Supplementary data: Cytosolic proteins (10,000 g supernatant) detected by proteomic analysis (LC-MS/MS) from cotyledons of 2 d old seedlings subjected to salt stress (120 mM NaCl) and NO donor (250 µM SNP) and exSNP.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  | Salt | | SNP (-NaCl) | | exSNP (-NaCl) | | SNP (+NaCl) | | exSNP (+NaCl) | |
| **Protein** | **Accession no.** | **kDa** | **Protein sequence (Ion score)** | **GO Biological process** | **Localization** | **Fold change** | **Log 2 Fold change** | **Fold change** | **Log 2 Fold change** | **Fold change** | **Log 2 Fold change** | **Fold change** | **Log 2 Fold change** | **Fold change** | **Log 2 Fold change** |
| **PRIMARY METABOLISM PROTEINS** | | | | | | |  |  |  |  |  |  |  |  |  |
| Phosphoenolpyruvate carboxylase 2 | Q9FV65 | 111 | FLDILQDLHGEGLK(53.0) KLEELGNVLTSLDPGDSIVIAK(43.9) | Tricarboxylic acid cycle | Cytoplasm | 1.2 | 0.2 | 1.3 | 0.4 | 1.7 | 0.7 | 0.3 | -1.7 | 0.3 | -2.0 |
| Serine hydroxymethyltransferase 1, mitochondrial | P49357 | 57 | ISAVSIFFETMPYR(101.4) QLNAPLEVVDPEIADIIELEK(37.2) | Glycine biosynthetic process | Mitochondria | 1.0 | -0.1 | 0.8 | -0.3 | 1.8 | 0.8 | 0.5 | -1.0 | 0.6 | -0.8 |
| Aspartate aminotransferase, mitochondrial | P46643 | 47 | GLDFSALMDDVK(45.6) VNVGVGAYR(44.3) | Aspartate metabolism | Mitochondrial matrix | 0.9 | -0.2 | 1.2 | 0.3 | 1.0 | 0 | 1.5 | 0.6 | 1.4 | 0.5 |
| Fructose-bisphosphate aldolase 4, cytosolic | F4KGQ0 | 42 | GILAADESTGTIGKR(51.8) EAGVLPGIK(39.9) | Gluconeogenesis | Cytoplasm | 1.7 | 0.8 | 1.1 | 0.1 | 1.7 | 0.8 | 0.8 | -0.3 | 0.8 | -0.3 |
| Peroxisomal acyl-coenzyme A oxidase 1 | O65202 | 74 | QASLANDQLR(52.0) VSTHAVVYAR(43.7) SLTTTATADGIEECRK(40.6) | Fatty acid metabolism | Peroxisome | 2.8 | 1.5 | 0.9 | -0.2 | 0.9 | -0.2 | 1.0 | 0.1 | 1.2 | 0.3 |
| Enolase | P42896 | 47 | YGQDATNVGDEGGFAPNIQENK(90.8) VNQIGSVTESIEAVR(87.7) | Glycolytic process | Cytoplasm | 0.7 | -0.5 | 1.2 | 0.2 | 1.1 | 0.2 | 1.8 | 0.8 | 1.8 | 0.8 |
| Glyceraldehyde-3-phosphate dehydrogenase, cytosolic | P34921 | 37 | VPTVDVSVVDLTVR(93.9) FGIVEGLmTTVHSITATQK(74.9) | Glycolytic process | Cytoplasm | 3.0 | 1.6 | 1.1 | 0.1 | 0.9 | -0.1 | 0.6 | -0.8 | 0.9 | -0.2 |
| Phosphoglucomutase, cytoplasmic 2 | P93805 | 63 | YDYENVDAGAAK(76.0) DSQEALAPLVDVALK(48.5) | Glucose metabolic process | Cytoplasm | 1.8 | 0.8 | 1.0 | 0 | 1.8 | 0.9 | 0.5 | -1.1 | 0.3 | -1.7 |
| Serine hydroxymethyltransferase 4 | O23254 | 52 | ISATSIYFESLPYK(69.3) NAVFGDSSALAPGGVR(65.0) | Glycine biosynthetic process | Cytoplasm | 1.1 | 0.1 | 1.0 | 0 | 1.1 | 0.2 | 0.9 | -0.1 | 0.9 | -0.1 |
| Aconitate hydratase, cytoplasmic | P49608 | 98 | NGVTATDLVLTVTQMLR(97.5) SENAVQANMELEFQR(77.2) DAYCLLNFGDSITTDHISPAGSIHK(44.5) | Glyoxylate cycle | Cytoplasm | 1.9 | 0.9 | 1.1 | 0.1 | 1.2 | 0.2 | 0.6 | -0.8 | 0.3 | -1.8 |
| Glyceraldehyde-3-phosphate dehydrogenase, cytosolic | P17878 | 37 | FGIVEGLMTTVHAMTATQK(59.9) AASFNIIPSSTGAAK(47.7) | Glycolytic process | Cytoplasm | 0.5 | -1.1 | 1.1 | 0.1 | 0.7 | -0.5 | 1.6 | 0.7 | 0.7 | -0.4 |
| Fumarate hydratase 2, chloroplastic | Q9FI53 | 54 | IYQLAQGGTAVGTGLNTK(70.6) SLQNFEIGGDR(37.8) | Tricarboxylic acid cycle | Chloroplast | 0.6 | -0.7 | 1.1 | 0.1 | 0.8 | -0.3 | 2.0 | 1.0 | 2.0 | 1.0 |
| Aconitate hydratase 1 | Q42560 | 98 | SDDTVSMIEAYLR(63.1) INPLVPVDLVIDHSVQVDVAR(69.5) | Tricarboxylic acid cycle | Cytoplasm, mitochondria | 1.1 | 0.1 | 1.1 | 0.1 | 1.2 | 0.3 | 0.9 | -0.2 | 0.8 | -0.3 |
| Putative aconitate hydratase, cytoplasmic | Q6YZX6 | 98 | LQNGVTATDLVLTVTQMLR(107.1) INPLVPVDLVIDHSVQVDVAR(67.5) | Glyoxylate cycle | Cytoplasm | 4.0 | 2.0 | 1.2 | 0.3 | 5.5 | 2.5 | 0.2 | -2.6 | 0.1 | -2.8 |
| S-adenosylmethionine synthase 2 | Q9FPL6 | 43 | VHTVLISTQHDETVTNEQIAADLK(41.2) | One-carbon metabolism | Cytoplasm | 0.4 | -1.4 | 1.0 | 0 | 0.7 | -0.6 | 1.4 | 0.5 | 0.9 | -0.1 |
| UDP-glucose 6-dehydrogenase 1 | Q96558 | 53 | VVASMFNTVSNK(65.1) | Glycosaminoglycan biosynthetic process | Cytosol, nuclueus | 2.0 | 1.0 | 1.7 | 0.7 | 2.0 | 1.0 | 0.8 | -0.3 | 0.7 | -0.5 |
| Phosphoglycerate kinase, cytosolic | Q42962 | 42 | LASLADLYVNDAFGTAHR(98.5) GVTTIIGGGDSVAAVEK(77.4) | Glycolysis | Cytoplasm | 1.5 | 0.6 | 0.8 | -0.2 | 2.1 | 1.1 | 0.3 | -1.7 | 0.3 | -1.6 |
| Aconitate hydratase 2, mitochondrial | Q9SIB9 | 108 | NGVTATDLVLTVTQMLR(94.3) FVEFYGNGMSGLSLADR(54.9) | Tricarboxylic acid cycle | Cytoplasm, mitochondria | 1.2 | 0.3 | 1.2 | 0.2 | 1.4 | 0.5 | 1.1 | 0.2 | 1.1 | 0.1 |
| Formate--tetrahydrofolate ligase | Q9SPK5 | 68 | SYGASGVEYSDQAEK(102.2) | One-carbon metabolism | Apoplast, chloroplast, cytosol, plasma membrane | 1.1 | 0.1 | 0.9 | -0.1 | 1.1 | 0.1 | 1.3 | 0.4 | 1.2 | 0.2 |
| Isocitrate dehydrogenase [NADP] | Q06197 | 46 | VTIESAEATLK(60.1) | Glyoxylate cycle | Cytoplasm | 0.7 | -0.5 | 1.0 | 0 | 0.8 | -0.3 | 2.4 | 1.3 | 0.7 | -0.5 |
| Serine hydroxymethyltransferase 5 | Q9SVM4 | 52 | IGTPAMTSR(34.0) | One-carbon metabolism | Cytoplasm | 0.9 | -0.2 | 1.0 | 0 | 0.8 | -0.3 | 1.1 | 0.1 | 1.1 | 0.1 |
| Phosphoglycerate kinase, chloroplastic | P12782 | 50 | GVTTIIGGGDSVAAVEK(78.8) VGVADVMSHISTGGGASLELLEGK(76.5) | Calvin cycle | Chloroplast | 1.1 | 0.1 | 1.1 | 0.2 | 1.3 | 0.4 | 1.0 | 0 | 2.0 | 1.0 |
| Acyl-coenzyme A oxidase 2, peroxisomal | O65201 | 77 | ESMNTYLSQPNPVTAR(44.1) | Fatty acid metabolism | Peroxisome | 0.7 | -0.6 | 1.0 | 0 | 0.9 | -0.2 | 1.0 | 0 | 1.1 | 0.2 |
| 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | P35493 | 61 | AHGTAVGLPTEDDMGNSEVGHNALGAGR(65.1) | Glycolysis | Cytoplasm | 0.6 | -0.8 | 1.0 | -0.1 | 0.7 | -0.6 | 2.3 | 1.2 | 1.6 | 0.7 |
| Aspartate aminotransferase, chloroplastic | P46248 | 50 | LNLGVGAYR(36.2) | Aspartate metabolism | Amyloplast, chloroplast | 1.2 | 0.3 | 1.2 | 0.3 | 1.1 | 0.1 | 1.1 | 0.1 | 1.4 | 0.5 |
| Aconitate hydratase 3, mitochondrial | Q94A28 | 108 | ANYLASPPLVVAYALAGTVDIDFEK(70.2) | Tricarboxylic acid cycle | Mitochondria | 1.4 | 0.5 | 1.4 | 0.5 | 1.5 | 0.6 | 1.2 | 0.2 | 1.0 | 0 |
| 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase | Q42662 | 85 | NDMVEYFGEQLSGFAFTANGWVQSYGSR(71.6) AGITVIQIDEAALR(64.8) | Methionine biosynthesis | Cytoplasm | 0.8 | -0.4 | 1.0 | 0 | 0.9 | -0.1 | 0.8 | -0.3 | 1.3 | 0.4 |
| Biotin carboxylase 2, chloroplastic | B9N843 | 57 | IQVEHPVTEMISSVDLIEEQIR(65.3) | Fatty acid biosynthetic process | Chloroplast | 1.2 | 0.3 | 0.9 | -0.1 | 1.2 | 0.3 | 0.6 | -0.7 | 0.6 | -0.7 |
| Transketolase-2, chloroplastic | F4IW47 | 80 | YPEEAAELK(40.0) | Reductive pentose-phosphate cycle | Chloroplast thylakoid membrane, chloroplast stroma | 1.1 | 0.1 | 0.8 | -0.3 | 1.8 | 0.8 | 0.9 | -0.2 | 0.9 | -0.2 |
| Isocitrate lyase | P49297 | 65 | TVQGGITSTAAMGK(82.1) FEAEVAEVQAWWNTER(73.3) | Tricarboxylic acid cycle | Glyoxysome | 0.7 | -0.4 | 1.1 | 0.1 | 0.7 | -0.4 | 1.0 | 0 | 1.1 | 0.1 |
| Aspartate aminotransferase, cytoplasmic | P28734 | 44 | LIFGADSPAIQENR(83.1) | Aspartate metabolism | Cytoplasm | 0.8 | -0.4 | 1.2 | 0.2 | 0.9 | -0.2 | 1.6 | 0.7 | 1.2 | 0.2 |
| Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic | P45621 | 50 | AGSGVATLGLPDSPGVPK(56.3) | Chlorophyll biosynthesis | Chloroplast | 1.3 | 0.4 | 1.0 | 0.1 | 1.5 | 0.6 | 1.0 | 0 | 0.9 | -0.1 |
| Fumarate hydratase 1, mitochondrial | P93033 | 53 | AIMQAAQEVAEGK(80.6) SQSSNDTFPTVMHIAAATEINSR(45.5) | Tricarboxylic acid cycle | Mitochondria | 0.9 | -0.1 | 0.9 | -0.2 | 1.3 | 0.3 | 1.1 | 0.1 | 0.9 | -0.2 |
| Aconitate hydratase, cytoplasmic (Fragment) | O04916 | 67 | ANNMFVDYNEPQQEK(37.7) | Glyoxylate cycle | Cytoplasm | 1.2 | 0.3 | 0.8 | -0.3 | 1.6 | 0.6 | 0.9 | -0.2 | 1.0 | 0 |
| Ribulose bisphosphate carboxylase small chain, chloroplastic | P08705 | 20 | KYETLSYLPPLTETQLAK(50.8) | Calvin cycle | Chloroplast | 1.3 | 0.4 | 0.9 | -0.2 | 1.5 | 0.6 | 0.5 | -0.9 | 1.1 | 0.1 |
| Ribulose-phosphate 3-epimerase, chloroplastic | Q43157 | 30 | SDIIVSPSILSANFAK(64.5) | Calvin cycle | Chloroplast thylakoid membrane | 1.5 | 0.5 | 0.9 | -0.2 | 1.9 | 1.0 | 0.2 | -2.2 | 1.3 | 0.3 |
| Geranylgeranyl diphosphate reductase, chloroplastic | Q9ZS34 | 51 | VAVVGGGPAGGAAAETLAK(43.2) | Photosynthesis | Chloroplast | 0.9 | -0.2 | 0.8 | -0.3 | 1.5 | 0.6 | 1.0 | 0 | 1.3 | 0.4 |
| Phosphoenolpyruvate carboxykinase (ATP) | P42066 | 74 | VFVNDQFLNWDPENR(54.7) NGDVALFFGLSGTGK(43.4) | Gluconeogenesis | Cytoplasm | 1.7 | 0.7 | 0.9 | -0.2 | 1.2 | 0.3 | 0.5 | -1.0 | 0.5 | -0.9 |
| S-adenosylmethionine synthase 2 | Q38JH8 | 43 | NDNGAMVPIR(46.1) | One-carbon metabolism | Cytoplasm | 0.7 | -0.5 | 0.9 | -0.1 | 0.8 | -0.3 | 1.6 | 0.7 | 1.4 | 0.4 |
| Citrate synthase, glyoxysomal | P49299 | 57 | LYPNVDFYSGLIYR(65.4) LAEEVFSIVGR(58.2) | Tricarboxylic acid cycle | Glyoxysome | 0.8 | -0.3 | 1.0 | 0 | 0.7 | -0.5 | 1.1 | 0.1 | 1.9 | 0.9 |
| Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial | Q6K9N6 | 45 | LEGTNVDQGK(62.2) | Tricarboxylic acid cycle | Mitochondrion | 1.0 | 0 | 0.9 | -0.2 | 1.3 | 0.3 | 1.1 | 0.2 | 0.8 | -0.3 |
| Triosephosphate isomerase, cytosolic | P21820 | 27 | ALLNESNEFVGDK(67.9) | Glycolysis | Cytoplasm | 0.7 | -0.4 | 1.1 | 0.1 | 0.8 | -0.4 | 2.0 | 1.0 | 1.7 | 0.8 |
| Malate dehydrogenase, cytoplasmic | Q7XDC8 | 36 | VLVVANPANTNALILK(77.2) | Tricarboxylic acid cycle | Cytoplasm | 0.9 | -0.1 | 0.9 | -0.1 | 1.0 | 0 | 1.2 | 0.3 | 1.2 | 0.3 |
| Phospholipase D alpha 1 | Q43007 | 92 | AYLPVQELLNGEEIDR(79.1) VLMLVWDDR(51.1) | Lipid catabolic process | Membrane | 0.5 | -0.9 | 0.8 | -0.4 | 0.9 | -0.2 | 1.0 | 0 | 0.7 | -0.6 |
| Nucleoside diphosphate kinase B | P47920 | 16 | IIGATNPAESAPGTIR(83.5) | GTP/CTP/UTP biosynthesis | Chloroplast, cytoplasm | 0.8 | -0.4 | 0.9 | -0.2 | 0.8 | -0.3 | 1.2 | 0.3 | 1.2 | 0.3 |
| Nucleoside diphosphate kinase IV, chloroplastic/mitochondrial | Q8LAH8 | 26 | NIIHGSDGPETAK(51.4) | Nucleotide metabolism | Chloroplast thylakoid membrane, mitochondrion intermembrane space | 0.7 | -0.4 | 0.9 | -0.2 | 0.8 | -0.3 | 1.2 | 0.3 | 1.2 | 0.3 |
| Formate--tetrahydrofolate ligase | P28723 | 68 | LDIDPDSITWR(54.9) | One-carbon metabolism | Apoplast, chloroplast, cytosol, plasma membrane | 1.19 | 0.3 | 1.2 | 0.2 | 1.5 | 0.5 | 0.9 | -0.1 | 1.0 | 0 |
| Adenosylhomocysteinase | Q01781 | 53 | ITGSLHMTIQTGVLIETLTALGAEVR(82.1) | One-carbon metabolism | Cytosol, membrane, vacuole | 0.9 | -0.2 | 1.1 | 0.1 | 1.0 | -0.1 | 1.3 | 0.4 | 1.2 | 0.2 |
| **STRESS-RESPONSE PROTEINS** | | | | | | |  |  |  |  |  |  |  |  |  |
| Heat shock 70 kDa protein, mitochondrial | P37900 | 72 | IINEPTAAAIAYGLDK(94.8) | Protein folding | Mitochondria | 0.19 | -2.4 | 1.0 | 0 | 1.9 | 0.9 | 2.0 | 1.0 | 0.2 | -2.7 |
| Adenosine kinase 1 | Q9SF85 | 38 | VHGWETDDVEQIAIK(45.5) | Stress response | Membrane, chloroplast, nuclues | 1.1 | 0.1 | 0.8 | -0.3 | 1.6 | 0.7 | 0.7 | -0.5 | 0.6 | -0.6 |
| 17.9 kDa class II heat shock protein | P46516 | 18 | NLHYILEATDDNTTGNK(86.4) FALPEDANTDK(46.9) | Stress response | Cytoplasm | 1.3 | 0.4 | 1.2 | 0.3 | 1.2 | 0.3 | 1.3 | 0.4 | 1.1 | 0.2 |
| Aldehyde dehydrogenase family 2 member B4, mitochondrial | Q9SU63 | 59 | DDMLIAQDEIFGPVQSILK(70.9) LAFTGSTDTGK(57.5) | Response to cadmium ion | Mitochondrion matrix | 1.0 | 0 | 1.0 | -0.1 | 1.1 | 0.1 | 1.1 | 0.2 | 1.0 | 0 |
| Obg-like ATPase 1 | Q9SA73 | 44 | AVDGIFHVLR(42.6) | Stress response | Cytosol | 0.9 | -0.1 | 1.0 | 0.1 | 1.2 | 0.2 | 0.9 | -0.2 | 1.1 | 0.2 |
| Annexin D1 | Q9SYT0 | 36 | TGTDEGALTR(63.9) | Stress response | Cytosol, membrane | 0.9 | -0.1 | 0.9 | -0.2 | 0.7 | -0.5 | 1.2 | 0.2 | 1.3 | 0.3 |
| Sucrose synthase 2 | Q00917 | 92 | SSSIGNGVQFLNR(47.2) | Stress response | Cytoplasm, plastid membrane | 2.0 | 1.0 | 3.8 | 1.9 | 2.0 | 1.0 | 0.6 | -0.6 | 0.6 | -0.8 |
| Catalase | P45739 | 57 | SSSAYNAPFWTTNSGAPVYNNNNSLTVGSR(70.7) GFFEVTHDITALTCADFLR(59.8) | Response to oxidative stress | Peroxisome | 1.1 | 0.1 | 1.1 | 0.1 | 1.2 | 0.3 | 0.9 | -0.1 | 1.1 | 0.1 |
| Chaperone protein ClpB1 | P42730 | 101 | LDEIVVFDPLSHDQLR(60.3) | Stress response | Nuclueus, cytosol | 0.8 | -0.3 | 1.1 | 0.2 | 0.8 | -0.4 | 1.5 | 0.6 | 1.4 | 0.4 |
| Heat shock protein 81-1 | A2YWQ1 | 80 | TMEINPENAIMEELR(71.8) HNDDEQYVWESQAGGSFTVTR(88.9) | Stress response | Cytoplasm | 1.4 | 0.5 | 1.0 | 0.1 | 1.9 | 0.9 | 0.5 | -0.9 | 0.5 | -0.9 |
| Heat shock 70 kDa protein | P26413 | 71 | SINPDEAVAYGAAVQAAILSGQGDEK(90.0) NQVAMNPQNTVFDAK(86.1) | Stress response | Mitochondrion, ribosome, nucleus | 1.7 | 0.8 | 1.3 | 0.4 | 1.2 | 0.2 | 0.9 | -0.1 | 0.8 | -0.4 |
| 17.6 kDa class I heat shock protein | P30693 | 18 | AMMENGVLTVVVPK(74.4) | Stress response | Cytoplasm | 1.2 | 0.2 | 1.4 | 0.5 | 0.9 | -0.1 | 1.1 | 0.2 | 1.1 | 0.2 |
| Probable mediator of RNA polymerase II transcription subunit 37c | Q9LHA8 | 71 | QFSAEEISSMVLIK(70.7) KIEDAIDQAIEWLDGnQLAEADEFEDK(48.0) | Stress response | Cytoplasm, Nucleus | 0.6 | -0.8 | 0.8 | -0.3 | 1.4 | 0.5 | 0.6 | -0.6 | 0.3 | -1.7 |
| **TRANSPORT PROTEINS** | | | | | | |  |  |  |  |  |  |  |  |  |
| ATP synthase subunit beta, mitochondrial | P37399 | 59 | GMDVIDTGAPLSVPVGGATLGR(93.1) | ATP synthesis coupled proton transport | Mitochondrion | 0.8 | -0.3 | 1.1 | 0.2 | 0.8 | -0.3 | 1.8 | 0.8 | 1.9 | 0.9 |
| Pyrophosphate-energized vacuolar membrane proton pump 1 | P31414;Q06572 | 80 | AAVIGDTIGDPLK (87.4) | Proton transport | Vacuolar membrane | 0.7 | -0.6 | 0.8 | -0.3 | 0.7 | -0.4 | 0.8 | -0.3 | 0.6 | -0.6 |
| Importin subunit alpha-1a | Q71VM4 | 57 | IENLQSHDNNEIYEK(64.3) SPPIEEVIQSGVVPR(48.7) | NLS-bearing protein import into nucleus | Cytoplasm | 1.0 | 0 | 0.9 | -0.1 | 1.6 | 0.7 | 0.9 | -0.2 | 0.6 | -0.7 |
| ATP synthase subunit beta, chloroplastic | Q1KXV2 | 54 | DVNEQDVLLFVDNIFR(87.8) IVGDEHYETAQQVK(56.3) | ATP synthesis coupled proton transport | Chloroplast thylakoid membrane | 0.7 | -0.6 | 0.7 | -0.5 | 0.9 | -0.1 | 0.6 | -0.8 | 0.6 | -0.6 |
| V-type proton ATPase catalytic subunit A | Q39291 | 69 | TTLVANTSNMPVAAR(95.4) EASIYTGITIAEYFR(89.5) | Ion transport | Proton-transporting V-type ATPase, V1 domain | 0.9 | -0.2 | 0.9 | -0.2 | 0.6 | -0.7 | 0.9 | -0.1 | 1.2 | 0.2 |
| Clathrin heavy chain 2 | Q0WLB5 | 193 | EAAELAAESPQGILR(69.3) | Endocytosis | Clathrin coat of trans-Golgi network vesicle | 0.9 | -0.1 | 0.9 | -0.1 | 0.6 | -0.6 | 1.1 | 0.1 | 1.0 | 0.1 |
| Probable mitochondrial-processing peptidase subunit beta, mitochondrial | Q42290 | 59 | EQTTYYAK(30.0) | Mitochondrial electron transport | Mitochondria | 1.1 | 0.1 | 1.1 | 0.2 | 1.1 | 0.2 | 0.7 | -0.5 | 0.8 | -0.2 |
| V-type proton ATPase subunit E | Q40272 | 26 | IEYSMQLNASR(57.9) | Ion transport | Proton-transporting two-sector ATPase complex, catalytic domain | 1.0 | 0 | 0.8 | -0.3 | 1.3 | 0.4 | 1.0 | 0 | 1.0 | 0 |
| ATP synthase subunit alpha, chloroplastic | Q1KXW5 | 56 | IVNTGTVLQVGDGIAR(83.9) ASSVAQVVTTFQEK(63.4) | Ion transport | Chloroplast thylakoid membrane | 0.8 | -0.4 | 0.8 | -0.3 | 1.4 | 0.5 | 0.9 | -0.1 | 1.5 | 0.6 |
| Importin subunit beta-1 | Q9FJD4 | 96 | NGILEAYSGIFQGFK(69.8) | Protein transport | Cytoplasm | 1.2 | 0.3 | 1.0 | 0.1 | 0.9 | -0.2 | 1.0 | 0 | 0.9 | -0.1 |
| ATP synthase subunit alpha, mitochondrial | P18260 | 55 | TELLQSLLEK(38.5) ISNFYTNFQVDEIGR(84.6) | ATP synthesis coupled proton transport | Mitochondria | 1.0 | 0 | 1.0 | 0.1 | 1.2 | 0.2 | 0.5 | -0.9 | 1.1 | 0.1 |
| NADH dehydrogenase [ubiquinone] iron-sulfur protein 2 | P93306 | 45 | LVDIGTVTAQQAK(78.4) | Electron transport | Mitochondrion | 0.8 | -0.3 | 1.1 | 0.1 | 0.8 | -0.3 | 1.1 | 0.1 | 1.4 | 0.5 |
| **TRANSLATION PROTEINS** | | | | | | | | | | | |  |  |  |  |
| Eukaryotic initiation factor 4A-3 | Q9CAI7 | 47 | MFVLDEADEMLSR(88.9) GLDVIQQAQSGTGK(83.5) | Translation initiation | Cytoplasm | 0.7 | -0.4 | 1.1 | 0.1 | 1.6 | 0.7 | 0.9 | -0.1 | 1.7 | 0.8 |
| 60S ribosomal protein L10 | Q9SPB3 | 25 | ENVSSEALEAAR(63.0) VSIGQVLLSVR(35.5) | Translation | Ribosome | 0.6 | -0.7 | 1.1 | 0.1 | 0.8 | -0.3 | 1.7 | 0.7 | 1.7 | 0.8 |
| 40S ribosomal protein S9-1 | Q9LXG1 | 23 | LDYVLALTVENFLER(60.2) YGLLDESQNK(32.7) | Translation | Cytosolic ribosome | 1.4 | 0.5 | 1.9 | 0.9 | 0.5 | -0.9 | 1.6 | 0.6 | 1.9 | 0.9 |
| 60S ribosomal protein L12 | O50003 | 18 | VTGGEVGAASSLAPK(73.1) | Translation | Ribosome | 0.6 | -0.8 | 1.2 | 0.2 | 0.7 | -0.5 | 1.9 | 0.9 | 2.1 | 1.1 |
| Elongation factor G, chloroplastic | Q9SI75 | 86 | INIIDTPGHVDFTLEVER(54.7) VEANVGAPQVNYR(48.6) | Protein biosynthesis | Chloroplast | 0.6 | -0.7 | 1.0 | -0.1 | 1.0 | 0 | 1.1 | 0.1 | 1.7 | 0.7 |
| 60S ribosomal protein L4 | Q9XF97 | 45 | AGHQTSAESWGTGR(73.6) | Translation | Ribosome | 1.0 | 0 | 1.1 | 0.1 | 1.1 | 0.2 | 1.0 | 0 | 1.2 | 0.3 |
| 60S ribosomal protein L15 | O82528 | 24 | VLNSYWINEDSTYK(73.0) | Translation | Ribosome | 0.7 | -0.5 | 1.2 | 0.3 | 0.8 | -0.3 | 1.4 | 0.4 | 1.9 | 1.0 |
| 60S acidic ribosomal protein P2 | P41099 | 12 | DITELIASGR(47.8) | Translation | Ribosome | 0.9 | -0.1 | 1.1 | 0.2 | 1.0 | 0 | 1.1 | 0.1 | 1.7 | 0.7 |
| Elongation factor 2 | Q9ASR1 | 94 | VENLYEGPLDDQYANAIR(79.4) DGNEYLINLIDSPGHVDFSSEVTAALR(51.3) | Protein biosynthesis | Cytoplasm | 0.9 | -0.2 | 1.0 | 0 | 1.0 | 0 | 1.1 | 0.1 | 1.1 | 0.2 |
| 40S ribosomal protein S6 | Q9M3V8 | 28 | ISQEVSGDALGEEFK(72.6) | Translation | Ribosome | 1.0 | 0 | 1.1 | 0.1 | 1.5 | 0.6 | 0.9 | -0.2 | 0.9 | -0.1 |
| 30S ribosomal protein S5, chloroplastic | P93014 | 33 | (QLGSNNALNNAR(77.2) | Chloroplast rRNA processing | Chloroplast | 0.5 | -1.1 | 0.9 | -0.1 | 1.1 | 0.1 | 1.5 | 0.5 | 2.7 | 1.4 |
| 40S ribosomal protein S3a | P49198 | 30 | VFEVSLADLQNDEDHSYR(61.8) | Translation | Cytoplasm | 1.1 | 0.2 | 1.1 | 0.1 | 0.9 | -0.1 | 0.6 | -0.7 | 0.8 | -0.3 |
| 40S ribosomal protein S13 | P62302 | 17 | GLTPSQIGVILR(49.0) | Translation | Cytosolic small ribosomal subunit, nucleolus | 0.8 | -0.3 | 1.2 | 0.2 | 1.0 | 0 | 0.8 | -0.3 | 1.6 | 0.6 |
| 60S ribosomal protein L5 | Q6UNT2 | 34 | ALLDVGLIR(43.3) | Translation | Cytoplasm, nucleus | 0.9 | -0.1 | 1.2 | 0.2 | 1.0 | 0 | 0.8 | -0.3 | 1.9 | 0.9 |
| 60S ribosomal protein L9 | P49210 | 21 | DELVLDGNDIELVSR(66.1) | Cytoplasmic translation | Cytosolic large ribosomal subunit | 1.2 | 0.3 | 1.1 | 0.1 | 1.5 | 0.6 | 0.7 | -0.4 | 0.9 | -0.1 |
| Serine--tRNA ligase | O81983 | 50 | LETVGNLVHDSVPVSNDEADNAVVR(72.1) | Protein biosynthesis | Cytoplasm | 0.8 | -0.3 | 1.0 | 0 | 0.9 | -0.1 | 1.7 | 0.7 | 0.8 | -0.3 |
| 60S ribosomal protein L6 | P34091 | 26 | ASITPGTVLIILAGR(79.5) | Translation | Ribosome | 1.2 | 0.3 | 1.0 | -0.1 | 1.5 | 0.6 | 0.9 | -0.2 | 0.9 | -0.1 |
| 60S ribosomal protein L3 | P35684 | 44 | DEMIDIIGVTK(60.5) DITPMGGFPHYGVVK(49.0) | Translation | Cytoplasm | 1.0 | 0 | 1.1 | 0.1 | 1.2 | 0.3 | 1.0 | 0 | 1.1 | 0.2 |
| 40S ribosomal protein S3-1 | Q9SIP7 | 28 | ELAEDGYSGVEVR(80.6) | Cytoplasmic translation | Cytosol | 1.4 | 0.5 | 1.3 | 0.4 | 1.5 | 0.6 | 0.9 | -0.2 | 1.3 | 0.3 |
| **PROTEOLYSIS PROTEINS** | | | | | | | | | | | |  |  |  |  |
| 26S proteasome regulatory subunit 4 homolog B | Q9SL67 | 49 | DYLLMEEEFVANQER(74.3) | Ubiquitin-dependent ERAD pathway | Cytoplasm, nucleus | 0.8 | -0.2 | 1.0 | 0 | 1.4 | 0.5 | 0.6 | -0.7 | 0.6 | -0.7 |
| 26S protease regulatory subunit 10B homolog A | Q9SEI3 | 44 | LAEGFnGADLR(51.8) SLQSVGQIIGEVLRPLDNER(50.8) | Ubiquitin-dependent ERAD pathway | Cytoplasm, nucleus | 1.5 | 0.6 | 1.3 | 0.4 | 1.0 | 0.1 | 1.2 | 0.2 | 1.1 | 0.1 |
| Tripeptidyl-peptidase 2 | F4JVN6 | 152 | GPVIDAVVWHDGEVWR(68.4) EAFYLGPPTK(39.8) | Proteolysis | Chloroplast, cytoplasm, cytosolic ribosome | 1.3 | 0.4 | 1.3 | 0.3 | 1.4 | 0.5 | 0.9 | -0.1 | 1.4 | 0.5 |
| Proteasome subunit alpha type-5 | Q9M4T8 | 26 | AIGSGSEGADSSLQEQFNK(52.1) | Proteasome-mediated ubiquitin-dependent protein catabolic process | Cytoplasm, nucleus | 1.2 | 0.3 | 1.1 | 0.2 | 1.3 | 0.3 | 1.2 | 0.2 | 0.9 | -0.2 |
| 26S proteasome non-ATPase regulatory subunit 11 homolog | Q9LP45 | 47 | LLLVDIDLLESK(73.0) | Protein catabolism | Cytosol, nucleus, plasmodesma, proteosome complex | 0.7 | -0.4 | 1.1 | 0.2 | 1.1 | 0.1 | 0.9 | -0.2 | 1.5 | 0.6 |
| 26S protease regulatory subunit 8 homolog B | Q94BQ2 | 47 | MESGSGNGDSEVQR(50.8) EHAPSIIFMDEIDSIGSAR(46.4) | Ubiquitin-dependent ERAD pathway | Cytoplasm, nuclueus | 1.1 | 0.2 | 1.1 | 0.1 | 1.1 | 0.2 | 0.7 | -0.5 | 0.8 | -0.3 |
| Presequence protease 1, chloroplastic/mitochondrial | Q9LJL3 | 121 | TLDIYDGTGDFLR(56.1) | Protein processing | Chloroplast stroma, mitochondrion matrix | 1.3 | 0.4 | 1.1 | 0.2 | 1.7 | 0.8 | 0.7 | -0.5 | 1.3 | 0.4 |
| 26S protease regulatory subunit 6B homolog | P85200 | 47 | ENAPAIIFIDEVDAIATAR(95.8) MNLSDEVDLEDYVSRPDK(64.6) | Protein catabolism | Cytoplasm, nucleus | 0.8 | -0.3 | 1.0 | 0 | 1.0 | -0.1 | 1.3 | 0.3 | 1.3 | 0.4 |
| Aminopeptidase M1 | Q8VZH2 | 98 | IWTQFLDESTEGLR(101.2) | Peptide catabolic process | Membrane, cytoplasm | 1.2 | 0.2 | 1.0 | 0 | 1.0 | 0 | 0.8 | -0.3 | 0.9 | -0.1 |
| Ubiquitin-conjugating enzyme E2 35 | Q94A97 | 17 | TVLLSIQALLSAPNPDDPLSENIAK(39.4) | Ubiquitin-dependent protein catabolic process | Cytoplasm, nucleus | 0.7 | -0.5 | 1.2 | 0.3 | 0.9 | -0.2 | 2.2 | 1.1 | 1.4 | 0.5 |
| 26S protease regulatory subunit 7 | Q41365 | 48 | TMLEIVNQLDGFDAR(99.8) | Protein catabolism | Cytoplasm, nucleus | 1.4 | 0.4 | 1.0 | 0 | 1.6 | 0.7 | 0.9 | -0.2 | 0.9 | -0.2 |
| Ubiquitin-conjugating enzyme E2 variant 1C | Q9SJ44 | 16 | GIGDGTVSYGMDDGDDIYMR(91.1) | Post replication repair | Cytosol, nucleus | 0.6 | -0.8 | 1.0 | 0 | 0.7 | -0.5 | 1.8 | 0.9 | 0.6 | -0.8 |
| **CHAPERONE PROTEINS** | | | | | | | | | | | |  |  |  |  |
| Peptidyl-prolyl cis-trans isomerase | P21569 | 18 | VFFDMTVGGAPAGR(70.0) | Protein folding | Cytoplasm | 1.0 | 0 | 1.1 | 0.1 | 0.7 | -0.5 | 1.1 | 0.1 | 1.5 | 0.5 |
| T-complex protein 1 subunit gamma | Q84WV1 | 60 | GENQTNAELVR(55.6) NLQDAMSVAR(31.3) | Protein folding | Cytoplasm | 0.7 | -0.4 | 1.1 | 0.1 | 0.7 | -0.5 | 1.5 | 0.6 | 1.8 | 0.8 |
| RuBisCO large subunit-binding protein subunit beta, chloroplastic | P08927 | 63 | LSGGVAVIQVGAQTETELK(71.6) SQYLDDIAILTGGTVIR(70.2) YGYNAATGK(38.5) | Protein refolding | Chloroplast | 0.8 | -0.3 | 1.0 | 0 | 1.2 | 0.2 | 0.9 | -0.1 | 1.0 | 0 |
| Peptidyl-prolyl cis-trans isomerase FKBP62 | Q38931 | 61 | VLLTVKPQYGFGEK(63.6) | Protein folding | Cytoplasm, nucleus | 1.7 | 0.7 | 1.2 | 0.3 | 1.6 | 0.7 | 0.8 | -0.3 | 0.9 | -0.2 |
| T-complex protein 1 subunit delta | Q9LV21 | 58 | TDIEQSIVVSDYTQMDR(58.4) | Protein folding | Cytoplasm | 0.6 | -0.8 | 1.0 | 0.1 | 0.7 | -0.5 | 2.3 | 1.2 | 1.3 | 0.3 |
| T-complex protein 1 subunit eta | Q9SF16 | 60 | LAIGDLATQYFADR(89.1) | Protein folding | Cytoplasm | 1.0 | -0.1 | 1.0 | 0.1 | 0.9 | -0.2 | 1.1 | 0.2 | 1.2 | 0.3 |
| Calreticulin | Q9ZPP1 | 48 | APMIDNPDFKDDPDIYVFPK(65.8) | Protein folding | Endoplasmic reticulum lumen | 1.0 | 0 | 0.8 | -0.3 | 1.3 | 0.4 | 0.7 | -0.5 | 0.8 | -0.4 |
| Endoplasmin homolog | P35016 | 93 | IMQSQTLSDASK(53.7) VFISDEFDELLPK(45.7) | Protein folding | Endoplasmic reticulum lumen | 0.9 | -0.1 | 1.0 | 0 | 0.8 | -0.4 | 1.3 | 0.3 | 1.1 | 0.1 |
| T-complex protein 1 subunit beta O | Q940P8 | 57 | DSFLDEGFILDK(55.9) | Protein folding | Cytoplasm | 0.7 | -0.5 | 1.1 | 0.1 | 0.8 | -0.4 | 1.1 | 0.1 | 0.9 | -0.2 |
| T-complex protein 1 subunit alpha | P28769 | 59 | EVGDGTTSVVIVAAELLK(85.8) | Protein folding | Cytoplasm | 0.9 | -0.2 | 0.9 | -0.2 | 0.9 | -0.1 | 1.2 | 0.2 | 1.2 | 0.3 |
| Calnexin homolog | Q39994 | 61 | GFDNESPYSIMFGPDK(52.0) SEGHDDYGLLVSDK(48.7) | Protein folding | Endoplasmic reticulum membrane | 1.1 | 0.2 | 1.0 | 0 | 1.3 | 0.4 | 0.7 | -0.5 | 0.9 | -0.2 |
| Heat shock protein 83 | P51819 | 81 | HNDDEQYIWESQAGGSFTVTR(46.8) | Protein folding | Cytoplasm | 1.3 | 0.3 | 1.2 | 0.2 | 0.8 | -0.4 | 0.8 | -0.3 | 0.9 | -0.2 |
| Heat shock protein 90-1 | P27323 | 81 | ADLVNNLGTIAR(61.1) KENEGEVEEVDEEK(71.2) | Protein folding | Cytoplasm | 1.1 | 0.2 | 0.8 | -0.3 | 1.5 | 0.6 | 0.8 | -0.3 | 0.3 | -1.6 |
| Heat shock protein 90-5, chloroplastic | Q9SIF2 | 89 | VFISDDFDGELFPR(86.3) | Protein folding | Chloroplast stroma | 0.9 | -0.1 | 0.7 | -0.6 | 1.4 | 0.5 | 1.0 | 0.1 | 0.6 | -0.7 |
| **REGULATORY PROTEINS** | | | | | | | | | | | |  |  |  |  |
| Oxygen-evolving enhancer protein 2, chloroplastic | P85189 | 28 | HQLISATVSDGK(51.8) | Photosynthesis | Chloroplast thylakoid membrane | 1.5 | 0.6 | 0.9 | -0.1 | 1.7 | 0.7 | 0.8 | -0.3 | 0.9 | -0.2 |
| Tubulin beta-7 chain | Q6VAF5 | 50 | VSEQFTVMFR(52.1) AVLMDLEPGTMDSLR(75.3) | Cell growth | Cytoplasm, microtubule | 0.6 | -0.7 | 1.0 | -0.1 | 0.7 | -0.4 | 0.8 | -0.4 | 1.2 | 0.2 |
| Oxygen-evolving enhancer protein 1, chloroplastic | P85194 | 34 | LTYTLDEIEGPLEVSSDGTIK(70.9) | Photosynthesis | Chloroplast thylakoid membrane | 1.4 | 0.4 | 0.9 | -0.2 | 1.6 | 0.7 | 0.8 | -0.4 | 1.0 | 0 |
| Protochlorophyllide reductase B, chloroplasti | P21218 | 43 | GLAGGLNGLNSSAMIDGGDFDGAK(98.7) | Photosynthesis | Chloroplast outer membrane, chloroplast thylakoid membrane | 0.3 | -1.7 | 0.6 | -0.7 | 1.1 | 0.1 | 1.0 | 0 | 2.4 | 1.3 |
| SKP1-like protein 1B | Q9FHW7 | 19 | NDFTPEEEEEVRR(35.1) | Auxin signaling pathway | Nucleus | 0.8 | -0.3 | 0.9 | -0.2 | 0.9 | -0.1 | 1.3 | 0.4 | 1.0 | -0.1 |
| Protochlorophyllide reductase B, chloroplastic | P21218 | 43 | GLAGGLNGLNSSAMIDGGDFDGAK(98.7) | Photosynthesis | Chloroplast outer membrane, chloroplast thylakoid membrane | 0.3 | -1.7 | 0.6 | -0.7 | 1.1 | 0.1 | 1.0 | 0 | 2.4 | 1.3 |
| 14-3-3-like protein | O65352 | 29 | VVAAADGGEELTIEER(101.8) QAFDEAIAELDTLGEDSYK(69.0) | Signaling | Nucleus | 2.1 | 1.0 | 1.1 | 0.1 | 2.1 | 1.1 | 0.6 | -0.7 | 0.5 | -0.9 |
| **OTHER METABOLIC PROTEINS** | | | | | | | | | | | |  |  |  |  |
| Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1 | Q9SYM5 | 75 | HPEGSGIGFK(43.8) | Cell wall biogenesis/degradation | Cytosol | 1.0 | 0 | 0.9 | -0.2 | 1.1 | 0.2 | 0.9 | -0.1 | 0.8 | -0.3 |
| Bifunctional dTDP-4-dehydrorhamnose 3,5-epimerase/dTDP-4-dehydrorhamnose reductase | Q9LQ04 | 34 | MPISSDLTNPR(72.7) | Cell wall biogenesis/degradation | Apoplast, plasmodesma, cytosol, plasma membrane | 0.7 | -0.4 | 1.0 | 0 | 0.7 | -0.6 | 1.7 | 0.8 | 1.6 | 0.7 |
| Adenylate kinase 4 | Q08480 | 26 | QTEPVIDYYSK(44.6) | Purine nucleotide metabolic process | Cytoplasm | 0.8 | -0.3 | 1.1 | 0.2 | 0.7 | -0.5 | 1.6 | 0.7 | 1.7 | 0.7 |
| Methionine S-methyltransferase | Q9SWR3 | 122 | ILQASDTDISALVEIEK(63.0) | Biosynthetic process | Cytoplasm | 1.1 | 0.1 | 0.9 | -0.1 | 1.2 | 0.3 | 0.8 | -0.2 | 0.8 | -0.4 |
| **STORAGE PROTEINS** | | | | | | | | | | | | | | | |
| Oleosin | P29529 | 19 | QTAGSVPESLDYVK(71.7) | Storage protein | Lipid droplet, Membrane | 0.9 | -0.1 | 1.5 | 0.2 | 0.9 | -0.2 | 0.9 | -0.2 | 0.9 | -0.1 |
| 11S globulin seed storage protein G3 | P19084 | 56 | TNDNAMIANLAGR(83.5) VQIVDNQGNSVFDNELR(80.5) EGQVVVIPQnFAVIK(55.0) | Storage protein | Protein body | 1.6 | 0.6 | 2.0 | 1.0 | 0.5 | -1.0 | 1.0 | 0 | 1.4 | 0.4 |
| **MISCELLANEOUS** | | | | | | | | | | | |  |  |  |  |
| Actin | Q05214 | 42 | IVLSGGSTMFPGIADR(103.4) AEYDESGPSIVHR(69.3) | Cytoplasmic streaming, cell growth | Cytoplasm, cytoskeleton | 9.6 | 3.3 | 1.3 | 0.4 | 10.9 | 3.4 | 0.2 | -2.5 | 0.4 | -1.4 |
| Cell division cycle protein 48 homolog | P54774 | 90 | VLNQLLTEMDGMSAK(63.4) EIDIGVPDEVGR(43.4) | Cell cycle | Cell membrane, peripheral membrane protein | 0.8 | -0.4 | 0.9 | -0.1 | 0.9 | -0.2 | 1.7 | 0.7 | 1.4 | 0.5 |
| Clathrin heavy chain 2 | Q2QYW2 | 193 | EGLVSEAIESFIR(64.8) YGLIYVITK(52.0) | Clathrin coat assembly | Cytoplasmic vesicle membrane, peripheral membrane protein | 0.9 | -0.1 | 0.9 | -0.1 | 0.6 | -0.6 | 1.1 | 0.1 | 1.0 | 0.1 |
| Non-specific lipid-transfer protein AP10 | P82007 | 12 | VRPDMASSLPGK(65.6) SGGKPTPACCAGAK(38.2) | Plant defense | Extracellular space, membrane | 1.4 | 0.5 | 1.1 | 0.1 | 1.1 | 0.1 | 1.0 | 0 | 0.7 | -0.5 |
| Leucine aminopeptidase 2, chloroplastic | Q944P7 | 61 | FDMGGSAAVLGAAK(80.8) | Leaf senescence | Chloroplast | 1.1 | 0.1 | 1.3 | 0.4 | 1.6 | 0.7 | 1.0 | 0 | 1.1 | 0.1 |
| Allene oxide synthase | Q40778 | 53 | SNFTIESHDATFEVK(78.9) VLSYLDPSEPR(61.7) | Oxylipin biosynthetic process | Chloroplast | 1.1 | 0.1 | 0.9 | -0.1 | 1.0 | 0 | 1.1 | 0.2 | 1.2 | 0.3 |
| Cysteine proteinase inhibitor A | Q10992 | 9 | QNALLEFGK(48.7) | Endopeptidase inhibitor protein | Vacuole, cell wall | 1.5 | 0.6 | 0.9 | -0.2 | 0.9 | -0.2 | 0.9 | -0.1 | 0.7 | -0.4 |