| Tree ID | Database | Accession | Annotation | Arabidopsis homolog | Acession | Chlamydiae homolog | Acession | Bootstrap | Plantae distn. | WoLF PSORT | TargetP | Predotar | ChloroP | PSLDoc | Prediction | UWE25 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Plantae-Arabidopsis_thaliana_15220982 | GenBank | 15220982 | PFC1 (PALEFACE 1) | PFC1 (PALEFACE 1) | 15220982 | dimethyladenosine transferase | 161611309 | 75 | G | chlo: 10.0 | chlo: 0.97 | chlo: 0.59 | chlo: 0.51 | chlo: 0.67 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_15225451 | GenBank | 15225451 | GAE4 (UDP-D-GLUCURONATE 4-EPIMERASE 4); catalytic | GAE4 (UDP-D-GLUCURONATE 4-EPIMERASE 4); catalytic | 15225451 | probable UDP-glucuronat epimerase | 46445713 | 75 | GR | chlo: 2.0 | none: 0.85 | none: 0.97 | chlo: 0.54 | chlo: 0.13 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_15237422 | GenBank | 15237422 | KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); fatty-acid synthase | KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); fatty-acid synthase | 15237422 | 3-oxoacyl-(acyl carrier protein) synthase II | 46446872 | 75 | GR | chlo: 9.5 | chlo: 0.89 | chlo: 0.54 | chlo: 0.58 | chlo: 0.82 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_15240411 | GenBank | 15240411 | Exonuclease family protein | Exonuclease family protein | 15240411 | DNA polymerase III subunit epsilon | 46446795 | 75 | G | chlo_mito: 5.8 | chlo: 0.78 | chlo: 0.81 |  | chlo: 0.05 | Chloroplast | N |
| Plantae-Arabidopsis_thaliana_18395376 | GenBank | 18395376 | ISPD (2-C-METHYL-D-ERYTHRITOL 4-PHOSPHATE CYTIDYLTRANSFERASE) | ISPD (2-C-METHYL-D-ERYTHRITOL 4-PHOSPHATE CYTIDYLTRANSFERASE) | 18395376 | putative 4-diphosphocytidyl-2C-methyl-D-erythritol synthase | 46445961 | 75 | GRC | chlo: 13.0 | mito: 0.26 | chlo: 0.5 | chlo: 0.53 | mito: 0.47 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_18396215 | GenBank | 18396215 | MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ oxidoreductase | MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ oxidoreductase | 18396215 | enoyl-(acyl carrier protein) reductase | 46446786 | 75 | GC | chlo: 11.0 | chlo: 0.89 | chlo: 0.91 | chlo: 0.55 | chlo: 0.37 | Chloroplast | N |
| Plantae-Arabidopsis_thaliana_18410414 | GenBank | 18410414 | Unknown protein (contains nucleotide-diphospho-sugar transferases domain) | Unknown protein (contains nucleotide-diphospho-sugar transferases domain) | 18410414 | hypothetical protein pc0324 | 46445958 | 75 | G | chlo: 7.0 | chlo: 0.95 | chlo: 0.63 | chlo: 0.59 | chlo: 0.06 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_18418270 | GenBank | 18418270 | AGD2 (ABERRANT GROWTH AND DEATH 2); transaminase | AGD2 (ABERRANT GROWTH AND DEATH 2); transaminase | 18418270 | L,L-diaminopimelate aminotransferase | 46446319 | 75 | GRCX | chlo: 13.0 | chlo: 0.86 | chlo: 0.51 | chlo: 0.57 | chlo: 0.58 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_22328517 | GenBank | 22328517 | ATISA3/ISA3 (ISOAMYLASE 3); alpha-amylase | ATISA3/ISA3 (ISOAMYLASE 3); alpha-amylase | 22328517 | probable isoamylase | 46446740 | 75 | GR | chlo: 11.5 | chlo: 0.98 | chlo: 0.67 | chlo: 0.59 | chlo: 0.14 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_30684861 | GenBank | 30684861 | Methylase-related | Methylase-related | 30684861 | hypothetical protein pc1620 | 46447254 | 50 | GRC | chlo: 6.0 | chlo: 0.83 | chlo: 0.79 | chlo: 0.55 | chlo: 0.07 | Chloroplast | N |
| Plantae-Arabidopsis_thaliana_30687794 | GenBank | 30687794 | Pseudouridine synthase family protein | Pseudouridine synthase family protein | 30687794 | putative ribosomal large chain pseudouridine synthase B | 46445794 | 75 | G | chlo: 11.0 | chlo: 0.68 | chlo: 0.97 | chlo: 0.57 | nucl: 0.14 | Chloroplast | N |
| Plantae-Arabidopsis_thaliana_30688378 | GenBank | 30688378 | PHT2;1 (phosphate transporter 2;1) | PHT2;1 (phosphate transporter 2;1) | 30688378 | Phosphate Permease | 15618590 | 75 | G | chlo: 8.0 | none: 0.45 | none: 0.99 | chlo: 0.50 | mito: 0.01 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_30691669 | GenBank | 30691669 | tRNA/rRNA methyltransferase (SpoU) family protein | tRNA/rRNA methyltransferase (SpoU) family protein | 30691669 | hypothetical protein pc0141 | 46445775 | 75 | GC | chlo: 12.0 | none: 0.25 | none: 0.86 |  | chlo: 0.79 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_30697049 | GenBank | 30697049 | Malate dehydrogenase (NADP) | Malate dehydrogenase (NADP) | 30697049 | malate dehydrogenase | 46447406 | 75 | G | chlo: 12.0 | chlo: 0.96 | chlo: 0.78 | chlo: 0.56 | chlo: 0.00 | Chloroplast | N |
| Plantae-Arabidopsis_thaliana_42563306 | GenBank | 42563306 | Phosphoglycerate/bisphosphoglycerate mutase family protein | Phosphoglycerate/bisphosphoglycerate mutase family protein | 42563306 | phosphoglyceromutase | 46445795 | 75 | G | chlo: 11.0 | chlo: 0.86 | chlo: 0.75 | chlo: 0.56 | nucl: 0.49 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_42565237 | GenBank | 42565237 | Unknown protein (contains domain S-adenosyl-L-methionine-dependent methyltransferases) | Unknown protein (contains domain S-adenosyl-L-methionine-dependent methyltransferases) | 42565237 | putative 23S rRNA (Uracil-5-)-methyltransferase | 46447632 | 75 | GC | chlo: 5.0 | chlo: 0.84 | chlo: 0.77 | chlo: 0.56 | cyto: 0.22 | Chloroplast | Y |
| Plantae-Arabidopsis_thaliana_42573275 | GenBank | 42573275 | PAI2 (PHOSPHORIBOSYLANTHRANILATE ISOMERASE 2); phosphoribosylanthranilate isomerase | PAI2 (PHOSPHORIBOSYLANTHRANILATE ISOMERASE 2); phosphoribosylanthranilate isomerase | 42573275 | N-(5'-phosphoribosyl)anthranilate isomerase | 15835220 | 75 | G | chlo: 13.0 | chlo: 0.83 | none: 0.85 | chlo: 0.56 | chlo: 0.72 | Chloroplast | N |
| Plantae-Arabidopsis_thaliana_42573371 | GenBank | 42573371 | CA2 (BETA CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | CA2 (BETA CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | 42573371 | putative carbonate dehydratase, cynT | 46446692 | 75 | X | cyto: 6.0 | none: 0.67 | chlo: 0.52 | chlo: 0.54 | chlo: 0.97 | Chloroplast | Y |
| Plantae-Chlamydomonas_reinhardtii_139405 | JGI | 139405 | Aminoacyl-tRNA synthetase, class Ib | tRNA synthetase class I (W and Y) family protein | 15232946 | probable tyrosine-tRNA ligase | 46446803 | 75 | GR | chlo: 13.0 | chlo: 0.86 | chlo: 0.84 | chlo: 0.58 | chlo: 0.62 | Chloroplast | Y |
| Plantae-Chlamydomonas_reinhardtii_155606 | JGI | 155606 | Conserved hypothetical protein | YebC-related | 18400953 | hypothetical protein CPn0573 | 15618484 | 75 | GRC | chlo: 8.0 | chlo: 0.58 | chlo: 0.45 | chlo: 0.57 | chlo: 0.16 | Chloroplast | N |
| Plantae-Chlamydomonas_reinhardtii_503 | JGI | 503 | Granule-bound starch synthase I (Glycosyl transferase) | Starch synthase | 15223331 | glycogen synthase | 46447230 | 75 | G | chlo: 13.0 | chlo: 0.91 | chlo: 0.92 | chlo: 0.56 | cyto: 0.10 | Chloroplast | Y |
| Plantae-Cyanidioschyzon_merolae_CMO211C | *C. merolae* | CMO211C | Conserved hypothetical protein | Unknown protein | 15238214 | hypothetical protein pc1708 | 46447342 | 75 | RC | chlo: 11.0 | mito: 0.60 | ER: 0.48 |  | chlo: 0.74 | Chloroplast | Y |
| Plantae-Cyanidioschyzon_merolae_CMR313C | *C. merolae* | CMR313C | Oligoendopeptidase F |  |  | putative oligoendopeptidase F | 46446812 | 50 | R | chlo: 12.0 | chlo: 0.77 | mito: 0.62 | chlo: 0.58 | cyto: 0.17 | Chloroplast | N |
| Plantae-Oryza_sativa_115438861 | GenBank | 115438861 | Plastidic ATP/ADP transporter | ADP/ATP translocase | 15218214 | ADP/ATP Translocase | 15604784 | 75 | G | plas: 10.0 | mito: 0.45 | none: 0.78 | chlo: 0.50 | chlo: 0.76 | Chloroplast | N |
| Plantae-Oryza_sativa_115460026 | GenBank | 115460026 | Copper/Zinc superoxide dismutase family protein | CCS1 (copper chaperone for superoxide dismutase 1); superoxide dismutase copper chaperone | 145335439 | putative Superoxide dismutase (Cu-Zn) | 46447393 | 75 | GCX | chlo: 6.0 | none: 0.87 | none: 0.98 |  | cyto: 0.66 | Chloroplast | Y |
| Plantae-Oryza_sativa_115463187 | GenBank | 115463187 | Rhodanese-like domain containing protein | Rhodanese-like domain-containing protein | 18405495 | hypothetical protein CCA00010 | 29839779 | 75 | GC | chlo: 9.5 | mito: 0.58 | mito: 0.47 | chlo: 0.56 | chlo: 0.40 | Chloroplast | N |
| Plantae-Oryza_sativa_115470767 | GenBank | 115470767 | Polyribonucleotide phophorylase | RIF10 (RESISTANT TO INHIBITION WITH FSM 10); 3'-5'-exoribonuclease/ RNA binding / nucleic acid binding | 30678905 | polynucleotide phosphorylase/polyadenylase | 46446277 | 75 | GRC | chlo: 14.0 | chlo: 0.97 | none: 0.86 | chlo: 0.57 | chlo: 0.60 | Chloroplast | N |
| Plantae-Oryza_sativa_115474235 | GenBank | 115474235 | D-alanine-D-alanine ligase B | D-alanine--D-alanine ligase family | 42572325 | putative D-alanine--D-alanine ligase | 46446032 | 75 | G | chlo: 4.0 | none: 0.65 | chlo: 0.63 | chlo: 0.50 | chlo: 0.35 | Chloroplast | Y |
| Plantae-Oryza_sativa_115483650 | GenBank | 115483650 | Glycerol-3-phosphate acyltransferase | ATS1 (ACYLTRANSFERASE 1) | 15222600 | glycerol-3-phosphate acyltransferase | 76789550 | 75 | GRC | chlo: 14.0 | chlo: 0.68 | chlo: 0.94 | chlo: 0.59 | chlo: 0.92 | Chloroplast | Y |
| Plantae-Ostreococcus_tauri_21840 | JGI | 21840 | 4-diphosphocytidyl-2C-methyl-D-erythritol kinase | ATCDPMEK (PIGMENT DEFECTIVE 277); 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase | 15225820 | probable isopentenyl monophosphate kinase (IPK) | 46447223 | 75 | GRC | chlo: 13.0 | chlo: 0.79 | chlo: 0.95 | chlo: 0.58 | chlo: 0.90 | Chloroplast | Y |
| Plantae-Ostreococcus_tauri_37113 | JGI | 37113 | Cytidylyltransferase family | cytidylyltransferase family | 30695393 | 3-deoxy-manno-octulosonate cytidylyltransferase | 89898215 | 75 | G | chlo: 11.0 | chlo: 0.61 | none: 0.77 | chlo: 0.50 | chlo: 0.35 | Chloroplast | N |
| Plantae-Ostreococcus_tauri_8662 | JGI | 8662 | Putative SAM dependent methyltransferases | mraW methylase family protein | 15238896 | probable S-adenosyl-methyltransferase | 46445945 | 75 | G | chlo: 11.0 | chlo: 0.67 | mito: 0.63 | chlo: 0.53 | chlo: 0.40 | Chloroplast | Y |
| Plantae-Physcomitrella_patens_218794 | JGI | 218794 | Pyrophosphate-dependent phosphofructokinase PfpB | pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | 15221156 | diphosphate--fructose-6-phosphate 1-phosphotransferase | 46446514 | 75 | GC | chlo: 8.0 | chlo: 0.59 | chlo: 0.63 |  | cyto: 0.31 | Chloroplast | N |
| Plantae-Physcomitrella_patens_219372 | JGI | 219372 | Anthranilate phosphoribosyl transferase | TRP1 (TRYPTOPHAN BIOSYNTHESIS 1); anthranilate phosphoribosyltransferase | 15238711 | anthranilate phosphoribosyltransferase | 89898246 | 75 | GRC | chlo: 11.0 | chlo: 0.81 | chlo: 0.9 | chlo: 0.56 | chlo: 0.64 | Chloroplast | N |
| Plantae-Physcomitrella_patens_55802 | JGI | 55802 | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase | GcpE (CHLOROPLAST BIOGENESIS 4); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase | 30697395 | probable gcpE protein | 46446374 | 75 | GC | chlo: 9.0 | chlo: 0.81 | chlo: 0.79 | chlo: 0.53 | cyto: 0.42 | Chloroplast | Y |
| Plantae-Physcomitrella_patens_60901 | JGI | 60901 | Sodium sulfate symporter and related arsenite permeases | ATNHD1 (Arabidopsis thaliana Na/H antiporter 1); sodium:hydrogen antiporter | 18402254 | Na+/H+ antiporter, putative | 16752011 | 75 | GRC | chlo: 11.5 | chlo: 0.95 | chlo: 0.83 | chlo: 0.58 | mito: 0.06 | Chloroplast | N |
| Plantae-Arabidopsis_thaliana_15235511 | GenBank | 15235511 | HMA1 (Heavy metal ATPase 1); copper-exporting ATPase | HMA1 (Heavy metal ATPase 1); copper-exporting ATPase | 15235511 | putative cation transport related membrane protein | 62185469 | 75 | GRX | plas: 7.0 | mito: 0.84 | none: 0.68 | chlo: 0.54 | chlo: 0.77 | Chloroplast envelope | N |
| Plantae-Arabidopsis_thaliana_15236554 | GenBank | 15236554 | 50S ribosomal protein-related | 50S ribosomal protein-related | 15236554 | 50S ribosomal protein L25/general stress protein Ctc | 76789542 | 50 | G | mito: 10.0 | mito: 0.74 | mito: 0.84 |  | cyto: 0.08 | Mitochondrion | N |
| Plantae-Chlamydomonas_reinhardtii_196649 | JGI | 196649 | Manganese and iron superoxide dismutase | MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); manganese superoxide dismutase | 15228407 | superoxide dismutase | 166154505 | 75 | RC | nucl: 7.0 | none: 0.51 | ER: 0.77 |  | chlo: 0.57 | Mitochondrion | N |
| Plantae-Ostreococcus_tauri_18978 | JGI | 18978 | Queuine tRNA-ribosyltransferase |  |  | queuine tRNA-ribosyltransferase | 46446428 | 75 | GRC | mito: 12.5 | mito: 0.64 | mito: 0.67 |  | chlo: 0.85 | Mitochondrion | N |
| Plantae-Arabidopsis_thaliana_18408421 | GenBank | 18408421 | glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative | glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative | 18408421 | probable regulatory protein uhpC | 46446021 | 75 | G | plas: 9.0 | none: 0.92 | none: 0.97 |  | chlo: 0.03 | Membrane | N |
| Plantae-Arabidopsis_thaliana_15223438 | GenBank | 15223438 | PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;3); water channel | PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;3); water channel | 15223438 | putative tonoplast intrinsic protein (Aquaporin) | 46446430 | 75 | G | plas: 12.0 | none: 0.94 | none: 0.99 |  | plas: 0.93 | Membrane | Y |
| Chromalveolata-Aureococcus_anophagefferens_65597 | JGI | 65597 | Prolyl 4-hydroxylase, alpha subunit |  |  | hypothetical protein pc1581 | 46447215 | 75 | GC | nucl: 8.0 | none: 0.81 | none: 0.99 |  | nucl: 0.95 | N-terminal extension | Y |
| Plantae-Arabidopsis_thaliana_15219361 | GenBank | 15219361 | Unknown protein | Unknown protein | 15219361 | hypothetical protein pc0850 | 46446484 | 75 | G | nucl: 10.0 | none: 0.86 | none: 0.99 |  | nucl: 0.63 |  | Y |
| Plantae-Arabidopsis_thaliana_15232565 | GenBank | 15232565 | Sugar isomerase (SIS) domain-containing protein | Sugar isomerase (SIS) domain-containing protein | 15232565 | putative Gut Q protein | 46447416 | 75 | G | nucl: 7.5 | none: 0.83 | none: 0.96 |  | chlo: 0.50 |  | Y |
| Plantae-Arabidopsis_thaliana_15237589 | GenBank | 15237589 | SAL2; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase | SAL2; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase | 15237589 | putative sulfur metabolism-related protein | 62185419 | 75 | GRC | ER: 5.0 | none: 0.26 | none: 0.99 |  | chlo: 0.17 |  | N |
| Plantae-Arabidopsis_thaliana_18396238 | GenBank | 18396238 | Unknown protein (similar to zinc finger family protein) | Unknown protein (similar to zinc finger family protein) | 18396238 | hypothetical protein pc1119 | 46446753 | 75 | G | nucl: 10.0 | none: 0.52 | none: 0.89 | chlo: 0.50 | golgi: 0.10 |  | Y |
| Plantae-Arabidopsis_thaliana_30687613 | GenBank | 30687613 | ATIPT9 (Arabidopsis thaliana isopentenyltransferase 9); ATP binding / tRNA isopentenyltransferase | ATIPT9 (Arabidopsis thaliana isopentenyltransferase 9); ATP binding / tRNA isopentenyltransferase | 30687613 | tRNA delta(2)-isopentenylpyrophosphate transferase | 46446877 | 75 | GRC | chlo: 7.5 | mito: 0.75 | mito: 0.48 | chlo: 0.51 | nucl: 0.80 |  | N |
| Plantae-Chlamydomonas_reinhardtii_104193 | JGI | 104193 | Dihydrouridine synthase, DuS | Dihydrouridine synthase family protein | 15234862 | putative protein involved in tRNA-dihydrouridine synthesis | 46447213 | 75 | G | nucl: 13.0 | none: 0.94 | none: 0.98 |  | nucl: 0.84 |  | Y |
| Plantae-Oryza_sativa_115452347 | GenBank | 115452347 | RNA-binding region containing protein | RNA recognition motif (RRM)-containing protein | 15232579 | probable nucleic acid-binding protein | 46446527 | 75 | G | nucl: 12.0 | none: 0.97 | none: 0.97 |  | mito: 0.03 |  | Y |
| Plantae-Oryza_sativa_115476574 | GenBank | 115476574 | Lipoate protein ligase-like protein | Unknown protein | 15228560 | putative lipoate-protein ligase | 46447472 | 75 | GC | cyto: 9.0 | none: 0.87 | none: 0.98 |  | chlo: 0.18 |  | Y |
| Plantae-Ostreococcus_lucimarinus_31465 | JGI | 31465 | FOG: PPR repeat | Pentatricopeptide (PPR) repeat-containing protein | 15222150 | tRNA (guanine-N(7))-methyltransferase | 62185355 | 75 | GRC | cyto: 9.0 | none: 0.73 | none: 0.99 |  | chlo: 0.02 |  | N |
| Plantae-Ostreococcus_tauri_31283 | JGI | 31283 | Predicted nucleic acid-binding protein ASMTL | Maf family protein | 22328154 | hypothetical protein CTL0603 | 166154561 | 75 | GRCX | cyto: 8.0 | mito: 0.59 | mito: 0.76 |  | cyto: 0.30 |  | N |
| Plantae-Physcomitrella_patens_70762 | JGI | 70762 | Cytidine/deoxycytidylate deaminase | Cytidine/deoxycytidylate deaminase family protein | 15221490 | cytosine/adenosine deaminases | 89898061 | 75 | GRC | nucl: 11.0 | mito: 0.68 | chlo: 0.66 |  | nucl: 0.40 |  | N |
| Plantae-Volvox_carteri_99233_jgi | JGI | 99233 | Leucine rich repeat proteins | Leucine-rich repeat family protein | 30684506 | hypothetical protein pc1032 | 46446666 | 75 | GC | nucl: 8.0 | none: 0.76 | none: 0.86 |  | chlo: 0.08 |  | Y |

**Table S1.** The list of 55 genes of Chlamydiae-like origin that were found in the 17 Plantae genomes analyzed in this study using phylogenomic methods. Shown are the tree IDs, the source of the sequences, the GI/accession numbers in the source database, the gene annotations in that database, the *Arabidopsis* homolog GI numbers and putative functions, the Chlamydiae homolog GI numbers and putative functions, the minimum bootstrap value that unites Chlamydiae and Plantae in each protein tree, the distribution of the genes in Plantae (G, R, C, and X indicate presence in green algae/plants, red algae, chromalveolates, and glaucophytes, respectively), the results of