| GenBank (dbEST) Accession Number | EST name | GO classification (1) | Gene product | Accession number | Cold | | Salinity | |
|---|---|---|---|---|---|---|---|---|
| | | | | | **Relative to control expression (2)** | **Fold change** | **Relative to control expression (2)** | **Fold change** |
| **Central metabolism/Photosynthesis (10)** | | | | | | | | |
| BU671793 | F175 | GO:0009523<br>(C, photosystem II) | photosystem II 22-K chlorophyll-binding protein - rice | BAA12337.1 | Down | -1.604 | NC | -1.060 |
| BU672070 | H124 | GO:0009765<br>(B, photosynthesis, light harvesting) | Q9SY97_ARATH PSI type III chlorophyll a/b-binding protein | AAD25555.1 | Down | -1.844 | Down | -1.412 |
| BU672060 | H125 | GO:0009765<br>(B, photosynthesis, light harvesting) | (AL132962) Lhca2 protein [*Arabidopsis thaliana*] | CAB71077.1 | Down | -2.246 | Down | -2.015 |
| BU672102 | H136 | GO:0009055<br>(M, electron carrier activity) | O04002_SOLTU CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) general metabolisms | O04002 | Down | -2.015 | NC | 1.186 |
| BU672078 | H302 | GO:0009507<br>(C, chloroplast) | Magnesium-protoporphyrin IX monomethyl este | Q9M591 | Down | -1.881 | Down | -1.314 |
| BU672090 | H385 | GO:0042132<br>(M, fructose-bisphosphatase activity) | fructose-1,6-bisphosphatase [*Pisum sativum*] | 5305145 | Down | -2.399 | Down | -1.749 |
| BU672091 | H411 | GO:0009538<br>(C, photosystem I reaction center) | SAF_FLATR PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) (*Flaveria trinerva*) | AAA33344.1 | Down | -2.453 | Down | -1.803 |
| BU671800 | T129 | GO:0009765<br>(B, photosynthesis, light harvesting) | Q9SDT2_DAUCA Chlorophyll a/b-binding protein. | AAF20948.1 | Up | 1.262 | Up | 1.269 |
| BU671843 | T340 | GO:0004356<br>(M, glutamate-ammonia ligase activity) | O04961_HELAN Chloroplastic glutamine synthetase (EC 6.3.1.2) (Fragment) general metabolism | AAN84537.1 | NC | -1.046 | Down | -1.522 |
| BU671801 | T411 | GO:0004332<br>(M, fructose-bisphosphate aldolase activity) | Q9SXX5_NICPA Plastidic aldolase general metabolism | BAA77603.1 | Up | 1.498 | Up | 1.282 |
| **Translation machinery (6)** | | | | | | | | |
| BU671926 | F230 | GO:0003735<br>(M, structural | *Solanum lycopersicon* ribosomal protein L2 protein | CAA45863.1 | NC | -1.071 | Down | -1.180 |

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| | | | | | Relative to control expression (2) | Fold change | Relative to control expression (2) | Fold change |
| | | constituent of ribosome) | | | | | | |
| BU672008 | F467 | GO:0003735 (M, structural constituent of ribosome) | *Arabidopsis thaliana* 60S ribosomal protein L13a protein | BAB09429.1 | Up | 1.660 | NC | 1.105 |
| BU672004 | F455 | No GO term | Q5I7K2_WHEAT Ribosomal protein S7 | Q5I7K2 | Up | 1.503 | Up | 1.323 |
| BU672017 | F550 | No GO term | Translation initiation factor B04 [*Helianthus annuus*] | 21842314 | Down | -1.366 | Down | .1.321 |
| BU671923 | F577 | GO:0003723 (M, RNA binding) | RS4_SOLTU 40S RIBOSOMAL PROTEIN S4 (potato) | AAC24585.1 | Up | 1.222 | Up | 1.306 |
| BU671873 | T111 | GO:0003746 (M, translation elongation factor activity) | *Solanum lycopersicon* elongation factor 1-alpha protein | CAA37212.1 | NC | -1.185 | Up | 1.376 |
| **No homology (1)** | | | | | | | | |
| BU672056 | H110 | No GO term | No homology in databases | | Down | -1.618 | Down | -1.208 |
| **Transcriptional machinery (4)** | | | | | | | | |
| BU671940 | F305 | GO:0003677 (M, DNA binding) | 41 kD chloroplast nucleid DNA binding protein (CND41) [*Nicotiana sylvestris*] | 24430421 | Up | 1.550 | NC | 1.171 |
| BU672034 | F561 | No GO term | Zinc finger family protein (Fragment) | Q5ULY2 | Up | 1.547 | NC | 1.138 |
| BU671817 | T187 | GO:0003677 (M, DNA binding) | MBD4; DNA binding [*Arabidopsis thaliana*] | 15229373 | NC | -1.025 | Up | 1.715 |
| BU671860 | T464 | GO:0006118 (B, electron transport) | Single-stranded DNA binding [*Medicago truncatula*] | ABD28355.1 | NC | 1.225 | Up | 1.306 |
| **Signaling machinery (2)** | | | | | | | | |
| BU671885 | EF127 | GO:0003924 (M, GTPase activity) | ADP-ribosylation factor 1. | Q7F270_ORYSA | Up | 1.759 | Up | 1.743 |
| BU671830 | T234 | No GO term | Extracellular Ca sensing receptor (*Arabidosis*) | Q9FN48 | Down | -2.181 | Down | -1.445 |
| **Protein turnover/folding/interactions (5)** | | | | | | | | |
| BU671886 | EF264 | GO:0004175 (M, endopeptidase activity) | *Arabidopsis thaliana* multicatalytic endopeptidase protein | CAA73619.1 | Up | 1.267 | NC | 1.162 |
| BU671928 | F231 | GO:0003755 (M, peptidyl-prolyl cis- | Q7XY71_9ROSI Cyclophilin (Fragment) | Q7XY71 | Up | -1.395 | NC | -1.089 |

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| | | | | | **Relative to control expression (2)** | **Fold change** | **Relative to control expression (2)** | **Fold change** |
| | | trans isomerase activity) | | | | | | |
| BU671999 | F443 | GO:0003743<br>(M, translation initiation factor activity) | Copper chaperone [*Lycopersicon esculentum*] | 30039180 | Down | -1.179 | Down | -1.103 |
| BU671806 | T124 | GO:0005524<br>(M, ATP binding activity) | Q8LKP8_SAUME Heat shock protein | Q8LKP8 | Up | 1.355 | Up | 1.520 |
| BU671835 | T289 | GO:0004374<br>(M, glycine cleavage system) | *Flaveria pringlei* P-protein of the glycine cleavage system protein | CAA85353.1 | Down | -1.395 | Down | -1.305 |
| **Transport (3)** | | | | | | | | |
| BU671910 | EF502 | GO:0016068<br>(B, type I hypersensitivity) | *Gossypium hirsutum* lipid transfer protein precursor protein transport | AAF35184.1 | Up | 1.101 | Down | -1.141 |
| BU672086 | H360 | GO:0046961<br>(M, hydrogen ion transporting ATPase activity, rotational mechanism) | ATP synthase beta subunit [*Helianthus annuus*] | CAB65035.1 | Up | 1.814 | Up | 1.246 |
| BU672042 | F557 | GO:0005488<br>(M, binding) | ARATH A_IG002N01.16 protein (Putative carrier protein) | AAL07192.1 | Up | 1.798 | Up | 1.368 |
| **Secondary metabolism (3)** | | | | | | | | |
| BU672069 | H123 | GO:0004512<br>(M, inositol-3-phosphate synthase activity | myo-inositol-1-phosphate synthase (EC 5.5.1.4) - common ice plant | BAA84084.1 | Down | -1.429 | Down | -1.515 |
| BU672083 | H322 | No GO term | Q43469_HELAN Delta-8 sphingolipid desaturase | Q9ZRP7 | Down | -1.288 | Down | -1.467 |
| BU671815 | T322 | GO:0004497<br>(M, monooxygenase activity) | *Glycine max* geranylgeranyl hydrogenase protein. | AAD28640.1 | NC | -1.041 | Up | 1.548 |
| **ROS machinery (7)** | | | | | | | | |
| BU672105 | H354 | GO:0008137<br>(M, NADH | NADH-plastoquinone oxidoreductase subunit 4 [*Oenothera elata subsp. hookeri*] | CAB67220.1 | Down | -1.381 | Down | -1.168 |

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| | | dehydrogenase (ubiquinote) activity) | | | | | | |
| BU671805 | T120 | GO:0009055 (M, electron carrier activity) | Q84LB8_ZANAE Glycolate oxidase (EC 1.1.3.15) (EC 1.1.3.1) ROS machinery | Q84LB8 | Up | 1.178 | Up | 1.292 |
| BU671812 | T155 | GO:0009055 (M, electron carrier activity) | Putative thioredoxin reductase [*Hordeum vulgare subsp. vulgare*] | 38174811 | Up | 1.467 | NC | 1.064 |
| BU671825 | T221 | GO:0004301 (M, epoxide hydrolase activity) | catalytic/ hydrolase [*Arabidopsis thaliana*] ROS machinery | NP_849507.1 | Down | -2.072 | Down | -1.337 |
| BU671832 | T243 | GO:0006986 (B, response to unfolded protein) | HSP7S_PEA Stromal 70 kDa heat shock-related protein, chloroplast precursor | Q02028 | Up | 1.509 | NC | 1.035 |
| BU671838 | T307 | GO:0004096 (M, catalase activity) | *Helianthus annuus* catalase protein | AAA69866 | Up | 1.730 | Up | 1.801 |
| BU671846 | T368 | GO:0009507 (C, chloroplast) | PSBQ2_ARATH Oxygen-evolving enhancer protein 3-2, chloroplast precursor (OEE3) (16 | Q41932 | Up | 1.225 | Up | 1.306 |
| **Unclassified** | | | | | | | | |
| BU672101 | EF432 | | No GO Term associated | | Down | -1.319 | Down | -1.307 |
| BU671912 | EF624 | | No GO Term associated | | Down | -1.751 | Down | -2.372 |
| BU671986 | F137 | | No GO Term associated | | NC | -1.185 | Down | -1.599 |
| BU671987 | F171 | | No GO Term associated | | Down | -1.797 | Up | 1.689 |
| BU671919 | F176 | | No GO Term associated | | Up | 1.280 | Up | 1.163 |
| BU671924 | F192 | | No GO Term associated | | NC | -1.085 | Up | 1.100 |
| BU671945 | F202 | | Q9SL05_ARATH Expressed protein (At2g05620/T20G20.3) | Q9SL05 | NC | 1.062 | Up | 1.669 |
| BU671949 | F209 | | No GO Term associated | | Down | -1.263 | NC | -1.044 |
| BU671950 | F210 | | No GO Term associated | | Down | -1.773 | NC | -1.165 |
| BU671927 | F216 | | No GO Term associated | | Down | -1.941 | Down | -1.938 |
| BU671931 | F295 | | No GO Term associated | | Up | 1.396 | NC | 1.091 |
| BU671961 | F319 | | No GO Term associated | | Up | 1.821 | NC | 1.029 |
| BU671965 | F340 | | No GO Term associated | | Up | 1.261 | NC | 1.085 |

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| | | | | | Relative to control expression (2) | Fold change | Relative to control expression (2) | Fold change |
| BU671980 | F373 | | No GO Term associated | | Up | 1.461 | NC | 1.085 |
| BU671983 | F379 | | No GO Term associated | | Up | 1.306 | NC | 1.191 |
| BU671988 | F401 | | No GO Term associated | | Down | -1.511 | Down | -1.265 |
| BU671788 | F406 | | No GO Term associated | | Up | 2.074 | Up | 1.677 |
| BU672039 | F426 | | No GO Term associated | | Up | 1.387 | NC | 1.172 |
| BU672013 | F482 | | No GO Term associated | | Up | 1.600 | Up | 1.238 |
| BU672016 | F489 | | No GO Term associated | | Up | 1.469 | Up | 1.519 |
| BU672017 | F491 | | No GO Term associated | | Up | 1.697 | Up | 1.314 |
| BU672019 | F494 | | No GO Term associated | | Up | 1.272 | Up | 1.288 |
| BU672020 | F496 | | No GO Term associated | | Up | 1.421 | Up | 1.328 |
| BU672110 | F514 | | No GO Term associated | | Up | 1.389 | Up | 1.240 |
| BU672026 | F543 | | similar to unknown protein [*Arabidopsis thaliana*] | BAB02703.1 | Down | -1.587 | Down | -1.271 |
| BU672028 | F549 | | No GO Term associated | | Down | -1.350 | Down | -1.213 |
| BU672032 | F554 | | No GO Term associated | | Up | 1.415 | NC | 1.155 |
| BU672046 | F572 | | No GO Term associated | | Up | 1.344 | Up | 1.237 |
| BU672051 | F593 | | No GO Term associated | | Up | 1.517 | NC | 1.126 |
| BU671789 | H111 | | No GO Term associated | | Down | -2.094 | NC | -1.198 |
| BU672074 | H209 | | No GO Term associated | | NC | -1.158 | Down | -1.624 |
| BU672079 | H304 | | No GO Term associated | | Down | -1.477 | Down | -1.908 |
| BU672084 | H329 | | No GO Term associated | | NC | 1.110 | Up | 1.527 |
| BU672087 | H368 | | No GO Term associated | | Up | 1.241 | Up | 1.687 |
| BU672092 | H387 | | No GO Term associated | | Down | -1.328 | Down | -1.329 |
| BU671799 | T107 | | No GO Term associated | | Down | -1.333 | Up | 1.348 |
| BU671868 | T253 | | No GO Term associated | | Down | -1.593 | Down | -1.645 |
| BU671875 | T283 | GO:0016740<br>(M, transferase activity) | Os03g0651000 [*Oryza sativa (japonica cultivar-group)*] | 115454377 | Up | 1.609 | NC | 1.105 |
| BU671862 | T479 | | | | Up | 1.794 | Up | 1.470 |