.720 |
| A2Y7R5 | 0.003 | 1.285 |
| A2Y7Y4 | 0.000 | 1.255 |
| A2Y8A0 | 0.001 | 1.303 |
| A2YBK1 | 0.000 | 1.267 |
| A2YBW4 | 0.002 | 0.707 |
| A2YG06 | 0.000 | 1.532 |
| A2YGS3 | 0.007 | 0.749 |
| A2YH08 | 0.000 | 1.455 |
| A2YP40 | 0.001 | 1.532 |
| A2YPX2 | 0.003 | 1.299 |
| A2YS08 | 0.000 | 1.266 |
| A2Z263 | 0.000 | 1.977 |
| A2Z3H3 | 0.008 | 1.234 |
| A2Z9J9 | 0.003 | 2.018 |
| A2Z9L8 | 0.001 | 1.202 |
| A2Z9L9 | 0.005 | 0.815 |
| A2ZAT2 | 0.000 | 1.212 |
| A2ZD01 | 0.000 | 0.659 |
| A2ZFY8 | 0.001 | 1.231 |
| A2ZIS0 | 0.000 | 0.724 |
| A2ZJH7 | 0.000 | 0.765 |
| A2ZK43 | 0.007 | 1.277 |
| A2ZLC1 | 0.002 | 0.812 |
| A2ZMY2 | 0.003 | 1.232 |
| A6N0M9 | 0.000 | 1.222 |
| B8A8F0 | 0.002 | 1.259 |
| B8A8H2 | 0.000 | 1.613 |
| B8AAT9 | 0.000 | 1.213 |
| B8ABU1 | 0.000 | 1.333 |
| B8ACF1 | 0.000 | 1.736 |
| B8ACF5 | 0.002 | 1.251 |
| B8ACL5 | 0.011 | 1.274 |
| B8AD25 | 0.007 | 1.568 |
| B8ADH7 | 0.000 | 1.202 |
| B8AED8 | 0.001 | 0.793 |
| B8AEX3 | 0.008 | 1.503 |
| B8AFN7 | 0.001 | 1.522 |
| B8AG23 | 0.000 | 0.617 |
| B8AGZ1 | 0.000 | 0.776 |
| B8AHM8 | 0.035 | 1.284 |
| B8AI32 | 0.001 | 1.240 |
| B8AIH2 | 0.000 | 1.299 |
| B8AKD7 | 0.001 | 1.333 |
| B8AKQ8 | 0.004 | 0.789 |
| B8ALD1 | 0.000 | 1.404 |
| B8ALJ1 | 0.000 | 0.797 |
| B8ALV6 | 0.003 | 0.793 |
| B8ANL0 | 0.001 | 1.352 |
| B8APD5 | 0.000 | 1.558 |
| B8ASD9 | 0.001 | 3.274 |
| B8ATG9 | 0.028 | 1.240 |
| B8AU81 | 0.002 | 0.752 |
| B8AW91 | 0.002 | 1.203 |
| B8AXG9 | 0.012 | 1.241 |
| B8AXU6 | 0.000 | 0.775 |
| B8AYJ5 | 0.003 | 1.360 |
| B8AZP1 | 0.001 | 1.231 |
| B8B107 | 0.000 | 1.224 |
| B8B2F2 | 0.001 | 1.282 |
| B8B3L5 | 0.002 | 0.736 |
| B8B5L9 | 0.000 | 1.242 |
| B8B764 | 0.006 | 0.784 |
| B8B8E2 | 0.000 | 1.331 |
| B8B9C5 | 0.010 | 1.340 |
| B8BAQ6 | 0.002 | 1.206 |
| B8BD60 | 0.000 | 2.101 |
| B8BHR1 | 0.009 | 1.225 |
| B8BIC2 | 0.004 | 1.766 |
| B8BMH5 | 0.020 | 1.259 |
| B8BMN2 | 0.002 | 0.773 |
| B9FSC8 | 0.006 | 1.233 |
| I1NKK9 | 0.003 | 1.297 |
| I1NMP4 | 0.000 | 1.423 |
| I1NQP6 | 0.000 | 1.237 |
| I1NRC3 | 0.000 | 1.608 |
| I1NRT6 | 0.000 | 1.394 |
| I1NRW1 | 0.000 | 1.308 |
| I1P1T4 | 0.016 | 1.212 |
| I1P2D6 | 0.000 | 1.812 |
| I1P526 | 0.008 | 1.232 |
| I1P5G4 | 0.000 | 1.325 |
| I1P5P0 | 0.000 | 0.674 |
| I1P782 | 0.002 | 0.833 |
| I1PA01 | 0.000 | 1.333 |
| I1PAF1 | 0.010 | 1.468 |
| I1PB43 | 0.000 | 0.638 |
| I1PBB4 | 0.000 | 1.257 |
| I1PC51 | 0.001 | 1.228 |
| I1PFI3 | 0.001 | 0.818 |
| I1PFN6 | 0.007 | 1.278 |
| I1PGU1 | 0.016 | 1.316 |
| I1PHB6 | 0.004 | 1.208 |
| I1PI01 | 0.001 | 0.797 |
| I1PLV0 | 0.000 | 0.678 |
| I1PM97 | 0.005 | 1.214 |
| I1PQ98 | 0.000 | 1.664 |
| I1PQC4 | 0.000 | 1.627 |
| I1PR89 | 0.000 | 0.728 |
| I1PRN9 | 0.001 | 1.633 |
| I1PSM1 | 0.000 | 1.233 |
| I1PSP2 | 0.039 | 1.247 |
| I1PT09 | 0.003 | 0.674 |
| I1PU82 | 0.000 | 1.251 |
| I1PU87 | 0.024 | 1.228 |
| I1PXT3 | 0.007 | 1.219 |
| I1PYW0 | 0.001 | 1.326 |
| I1PYX1 | 0.005 | 0.820 |
| I1PZA2 | 0.002 | 1.214 |
| I1PZV7 | 0.014 | 1.208 |
| I1Q096 | 0.004 | 1.297 |
| I1Q1X7 | 0.001 | 0.753 |
| I1Q461 | 0.002 | 1.760 |
| I1Q6C6 | 0.001 | 0.720 |
| I1QCH6 | 0.000 | 0.781 |
| I1QF99 | 0.000 | 1.428 |
| I1QJW3 | 0.003 | 1.241 |
| I1QK10 | 0.000 | 2.200 |
| I1QKV4 | 0.000 | 0.647 |
| I1QLP7 | 0.029 | 1.209 |
| I1QN54 | 0.001 | 0.740 |
| I1QTD1 | 0.003 | 1.224 |
| I1QUH7 | 0.000 | 1.284 |
| I1QV49 | 0.002 | 1.369 |
| I1QVB5 | 0.007 | 1.231 |
| I1QXY9 | 0.001 | 1.212 |
| I1R1E2 | 0.010 | 1.276 |
| I1R408 | 0.004 | 1.239 |
| I1R446 | 0.008 | 1.212 |
| O22386 | 0.002 | 0.700 |
| P0C2Z0 | 0.000 | 0.706 |
| P0C2Z5 | 0.000 | 0.831 |
| P0C457 | 0.000 | 0.795 |
| P0C490 | 0.000 | 0.734 |
| P0C497 | 0.000 | 0.681 |
| P0DKK0 | 0.000 | 1.216 |
| P83646 | 0.008 | 0.820 |
| P93431 | 0.000 | 0.828 |
| Q0DZE5 | 0.034 | 1.339 |
| Q0E446 | 0.002 | 0.803 |
| Q0J2H4 | 0.000 | 1.235 |
| Q0JM17 | 0.000 | 1.214 |
| Q0JR29 | 0.005 | 1.222 |
| Q1KL27 | 0.000 | 1.293 |
| Q2QNN5 | 0.000 | 1.265 |
| Q2QYW2 | 0.000 | 1.306 |
| Q33E23 | 0.000 | 1.409 |
| Q53RM0 | 0.003 | 0.739 |
| Q5JMS4 | 0.000 | 1.349 |
| Q5Z4M6 | 0.000 | 0.782 |
| Q65XE5 | 0.000 | 1.862 |
| Q6H748 | 0.002 | 0.802 |
| Q6L4S0 | 0.001 | 1.351 |
| Q6L5I5 | 0.000 | 1.417 |
| Q6Z2T6 | 0.002 | 0.680 |
| Q6Z7B0 | 0.000 | 1.420 |
| Q6ZBX9 | 0.000 | 1.352 |
| Q75GR6 | 0.009 | 0.788 |
| Q7GCH3 | 0.001 | 1.249 |
| Q7XDC8 | 0.004 | 1.230 |
| Q84M68 | 0.001 | 0.795 |
| Q84PB4 | 0.002 | 0.797 |
| Q8H4V1 | 0.000 | 1.380 |
| Q8H903 | 0.005 | 1.223 |
| Q8L4V6 | 0.000 | 1.849 |
| Q942L2 | 0.000 | 1.452 |
| Q9AS12 | 0.000 | 1.217 |
| Q9LST8 | 0.000 | 1.264 |
| Q9LSU1 | 0.000 | 1.291 |
| Q9SDG5 | 0.003 | 1.263 |
| Q9SDJ2 | 0.002 | 0.624 |
| Q9XGP7 | 0.000 | 1.698 |

Table S3: Pathways and functions enrichment analysis of differentially expressed proteins after Cd treatment

Bancanggennuo:

KEGG:

|  |  |  |  |
| --- | --- | --- | --- |
| Pathway Name | Pathway ID | Pvalue |  |
| Porphyrin and chlorophyll metabolism | osa00860 | 4.61E-07 | down |
| Biosynthesis of secondary metabolites | osa01110 | 1.36E-02 | down |
| Vitamin B6 metabolism | osa00750 | 1.62E-02 | down |
| Metabolic pathways | osa01100 | 4.88E-02 | down |
| Linoleic acid metabolism | osa00591 | 1.36E-04 | up |
| alpha-Linolenic acid metabolism | osa00592 | 9.49E-04 | up |
| Metabolic pathways | osa01100 | 1.00E-02 | up |
| Thiamine metabolism | osa00730 | 1.27E-02 | up |
| Propanoate metabolism | osa00640 | 2.53E-02 | up |
| Carbon metabolism | osa01200 | 3.18E-02 | up |
| beta-Alanine metabolism | osa00410 | 4.02E-02 | up |
| Pyruvate metabolism | osa00620 | 4.46E-02 | up |

MF:

|  |  |  |  |
| --- | --- | --- | --- |
| GO\_Name | GO\_ID | Pvalue |  |
| oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | GO:0016702 | 2.78E-04 | up |
| methylmalonate-semialdehyde dehydrogenase (acylating) activity | GO:0004491 | 4.83E-04 | up |
| oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | GO:0016701 | 5.78E-04 | up |
| phosphoenolpyruvate carboxylase activity | GO:0008964 | 3.86E-03 | up |
| dioxygenase activity | GO:0051213 | 4.61E-03 | up |
| phosphoenolpyruvate carboxykinase activity | GO:0004611 | 6.26E-03 | up |
| protein homodimerization activity | GO:0042803 | 1.63E-02 | up |
| oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | GO:0016620 | 2.86E-02 | up |
| O-methyltransferase activity | GO:0008171 | 2.86E-02 | up |
| identical protein binding | GO:0042802 | 2.86E-02 | up |
| serine-type endopeptidase inhibitor activity | GO:0004867 | 3.05E-02 | up |
| oxidoreductase activity, acting on the aldehyde or oxo group of donors | GO:0016903 | 3.70E-02 | up |
| peptidase regulator activity | GO:0061134 | 3.80E-02 | up |
| endopeptidase regulator activity | GO:0061135 | 3.80E-02 | up |
| peptidase inhibitor activity | GO:0030414 | 3.80E-02 | up |
| endopeptidase inhibitor activity | GO:0004866 | 3.80E-02 | up |
| carboxy-lyase activity | GO:0016831 | 4.26E-02 | up |
| oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor | GO:0016628 | 3.50E-05 | down |
| oxidoreductase activity, acting on the CH-CH group of donors | GO:0016627 | 2.80E-04 | down |
| magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase activity | GO:0048529 | 3.51E-04 | down |
| geranylgeranyl reductase activity | GO:0045550 | 7.03E-04 | down |
| protochlorophyllide reductase activity | GO:0016630 | 7.03E-04 | down |
| fructokinase activity | GO:0008865 | 1.05E-03 | down |
| ligase activity, forming nitrogen-metal bonds | GO:0051002 | 1.76E-03 | down |
| ligase activity, forming nitrogen-metal bonds, forming coordination complexes | GO:0051003 | 1.76E-03 | down |
| magnesium chelatase activity | GO:0016851 | 1.76E-03 | down |
| hexokinase activity | GO:0004396 | 7.36E-03 | down |
| carbohydrate kinase activity | GO:0019200 | 2.05E-02 | down |
| oxidoreductase activity | GO:0016491 | 3.65E-02 | down |
| pyridoxal phosphate binding | GO:0030170 | 4.38E-02 | down |
|  |  |  |  |

BP:

|  |  |  |  |
| --- | --- | --- | --- |
| GO\_Name | GO\_ID | Pvalue |  |
| pigment catabolic process | GO:0046149 | 1.18E-04 | up |
| chlorophyll catabolic process | GO:0015996 | 1.18E-04 | up |
| porphyrin-containing compound catabolic process | GO:0006787 | 1.34E-04 | up |
| cofactor catabolic process | GO:0051187 | 1.34E-04 | up |
| tetrapyrrole catabolic process | GO:0033015 | 1.34E-04 | up |
| oxylipin biosynthetic process | GO:0031408 | 2.68E-04 | up |
| oxylipin metabolic process | GO:0031407 | 2.79E-04 | up |
| oxazole or thiazole metabolic process | GO:0046484 | 5.15E-04 | up |
| oxazole or thiazole biosynthetic process | GO:0018131 | 5.15E-04 | up |
| chlorophyll metabolic process | GO:0015994 | 1.50E-03 | up |
| porphyrin-containing compound metabolic process | GO:0006778 | 2.16E-03 | up |
| small molecule metabolic process | GO:0044281 | 2.22E-03 | up |
| tetrapyrrole metabolic process | GO:0033013 | 2.28E-03 | up |
| heterocycle catabolic process | GO:0046700 | 2.72E-03 | up |
| cellular nitrogen compound catabolic process | GO:0044270 | 2.75E-03 | up |
| photosystem II repair | GO:0010206 | 3.08E-03 | up |
| organonitrogen compound catabolic process | GO:1901565 | 3.30E-03 | up |
| pigment metabolic process | GO:0042440 | 3.69E-03 | up |
| aromatic compound catabolic process | GO:0019439 | 3.77E-03 | up |
| organic cyclic compound catabolic process | GO:1901361 | 4.06E-03 | up |
| PSII associated light-harvesting complex II catabolic process | GO:0010304 | 4.11E-03 | up |
| fatty acid biosynthetic process | GO:0006633 | 4.23E-03 | up |
| oxoacid metabolic process | GO:0043436 | 4.36E-03 | up |
| organic acid metabolic process | GO:0006082 | 4.37E-03 | up |
| thiamine biosynthetic process | GO:0009228 | 5.13E-03 | up |
| thiamine-containing compound biosynthetic process | GO:0042724 | 5.13E-03 | up |
| small molecule biosynthetic process | GO:0044283 | 5.83E-03 | up |
| sulfur compound biosynthetic process | GO:0044272 | 5.95E-03 | up |
| protein repair | GO:0030091 | 7.18E-03 | up |
| thiamine metabolic process | GO:0006772 | 7.69E-03 | up |
| thiamine-containing compound metabolic process | GO:0042723 | 7.69E-03 | up |
| fatty acid metabolic process | GO:0006631 | 8.76E-03 | up |
| monocarboxylic acid biosynthetic process | GO:0072330 | 8.94E-03 | up |
| sulfur compound metabolic process | GO:0006790 | 1.09E-02 | up |
| carbon fixation | GO:0015977 | 1.23E-02 | up |
| single-organism biosynthetic process | GO:0044711 | 1.32E-02 | up |
| photosynthesis, light harvesting | GO:0009765 | 1.53E-02 | up |
| regulation of proton transport | GO:0010155 | 1.84E-02 | up |
| generation of precursor metabolites and energy | GO:0006091 | 2.11E-02 | up |
| regulation of catalytic activity | GO:0050790 | 2.13E-02 | up |
| regulation of molecular function | GO:0065009 | 2.19E-02 | up |
| glucosinolate biosynthetic process | GO:0019761 | 2.29E-02 | up |
| glycosinolate biosynthetic process | GO:0019758 | 2.29E-02 | up |
| S-glycoside biosynthetic process | GO:0016144 | 2.29E-02 | up |
| response to blue light | GO:0009637 | 2.69E-02 | up |
| water-soluble vitamin biosynthetic process | GO:0042364 | 2.74E-02 | up |
| tricarboxylic acid cycle | GO:0006099 | 2.74E-02 | up |
| cofactor metabolic process | GO:0051186 | 2.77E-02 | up |
| citrate metabolic process | GO:0006101 | 2.79E-02 | up |
| oxidation-reduction process | GO:0055114 | 2.86E-02 | up |
| carboxylic acid metabolic process | GO:0019752 | 2.91E-02 | up |
| tricarboxylic acid metabolic process | GO:0072350 | 2.94E-02 | up |
| water-soluble vitamin metabolic process | GO:0006767 | 2.99E-02 | up |
| glycosinolate metabolic process | GO:0019757 | 3.14E-02 | up |
| glucosinolate metabolic process | GO:0019760 | 3.14E-02 | up |
| S-glycoside metabolic process | GO:0016143 | 3.14E-02 | up |
| vitamin biosynthetic process | GO:0009110 | 3.24E-02 | up |
| single-organism catabolic process | GO:0044712 | 3.27E-02 | up |
| aerobic respiration | GO:0009060 | 3.39E-02 | up |
| maltose metabolic process | GO:0000023 | 3.44E-02 | up |
| organic acid biosynthetic process | GO:0016053 | 3.88E-02 | up |
| carboxylic acid biosynthetic process | GO:0046394 | 3.88E-02 | up |
| lipid biosynthetic process | GO:0008610 | 3.96E-02 | up |
| defense response to bacterium | GO:0042742 | 3.99E-02 | up |
| regulation of peptidase activity | GO:0052547 | 4.04E-02 | up |
| negative regulation of peptidase activity | GO:0010466 | 4.04E-02 | up |
| regulation of endopeptidase activity | GO:0052548 | 4.04E-02 | up |
| negative regulation of endopeptidase activity | GO:0010951 | 4.04E-02 | up |
| negative regulation of hydrolase activity | GO:0051346 | 4.29E-02 | up |
| single-organism metabolic process | GO:0044710 | 4.36E-02 | up |
| vitamin metabolic process | GO:0006766 | 4.39E-02 | up |
| negative regulation of proteolysis | GO:0045861 | 4.44E-02 | up |
| response to bacterium | GO:0009617 | 4.49E-02 | up |
| regulation of ion transport | GO:0043269 | 4.58E-02 | up |
| cellular respiration | GO:0045333 | 4.83E-02 | up |
| starch biosynthetic process | GO:0019252 | 4.93E-02 | up |
| pigment biosynthetic process | GO:0046148 | 3.06E-09 | down |
| pigment metabolic process | GO:0042440 | 9.75E-09 | down |
| chlorophyll biosynthetic process | GO:0015995 | 3.05E-08 | down |
| porphyrin-containing compound biosynthetic process | GO:0006779 | 7.85E-08 | down |
| tetrapyrrole biosynthetic process | GO:0033014 | 9.64E-08 | down |
| chlorophyll metabolic process | GO:0015994 | 1.57E-07 | down |
| porphyrin-containing compound metabolic process | GO:0006778 | 3.29E-07 | down |
| tetrapyrrole metabolic process | GO:0033013 | 3.69E-07 | down |
| cofactor biosynthetic process | GO:0051188 | 2.30E-06 | down |
| photosynthesis | GO:0015979 | 1.14E-05 | down |
| cofactor metabolic process | GO:0051186 | 6.27E-05 | down |
| single-organism biosynthetic process | GO:0044711 | 8.34E-05 | down |
| organonitrogen compound metabolic process | GO:1901564 | 1.36E-04 | down |
| organonitrogen compound biosynthetic process | GO:1901566 | 3.46E-04 | down |
| light-independent chlorophyll biosynthetic process | GO:0036068 | 4.68E-04 | down |
| starch biosynthetic process | GO:0019252 | 9.14E-04 | down |
| starch metabolic process | GO:0005982 | 1.23E-03 | down |
| plastid membrane organization | GO:0009668 | 1.39E-03 | down |
| thylakoid membrane organization | GO:0010027 | 1.39E-03 | down |
| chloroplast organization | GO:0009658 | 1.55E-03 | down |
| isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | GO:0019288 | 1.83E-03 | down |
| isopentenyl diphosphate metabolic process | GO:0046490 | 1.85E-03 | down |
| isopentenyl diphosphate biosynthetic process | GO:0009240 | 1.85E-03 | down |
| cellular biosynthetic process | GO:0044249 | 2.24E-03 | down |
| regulation of tetrapyrrole metabolic process | GO:1901401 | 2.34E-03 | down |
| nitrogen compound metabolic process | GO:0006807 | 2.55E-03 | down |
| organic substance biosynthetic process | GO:1901576 | 2.78E-03 | down |
| chloroplast RNA processing | GO:0031425 | 3.27E-03 | down |
| glucan biosynthetic process | GO:0009250 | 3.41E-03 | down |
| glyceraldehyde-3-phosphate metabolic process | GO:0019682 | 3.88E-03 | down |
| plastid organization | GO:0009657 | 4.14E-03 | down |
| biosynthetic process | GO:0009058 | 4.16E-03 | down |
| fat-soluble vitamin metabolic process | GO:0006775 | 4.67E-03 | down |
| fat-soluble vitamin biosynthetic process | GO:0042362 | 4.67E-03 | down |
| vitamin E biosynthetic process | GO:0010189 | 4.67E-03 | down |
| vitamin E metabolic process | GO:0042360 | 4.67E-03 | down |
| single-organism metabolic process | GO:0044710 | 4.82E-03 | down |
| cellular polysaccharide biosynthetic process | GO:0033692 | 5.15E-03 | down |
| phospholipid biosynthetic process | GO:0008654 | 5.99E-03 | down |
| single-organism membrane organization | GO:0044802 | 6.12E-03 | down |
| cellular aldehyde metabolic process | GO:0006081 | 6.26E-03 | down |
| isoprenoid biosynthetic process | GO:0008299 | 6.40E-03 | down |
| polysaccharide biosynthetic process | GO:0000271 | 6.64E-03 | down |
| cellular carbohydrate biosynthetic process | GO:0034637 | 7.03E-03 | down |
| pyruvate metabolic process | GO:0006090 | 7.03E-03 | down |
| isoprenoid metabolic process | GO:0006720 | 7.23E-03 | down |
| glucan metabolic process | GO:0044042 | 7.63E-03 | down |
| cellular glucan metabolic process | GO:0006073 | 7.63E-03 | down |
| membrane organization | GO:0061024 | 7.63E-03 | down |
| cellular polysaccharide metabolic process | GO:0044264 | 1.01E-02 | down |
| phospholipid metabolic process | GO:0006644 | 1.07E-02 | down |
| cellular nitrogen compound metabolic process | GO:0034641 | 1.07E-02 | down |
| small molecule metabolic process | GO:0044281 | 1.08E-02 | down |
| regulation of lipid metabolic process | GO:0019216 | 1.12E-02 | down |
| carbohydrate biosynthetic process | GO:0016051 | 1.21E-02 | down |
| cellular nitrogen compound biosynthetic process | GO:0044271 | 1.45E-02 | down |
| ncRNA metabolic process | GO:0034660 | 1.50E-02 | down |
| polysaccharide metabolic process | GO:0005976 | 1.57E-02 | down |
| unsaturated fatty acid metabolic process | GO:0033559 | 1.58E-02 | down |
| unsaturated fatty acid biosynthetic process | GO:0006636 | 1.58E-02 | down |
| stomatal complex morphogenesis | GO:0010103 | 1.76E-02 | down |
| single-organism cellular process | GO:0044763 | 1.95E-02 | down |
| cellular process | GO:0009987 | 2.05E-02 | down |
| cellular carbohydrate metabolic process | GO:0044262 | 2.07E-02 | down |
| carboxylic acid metabolic process | GO:0019752 | 2.22E-02 | down |
| oxylipin biosynthetic process | GO:0031408 | 2.22E-02 | down |
| oxylipin metabolic process | GO:0031407 | 2.27E-02 | down |
| stomatal complex development | GO:0010374 | 2.31E-02 | down |
| oxoacid metabolic process | GO:0043436 | 2.46E-02 | down |
| organic acid metabolic process | GO:0006082 | 2.46E-02 | down |
| cellular metabolic process | GO:0044237 | 2.59E-02 | down |
| mRNA modification | GO:0016556 | 2.68E-02 | down |
| organophosphate biosynthetic process | GO:0090407 | 2.79E-02 | down |
| carotenoid biosynthetic process | GO:0016117 | 2.86E-02 | down |
| tetraterpenoid biosynthetic process | GO:0016109 | 2.86E-02 | down |
| carbohydrate phosphorylation | GO:0046835 | 2.91E-02 | down |
| plastid localization | GO:0051644 | 2.91E-02 | down |
| chloroplast relocation | GO:0009902 | 2.91E-02 | down |
| establishment of plastid localization | GO:0051667 | 2.91E-02 | down |
| chloroplast localization | GO:0019750 | 2.91E-02 | down |
| heterocycle metabolic process | GO:0046483 | 2.94E-02 | down |
| tetraterpenoid metabolic process | GO:0016108 | 2.95E-02 | down |
| vitamin biosynthetic process | GO:0009110 | 2.95E-02 | down |
| carotenoid metabolic process | GO:0016116 | 2.95E-02 | down |
| cellular amino acid metabolic process | GO:0006520 | 3.02E-02 | down |
| maltose metabolic process | GO:0000023 | 3.14E-02 | down |
| establishment of organelle localization | GO:0051656 | 3.14E-02 | down |
| cellular aromatic compound metabolic process | GO:0006725 | 3.20E-02 | down |
| heterocycle biosynthetic process | GO:0018130 | 3.24E-02 | down |
| lipid biosynthetic process | GO:0008610 | 3.31E-02 | down |
| organic cyclic compound metabolic process | GO:1901360 | 3.43E-02 | down |
| aromatic compound biosynthetic process | GO:0019438 | 3.47E-02 | down |
| organelle localization | GO:0051640 | 3.50E-02 | down |
| response to reactive oxygen species | GO:0000302 | 3.68E-02 | down |
| cysteine biosynthetic process | GO:0019344 | 3.68E-02 | down |
| cysteine metabolic process | GO:0006534 | 3.77E-02 | down |
| photosystem II assembly | GO:0010207 | 3.82E-02 | down |
| plant epidermis morphogenesis | GO:0090626 | 3.91E-02 | down |
| organic cyclic compound biosynthetic process | GO:1901362 | 3.93E-02 | down |
| vitamin metabolic process | GO:0006766 | 4.00E-02 | down |
| RNA processing | GO:0006396 | 4.06E-02 | down |
| serine family amino acid biosynthetic process | GO:0009070 | 4.09E-02 | down |
| small molecule biosynthetic process | GO:0044283 | 4.63E-02 | down |
| monocarboxylic acid metabolic process | GO:0032787 | 4.74E-02 | down |

CC:

|  |  |  |  |
| --- | --- | --- | --- |
| GO\_Name | GO\_ID | Pvalue |  |
| stromule | GO:0010319 | 5.35E-03 | up |
| thylakoid | GO:0009579 | 6.26E-03 | up |
| thylakoid lumen | GO:0031977 | 9.67E-03 | up |
| chloroplast part | GO:0044434 | 1.34E-02 | up |
| plastid part | GO:0044435 | 1.38E-02 | up |
| chloroplast | GO:0009507 | 4.11E-02 | up |
| plastid | GO:0009536 | 4.35E-02 | up |
| chloroplast | GO:0009507 | 1.10E-05 | down |
| plastid | GO:0009536 | 1.31E-05 | down |
| cytoplasmic part | GO:0044444 | 1.23E-03 | down |
| cytoplasm | GO:0005737 | 4.57E-03 | down |
| chloroplast part | GO:0044434 | 5.41E-03 | down |
| plastid part | GO:0044435 | 5.67E-03 | down |
| anchored component of plasma membrane | GO:0046658 | 6.68E-03 | down |
| chloroplast envelope | GO:0009941 | 1.16E-02 | down |
| chloroplast stroma | GO:0009570 | 1.18E-02 | down |
| plastid stroma | GO:0009532 | 1.24E-02 | down |
| plastid envelope | GO:0009526 | 1.26E-02 | down |
| anchored component of membrane | GO:0031225 | 2.84E-02 | down |
| intracellular organelle | GO:0043229 | 3.14E-02 | down |
| organelle | GO:0043226 | 3.21E-02 | down |
| organelle envelope | GO:0031967 | 3.44E-02 | down |
| envelope | GO:0031975 | 3.52E-02 | down |
| small ribosomal subunit | GO:0015935 | 4.14E-02 | down |

Yuzenxiang:

KEGG:

|  |  |  |  |
| --- | --- | --- | --- |
| Pathway Name | Pathway ID | Pvalue |  |
| Porphyrin and chlorophyll metabolism | osa00860 | 6.28E-05 | down |
| Ribosome | osa03010 | 4.30E-03 | down |
| Photosynthesis | osa00195 | 1.05E-02 | down |
| Biosynthesis of secondary metabolites | osa01110 | 3.97E-02 | down |
| Proteasome | osa03050 | 1.83E-03 | up |
| Citrate cycle (TCA cycle) | osa00020 | 1.78E-02 | up |
| Carbon fixation in photosynthetic organisms | osa00710 | 3.48E-02 | up |
| Pyruvate metabolism | osa00620 | 3.84E-02 | up |
| Cysteine and methionine metabolism | osa00270 | 5.72E-02 | up |
| Linoleic acid metabolism | osa00591 | 4.97E-02 | up |

MF:

|  |  |  |  |
| --- | --- | --- | --- |
| GO\_Name | GO\_ID | Pvalue |  |
| structural constituent of ribosome | GO:0003735 | 1.14E-06 | down |
| structural molecule activity | GO:0005198 | 2.26E-06 | down |
| magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase activity | GO:0048529 | 4.83E-04 | down |
| geranylgeranyl reductase activity | GO:0045550 | 9.66E-04 | down |
| ligase activity, forming nitrogen-metal bonds | GO:0051002 | 2.41E-03 | down |
| ligase activity, forming nitrogen-metal bonds, forming coordination complexes | GO:0051003 | 2.41E-03 | down |
| magnesium chelatase activity | GO:0016851 | 2.41E-03 | down |
| oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor | GO:0016628 | 1.25E-02 | down |
| proton-transporting ATP synthase activity, rotational mechanism | GO:0046933 | 1.44E-02 | down |
| chlorophyll binding | GO:0016168 | 1.92E-02 | down |
| ATPase activity, coupled to transmembrane movement of ions, rotational mechanism | GO:0044769 | 2.15E-02 | down |
| rRNA binding | GO:0019843 | 3.10E-02 | down |
| oxidoreductase activity, acting on the CH-CH group of donors | GO:0016627 | 3.47E-02 | down |
| cation-transporting ATPase activity | GO:0019829 | 3.75E-02 | down |
| ATPase coupled ion transmembrane transporter activity | GO:0042625 | 3.80E-02 | down |
| threonine-type endopeptidase activity | GO:0004298 | 4.07E-04 | up |
| threonine-type peptidase activity | GO:0070003 | 4.07E-04 | up |
| adenosine kinase activity | GO:0004001 | 3.86E-03 | up |
| isocitrate dehydrogenase (NAD+) activity | GO:0004449 | 3.86E-03 | up |
| oxidoreductase activity | GO:0016491 | 3.98E-03 | up |
| phosphoenolpyruvate carboxylase activity | GO:0008964 | 7.70E-03 | up |
| porin activity | GO:0015288 | 8.66E-03 | up |
| wide pore channel activity | GO:0022829 | 8.66E-03 | up |
| isocitrate dehydrogenase activity | GO:0004448 | 8.66E-03 | up |
| L-malate dehydrogenase activity | GO:0030060 | 1.15E-02 | up |
| phosphoenolpyruvate carboxykinase activity | GO:0004611 | 1.25E-02 | up |
| protein disulfide isomerase activity | GO:0003756 | 1.44E-02 | up |
| intramolecular oxidoreductase activity, transposing S-S bonds | GO:0016864 | 1.44E-02 | up |
| nucleoside kinase activity | GO:0019206 | 1.44E-02 | up |
| oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | GO:0016616 | 1.67E-02 | up |
| dioxygenase activity | GO:0051213 | 1.81E-02 | up |
| peroxidase activity | GO:0004601 | 2.22E-02 | up |
| oxidoreductase activity, acting on peroxide as acceptor | GO:0016684 | 2.28E-02 | up |
| malate dehydrogenase activity | GO:0016615 | 2.29E-02 | up |
| oxidoreductase activity, acting on CH-OH group of donors | GO:0016614 | 2.42E-02 | up |
| antioxidant activity | GO:0016209 | 2.62E-02 | up |
| FMN binding | GO:0010181 | 4.17E-02 | up |
| nucleobase-containing compound kinase activity | GO:0019205 | 4.17E-02 | up |
| oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | GO:0016702 | 4.91E-02 | up |

BP:

|  |  |  |  |
| --- | --- | --- | --- |
| GO\_Name | GO\_ID | Pvalue |  |
| organonitrogen compound biosynthetic process | GO:1901566 | 8.03E-10 | down |
| pigment biosynthetic process | GO:0046148 | 1.54E-08 | down |
| organonitrogen compound metabolic process | GO:1901564 | 1.87E-08 | down |
| photosynthesis | GO:0015979 | 2.18E-08 | down |
| pigment metabolic process | GO:0042440 | 4.88E-08 | down |
| chlorophyll biosynthetic process | GO:0015995 | 1.03E-07 | down |
| porphyrin-containing compound biosynthetic process | GO:0006779 | 2.65E-07 | down |
| tetrapyrrole biosynthetic process | GO:0033014 | 3.25E-07 | down |
| chlorophyll metabolic process | GO:0015994 | 5.28E-07 | down |
| porphyrin-containing compound metabolic process | GO:0006778 | 1.10E-06 | down |
| isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | GO:0019288 | 1.17E-06 | down |
| isopentenyl diphosphate metabolic process | GO:0046490 | 1.20E-06 | down |
| isopentenyl diphosphate biosynthetic process | GO:0009240 | 1.20E-06 | down |
| tetrapyrrole metabolic process | GO:0033013 | 1.24E-06 | down |
| single-organism biosynthetic process | GO:0044711 | 3.79E-06 | down |
| cellular biosynthetic process | GO:0044249 | 5.19E-06 | down |
| glyceraldehyde-3-phosphate metabolic process | GO:0019682 | 5.38E-06 | down |
| organic substance biosynthetic process | GO:1901576 | 7.46E-06 | down |
| cofactor biosynthetic process | GO:0051188 | 7.65E-06 | down |
| phospholipid biosynthetic process | GO:0008654 | 1.30E-05 | down |
| cellular aldehyde metabolic process | GO:0006081 | 1.42E-05 | down |
| organophosphate biosynthetic process | GO:0090407 | 1.45E-05 | down |
| biosynthetic process | GO:0009058 | 1.47E-05 | down |
| isoprenoid biosynthetic process | GO:0008299 | 1.49E-05 | down |
| pyruvate metabolic process | GO:0006090 | 1.80E-05 | down |
| isoprenoid metabolic process | GO:0006720 | 1.90E-05 | down |
| cellular nitrogen compound biosynthetic process | GO:0044271 | 3.26E-05 | down |
| phospholipid metabolic process | GO:0006644 | 4.20E-05 | down |
| translation | GO:0006412 | 6.47E-05 | down |
| peptide biosynthetic process | GO:0043043 | 6.92E-05 | down |
| small molecule metabolic process | GO:0044281 | 7.28E-05 | down |
| peptide metabolic process | GO:0006518 | 7.88E-05 | down |
| amide biosynthetic process | GO:0043604 | 8.40E-05 | down |
| cellular amide metabolic process | GO:0043603 | 1.09E-04 | down |
| carbohydrate derivative metabolic process | GO:1901135 | 1.26E-04 | down |
| nitrogen compound metabolic process | GO:0006807 | 1.41E-04 | down |
| organophosphate metabolic process | GO:0019637 | 1.60E-04 | down |
| cofactor metabolic process | GO:0051186 | 2.02E-04 | down |
| photosynthesis, light reaction | GO:0019684 | 2.03E-04 | down |
| lipid biosynthetic process | GO:0008610 | 4.24E-04 | down |
| light-independent chlorophyll biosynthetic process | GO:0036068 | 6.08E-04 | down |
| cellular nitrogen compound metabolic process | GO:0034641 | 6.60E-04 | down |
| carboxylic acid metabolic process | GO:0019752 | 8.79E-04 | down |
| monocarboxylic acid metabolic process | GO:0032787 | 8.94E-04 | down |
| oxoacid metabolic process | GO:0043436 | 1.05E-03 | down |
| organic acid metabolic process | GO:0006082 | 1.05E-03 | down |
| cysteine biosynthetic process | GO:0019344 | 1.05E-03 | down |
| cellular lipid metabolic process | GO:0044255 | 1.06E-03 | down |
| cysteine metabolic process | GO:0006534 | 1.10E-03 | down |
| photosystem II assembly | GO:0010207 | 1.13E-03 | down |
| serine family amino acid biosynthetic process | GO:0009070 | 1.30E-03 | down |
| ncRNA metabolic process | GO:0034660 | 1.75E-03 | down |
| generation of precursor metabolites and energy | GO:0006091 | 2.21E-03 | down |
| plastid membrane organization | GO:0009668 | 2.38E-03 | down |
| thylakoid membrane organization | GO:0010027 | 2.38E-03 | down |
| serine family amino acid metabolic process | GO:0009069 | 2.58E-03 | down |
| chloroplast organization | GO:0009658 | 2.66E-03 | down |
| sulfur amino acid biosynthetic process | GO:0000097 | 2.70E-03 | down |
| lipid metabolic process | GO:0006629 | 2.74E-03 | down |
| regulation of tetrapyrrole metabolic process | GO:1901401 | 3.04E-03 | down |
| sulfur amino acid metabolic process | GO:0000096 | 3.77E-03 | down |
| cellular metabolic process | GO:0044237 | 5.69E-03 | down |
| fat-soluble vitamin metabolic process | GO:0006775 | 6.07E-03 | down |
| vitamin E biosynthetic process | GO:0010189 | 6.07E-03 | down |
| fat-soluble vitamin biosynthetic process | GO:0042362 | 6.07E-03 | down |
| vitamin E metabolic process | GO:0042360 | 6.07E-03 | down |
| rRNA metabolic process | GO:0016072 | 6.91E-03 | down |
| rRNA processing | GO:0006364 | 6.91E-03 | down |
| plastid organization | GO:0009657 | 7.04E-03 | down |
| single-organism metabolic process | GO:0044710 | 7.92E-03 | down |
| sulfur compound biosynthetic process | GO:0044272 | 8.31E-03 | down |
| small molecule biosynthetic process | GO:0044283 | 9.59E-03 | down |
| ribosome biogenesis | GO:0042254 | 9.83E-03 | down |
| single-organism membrane organization | GO:0044802 | 1.04E-02 | down |
| cellular protein metabolic process | GO:0044267 | 1.04E-02 | down |
| alpha-amino acid biosynthetic process | GO:1901607 | 1.15E-02 | down |
| membrane organization | GO:0061024 | 1.29E-02 | down |
| ribonucleoprotein complex biogenesis | GO:0022613 | 1.35E-02 | down |
| cellular macromolecule biosynthetic process | GO:0034645 | 1.35E-02 | down |
| ncRNA processing | GO:0034470 | 1.41E-02 | down |
| regulation of lipid metabolic process | GO:0019216 | 1.45E-02 | down |
| macromolecule biosynthetic process | GO:0009059 | 1.46E-02 | down |
| cellular protein complex assembly | GO:0043623 | 1.47E-02 | down |
| gene expression | GO:0010467 | 1.48E-02 | down |
| sulfur compound metabolic process | GO:0006790 | 1.52E-02 | down |
| photosynthesis, light harvesting | GO:0009765 | 1.81E-02 | down |
| cellular amino acid biosynthetic process | GO:0008652 | 1.86E-02 | down |
| protein targeting to chloroplast | GO:0045036 | 1.99E-02 | down |
| protein localization to chloroplast | GO:0072598 | 1.99E-02 | down |
| establishment of protein localization to chloroplast | GO:0072596 | 1.99E-02 | down |
| heterocycle biosynthetic process | GO:0018130 | 2.01E-02 | down |
| unsaturated fatty acid metabolic process | GO:0033559 | 2.05E-02 | down |
| unsaturated fatty acid biosynthetic process | GO:0006636 | 2.05E-02 | down |
| protein complex assembly | GO:0006461 | 2.13E-02 | down |
| protein complex biogenesis | GO:0070271 | 2.15E-02 | down |
| aromatic compound biosynthetic process | GO:0019438 | 2.19E-02 | down |
| stomatal complex morphogenesis | GO:0010103 | 2.29E-02 | down |
| alpha-amino acid metabolic process | GO:1901605 | 2.31E-02 | down |
| cellular macromolecular complex assembly | GO:0034622 | 2.45E-02 | down |
| organic cyclic compound biosynthetic process | GO:1901362 | 2.55E-02 | down |
| protein-chromophore linkage | GO:0018298 | 2.82E-02 | down |
| oxylipin biosynthetic process | GO:0031408 | 2.88E-02 | down |
| macromolecular complex assembly | GO:0065003 | 2.92E-02 | down |
| energy coupled proton transport, down electrochemical gradient | GO:0015985 | 2.94E-02 | down |
| oxylipin metabolic process | GO:0031407 | 2.94E-02 | down |
| ATP synthesis coupled proton transport | GO:0015986 | 2.94E-02 | down |
| stomatal complex development | GO:0010374 | 3.00E-02 | down |
| protein complex subunit organization | GO:0071822 | 3.01E-02 | down |
| single-organism cellular process | GO:0044763 | 3.43E-02 | down |
| mRNA modification | GO:0016556 | 3.47E-02 | down |
| protein metabolic process | GO:0019538 | 3.68E-02 | down |
| carotenoid biosynthetic process | GO:0016117 | 3.71E-02 | down |
| tetraterpenoid biosynthetic process | GO:0016109 | 3.71E-02 | down |
| ATP biosynthetic process | GO:0006754 | 3.76E-02 | down |
| plastid localization | GO:0051644 | 3.76E-02 | down |
| establishment of plastid localization | GO:0051667 | 3.76E-02 | down |
| chloroplast relocation | GO:0009902 | 3.76E-02 | down |
| chloroplast localization | GO:0019750 | 3.76E-02 | down |
| tetraterpenoid metabolic process | GO:0016108 | 3.82E-02 | down |
| vitamin biosynthetic process | GO:0009110 | 3.82E-02 | down |
| carotenoid metabolic process | GO:0016116 | 3.82E-02 | down |
| purine ribonucleoside triphosphate biosynthetic process | GO:0009206 | 4.06E-02 | down |
| maltose metabolic process | GO:0000023 | 4.06E-02 | down |
| establishment of organelle localization | GO:0051656 | 4.06E-02 | down |
| purine nucleoside triphosphate biosynthetic process | GO:0009145 | 4.06E-02 | down |
| organelle localization | GO:0051640 | 4.53E-02 | down |
| cellular process | GO:0009987 | 4.58E-02 | down |
| ribonucleoside triphosphate biosynthetic process | GO:0009201 | 4.64E-02 | down |
| nucleoside triphosphate biosynthetic process | GO:0009142 | 4.70E-02 | down |
| cellular component assembly | GO:0022607 | 4.89E-02 | down |
| cellular amino acid metabolic process | GO:0006520 | 4.95E-02 | down |
| tricarboxylic acid cycle | GO:0006099 | 1.68E-05 | up |
| citrate metabolic process | GO:0006101 | 1.78E-05 | up |
| tricarboxylic acid metabolic process | GO:0072350 | 2.09E-05 | up |
| aerobic respiration | GO:0009060 | 3.23E-05 | up |
| cellular respiration | GO:0045333 | 9.46E-05 | up |
| energy derivation by oxidation of organic compounds | GO:0015980 | 1.54E-04 | up |
| oxylipin biosynthetic process | GO:0031408 | 9.14E-04 | up |
| oxylipin metabolic process | GO:0031407 | 9.52E-04 | up |
| oxidation-reduction process | GO:0055114 | 9.90E-04 | up |
| purine ribonucleoside salvage | GO:0006166 | 3.74E-03 | up |
| AMP biosynthetic process | GO:0006167 | 6.53E-03 | up |
| AMP metabolic process | GO:0046033 | 6.53E-03 | up |
| carboxylic acid metabolic process | GO:0019752 | 7.29E-03 | up |
| nucleoside salvage | GO:0043174 | 7.46E-03 | up |
| generation of precursor metabolites and energy | GO:0006091 | 7.90E-03 | up |
| oxoacid metabolic process | GO:0043436 | 8.54E-03 | up |
| organic acid metabolic process | GO:0006082 | 8.56E-03 | up |
| small molecule metabolic process | GO:0044281 | 8.97E-03 | up |
| protein catabolic process | GO:0030163 | 1.00E-02 | up |
| purine-containing compound salvage | GO:0043101 | 1.12E-02 | up |
| fatty acid biosynthetic process | GO:0006633 | 1.38E-02 | up |
| protein refolding | GO:0042026 | 2.22E-02 | up |
| malate metabolic process | GO:0006108 | 2.22E-02 | up |
| carbon fixation | GO:0015977 | 2.22E-02 | up |
| protein folding | GO:0006457 | 2.27E-02 | up |
| macromolecule catabolic process | GO:0009057 | 2.33E-02 | up |
| fatty acid metabolic process | GO:0006631 | 2.80E-02 | up |
| monocarboxylic acid biosynthetic process | GO:0072330 | 2.85E-02 | up |
| mRNA transport | GO:0051028 | 4.04E-02 | up |
| response to oxidative stress | GO:0006979 | 4.07E-02 | up |
| establishment of RNA localization | GO:0051236 | 4.31E-02 | up |
| RNA transport | GO:0050658 | 4.31E-02 | up |
| nucleic acid transport | GO:0050657 | 4.31E-02 | up |
| RNA localization | GO:0006403 | 4.40E-02 | up |
| response to endoplasmic reticulum stress | GO:0034976 | 4.85E-02 | up |

CC:

|  |  |  |  |
| --- | --- | --- | --- |
| GO\_Name | GO\_ID | Pvalue |  |
| chloroplast | GO:0009507 | 2.27E-13 | down |
| plastid | GO:0009536 | 3.35E-13 | down |
| chloroplast part | GO:0044434 | 7.18E-08 | down |
| plastid part | GO:0044435 | 8.20E-08 | down |
| chloroplast stroma | GO:0009570 | 2.37E-07 | down |
| plastid stroma | GO:0009532 | 2.78E-07 | down |
| cytoplasmic part | GO:0044444 | 1.46E-06 | down |
| ribosome | GO:0005840 | 1.57E-05 | down |
| cytoplasm | GO:0005737 | 1.78E-05 | down |
| thylakoid | GO:0009579 | 6.02E-05 | down |
| intracellular ribonucleoprotein complex | GO:0030529 | 1.15E-04 | down |
| intracellular membrane-bounded organelle | GO:0043231 | 1.52E-04 | down |
| membrane-bounded organelle | GO:0043227 | 1.60E-04 | down |
| chloroplast envelope | GO:0009941 | 1.69E-04 | down |
| chloroplast thylakoid | GO:0009534 | 1.79E-04 | down |
| plastid thylakoid | GO:0031976 | 1.82E-04 | down |
| plastid envelope | GO:0009526 | 1.99E-04 | down |
| macromolecular complex | GO:0032991 | 2.65E-04 | down |
| intracellular organelle part | GO:0044446 | 3.05E-04 | down |
| organelle part | GO:0044422 | 3.34E-04 | down |
| organelle subcompartment | GO:0031984 | 6.05E-04 | down |
| intracellular organelle | GO:0043229 | 7.30E-04 | down |
| organelle | GO:0043226 | 7.64E-04 | down |
| intracellular part | GO:0044424 | 8.54E-04 | down |
| non-membrane-bounded organelle | GO:0043228 | 1.24E-03 | down |
| intracellular non-membrane-bounded organelle | GO:0043232 | 1.24E-03 | down |
| organelle envelope | GO:0031967 | 1.49E-03 | down |
| envelope | GO:0031975 | 1.57E-03 | down |
| photosystem I | GO:0009522 | 1.63E-03 | down |
| intracellular | GO:0005622 | 2.12E-03 | down |
| photosynthetic membrane | GO:0034357 | 5.09E-03 | down |
| thylakoid part | GO:0044436 | 6.01E-03 | down |
| photosystem I reaction center | GO:0009538 | 8.17E-03 | down |
| plastoglobule | GO:0010287 | 1.05E-02 | down |
| photosystem | GO:0009521 | 1.12E-02 | down |
| proton-transporting ATP synthase complex, coupling factor F(o) | GO:0045263 | 1.40E-02 | down |
| membrane protein complex | GO:0098796 | 1.68E-02 | down |
| cell part | GO:0044464 | 1.78E-02 | down |
| cell | GO:0005623 | 2.14E-02 | down |
| chloroplast thylakoid membrane | GO:0009535 | 2.22E-02 | down |
| plastid thylakoid membrane | GO:0055035 | 2.24E-02 | down |
| proton-transporting two-sector ATPase complex, proton-transporting domain | GO:0033177 | 3.01E-02 | down |
| thylakoid membrane | GO:0042651 | 3.22E-02 | down |
| proton-transporting ATP synthase complex | GO:0045259 | 4.36E-02 | down |
| proteasome complex | GO:0000502 | 6.76E-05 | up |
| proteasome core complex | GO:0005839 | 5.32E-04 | up |
| clathrin coat of trans-Golgi network vesicle | GO:0030130 | 5.43E-03 | up |
| trans-Golgi network transport vesicle membrane | GO:0012510 | 6.51E-03 | up |
| clathrin coat of coated pit | GO:0030132 | 6.51E-03 | up |
| clathrin-coated pit | GO:0005905 | 6.51E-03 | up |
| trans-Golgi network transport vesicle | GO:0030140 | 6.51E-03 | up |
| clathrin vesicle coat | GO:0030125 | 6.51E-03 | up |
| clathrin-coated vesicle membrane | GO:0030665 | 7.59E-03 | up |
| intracellular part | GO:0044424 | 1.35E-02 | up |
| membrane region | GO:0098589 | 1.41E-02 | up |
| cytoplasm | GO:0005737 | 1.64E-02 | up |
| proteasome core complex, alpha-subunit complex | GO:0019773 | 1.83E-02 | up |
| protein complex | GO:0043234 | 2.08E-02 | up |
| clathrin coat | GO:0030118 | 2.16E-02 | up |
| mitochondrial outer membrane | GO:0005741 | 2.16E-02 | up |
| clathrin-coated vesicle | GO:0030136 | 2.47E-02 | up |
| intracellular | GO:0005622 | 2.69E-02 | up |
| Golgi-associated vesicle | GO:0005798 | 3.01E-02 | up |
| Golgi-associated vesicle membrane | GO:0030660 | 3.01E-02 | up |
| transport vesicle membrane | GO:0030658 | 3.11E-02 | up |
| transport vesicle | GO:0030133 | 3.11E-02 | up |
| pore complex | GO:0046930 | 3.53E-02 | up |
| vesicle coat | GO:0030120 | 3.85E-02 | up |
| organelle outer membrane | GO:0031968 | 3.85E-02 | up |
| whole membrane | GO:0098805 | 4.23E-02 | up |
| plasma membrane protein complex | GO:0098797 | 4.27E-02 | up |
| coated vesicle membrane | GO:0030662 | 4.89E-02 | up |
| outer membrane | GO:0019867 | 4.89E-02 | up |