***Supporting Information***

**Proteomic analysis for phenanthrene-elicited wheat chloroplast deformation**

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**Table S1 Proteins, genes and primers, and characteristics**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Protein name** | **Accession** | **Primer sequences**  **(forward/reverse)** | **Length (bp)** | **Chloroplast**  **component** |
| W5ALR1 | UPI0003D4A47A | CCAAGAGAACCCAGACGGAC  TGCACGATGCCACAGTACAT | 20 | thylakoid membrane |
| W5HA90 | UPI0003D42B15 | TCGGCCACTCTCAACAGAAC  GCGGTTGCCAATATAGCTGC | 20 | envelope |
| W5FHC5 | UPI0003D4AFC7 | CGGGATGCAGACGAGGTATC  TGCGTCCAGAACGATGAACA | 20 | envelope  and stroma |
| W5HNV3 | UPI0003D55414 | TGCGAGCTAATCAAGGCCAA  TCCTGAGCATCTGGTTGCAG | 20 | stroma |
| W5EKY8 | UPI0003D58A81 | GTGCTGGGGCATTATCCACT  ACGGTCCTTGAACGCTGAAT | 20 | thylakoid membrane |
| W5FZJ6 | UPI0003D531CF | AGCATGGAGGCAATCCACTC  ACAGCAGCGTCAACAAGGTA | 20 | stroma |
| W5GWH6 | UPI0003D51983 | AAGCTCTGCGACATGGACTT  GAACCTCGCCGTGTAGTGTA | 20 | thylakoid lumen |
| W5HI59 | UPI0003D43D38 | TTGAGGACAAGCCGACCTTC  ATGTCGGTGGCCAACTCTTT | 20 | thylakoid |
| W5D4R0 | UPI00016F0C0B | GAGGACGGTATCTTCGGCAC  GATGGCCTCTCCCAAGATCG | 20 | integral component of thylakoid membrane |
| W5EZT3 | UPI0003D544F7 | AGTCAATCAGAATGGCCGCA  GTAACCTGCTTGGCCTTTGC | 20 | thylakoid membrane |
| W5A296 | UPI0003D4985E | CTATGGGTGGGACACTGCTG  GCTGGGGTTGCCAAGATAGT | 20 | integral component of thylakoid membrane |
| W5C1B8 | UPI0003D52D6F | CTTCTTCAACCCGGACTCCC  TTGATCTCGGCCACCTTGAG | 20 | thylakoid membrane and envelope |

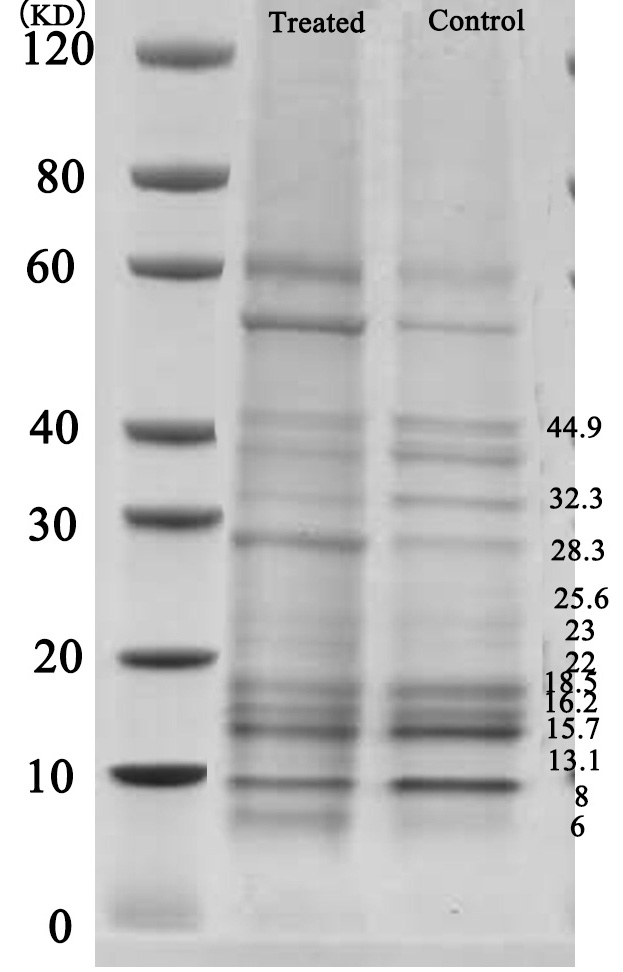
**Table S2 Protein information through iTRAQ**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| No. | Protein Accession | Description | MW (kDa) | pI | Coverage (%) | Control/Treated |
| 1 | Q03387 | Translation initiation factor | 86.2 | 8.02 | 2.54 | - |
| 2 | W5AJT0 | Translation | 5.5 | 9.83 | 19.61 | - |
| 3 | W5FWD3 | Complete proteome, Reference proteome | 22.5 | 5.43 | 7.84 | - |
| 4 | W5BTZ9 | Cellular component, membrane | 21.0 | 6.06 | 8.76 | - |
| 5 | W5GL40 | Coproporphyrinogen oxidase | 10.0 | 6.54 | 15.66 | - |
| 6 | W4ZLQ2 | Hydrolase | 25.4 | 5.45 | 7.50 | - |
| 7 | W5DNS9 | Complete proteome, Reference proteome | 15.1 | 5.80 | 9.93 | - |
| 8 | J3NFZ0 | Oxidoreductase | 67.9 | 8.90 | 1.92 | 0.119476 |
| 9 | W4ZWJ2 | 6-phosphofructo-2-kinase | 47.7 | 5.74 | 3.13 | 0.182567 |
| 10 | W5BHE1 | Complete proteome, Reference proteome | 177.9 | 4.67 | 0.63 | 0.202301 |
| 11 | W5AQ91 | Hydrogen peroxide catabolic process, response to oxidative stress | 31.7 | 8.79 | 4.78 | 0.27519 |
| 12 | W5E6P3 | Signal protein | 17.9 | 7.53 | 14.20 | 0.330014 |
| 13 | W5B1X6 | Calcium ion binding | 22.9 | 9.77 | 24.88 | 0.396033 |
| 14 | W5F0N8 | Nucleic acid binding, nucleotide binding | 5.8 | 8.73 | 43.40 | 0.40454 |
| 15 | W5G8S4 | Structural constituent of ribosome | 22.3 | 7.75 | 4.88 | 0.413771 |
| 16 | W5AX02 | Structural constituent of ribosome | 15.7 | 10.27 | 6.21 | 0.422891 |
| 17 | W5H575 | Structural constituent of ribosome | 16.4 | 10.77 | 5.63 | 0.432186 |
| 18 | W5GRU1 | DNA binding | 5.2 | 9.99 | 17.78 | 0.44111 |
| 19 | W5HAX6 | Response to cytokinin | 15.2 | 5.03 | 15.38 | 0.451884 |
| 20 | W5HQS2 | Structural constituent of ribosome | 16.9 | 9.67 | 16.11 | 0.461038 |
| 21 | W5CKC4 | Nucleic acid binding, nucleotide binding, zinc ion binding | 21.9 | 10.02 | 4.21 | 0.461309 |
| 22 | W5FEC0 | Nucleic acid binding, nucleotide binding | 22.8 | 4.61 | 26.11 | 0.476179 |
| 23 | W5HPP3 | Transferase , transferring acyl groups | 24.6 | 7.97 | 4.89 | 0.479091 |
| 24 | W5H8Z3 | 2S-2Fe(Iron, Iron-sulfur, Metal-binding) cluster binding, electron carrier | 6.6 | 4.35 | 16.13 | 0.491994 |
| 25 | W5C4T7 | Nucleic acid binding, nucleotide binding, zinc ion binding | 31.9 | 9.04 | 7.17 | 0.492123 |
| 26 | W5GYE4 | Proton-transporting ATP synthase , rotational mechanism | 17.7 | 4.54 | 52.83 | 0.493182 |
| 27 | W5GBM7 | DNA-templated transcription, termination | 42.1 | 5.50 | 2.84 | 0.497164 |
| 28 | W5BTL4 | Structural constituent of ribosome | 13.6 | 11.08 | 7.32 | 0.506052 |
| 29 | W5AWB7 | Hydrogen ion transmembrane transporter | 19.5 | 6.14 | 12.57 | 0.516889 |
| 30 | W5AH72 | Structural constituent of ribosome | 13.7 | 9.52 | 6.67 | 0.519526 |
| 31 | W5FY59 | Sulfate adenylyltransferase (ATP) | 35.8 | 6.93 | 2.80 | 0.522117 |
| 32 | W4ZPA7 | Uncharacteristic | 11.0 | 4.75 | 62.38 | 0.529132 |
| 33 | P60577 | rRNA binding | 10.7 | 10.29 | 21.51 | 0.53592 |
| 34 | W5AQ04 | Structural constituent of ribosome | 25.0 | 10.45 | 19.37 | 0.541854 |
| 35 | Q75QN9 | DNA binding | 19.2 | 5.91 | 12.20 | 0.542879 |
| 36 | W5GRX7 | Pollen development | 26.2 | 5.71 | 4.37 | 0.554468 |
| 37 | W5DYL6 | Uncharacteristic | 21.1 | 5.52 | 4.10 | 0.555658 |
| 38 | W5I159 | Protein folding | 7.4 | 4.94 | 20.27 | 0.565166 |
| 39 | W5E889 | RNA binding ribosome | 34.5 | 7.23 | 3.97 | 0.573101 |
| 40 | A0A0M5J8Z4 | Photosynthesis | 8.1 | 8.47 | 50.70 | 0.573192 |
| 41 | W5F6H4 | Oxidoreductase (dehydrogenases/reductases) | 23.1 | 6.39 | 7.41 | 0.574681 |
| 42 | W5DJH7 | Small heat shock protein (HSP20) family | 14.4 | 5.68 | 22.05 | 0.576453 |
| 43 | W5HR23 | Photosynthesis (photosystem II oxygen evolving complex | 23.4 | 8.66 | 9.18 | 0.5771 |
| 44 | Q5S1S6 | Peroxiredoxin Q, peroxidase , peroxiredoxin | 23.3 | 9.67 | 22.12 | 0.580064 |
| 45 | W5F0U1 | Metal ion binding | 30.7 | 6.55 | 4.10 | 0.58701 |
| 46 | W5FH17 | Nucleus, nucleosome, DNA binding | 6.8 | 11.47 | 14.29 | 0.596905 |
| 47 | W5E0V4 | Structural constituent of ribosome, ribosome | 28.0 | 5.21 | 16.86 | 0.597182 |
| 48 | A0A077S298 | Structural constituent of ribosome | 18.1 | 5.68 | 39.20 | 0.598034 |
| 49 | W5B9L0 | Ca ion binding | 34.4 | 5.90 | 53.35 | 0.599516 |
| 50 | Q7X9A6 | Photosynthesis, electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II | 23.7 | 8.18 | 37.84 | 0.602179 |
| 51 | W5EBH1 | Uncharacteristic | 14.4 | 5.60 | 22.39 | 0.603468 |
| 52 | W5G637 | Protein disulfide oxidoreductase | 32.4 | 7.18 | 11.07 | 0.605631 |
| 53 | W5FHZ8 | Isochorismate synthase | 87.1 | 6.28 | 7.22 | 0.612015 |
| 54 | Q5XUU9 | Structural constituent of ribosome | 17.1 | 10.54 | 13.91 | 0.613219 |
| 55 | A0A077RYA3 | 4S-4Fe(Iron, Iron-sulfur, Metal-binding) cluster binding | 8.9 | 7.50 | 64.20 | 0.617241 |
| 56 | W5DPW0 | Photosystem II oxygen evolving complex | 25.7 | 9.36 | 31.09 | 0.627383 |
| 57 | W5G8V1 | Mitochondrial matrix | 24.0 | 4.48 | 6.57 | 0.628119 |
| 58 | W5FFQ1 | HSP20 | 32.7 | 9.61 | 16.33 | 0.629157 |
| 59 | W5EED6 | Calcium ion binding | 25.4 | 9.47 | 31.36 | 0.633507 |
| 60 | W5C5N9 | Structural constituent of ribosome | 14.3 | 9.55 | 6.98 | 0.636943 |
| 61 | W5A7A6 | Uncharacteristic | 8.7 | 4.77 | 63.29 | 0.641557 |
| 62 | W5A3C5 | Structural constituent of ribosome | 23.1 | 10.21 | 6.80 | 0.642468 |
| 63 | A0A096UKU5 | Structural constituent of ribosome | 11.4 | 4.34 | 10.71 | 0.645325 |
| 64 | W4ZVZ5 | NAD(P)- binding | 9.0 | 5.01 | 14.46 | 0.6471 |
| 65 | W5G616 | Integral component of membrane | 50.6 | 8.72 | 3.33 | 0.648857 |
| 66 | W5A3U7 | RNA binding | 20.7 | 8.51 | 36.65 | 0.650657 |
| 67 | W5DZQ3 | Nucleic acid binding | 43.1 | 4.75 | 11.31 | 0.651022 |
| 68 | W5B543 | Regulation of reactive oxygen species metabolic process | 28.4 | 6.86 | 12.69 | 0.654743 |
| 69 | Q0IJ88 | Response to biotic stimulus, defense response | 17.1 | 4.82 | 18.30 | 0.658006 |
| 70 | Q00434 | Calcium ion binding | 27.3 | 8.70 | 43.41 | 0.660521 |
| 71 | W5DDK2 | Structural constituent of ribosome | 6.8 | 9.03 | 18.64 | 0.661965 |
| 72 | W5F4R0 | 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase | 75.7 | 6.07 | 1.46 | 0.662747 |
| 73 | W5EHT8 | Photosystem II assembly | 18.5 | 10.17 | 11.11 | 0.66481 |
| 74 | W5BDE7 | Intracellular sterol transport | 16.4 | 5.03 | 8.55 | 0.665742 |
| 75 | W5B0W3 | Ribonucleoprotein, Ribosomal protein | 32.9 | 4.96 | 5.92 | 0.668699 |
| 76 | W5HR45 | NAD(P)-binding | 22.2 | 6.79 | 24.27 | 0.679642 |
| 77 | A0A0C4BK40 | Glycine decarboxylation via glycine cleavage system, glycine cleavage complex | 17.3 | 5.15 | 10.37 | 0.680391 |
| 78 | B2B9U2 | Hydrolase , acting on acid anhydrides, catalyzing transmembrane movement of substances | 12.4 | 8.50 | 35.45 | 0.685215 |
| 79 | W5B5M5 | Dihydrolipoyllysine-residue succinyltransferase | 48.7 | 8.94 | 4.49 | 0.68934 |
| 80 | W5EGE3 | NADH dehydrogenase (ubiquinone) | 12.2 | 8.47 | 10.81 | 0.69108 |
| 81 | W5BAB9 | NAD(P)-binding | 43.4 | 7.68 | 21.81 | 0.69145 |
| 82 | A6XMY5 | L-serine metabolic process and glycine metabolic process | 56.1 | 8.21 | 16.47 | 0.692019 |
| 83 | W5BYZ6 | Lipocln\_cytosolic\_FA-bd\_dom | 24.1 | 5.10 | 7.37 | 0.697808 |
| 84 | Q9ZSR6 | HSP26.6, stress response | 26.5 | 9.33 | 9.66 | 0.700757 |
| 85 | W5I1S8 | Uncharacteristic | 4.3 | 5.11 | 80.00 | 0.704572 |
| 86 | W5HWS4 | Protein folding | 15.5 | 8.29 | 6.99 | 0.706249 |
| 87 | W5BY17 | Adenyl-nucleotide exchange factor | 23.6 | 5.05 | 18.87 | 0.706575 |
| 88 | W5IB66 | Photosynthesis, photosystem II oxygen evolving complex | 17.2 | 5.94 | 32.47 | 0.706925 |
| 89 | Q8L806 | Ribosome, structural constituent of ribosome | 17.7 | 10.74 | 11.18 | 0.712275 |
| 90 | W5G9Q5 | Structural constituent of ribosome | 16.5 | 6.54 | 6.16 | 0.712396 |
| 91 | W5HWV0 | Electron carrier , photosynthetic electron transport in photosystem I | 8.8 | 6.92 | 62.50 | 0.717818 |
| 92 | U5HTF2 | Translation initiation factor for protein biosynthesis | 31.5 | 7.03 | 11.42 | 0.718014 |
| 93 | W5GWJ4 | Fe-S rdtase | 56.2 | 6.20 | 2.96 | 0.720367 |
| 94 | A7XDG5 | PPIases accelerate the folding of proteins. | 25.9 | 9.33 | 18.37 | 0.721027 |
| 95 | W5FCR1 | Uncharacteristic | 31.3 | 8.76 | 12.76 | 0.722017 |
| 96 | W5BKV5 | PPIase for protein folding | 18.2 | 8.03 | 17.68 | 0.723257 |
| 97 | W5AP83 | ATP synthesis coupled proton transport | 26.0 | 8.65 | 4.05 | 0.723282 |
| 98 | W5EUA2 | Integral component of membrane | 19.0 | 9.70 | 22.95 | 0.723656 |
| 99 | W5AQ58 | Uncharacteristic | 16.9 | 6.77 | 6.21 | 0.7247 |
| 100 | W5HC08 | Uncharacteristic | 9.4 | 10.08 | 16.47 | 0.725358 |
| 101 | W5H9W9 | Structural constituent of ribosome for translational elongation | 9.2 | 4.68 | 12.22 | 0.726207 |
| 102 | A0A077RQG8 | Small heat shock protein (HSP20) family | 17.7 | 6.24 | 11.11 | 0.726462 |
| 103 | W5G736 | Mg-binding | 31.8 | 5.64 | 28.92 | 0.732447 |
| 104 | W5HDP4 | ATP binding | 63.9 | 5.66 | 25.08 | 0.73629 |
| 105 | Q8LRU5 | HMG-I/Y protein HMGa and DNA-binding | 19.3 | 10.43 | 5.29 | 0.737952 |
| 106 | W5B1K1 | Glutamate synthase | 164.7 | 6.13 | 1.06 | 0.742217 |
| 107 | W5C4J9 | Uncharacteristic | 8.7 | 4.97 | 12.35 | 0.749225 |
| 108 | Q2L9B8 | Proton-transporting ATPase | 26.1 | 6.87 | 11.89 | 0.75252 |
| 109 | A0A075VWW4 | Produces ATP from ADP in the presence of a proton gradient across the membrane | 53.9 | 5.16 | 58.43 | 0.761021 |
| 110 | W5BH99 | Adenyl-nucleotide exchange factor | 31.3 | 6.01 | 20.56 | 0.762875 |
| 111 | W5H3F9 | Oxidoreductase | 18.1 | 4.88 | 48.85 | 0.76341 |
| 112 | W5H4D7 | Structural constituent of ribosome | 23.2 | 10.24 | 24.19 | 0.764464 |
| 113 | W5AU48 | Response to oxidative stress peroxidase | 41.2 | 8.29 | 23.70 | 0.765654 |
| 114 | A0A077RVF8 | Uncharacteristic | 21.1 | 7.77 | 4.23 | 0.766447 |
| 115 | A0A096URE2 | Uncharacteristic | 38.2 | 6.11 | 3.65 | 0.767162 |
| 116 | C3V134 | Nucleic acid binding | 19.0 | 4.94 | 43.53 | 0.76793 |
| 117 | W5DXN4 | Voltage-gated anion channel | 29.4 | 9.25 | 14.44 | 0.768305 |
| 118 | W5ATV6 | Oxidoreductase , acting on the aldehyde or oxo group of donors for NAD or NADP | 43.3 | 7.37 | 21.81 | 0.77282 |
| 119 | W5CHL5 | Uncharacteristic | 22.5 | 7.06 | 5.85 | 0.773658 |
| 120 | W5GSK4 | Nucleic acid binding | 22.1 | 7.08 | 13.00 | 0.774195 |
| 121 | M9T150 | Pyridoxal phosphate | 34.1 | 5.57 | 9.23 | 0.774565 |
| 122 | W5DL12 | Structural constituent of ribosome | 6.2 | 4.72 | 21.43 | 0.775103 |
| 123 | W5FJ26 | Regulation of proton transport | 69.9 | 9.01 | 4.52 | 0.775624 |
| 124 | Q2TN84 | Response to stress | 17.9 | 6.19 | 7.23 | 0.777745 |
| 125 | W5FSA9 | Small heat shock protein (HSP20) family. | 27.5 | 6.35 | 28.74 | 0.778465 |
| 126 | W5CMF5 | Uncharacteristic | 83.3 | 5.17 | 12.92 | 0.779611 |
| 127 | W5BDH1 | Hydrolase , hydrolyzing O-glycosyl compounds | 47.3 | 7.53 | 3.44 | 0.781792 |
| 128 | W5AEG9 | Serine-type endopeptidase | 27.5 | 5.21 | 4.15 | 0.783396 |
| 129 | A0A096URP4 | RNA binding | 55.4 | 4.92 | 1.95 | 0.783649 |
| 130 | W5F164 | Oxidoreductase , acting on the aldehyde or oxo group of donors for NAD or NADP | 4.3 | 5.87 | 22.50 | 0.787238 |
| 131 | P12782 | Reductive pentose-phosphate cycle, phosphoglycerate kinase | 49.8 | 7.03 | 26.88 | 0.79177 |
| 132 | W5IB10 | Pyruvate dehydrogenase (acetyl-transferring) | 35.3 | 5.08 | 12.50 | 0.793231 |
| 133 | P46274 | Voltage-gated anion channel | 28.9 | 8.44 | 19.64 | 0.793913 |
| 134 | W5CBD9 | Cytochrome-c oxidase | 11.9 | 4.68 | 12.38 | 0.79443 |
| 135 | Q9SAU8 | ATP binding | 71.0 | 5.25 | 5.86 | 0.795562 |
| 136 | W5E8I4 | Metal ion binding | 53.6 | 5.66 | 7.08 | 0.795603 |
| 137 | W5EN32 | Oxidoreductase , acting on the aldehyde or oxo group of donors for NAD or NADP | 9.2 | 4.36 | 29.41 | 0.7958 |
| 138 | W5FWF5 | Structural constituent of ribosome | 17.1 | 9.89 | 28.39 | 0.795836 |
| 139 | A0A096UQ06 | Structural constituent of ribosome | 13.2 | 10.74 | 14.66 | 0.795861 |
| 140 | Q9ZP21 | cell redox homeostasis, glycerol ether metabolic process | 19.1 | 8.31 | 11.43 | 0.796044 |
| 141 | Q6EZA4 | Uncharacteristic | 7.7 | 5.38 | 55.88 | 0.796866 |
| 142 | W5FXC4 | IMP dehydrogenase | 19.7 | 9.10 | 19.68 | 0.798174 |
| 143 | W5DSD5 | Uncharacteristic | 20.4 | 9.50 | 4.40 | 0.798519 |
| 144 | A0A077RR71 | Peptidyl-prolyl cis-trans isomerase | 29.9 | 9.72 | 26.80 | 0.799458 |
| 145 | W5D898 | Mg- binding | 48.2 | 5.69 | 4.33 | 0.800912 |
| 146 | Q7XJJ1 | Oxidoreductase , acting on the aldehyde or oxo group of donors for NAD or NADP | 18.2 | 6.80 | 33.33 | 0.804719 |
| 147 | W5G105 | Structural constituent of ribosome (5S rRNA binding) | 34.5 | 9.35 | 6.95 | 0.807241 |
| 148 | W5GVP7 | Structural constituent of ribosome | 17.6 | 8.91 | 18.18 | 0.808968 |
| 149 | W5DT48 | RNA binding | 34.6 | 5.36 | 10.28 | 0.811751 |
| 150 | W5ALR1 | Chloroplast thylakoid membrane | 25.6 | 5.34 | 13.22 | 0.812315 |
| 151 | W5I9F9 | Uncharacteristic | 21.4 | 9.52 | 4.57 | 0.813094 |
| 152 | W5HA90 | Chloroplast envelope | 32.3 | 7.40 | 11.22 | 0.816049 |
| 153 | W5B3S3 | Uncharacteristic | 12.4 | 5.67 | 10.43 | 0.817707 |
| 154 | W5D7Q4 | Oxidoreductase | 14.7 | 7.43 | 15.79 | 0.818672 |
| 155 | W5CQE4 | Signal | 23.8 | 5.24 | 3.62 | 0.819489 |
| 156 | W5E8I6 | Uncharacteristic | 33.1 | 8.65 | 3.05 | 0.821495 |
| 157 | W5G2H9 | Nucleic acid binding | 7.1 | 4.78 | 22.22 | 0.822468 |
| 158 | W5F9P6 | Glycerol ether metabolic process | 29.1 | 5.96 | 7.87 | 0.823033 |
| 159 | W5FX49 | ADP binding | 132.6 | 6.55 | 2.13 | 0.823717 |
| 160 | W5FHC5 | Chloroplast stroma | 44.9 | 8.44 | 4.53 | 0.823721 |
| 161 | W5CAD8 | Glycine dehydrogenase (decarboxylating) | 42.5 | 6.73 | 2.78 | 0.827462 |
| 162 | W5GIK1 | Cobalamin (vitamin B12) biosynthesis | 34.8 | 5.99 | 5.26 | 0.828479 |
| 163 | W5C547 | Peptidyl-prolyl cis-trans isomerase ; | 16.7 | 4.74 | 29.68 | 0.829539 |
| 164 | W5ABP1 | Structural constituent of ribosome | 27.9 | 9.96 | 7.69 | 0.833461 |
| 165 | W5C302 | Peptidyl-prolyl cis-trans isomerase | 21.0 | 9.95 | 20.83 | 0.836923 |
| 166 | W5HNV3 | Adenylate kinase in chloroplast stroma; | 23.7 | 5.07 | 10.33 | 0.838295 |
| 167 | A0A077RXS4 | Hydrolase | 48.2 | 4.94 | 7.83 | 0.838515 |
| 168 | B9VGW3 | Cysteine-type endopeptidase inhibitor | 11.3 | 5.53 | 24.51 | 0.840996 |
| 169 | W5B4Z9 | Serine-type endopeptidase inhibitor | 7.5 | 5.45 | 13.43 | 0.845007 |
| 170 | W5E9B7 | Adenyl nucleotide binding ATP | 11.1 | 9.57 | 9.18 | 0.84755 |
| 171 | W4ZT48 | Uncharacteristic | 16.4 | 7.18 | 7.69 | 0.849098 |
| 172 | W5GNI5 | Uncharacteristic | 59.9 | 8.95 | 2.45 | 0.850157 |
| 173 | W4ZS00 | Structural constituent of ribosome | 13.8 | 8.43 | 39.84 | 0.851831 |
| 174 | Q6XPZ4 | Peptidyl-prolyl cis-trans isomerase | 25.9 | 9.57 | 18.37 | 0.851854 |
| 175 | A3FKE5 | Superoxide dismutase | 19.3 | 7.27 | 22.41 | 0.855199 |
| 176 | P08823 | ATP binding | 57.5 | 4.91 | 27.26 | 0.855473 |
| 177 | W5ACA2 | ATP binding | 56.2 | 5.22 | 14.02 | 0.857311 |
| 178 | W4ZRT8 | Nucleic acid binding | 57.8 | 10.14 | 5.46 | 0.857454 |
| 179 | P12112 | ATP synthase subunit alpha, chloroplastic | 55.3 | 6.48 | 36.11 | 0.858333 |
| 180 | A0A077RPB8 | Fe-S cluster assembly | 51.3 | 7.09 | 1.68 | 0.859764 |
| 181 | W5HVV0 | Uncharacteristic | 37.8 | 8.95 | 3.89 | 0.860006 |
| 182 | W5EGQ1 | Uncharacteristic | 9.5 | 10.26 | 13.64 | 0.862543 |
| 183 | B5B1F8 | L-aspartate (2-oxoglutarate aminotransferase) | 40.8 | 7.11 | 10.05 | 0.866715 |
| 184 | W5B8G5 | Translation elongation factor | 75.2 | 5.05 | 2.05 | 0.866925 |
| 185 | W5FSV2 | Uncharacteristic | 11.4 | 5.49 | 8.33 | 0.869145 |
| 186 | W5DIB3 | Cysteine-type endopeptidase inhibitor | 12.2 | 6.68 | 22.02 | 0.869706 |
| 187 | P69555 | Phosphate ion binding | 7.8 | 8.57 | 23.29 | 0.870377 |
| 188 | W5FRZ6 | ATP binding | 61.8 | 5.58 | 12.61 | 0.871758 |
| 189 | W5H7Z1 | Nucleic acid binding | 43.2 | 6.10 | 2.53 | 0.874039 |
| 190 | W5DX53 | rRNA binding in ribosome | 12.8 | 9.89 | 44.74 | 0.875206 |
| 191 | W5H8V6 | Structural constituent of ribosome | 12.1 | 4.55 | 15.00 | 0.878755 |
| 192 | D3K4D8 | Proton-transporting ATP synthase | 39.7 | 8.02 | 21.23 | 0.880665 |
| 193 | W5AIM5 | FMN binding | 11.7 | 5.45 | 10.19 | 0.881125 |
| 194 | W5I4U0 | Calcium ion binding | 16.7 | 5.16 | 10.81 | 0.881279 |
| 195 | W5HXU9 | Mg chelatase | 45.7 | 5.16 | 9.29 | 0.888328 |
| 196 | C7ENF7 | ATP binding | 73.5 | 5.15 | 17.97 | 0.892104 |
| 197 | I3NM60 | RNA binding in ribosome | 19.1 | 10.45 | 7.60 | 0.894269 |
| 198 | W5DUE4 | Dihydrolipoyllysine-residue succinyltransferase | 39.0 | 6.30 | 3.89 | 0.896869 |
| 199 | W5I9U0 | ATP binding | 21.5 | 5.49 | 38.24 | 0.897231 |
| 200 | W5GUK3 | GTPase | 41.0 | 5.01 | 27.13 | 0.899454 |
| 201 | Q94F69 | Peptidyl-prolyl cis-trans isomerase | 14.1 | 8.18 | 22.14 | 0.900595 |
| 202 | Q7XY25 | Electron carrier | 11.7 | 7.85 | 15.04 | 0.901696 |
| 203 | W5F5B3 | Isopentenyl diphosphate biosynthetic process | 105.0 | 5.12 | 8.13 | 0.901944 |
| 204 | W5DAM0 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | 23.4 | 5.22 | 12.32 | 0.903209 |
| 205 | C9EF64 | Glutathione dehydrogenase (ascorbate) | 23.3 | 6.29 | 23.11 | 0.90419 |
| 206 | W5EWM6 | Structural constituent of ribosome | 4.2 | 9.70 | 21.62 | 0.904418 |
| 207 | W5H155 | Structural constituent of ribosome | 14.8 | 9.66 | 30.77 | 0.90537 |
| 208 | W5HJL0 | Uncharacteristic | 27.4 | 5.82 | 6.12 | 0.905582 |
| 209 | W5H454 | ATP binding | 72.6 | 5.16 | 12.58 | 0.906751 |
| 210 | W5E6U7 | Ribosome biogenesis | 24.1 | 8.41 | 16.82 | 0.915764 |
| 211 | W5F3P8 | Mg- binding | 46.7 | 5.54 | 11.06 | 0.916722 |
| 212 | Q41590 | Transmembrane transport | 29.3 | 9.32 | 24.91 | 0.91747 |
| 213 | W5GM35 | Fe-S cluster binding in photosynthesis | 6.8 | 5.97 | 27.59 | 0.922803 |
| 214 | W5E5N6 | Uncharacteristic | 44.7 | 7.78 | 2.64 | 0.925543 |
| 215 | W5ETS4 | structural constituent of ribosome | 17.3 | 10.18 | 11.46 | 0.929549 |
| 216 | A0A078BTE9 | Phosphopantothenoylcysteine decarboxylase | 41.2 | 5.43 | 39.46 | 0.930433 |
| 217 | W5FBC6 | DNA binding | 4.6 | 9.99 | 21.43 | 0.930806 |
| 218 | W5H9C6 | Proton-transporting ATPase | 62.2 | 5.71 | 2.12 | 0.932373 |
| 219 | W5GCH5 | Uncharacteristic | 11.8 | 4.79 | 24.07 | 0.935332 |
| 220 | W5CP37 | Uncharacteristic | 11.6 | 9.44 | 14.85 | 0.93555 |
| 221 | P12862 | Proton-transporting ATP synthase | 55.2 | 5.90 | 13.56 | 0.93625 |
| 222 | W5B0S2 | Cofactor binding | 34.3 | 8.00 | 6.67 | 0.937823 |
| 223 | W5EG56 | Fructose 1,6-bisphosphate 1-phosphatase | 44.3 | 5.20 | 5.62 | 0.938945 |
| 224 | W5CKU6 | Catalytic ; | 54.0 | 6.55 | 5.89 | 0.93957 |
| 225 | W5FU40 | Nucleic acid binding | 26.2 | 9.19 | 25.71 | 0.94029 |
| 226 | W5BCG1 | Nucleic acid binding | 30.6 | 5.50 | 11.97 | 0.940586 |
| 227 | A0A0C4BJJ8 | Fumarate hydratase | 53.1 | 7.61 | 2.23 | 0.941583 |
| 228 | W4ZPF8 | Uncharacteristic | 26.3 | 6.40 | 15.79 | 0.942576 |
| 229 | A0A077RX13 | Uncharacteristic | 86.5 | 5.10 | 13.40 | 0.946343 |
| 230 | W5AWW1 | Serine-type endopeptidase | 33.8 | 8.12 | 3.44 | 0.946473 |
| 231 | W5FW68 | Primary metabolic process | 24.9 | 5.16 | 9.91 | 0.95348 |
| 232 | W5H883 | Nucleic acid binding | 25.6 | 4.70 | 23.50 | 0.954974 |
| 233 | P12783 | Phosphoglycerate kinase | 42.1 | 5.86 | 26.43 | 0.959787 |
| 234 | A0A096UUU5 | Oxidoreductase | 39.8 | 8.25 | 36.55 | 0.963011 |
| 235 | W5F377 | Nucleotide binding | 61.7 | 8.28 | 6.96 | 0.963229 |
| 236 | W5GPK3 | Uncharacteristic | 97.3 | 5.03 | 1.37 | 0.963274 |
| 237 | P26302 | ATP binding | 45.1 | 6.05 | 11.63 | 0.964133 |
| 238 | A0A024FR39 | Protein disulfide isomerase | 53.8 | 5.24 | 9.28 | 0.964669 |
| 239 | W5BAH6 | GTP binding and GTPase | 42.0 | 6.43 | 2.48 | 0.966003 |
| 240 | W5GZ57 | DNA translation initiation factor | 18.6 | 4.61 | 16.17 | 0.967328 |
| 241 | A0A0M4FLM5 | Aspartic-type endopeptidase | 10.2 | 4.84 | 10.53 | 0.970169 |
| 242 | W5C0J3 | Glycerol ether metabolic process | 8.2 | 6.61 | 21.92 | 0.970566 |
| 243 | A0A077RSZ8 | Integral component of membrane S | 29.5 | 5.26 | 3.09 | 0.970762 |
| 244 | Q8RVZ8 | Oxidoreductase | 40.2 | 7.31 | 40.50 | 0.975422 |
| 245 | W5BBF4 | Oxidoreductase | 101.8 | 6.35 | 1.73 | 0.975868 |
| 246 | W5HYN5 | L-malate dehydrogenase | 41.1 | 8.34 | 9.14 | 0.977321 |
| 247 | W5F2Z6 | Uncharacteristic | 12.1 | 7.18 | 10.43 | 0.977763 |
| 248 | C7AE91 | Electron carrier | 17.4 | 5.31 | 7.39 | 0.978291 |
| 249 | W5AGK9 | ATP binding | 16.7 | 6.80 | 22.52 | 0.978477 |
| 250 | A1XC19 | ATP binding | 26.2 | 8.12 | 6.28 | 0.979908 |
| 251 | W5E091 | Carbohydrate binding | 37.7 | 6.70 | 11.42 | 0.981949 |
| 252 | A0A096UUG6 | ATP Chaperone | 101.5 | 6.10 | 8.19 | 0.982676 |
| 253 | Q38JE5 | Transporter | 20.8 | 6.35 | 5.49 | 0.983875 |
| 254 | W4ZRP4 | Response to stress | 22.8 | 5.07 | 7.48 | 0.98626 |
| 255 | W5DNQ1 | Membrane composition | 18.0 | 9.41 | 11.59 | 0.987723 |
| 256 | B6UZ80 | Ferric hydroxides | 8.9 | 5.36 | 20.51 | 0.992238 |
| 257 | B2W290 | Membrane composition | 47.8 | 7.28 | 2.76 | 0.994055 |
| 258 | M4Q9V8 | Tetratricopeptide repeat | 36.1 | 7.58 | 16.26 | 0.994075 |
| 259 | W5EGD6 | B, structural constituent of ribosome | 34.0 | 7.50 | 13.74 | 0.99485 |
| 260 | W5BVX4 | Pyridoxal phosphate binding | 25.2 | 6.58 | 7.39 | 0.995602 |
| 261 | W5DSM4 | ATP binding | 50.9 | 7.30 | 41.38 | 0.999053 |
| 262 | W5I663 | Glutathione-S-Transferase | 22.6 | 5.27 | 9.31 | 1.000948 |
| 263 | W5HIH7 | Protein transport | 51.8 | 4.93 | 6.13 | 1.002283 |
| 264 | W5AWM3 | Oxidoreductase | 42.0 | 6.18 | 4.62 | 1.003667 |
| 265 | W5I767 | Uncharacteristic | 41.1 | 10.61 | 8.00 | 1.00428 |
| 266 | W5B3P3 | Oxidoreductase , acting on the aldehyde or oxo group of donors for NAD or NADP | 46.6 | 7.01 | 3.42 | 1.004361 |
| 267 | W5FAX3 | Photosynthesis | 10.9 | 9.99 | 15.46 | 1.004582 |
| 268 | W5FCR5 | Uncharacteristic | 5.7 | 7.03 | 22.92 | 1.005266 |
| 269 | W5DYM3 | Participate in protein metabolic process | 24.5 | 9.58 | 3.93 | 1.005478 |
| 270 | B2BAL3 | ATP binding | 54.0 | 5.25 | 13.73 | 1.006844 |
| 271 | W5E0M2 | Uncharacteristic | 9.4 | 5.86 | 42.70 | 1.006922 |
| 272 | W5GBY0 | Uncharacteristic | 29.8 | 9.23 | 4.98 | 1.010937 |
| 273 | W5IAC3 | Aminoacylase | 34.9 | 5.62 | 3.19 | 1.011198 |
| 274 | L7P617 | Translation initiation factor | 36.1 | 6.96 | 17.18 | 1.011748 |
| 275 | A0A096UKY2 | Uncharacteristic | 32.8 | 5.55 | 2.78 | 1.01336 |
| 276 | W5DFI7 | HSP20-like\_chaperone | 16.3 | 5.72 | 19.73 | 1.015979 |
| 277 | A7WK82 | 4-hydroxyphenylpyruvate dioxygenase | 40.5 | 6.24 | 7.09 | 1.018338 |
| 278 | W5DYW7 | Peroxidase | 27.5 | 6.24 | 10.80 | 1.01841 |
| 279 | W5HDA6 | Pentose-phosphate shunt | 45.6 | 4.72 | 13.32 | 1.018616 |
| 280 | W5HIR3 | Actin cytoskeleton organization | 10.0 | 5.38 | 24.73 | 1.019043 |
| 281 | W4ZY98 | ATP binding | 73.2 | 5.19 | 20.91 | 1.019834 |
| 282 | W5AIY0 | Uncharacteristic | 5.6 | 4.55 | 20.00 | 1.022848 |
| 283 | Q43655 | Actin filament depolymerization | 15.8 | 4.64 | 9.86 | 1.024048 |
| 284 | W5EP77 | Uncharacteristic | 17.2 | 7.21 | 12.26 | 1.029775 |
| 285 | W5F4C1 | NAD(P)-binding | 8.9 | 5.87 | 37.50 | 1.030317 |
| 286 | W5HGR2 | Ribulose-bisphosphate carboxylase | 52.4 | 6.80 | 28.90 | 1.031856 |
| 287 | W5GRE0 | pentose-phosphate shunt, non-oxidative branch | 9.2 | 5.10 | 15.29 | 1.033577 |
| 288 | W5F5Z9 | Acid-amino acid ligase | 16.6 | 6.54 | 11.89 | 1.034405 |
| 289 | A0A077RVD7 | Uncharacteristic | 15.4 | 8.73 | 12.41 | 1.036749 |
| 290 | W5EI90 | Uncharacteristic | 38.6 | 6.77 | 7.49 | 1.03748 |
| 291 | W5DNW1 | Uncharacteristic | 11.1 | 6.55 | 10.53 | 1.038204 |
| 292 | W5EPV5 | dUTP diphosphatase | 16.7 | 6.18 | 12.88 | 1.038805 |
| 293 | W5GSL5 | Participate in protein folding | 6.5 | 5.95 | 14.04 | 1.041595 |
| 294 | W5HT06 | Uncharacteristic | 83.6 | 6.13 | 1.84 | 1.04267 |
| 295 | C3V133 | Heat shock protein 70 | 45.1 | 5.02 | 11.82 | 1.044321 |
| 296 | W5DM75 | Uncharacteristic | 55.4 | 4.89 | 2.48 | 1.045222 |
| 297 | Q8GZC0 | Peroxidase | 41.2 | 5.57 | 16.84 | 1.047328 |
| 298 | W5D8U4 | Voltage-gated anion channel | 29.5 | 8.03 | 4.06 | 1.050644 |
| 299 | W5C8D1 | Translation elongation factor | 23.3 | 4.67 | 19.72 | 1.050767 |
| 301 | W5GCG0 | NAD binding | 42.0 | 7.83 | 5.96 | 1.055327 |
| 302 | W5AYA4 | Uncharacteristic | 23.4 | 4.88 | 7.62 | 1.057434 |
| 303 | W5AIQ9 | Uncharacteristic | 11.8 | 6.06 | 16.19 | 1.058695 |
| 304 | Q9ZTU7 | Electron carrier | 17.4 | 5.83 | 13.64 | 1.059041 |
| 305 | W5CRM8 | Nucleic acid binding, nucleotide binding | 17.1 | 7.34 | 10.29 | 1.05986 |
| 306 | W5GRV6 | Hydroxymethylbilane synthase | 28.6 | 5.40 | 6.06 | 1.065344 |
| 307 | W5DNV0 | Participate in metabolic process | 54.6 | 5.54 | 8.13 | 1.066364 |
| 308 | W5B9R1 | Uncharacteristic | 16.4 | 9.57 | 7.69 | 1.068023 |
| 309 | A0A075TDV1 | RNA helicases | 59.3 | 6.28 | 2.36 | 1.068773 |
| 310 | W5I9I6 | Damaged DNA binding for nucleotide-excision repair | 42.4 | 4.73 | 12.53 | 1.070624 |
| 311 | W5F2Z7 | Uncharacteristic | 25.6 | 8.76 | 6.11 | 1.072358 |
| 312 | W5FL09 | Fructose-bisphosphate aldolase | 41.6 | 6.40 | 14.03 | 1.073417 |
| 313 | W5DPZ4 | Catalytic | 21.7 | 8.10 | 8.12 | 1.076208 |
| 314 | Q8S9H0 | Response to the temperature | 21.8 | 5.71 | 15.79 | 1.078115 |
| 315 | A0A077RST2 | Reversible hydration of carbon dioxide | 27.9 | 8.07 | 17.44 | 1.07889 |
| 316 | W5BKY5 | Uncharacteristic | 29.3 | 9.47 | 14.49 | 1.082533 |
| 317 | W5FV90 | Extrinsic component of membrane | 3.9 | 4.73 | 25.71 | 1.083608 |
| 318 | W5EKY8 | Chloroplast thylakoid membrane component | 22.1 | 5.71 | 7.22 | 1.084557 |
| 319 | W5EWT8 | Electron carrier | 16.0 | 6.38 | 9.52 | 1.086707 |
| 320 | W5F1W5 | Serine-type peptidase | 27.2 | 6.60 | 2.77 | 1.092493 |
| 321 | W5BA08 | Structural constituent of ribosome | 10.8 | 10.48 | 7.53 | 1.093059 |
| 322 | W5HV87 | Damaged DNA binding | 42.5 | 4.69 | 12.53 | 1.094533 |
| 323 | W5H3C5 | Fd\_ Reductase in FAD-binding | 45.6 | 7.75 | 35.94 | 1.096167 |
| 324 | W5FGU1 | Glutathione S-transferase | 25.0 | 6.40 | 6.76 | 1.097927 |
| 325 | W5BGU3 | Plasminogen activator, tissue type (PLAT) | 27.4 | 6.96 | 7.84 | 1.099787 |
| 326 | C3VQ50 | Cu-Zn superoxide dismutase | 15.1 | 6.18 | 13.16 | 1.102241 |
| 327 | W5H103 | Participate in S-adenosylmethionine biosynthetic process | 39.4 | 5.71 | 8.24 | 1.105309 |
| 328 | W5DNL2 | Nucleic acid binding | 34.5 | 9.03 | 3.15 | 1.106641 |
| 329 | W5FQW0 | Photosystem I reaction center | 8.2 | 5.97 | 28.38 | 1.106707 |
| 330 | Q9LDX4 | Protein disulfide oxidoreductase | 13.3 | 5.22 | 8.80 | 1.10796 |
| 331 | W5E7A0 | Glutathione-S-Transferase | 20.3 | 5.08 | 3.78 | 1.108396 |
| 332 | Q41534 | Adenosinetriphosphatase | 59.2 | 5.86 | 21.52 | 1.109176 |
| 333 | W5EVF4 | Atructural constituent of ribosome | 10.4 | 10.24 | 13.73 | 1.109928 |
| 334 | W5B2V5 | Electron carrier | 12.8 | 8.91 | 23.14 | 1.111525 |
| 335 | W5AJE1 | 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase | 26.9 | 7.88 | 3.97 | 1.115815 |
| 336 | W5D9G4 | Uncharacteristic | 20.8 | 4.70 | 20.00 | 1.116779 |
| 337 | W5AMZ5 | Uncharacteristic | 6.9 | 6.01 | 19.35 | 1.119182 |
| 338 | A0A077RU36 | NADP binding | 52.5 | 5.67 | 14.06 | 1.121021 |
| 339 | W5DG48 | Tryptophan synthase | 4.7 | 6.51 | 21.28 | 1.122827 |
| 340 | W5FKS2 | GTP binding | 26.2 | 9.26 | 16.12 | 1.12386 |
| 341 | W5A6T2 | RNA binding | 39.7 | 5.67 | 4.61 | 1.130391 |
| 342 | W5B7A5 | Structural constituent of ribosome | 10.6 | 6.28 | 14.43 | 1.131198 |
| 343 | W5AV94 | Oxidoreductase | 15.2 | 5.54 | 25.58 | 1.140601 |
| 344 | W5F095 | Transition metal ion binding | 23.9 | 5.33 | 45.33 | 1.141469 |
| 345 | W5HM46 | Response to cytokinin | 27.4 | 5.50 | 4.71 | 1.144985 |
| 346 | W5I1N1 | Serine-type peptidase | 32.4 | 9.00 | 5.44 | 1.145851 |
| 347 | W5EWV0 | Integral component of membrane | 25.0 | 8.78 | 10.36 | 1.149226 |
| 348 | W5EBJ4 | Integral component of membrane | 18.9 | 8.09 | 8.79 | 1.157009 |
| 349 | W5BRW8 | Uncharacteristic | 17.4 | 5.33 | 10.60 | 1.159285 |
| 350 | W5FZJ6 | Chloroplast stroma; | 18.5 | 6.39 | 10.53 | 1.161134 |
| 351 | W5EZT4 | Cysteine synthase | 29.0 | 5.69 | 4.04 | 1.166187 |
| 352 | M1MQ57 | Nucleotide binding | 55.0 | 9.06 | 2.62 | 1.168836 |
| 353 | W5GM11 | Adenyl nucleotide binding ATP | 10.5 | 9.33 | 16.33 | 1.176085 |
| 354 | W5AGI7 | Aspartic-type endopeptidase | 46.0 | 5.14 | 6.28 | 1.180047 |
| 355 | Q5XUV3 | Photosystem II assembly | 32.3 | 9.19 | 4.90 | 1.182714 |
| 356 | Q45FE7 | FAD binding | 50.5 | 9.17 | 16.45 | 1.183439 |
| 357 | W5AU55 | Uncharacteristic | 45.7 | 5.38 | 5.18 | 1.185823 |
| 358 | W5A2E7 | Uncharacteristic | 25.1 | 6.77 | 3.72 | 1.189659 |
| 359 | W5EVZ9 | L-malate dehydrogenase | 28.7 | 7.99 | 6.25 | 1.191222 |
| 360 | W5GVP4 | Uncharacteristic | 51.2 | 5.72 | 2.93 | 1.192479 |
| 361 | Q41628 | Transporter | 35.9 | 9.79 | 3.63 | 1.193527 |
| 362 | W5C7V9 | Proton-transporting ATPase | 37.4 | 5.12 | 35.19 | 1.198827 |
| 363 | A0A077RSI3 | Triose-phosphate isomerase | 26.8 | 5.69 | 9.88 | 1.201568 |
| 364 | W5GBV6 | Uncharacteristic | 19.4 | 4.86 | 10.47 | 1.204929 |
| 365 | W5I3H6 | Hydrolase | 34.0 | 7.12 | 3.13 | 1.205178 |
| 366 | W5ES91 | Uncharacteristic | 17.4 | 4.86 | 5.84 | 1.208917 |
| 367 | W5EVN6 | Amino acid binding | 29.4 | 5.43 | 3.85 | 1.216899 |
| 368 | W5HZZ4 | Component of membrane | 51.7 | 5.38 | 28.33 | 1.222677 |
| 369 | W5GWH6 | Chloroplast thylakoid lumen | 13.1 | 9.14 | 13.71 | 1.223136 |
| 370 | W5B2J4 | Uncharacteristic | 22.9 | 6.35 | 5.53 | 1.223715 |
| 371 | W5FB83 | Transition metal ion binding | 26.0 | 7.33 | 40.64 | 1.225128 |
| 372 | W5AMH9 | ATP binding | 48.1 | 4.69 | 18.14 | 1.226903 |
| 373 | W5IBN6 | Electron carrier | 13.2 | 5.38 | 18.46 | 1.227515 |
| 374 | J3NFL5 | Polyubiquitin | 34.3 | 7.53 | 49.84 | 1.236693 |
| 375 | W5FKC9 | Actin filament depolymerization | 13.4 | 5.17 | 13.27 | 1.245061 |
| 376 | W5D1S8 | Structural constituent of ribosome | 19.9 | 10.02 | 8.11 | 1.245732 |
| 377 | H9NAV2 | Superoxide dismutase | 17.5 | 5.43 | 6.32 | 1.24854 |
| 378 | D2KZ12 | Transferase | 47.9 | 7.96 | 3.27 | 1.258026 |
| 379 | W5C4R5 | Oxidoreductase | 19.4 | 5.21 | 18.13 | 1.258911 |
| 380 | W5E1M7 | Response to oxidative stress | 27.4 | 6.93 | 6.25 | 1.267975 |
| 381 | I1RU42 | Arylsulfatase | 68.3 | 5.95 | 1.82 | 1.268323 |
| 382 | W4ZUZ6 | Dihydrolipoyl dehydrogenase | 52.7 | 7.18 | 2.19 | 1.292344 |
| 383 | W5DSC6 | Intramolecular transferase and phosphotransferases | 54.4 | 5.19 | 2.38 | 1.298016 |
| 384 | W5GX51 | Uncharacteristic | 12.2 | 5.14 | 13.51 | 1.302251 |
| 385 | W5FWR2 | Structural constituent of ribosome | 11.4 | 8.31 | 28.85 | 1.302951 |
| 386 | W5B7Y9 | Aminomethyltransferase and transaminase | 38.6 | 8.00 | 3.08 | 1.306248 |
| 387 | W5EAE9 | Fructose 1,6-bisphosphate 1-phosphatase | 38.5 | 4.86 | 6.52 | 1.317456 |
| 388 | W4ZSC8 | Protochlorophyllide reductase | 42.2 | 9.17 | 6.58 | 1.31777 |
| 389 | W5D8S6 | Fructose-bisphosphate aldolase | 24.6 | 5.44 | 12.72 | 1.324671 |
| 390 | W5GSD9 | Protein about serine/threonine phosphatase | 28.3 | 4.84 | 8.33 | 1.325659 |
| 391 | W5HF52 | Glutathione peroxidase | 16.7 | 8.97 | 8.05 | 1.338219 |
| 392 | W5GJ32 | Integral component of membrane | 9.1 | 8.87 | 11.90 | 1.347995 |
| 393 | W5I1P4 | Metalloendopeptidase | 71.8 | 5.82 | 19.02 | 1.348996 |
| 394 | C7DPL4 | Glutamate-ammonia ligase | 46.6 | 6.09 | 9.37 | 1.350248 |
| 395 | W5G8A5 | Rhodanese | 40.2 | 9.58 | 19.28 | 1.362038 |
| 396 | W5F4M9 | Integral component of membrane | 12.9 | 6.77 | 30.91 | 1.362349 |
| 397 | W5F5I6 | Integral component of membrane | 12.7 | 4.65 | 7.41 | 1.371475 |
| 398 | W5BP68 | Uncharacteristic | 9.1 | 4.50 | 18.07 | 1.374301 |
| 399 | W5GN97 | Photosystem II oxygen evolving complex | 4.3 | 4.55 | 81.58 | 1.378334 |
| 400 | W5GKS4 | Peroxidase | 39.6 | 5.66 | 12.53 | 1.381524 |
| 401 | W5CAY0 | Integral component of membrane | 10.5 | 4.18 | 13.40 | 1.382403 |
| 402 | W5FP32 | Uncharacteristic | 20.5 | 5.30 | 4.21 | 1.384192 |
| 403 | W5F021 | Triose-phosphate isomerase | 25.8 | 5.03 | 4.98 | 1.386045 |
| 404 | W5DTC2 | Fructose-bisphosphate aldolase | 41.9 | 6.16 | 10.57 | 1.387557 |
| 405 | W5GTE2 | NAD binding | 15.3 | 8.13 | 11.64 | 1.389211 |
| 406 | W5DEI7 | Uncharacteristic | 23.2 | 5.05 | 11.74 | 1.39543 |
| 407 | W5G8U0 | Uncharacteristic | 31.5 | 8.53 | 3.97 | 1.410623 |
| 408 | W4ZXN4 | Regulation of nitrogen utilization | 10.3 | 5.91 | 11.83 | 1.418032 |
| 409 | W5B5T6 | Pyruvate dehydrogenase (acetyl-transferring) | 43.9 | 5.97 | 3.55 | 1.418604 |
| 410 | Q8S2Z6 | Ribonuclease T2 | 27.7 | 6.76 | 7.35 | 1.420574 |
| 411 | W5FRU9 | Uncharacteristic | 10.7 | 8.68 | 14.14 | 1.426532 |
| 412 | W5FSC8 | Photosystem I reaction center | 25.0 | 10.68 | 8.81 | 1.429052 |
| 413 | P80602 | May be an antioxidant enzyme particularly in the developing shoot and photosynthesizing leaf. | 23.3 | 5.99 | 10.00 | 1.43914 |
| 414 | W5E0U7 | Integral component of membrane | 27.8 | 9.73 | 6.06 | 1.44451 |
| 415 | W5AZC3 | Integral component of membrane | 30.4 | 8.84 | 3.91 | 1.455512 |
| 416 | W5BXI3 | Nucleotide binding | 13.9 | 4.56 | 8.00 | 1.460888 |
| 417 | W5FYL8 | Transporter | 9.0 | 9.70 | 19.75 | 1.471048 |
| 418 | O80370 | Dirigent proteins impart stereoselectivity on the phenoxy radical-coupling reaction | 32.4 | 7.18 | 3.33 | 1.477758 |
| 419 | W5FTM2 | Pyruvate catalytic | 34.0 | 5.63 | 3.23 | 1.482661 |
| 420 | A0A077S2L1 | Uncharacteristic | 52.0 | 8.90 | 4.14 | 1.487533 |
| 421 | W5HRK9 | Uncharacteristic | 7.8 | 7.28 | 14.93 | 1.498894 |
| 422 | W5DSZ0 | Reduced ferredoxin hydrolase | 28.7 | 5.60 | 29.02 | 1.505329 |
| 423 | A7J2I2 | Transporter | 30.4 | 8.15 | 7.93 | 1.512649 |
| 424 | Q8RVZ9 | Reduced ferredoxin hydrolase | 38.8 | 8.10 | 24.36 | 1.513358 |
| 425 | A0A077RT18 | Helicalase | 19.7 | 6.15 | 6.88 | 1.518306 |
| 426 | P43650 | Hydrolase | 18.0 | 9.74 | 4.49 | 1.519547 |
| 427 | W5HVV2 | Pyridoxal phosphate binding | 34.8 | 6.35 | 4.27 | 1.521268 |
| 428 | W5G0E8 | FMN binding | 38.0 | 8.82 | 5.73 | 1.533396 |
| 429 | W5EBA5 | Electron carrier | 30.1 | 8.59 | 28.62 | 1.53414 |
| 430 | W5E8X2 | Structural constituent of ribosome | 7.5 | 11.17 | 24.62 | 1.534581 |
| 431 | W5DP52 | NAD+ and ADP ribosyltransferase | 63.5 | 8.78 | 1.92 | 1.54318 |
| 432 | W5D936 | Uncharacteristic | 39.2 | 8.73 | 6.03 | 1.560205 |
| 433 | W5FQS4 | Photosynthetic electron transport chain | 9.7 | 5.14 | 40.00 | 1.581478 |
| 434 | W5DE07 | Threonine-type endopeptidase | 6.1 | 9.86 | 19.23 | 1.581549 |
| 435 | W5GGG6 | Uncharacteristic | 27.3 | 7.05 | 11.51 | 1.581615 |
| 436 | W5G8J8 | Uncharacteristic | 118.2 | 5.26 | 1.36 | 1.583828 |
| 437 | W5DXY3 | Proton-transporting ATP synthase complex, coupling factor F(o) | 22.5 | 5.34 | 27.49 | 1.586781 |
| 438 | W5HS38 | Iron ion binding; | 14.7 | 8.69 | 11.68 | 1.588325 |
| 439 | W4ZSM1 | Photosynthesis | 14.9 | 10.37 | 7.69 | 1.595105 |
| 440 | W5IBM7 | NAD(P)-binding | 24.9 | 7.21 | 5.05 | 1.605145 |
| 441 | H9CDF7 | Membrane component | 30.7 | 5.78 | 13.26 | 1.606222 |
| 442 | A0A0C4B3H7 | Uncharacteristic | 8.5 | 10.74 | 11.69 | 1.616008 |
| 443 | A0A060AIU4 | Endoplasmic reticulum membrane | 25.8 | 7.68 | 3.78 | 1.618585 |
| 444 | F6K744 | Chlorophyll binding | 28.2 | 5.27 | 8.65 | 1.621853 |
| 445 | W5FDX1 | NAD(P)-binding | 11.2 | 6.70 | 7.41 | 1.626803 |
| 446 | W5BU82 | Transferase | 7.5 | 9.47 | 18.57 | 1.629173 |
| 447 | W5HZ47 | Fructose-bisphosphate aldolase | 37.9 | 6.80 | 11.39 | 1.645444 |
| 448 | W5EB01 | Protein kinase | 75.5 | 5.63 | 1.63 | 1.646294 |
| 449 | W5CDG6 | Rhodanese | 39.5 | 8.47 | 5.99 | 1.648576 |
| 450 | W5HI59 | Thylakoid component | 6.0 | 8.76 | 19.23 | 1.65467 |
| 451 | W5DMM5 | Uncharacteristic | 19.0 | 5.01 | 14.62 | 1.667345 |
| 452 | W5HW46 | Uncharacteristic | 4.1 | 4.44 | 27.03 | 1.670339 |
| 453 | C1K5B6 | Chlorophyll binding The light-harvesting complex (LHC) functions as a light receptor | 21.2 | 5.83 | 11.22 | 1.675801 |
| 454 | W5F8Y0 | NAD(P)-binding | 57.4 | 8.75 | 3.70 | 1.679399 |
| 455 | W5GZB9 | Calcium ion binding | 23.5 | 9.73 | 6.60 | 1.68178 |
| 456 | A0A0C4BJ37 | Photosynthesis for light harvesting The light-harvesting complex (LHC) functions as a light receptor | 31.1 | 5.35 | 8.39 | 1.688715 |
| 457 | W5GF02 | Helical | 28.7 | 9.99 | 3.62 | 1.692804 |
| 458 | W5BUR2 | Peroxidase | 13.8 | 7.06 | 7.52 | 1.701641 |
| 459 | W5GH91 | Uncharacteristic | 5.2 | 7.88 | 30.43 | 1.705592 |
| 460 | W5FIZ2 | Photosynthesis for light harvesting | 26.7 | 6.11 | 5.71 | 1.707318 |
| 461 | A0A077RAG2 | Metal ion binding | 15.0 | 5.30 | 33.58 | 1.711933 |
| 462 | N0E6S4 | Small GTPase mediated signal transduction | 18.7 | 7.06 | 9.47 | 1.718827 |
| 463 | A0A096UW12 | Nucleic acid binding | 29.5 | 9.28 | 15.86 | 1.724167 |
| 464 | A0A096UJV2 | Chlorophyll binding for The light-harvesting complex (LHC) functions as a light receptor | 28.1 | 5.43 | 8.68 | 1.726114 |
| 465 | W5D4R0 | Chloroplast thylakoid membrane component | 28.3 | 8.82 | 16.18 | 1.72629 |
| 466 | P69386 | Electron carrier | 9.4 | 4.78 | 37.35 | 1.746109 |
| 467 | P60125 | Electron carrier | 4.5 | 10.74 | 20.51 | 1.749738 |
| 468 | W5HMD2 | Oxidoreductase , acting on NAD(P)H | 11.1 | 6.79 | 9.89 | 1.765374 |
| 469 | W5ERY2 | Photosystem I and photosystem II binding | 25.3 | 5.30 | 4.29 | 1.765876 |
| 470 | W5EZT3 | Chloroplast thylakoid membrane component | 8.1 | 9.52 | 16.88 | 1.769799 |
| 471 | W5EGM5 | Hydrogen ion transmembrane transporter | 75.5 | 6.21 | 3.47 | 1.793066 |
| 472 | P06528 | F1F0-ATP synthase produces ATP from ADP in the presence of a proton or sodium gradient | 21.0 | 9.61 | 31.69 | 1.795622 |
| 473 | W5H1Y5 | Oxidoreductase , acting on paired donors, with incorporation or reduction of molecular oxygen | 9.5 | 4.81 | 12.94 | 1.807411 |
| 474 | W5G6S0 | Photosystem II oxygen evolving complex | 14.4 | 9.80 | 7.19 | 1.822421 |
| 475 | W5EBL4 | Helical | 62.6 | 6.07 | 2.76 | 1.849473 |
| 476 | W5AI13 | Electron carrier | 9.0 | 7.11 | 26.92 | 1.854393 |
| 477 | W5E5Z3 | Divalent metal cation | 28.9 | 8.15 | 12.82 | 1.857345 |
| 478 | W5BCQ3 | Integral component of membrane | 26.1 | 7.50 | 5.76 | 1.883042 |
| 479 | W5FMA5 | Oxygen-dependent protoporphyrinogen oxidase | 56.3 | 9.14 | 2.26 | 1.890825 |
| 480 | A9UEC1 | Transporter | 7.0 | 10.17 | 15.15 | 1.898771 |
| 481 | W5GGQ5 | Proton-transporting ATP synthase complex, catalytic core F1 | 44.3 | 5.35 | 3.66 | 1.907535 |
| 482 | W5CPX1 | Orotidine-5'-phosphate decarboxylase | 50.4 | 7.06 | 2.33 | 1.917351 |
| 483 | W5FCF5 | Dirigent proteins impart stereoselectivity on the phenoxy radical-coupling reaction | 17.1 | 7.44 | 7.27 | 1.918173 |
| 484 | A0A096USS5 | The light-harvesting complex (LHC) functions as a light receptor | 28.0 | 5.43 | 7.92 | 1.93107 |
| 485 | W5A296 | Chloroplast thylakoid membrane component | 15.7 | 5.20 | 14.38 | 1.951225 |
| 486 | W5G2H8 | Transferase | 41.9 | 9.41 | 7.91 | 1.96298 |
| 487 | P26667 | Hydrolase of 3-phospho-D-glycerate | 19.4 | 8.24 | 25.71 | 1.997783 |
| 488 | W4ZQ27 | Integral component of chloroplast thylakoid membrane | 28.0 | 5.43 | 8.68 | 2.00581 |
| 489 | W5DM32 | Fe - S cluster binding | 24.5 | 5.05 | 7.08 | 2.021048 |
| 490 | H9NAL7 | Hydrogen-translocating pyrophosphatase | 22.6 | 6.10 | 5.05 | 2.025789 |
| 491 | Q575T3 | Hydrolase of 3-phospho-D-glycerate | 19.0 | 8.32 | 26.47 | 2.059798 |
| 492 | Q2L3V4 | Chlorophyll binding | 15.2 | 9.60 | 4.90 | 2.126267 |
| 493 | W5C1B8 | Chloroplast thylakoid membrane component | 16.2 | 5.01 | 28.86 | 2.127137 |
| 494 | W5EWC8 | The light-harvesting complex (LHC) functions as a light receptor | 28.3 | 5.43 | 7.89 | 2.171653 |
| 495 | P07398 | Hydrolase of 3-phospho-D-glycerate | 13.0 | 6.06 | 21.24 | 2.189755 |
| 496 | W5HU96 | Chlorophyll binding for photosynthesis and light harvesting | 28.2 | 5.43 | 7.89 | 2.225233 |
| 497 | W5A9P1 | Electron transporter | 17.3 | 4.78 | 46.45 | 2.231389 |
| 498 | W5FVP1 | Helical | 35.8 | 5.33 | 7.72 | 2.233973 |
| 499 | W5HNJ3 | Uncharacteristic | 17.8 | 5.83 | 5.16 | 2.255513 |
| 500 | W5G7G2 | Electron transporter | 20.9 | 5.60 | 15.79 | 2.280604 |
| 501 | H6UV51 | Oxidoreductase , acting on paired donors with incorporation or reduction of molecular oxygen | 45.3 | 8.66 | 5.60 | 2.281999 |
| 502 | H9ZWY8 | Phosphoglycerate kinase | 31.4 | 5.01 | 25.50 | 2.285922 |
| 503 | W5FL28 | Oxidoreductase | 105.4 | 6.11 | 4.09 | 2.33199 |
| 504 | W5AYW5 | Ccatalytic | 33.9 | 5.49 | 5.75 | 2.459998 |
| 505 | A0A075VTX2 | One of the components of the core complex of photosystem II | 52.1 | 7.21 | 21.56 | 2.466916 |
| 506 | W5B474 | The light-harvesting complex (LHC) functions as a light receptor | 27.4 | 5.94 | 14.40 | 2.473347 |
| 507 | W5GFA4 | The light-harvesting complex (LHC) functions as a light receptor | 29.3 | 8.75 | 25.65 | 2.509744 |
| 508 | A0A077RSR2 | Uncharacteristic | 54.3 | 6.77 | 2.96 | 2.536007 |
| 509 | W5GBZ1 | Integral component of membrane | 49.9 | 8.25 | 5.76 | 2.568946 |
| 510 | P58386 | The primary electron donor (PsaA and PsaB bind in P700) of photosystem I (PSI) | 82.5 | 7.15 | 9.26 | 2.577056 |
| 511 | A0A077S3F8 | Integral component of membrane | 20.4 | 6.02 | 7.96 | 2.677596 |
| 512 | W5ELP3 | Cytoskeleton organization | 20.7 | 5.08 | 8.81 | 2.824053 |
| 513 | W5G545 | Integral component of membrane | 21.0 | 5.27 | 32.80 | 2.847804 |
| 514 | W5HG98 | Damaged DNA binding | 38.3 | 4.69 | 8.38 | 3.076707 |
| 515 | Q5I3F2 | Phenolic donor | 34.7 | 8.18 | 5.28 | 3.361736 |
| 516 | A0A075VX44 | The primary electron donor (PsaA and PsaB bind in P700) of photosystem I (PSI) | 83.1 | 7.11 | 7.20 | 4.10309 |
| 517 | W5EXW7 | Integral component of membrane | 8.2 | 5.17 | 11.84 | 4.285227 |
| Note: - , not detected in 1.0 mg L-1 phenantherene treated group. | | | | | | |

**Chloroplast Protein Verification**

The molecular mass of the purified protease was determined using 4–12% (w/v) sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) (Laemmli, 1970), under denaturing and reducing conditions. The gels were stained with 0.1% (w/v) Coomassie brilliant blue R-250. The molecular mass was calculated by comparison with standard protein markers. Protein markers were purchased from Genscript (M00516, China), and marker labels are 0, 10, 20, 30, 40, 60, 80 and 120 KD. Each chloroplast protein sample solution was 10 μL for SDS-PAGE.

We tested the 12 proteins related with chloroplast structure (Fig. S1). In details, W5FHC5 (44.9 KD), W5HA90 (32.3 KD) and W5ALR1 (25.6 KD) were up-regulated obviously, while W5HNV3 (23.7 KD) was not clearly. Meanwhile, W5D4R0 (28.3 KD), W5EKY8 (22.1KD), W5FZJ6 (18.5 KD), W5C1B8 (16.2 KD), W5A296 (15.7 KD), W5GWH6 (13.1 KD), W5EZT3 (8.1 KD) and W5HI59 (6.0 KD) became down-regulated in wheat leaf exposed to phenanthrene.

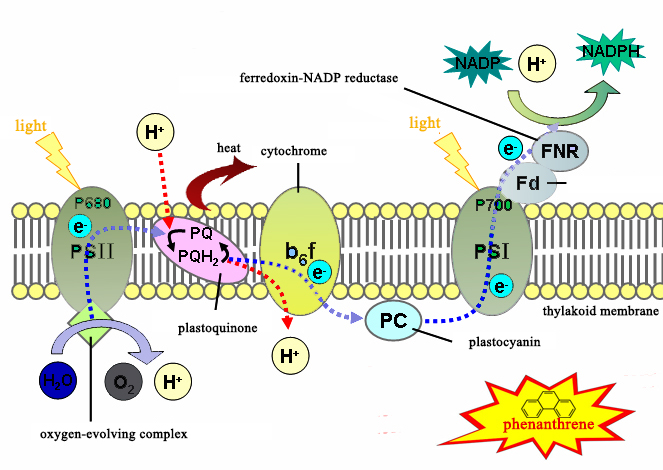
**Fig. S1.** Representative SDS-PAGE of chloroplast proteins. Positions of molecular weight standards (in kDa) are indicated.

**Three Major Biological Processes from Proteomics**

**Photosynthesis System Response.** Chloroplast is an independent, endosymbiotic union in plant cells, and its genome most commonly includes photosynthesis and protein pipeline (Clegg *et al*. 1994; McFadden 2001). Recently, there are many reports about the photosystem response under phenanthrene treatment (Jajoo *et al*. 2014; Jin *et al*. 2017). In light reaction state, the accumulation of PAHs would restrict the free light harvesting complex (LHC) to obtain light quantum in Photosystem II (PS II) (Jajoo *et al.* 2014). The energy transfer from light to electron would be weakened and only 60% electrons were able to transfer to Photosystem I (PS I) when PS II was damaged under PAH treatment, and the oxygen released would be also reduced under this condition (Thomas & Donald 1984; Kreslavski *et al*. 2014). In addition, the electron transfer of chlorophyll fluorescence in light reaction would be interrupted in aquatic macrophytes and pea under PAH treatment (Kummerova *et al*. 2001). However, there are no systematic and comprehensive reports about photosynthesis system response to date.

In our results, it was detected that 20 proteins turned up-regulated and 56 proteins turned down-regulated under phenanthrene treatment through proteomic analysis. Among proteins in photosynthesis systems, five proteins related with PS II and one protein related with PS I became down-regulated, while three proteins related with PS II and two proteins related with PS I were up-regulated under phenanthrene treatment (Fig. 3 and Table S2). Eight proteins associated with light harvesting complex and two proteins in P700 (700 nm wavelength light acceptors) of PS I turned down-regulated in the treatment (Table S2). In the energy chain, one protein in cytochrome complex (b6f), two ferredoxins, four electronic carriers and two photo proton transfer proteins were down-regulated, while 1 ferredoxin, one protein in cytochrome complex, 2 electronic carriers and 4 photo proton transfer proteins were up-regulated when phenanthrene accumulated in chloroplast (Table S1).

Combined with the previous results, an improved Z-schema (Zigzag schema) of photosynthetic electron transport chain is proposed under phenanthrene treatment (Fig. S2). In detail, at the start, because thylakoid structure becomes weakened and the chlorophyll concentration decreases (Shen *et al.* 2017), the thylakoid membrane becomes yellow, PS II and PS I turn chlorosis and cytochrome complex gets recessive white. Since the plant cell would absorb more H+ from outer environment under PAH treatment (Zhan *et al*. 2015), the participation of H+ is active in photosynthesis. Then the electron transfer chain is weakened in the photosynthesis. Based on ATP or NADPH proteins in heatmaps (Fig. 3), 54.72% proteins as ATP and NADPH components are down-regulated under phenanthrene treatment. In addition, it was reported that the values of fast fluorescence of inactive centers of PS II and chlorophyll fluorescence of non-photochemical quenching would increase when plants are exposed to organic pollutants (Kreslavski *et al*. 2006; Zhang *et al*. 2016). It is suggested that the electronic flow is inferred and weakened from PS II to pheophytin- plastoquinone (PQ-PQH2) and the heat is the major energy loss in PAH treatment. The changes are presented in Fig. S1.

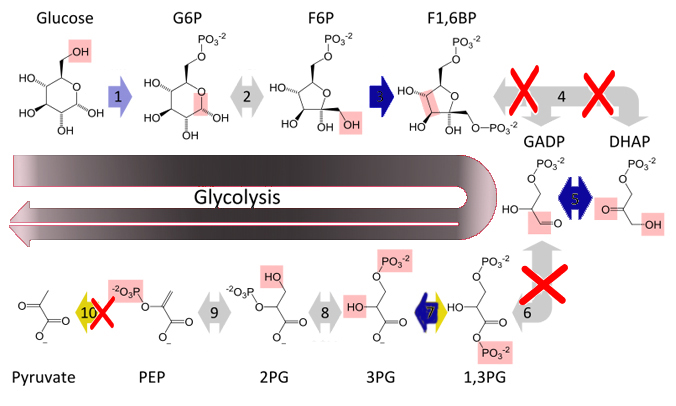


**Fig. S2.** The improved Z-schema (Zigzag schema) of photosynthetic electron transport chain in wheat leaf chloroplast under phenanthrene treatment. The gradient color in the arrows and photosystem units means turning weakness.

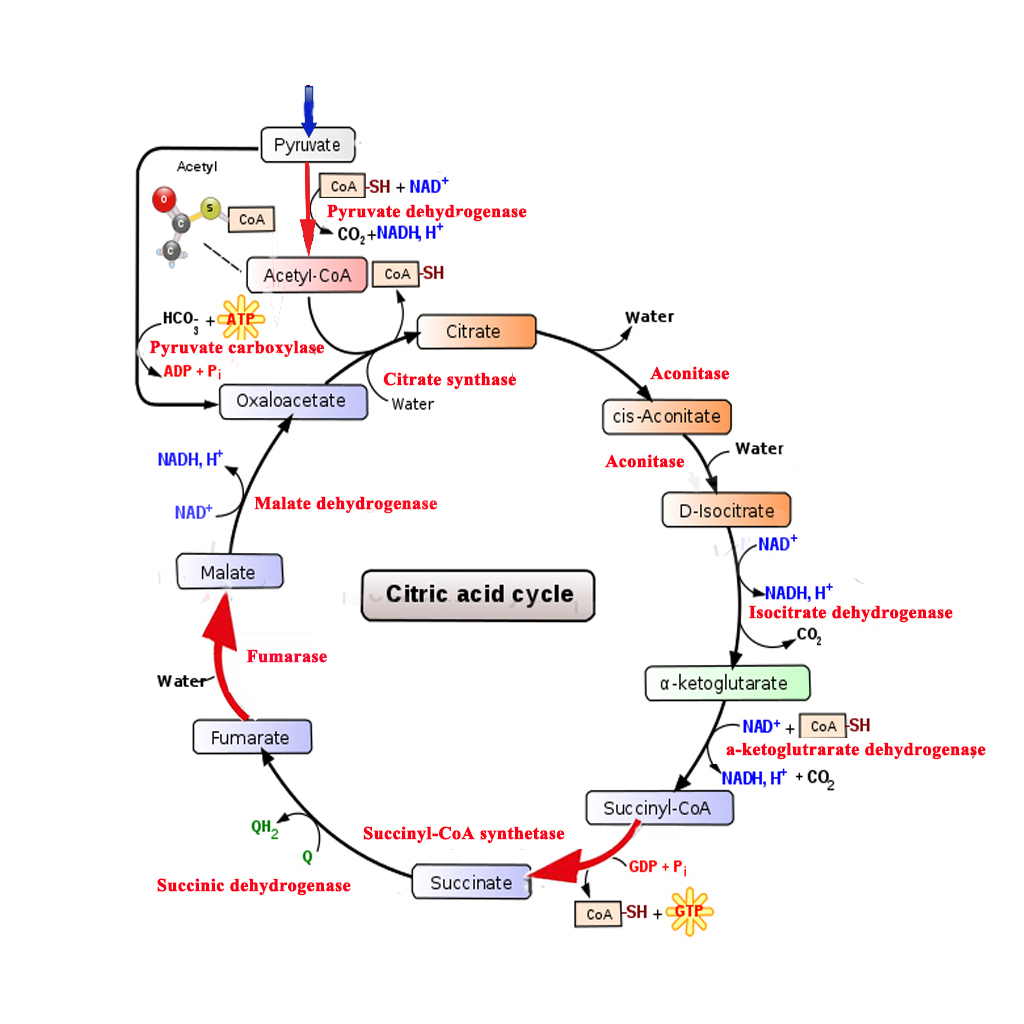
**Energy Conversion Changes.** The chemical energy from photosynthesis is the major energy source for life on earth (Kreslavski *et al.* 2006), and glycolysis and tricarboxylic acid (TCA) cycle are the most important processes in the respiration (Owen *et al*. 2002). But there are other carbohydrate metabolisms in plant cells. In previous research, we have detected that malate metabolism would be strengthened with the accumulation of phenanthrene (Zhan *et al.* 2015). In this study, 15 proteins related with carbohydrate metabolism were up-regulated and 10 proteins were down-regulated, and we applied glycolysis process pathway (Fig. S3) to analyze the chloroplast protein response under phenanthrene treatment. Combined with heatmaps (Fig. S3), pyruvate synthesis, which is the key point in glycolysis process, was inactivated when phenanthrene accumulated in leaf cells. The enzyme of pyruvate production, i.e. pyruvate catalyst (W5FTM2), is down-regulated. Thus, the important raw substance for the aerobic and anaerobic metabolism becomes less. Moreover, W5FL09 (fructose-bisphosphate aldolase) and W5EAE9 (fructose 1,6-bisphosphate phosphatase (F 1,6 BP) activity) turned down-regulated and their related process of F 1,6 BP conversion broke down under phenanthrene treatment. The conversion enzymes, A0A077RSI3 and W5F021 (triose-phosphate isomerase) between glyceraldehyde phosphate (GADP) and 1,3-bisphosphoglycerate (1,3 PG) were also suppressed in chloroplast under phenanthrene treatment. In previous proteomic study, we found that the process in glyceraldehyde 3-phosphate production is blocked (Shen *et al.* 2016), which is an important stage for energy release in glycolysis. It has been reported that phenanthrene would suppress the glycolysis process in *Arabidopsis thaliana* (Weisman *et al*. 2010), and the inhibition of glycolysis process is detected in the chloroplast in *Gammarus pulex* (Leroy *et* *al*. 2010). We also detected W4ZWJ2 (6-phosphofructo-2-kinase), an enzyme associated with F 1,6 BP generation, and P12782 (phosphoglycerate kinase), an enzyme that catalyzes the reversible transfer of a phosphate group from 1,3 PG to ADP producing 3-phosphoglycerate (3 PG) and ATP, as well as a mutual conversion enzyme participating in GADP and dihydroxyacetone phosphate (DHAP). W4ZWJ2 and P12782 were up-regulated under the treatment. These two up-regulated enzymes are not the key points in glycolysis, and they would not alter the pyruvate formation in the chain reaction. Meanwhile, another reason for pyruvate decrease is that photosynthesis becomes weak under phenanthrene treatment.

TCA cycle is the most important energy conversion in biology, and it appears to be the most efficient one in evolution now (Ebenhoh & Heinrich 2001). Hence, TCA cycle was applied in Fig. S4 to analyze the change in chloroplast under phenanthrene treatment. As is mentioned above, the pyruvate decrease leads to be short of substrate at the start of the TCA cycle. However, the protein related to the start of TCA cycle, W5IB10 (pyruvate dehydrogenase (acetyl-transferring)), is up-regulated under phenanthrene treatment. In this study, two enzymes in TCA cycle turned up-regulated in chloroplast under phenanthrene treatment. In the conversion from succinyl-CoA to succinate and fumarate to malate, W5B5M (dihydrolipoyllysine-residue succinyltransferase) and A0A0C4BJJ8 (fumarate hydratase) were also up-regulated in TCA cycle. Due to no reports associated with TCA cycle response under PAH treatment, we describe the pathway to offer a reference to the future research here.

Besides glycolysis and TCA cycle, the proteins related with pentose-phosphate cycle (P12782, W5HDA6 and W5GRE0) and glycerol ether metabolism (Q9ZP21, W5F9P6 and W5C0J3) became active in wheat chloroplasts under phenanthrene treatment. Due to the reduction of glucose and pyruvate in glycolysis and TCA cycle, the energy conversion is weak, and there should be some other energy conversions turning active to keep physiological metabolism in chloroplasts and plant cells. Pentose-phosphate cycle is a metabolic pathway parallel to glycolysis. It generates NADPH and pentoses (5-carbon sugars) as well as ribose 5-phosphate (Kruger *et al*. 2003). The two proteins (P12782 and P12783) were up-regulated and one protein (H9ZWY8) was down-regulated in pentose-phosphate cycle. Generally, pentose-phosphate cycle involves oxidation of glucose, and its primary role is anabolic rather than catabolic (Xu *et al*. 2016). Herein, it is inferred that the accumulation of phenanthrene stimulates pentose-phosphate cycle to store some substances to defend the stress when the primary metabolism is low. However, there is no information about glycerol ether metabolic process under PAH exposure, and this process would enrich the energy conversion change when plants are exposed to PAHs.



**Fig. S3.** The metabolic pathway of glycolysis from glucose to pyruvate in wheat leaf chloroplast under phenanthrene treatment. The dark arrow means that the conversion gets stronger, and the cross indicates the block of the reaction.



**Fig. S4.** The improved citric acid cycle (TCA) of chemical transport chain in wheat leaf chloroplast under phenanthrene treatment. The red arrow is the chain reaction turning stronger and the blue arrow means the reaction getting weakness.

**Amino Acid Metabolism Response.** Chloroplasts alone make almost all of a plant cell's amino acids in their stroma except the sulfur-containing ones like cysteine and methionine (Rolland *et al*. 1991; Ferro *et al*. 2002). When exposed to stress conditions, plants accumulate an array of metabolites, particularly amino acids (Arbona *et al*. 2013). Amino acids are considered traditionally as precursors to and constituents of proteins, and play an important role in plant metabolism and development (Sun *et al*. 2016). In our results, the proteins related with proline and tryptophan synthesis and glycine metabolism were up-regulated under phenanthrene treatment. Proline plays a highly beneficial role in plants exposed to various stress conditions. Besides acting as an excellent osmolyte, proline plays three major roles during stress, i.e., as a metal chelator, an anti-oxidative defense molecule and a signaling molecule (Hayat *et al*. 2012; Liang *et al*. 2013). Numerous data suggest a positive correlation between proline accumulation and plant stress. In PAH pollution, it was reported that proline concentrations would increase in *Bruguiera gymnorrhiza* treated with pyrene (Song *et al*. 2012). The same phenomenon was also found in *Kandelia candel* under pyrene and *p*-terphenyl combined treatment (Song *et al*. 2011). Together with glycine metabolism, the increase of glycine betaine and proline concentration would improve plant abiotic stress resistance (Ashraf & Foolad 2007). Glycine betaine (trimethylglycine) is an amino acid derivative that occurs in plants. Hence, it is inferred that glycine metabolism also gets active in stressed plants (Sakamoto & Murata 2002). It was found that the glycine betaine proteins increased under petroleum contamination (Chen *et al*. 2017), and the glycine betaine metabolism increased in the oil-contaminated saline environment (Husseina & Terry 2002). The glycine-rich proteins play key roles in the adaptation of organisms to biotic and abiotic stresses including pathogenesis, alterations in the osmotic, saline and oxidative environment, and changes in temperature (Ciuzan *et al*. 2015). In addition, the proteins related with histidine, threonine and arginine metabolism were down-regulated when wheat was treated with phenanthrene (Fig. 3). Histidine and threonine concentrations increase significantly in *Quercus ilex* in PAH polluted air, but arginine concentration would not increase (Papa *et al*. 2012). In heavy metal and salt stress, the threonine concentration always increases in plants (Pavlik *et al*. 2010; Shabala *et al*. 2015). Moreover, threonine/serine kinase plays a role in the regulation of cell proliferation and programmed death under environmental stress (Rai, 2002), and its activity would increase under environmental stress (Mizoguchi *et al*. 1997; Shabala *et al.* 2015). Based on the results (Fig. 3 and Table S2), the protein metabolism of aspartate, cysteine, glutamate, serine and methionine is unclear here. In our previous results, the glutamate concentration would increase under phenanthrene treatment (Shen *et al*., 2017), and the glutamate metabolism needs more detection on intermediate change. Cysteine is formed in the chloroplast, and it is also synthesized in the cytosol and mitochondria (Rolland *et al*. 1992), probably because it has trouble in crossing membranes to chloroplast under phenanthrene treatment. The chloroplast is known to produce the precursors to methionine, but it is unclear whether the organelle carries out the steps of the pathway or whether it happens in the cytosol (Ravanel *et al*. 1998). However, our proteomic results are different from the previous reports in which the methionine metabolism would be weakened under PAH pollution (Dupuy *et al*. 2014; Elie *et al*. 2015). Therefore, PAHs are a kind of environmental stress that would change amino acid metabolism.

**References**

Arbona V., Manzi M., Ollas C. & Gomez-Cadenas A. (2013) Metabolomics as a tool to investigate abiotic stress tolerance in plants. *International Journal of Molecular Science* **14**, 4885-4911.

Ashraf M. & Foolad M.R. (2007) Roles of glycine betaine and proline in improving plant abiotic stress resistance. *Environmental and Experimental Botany* **59**, 206-216.

Chen S., Ma H., Guo Z., Feng Y., Lin J., Zhang M. & Zhong M. (2017) Quantitative proteomics analysis reveals the tolerance of Mirabilis jalapa L. to petroleum contamination. *Environment Science and Pollution Research* **24**, 7375-7382.

Ciuzan O., Hancock J., Pamfil D., Wilson I. & Ladomery M. (2015) The evolutionarily conserved multifunctional glycine-rich RNA-binding proteins play key roles in development and stress adaptation. *Physiologia Plantarum* **153**, 1-11.

Clegg M.T., Gaut B.S., Gerald H. Learn J. & Morton B.R. (1994) Rates and patterns of chloroplast DNA evolution. *Proceedings of the National Academy of Sciences* **91**, 6795-6801.

Dupuy C., Galland C., Devaux A., Bony S., Loizeau V., Danion M., Pichereau V., Fournier M. & Laroche J. (2014) Responses of the European flounder (Platichthys flesus) to a mixture of PAHs and PCBs in experimental conditions. *Environment Science and Pollution Research* **21**, 13789-13803.

Ebenhoh O. & Heinrich R. (2001) Evolutionary optimization of metabolic pathways. Theoretical reconstruction of the stoichiometry of ATP and NADH producing systems. *Bulletin of Mathematical Biology* **63**, 21-55.

Elie M.R., Choi J., Nkrumah-Elie Y.M., Gonnerman G.D., Stevens J.F. & Tanguay R.L. (2015) Metabolomic analysis to define and compare the effects of PAHs and oxygenated PAHs in developing zebrafish. *Environment Res*e*arch* **140**, 502-510.

Ferro M., Salvi D., Riviere-Rolland H., Vermat T., Seigneurin-Berny D., Grunwald D., Garin J., Joyard J. & Rolland N. (2002) Integral membrane proteins of the chloroplast envelope: identification and subcellular localization of new transporters. *Proceedings of the National Academy of Sciences* **99**, 11487-11492.

Hayat S., Hayat Q., Alyemeni M.N., Wani A.S., Pichtel J. & Ahmad A. (2012) Role of proline under changing environments: a review. *Plant Signaling & Behavior* **7**, 1456-1466.

Husseina H.S. & Terry N. (2002) Phytomonitoring the unique colonization of oil-contaminated saline environment by *Limoniastrum monopetalum* (L.) Boiss in Egypt. *Environmental International* **28**, 127-135.

Jajoo A., Mekala N.R., Tomar R.S., Grieco M., Tikkanen M. & Aro E.M. (2014) Inhibitory effects of polycyclic aromatic hydrocarbons (PAHs) on photosynthetic performance are not related to their aromaticity. *Journal of Photochemistry and Photobiology, Biology* **137**, 151-155.

Jin L., Che X., Zhang Z., Li Y., Gao H. & Zhao S. (2017) The mechanisms by which phenanthrene affects the photosynthetic apparatus of cucumber leaves. *Chemosphere* **168**, 1498-1505.

Kreslavski V.D., Brestic M., Zharmukhamedov S.K., Lyubimov V.Y., Lankin A.V., Jajoo A. & Allakhverdiev S.I. (2006) Mechanisms of inhibitory effects of polycyclic aromatic hydrocarbons in photosynthetic primary processes in pea leaves and thylakoid preparations. *Trends in Microbiology* **19**, 683-688.

Kreslavski V.D., Lankin A.V., Vasilyeva G.K., Luybimov V.Y., Semenova G.N., Schmitt F.J., Friedrich T. & Allakhverdiev S.I. (2014) Effects of polyaromatic hydrocarbons on photosystem II activity in pea leaves. *Plant Physiology and Biochemistry* **81**, 135-142.

Kruger N.J. & von Schaewen A. (2003) The oxidative pentose phosphate pathway: structure and organisation. *Current Opinion in Plant Biology* **6**, 236-246.

Kummerova M., Krulova J., Zezulka S. & Triska J. (2006) Evaluation of fluoranthene phytotoxicity in pea plants by Hill reaction and chlorophyll fluorescence. *Chemosphere* **65**, 489-496.

Laemmli U K. (1970) Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature* **227**, 680.

Leroy D., Haubruge E., De Pauw E., Thome J.P. & Francis F. (2010) Development of ecotoxicoproteomics on the freshwater amphipod Gammarus pulex: identification of PCB biomarkers in glycolysis and glutamate pathways. *Ecotoxicology and Environmental Safety* **73**, 343-352.

Liang X., Zhang L., Natarajan S.K. & Becker D.F. (2013) Proline mechanisms of stress survival. *Antioxidants and Redox Signaling* **19**, 998-1011.

McFadden G.I. (2001) Chloroplast Origin and Integration. *Plant Physiology*, **125**, 50-53.

Mizoguchi T., Lchimura K. & Shinozaki K. (1997) Environmental stress response in plants: the role of mitogen-activated protein kinases. *Trends in Biotechnology* **15**, 15-19.

Owen O.E., Kalhan S.C. & Hanson R.W. (2002) The key role of anaplerosis and cataplerosis for citric acid cycle function. *The Journal of Biological Chemistry* **277**, 30409-30412.

Papa S., Bartoli G., Nacca F., D'Abrosca B., Cembrola E., Pellegrino A., Fiorentino A., Fuggi A. & Fioretto A. (2012) Trace metals, peroxidase activity, PAHs contents and ecophysiological changes in Quercus ilex leaves in the urban area of Caserta (Italy). *Journal of Environmental Management* **113**, 501-509.

Pavlik M., Pavlikova D., Staszkova L., Neuberg M., Kaliszova R., Szakova J. & Tlustos P. (2010) The effect of arsenic contamination on amino acids metabolism in *Spinacia oleracea* L. *Ecotoxicology and Environmental Safety* **73**, 1309-1313.

Rai V.K. (2002) Role of amino acids in plant responses to stresses. *Biologia Plantarum* **45**, 481-487.

Ravanel S., Gakière B., Job D. & Douce R. (1998) The specific features of methionine biosynthesis and metabolism in plants. *Proceedings of the National Academy of Sciences* **95**, 7805–7812.

Rolland N., Droux M. & Douce R. (1991) Subcellular distribution of o-acetylserine(thiol)lyase in cauliflower (*Brassica oleracea* L.) inflorescence. *Plant Physiology* **98**, 927-935.

Rolland, N., Droux, M., & Douce, R. (1992). Subcellular distribution of O-acetylserine (thiol) lyase in cauliflower (Brassica oleracea L.) inflorescence. *Plant Physiology* **98**, 927-935.

Shabala S., Wu H. & Bose J. (2015) Salt stress sensing and early signalling events in plant roots: Current knowledge and hypothesis. *Plant Science* **241**, 109-119.

Shen Y., Du J., Yue L. & Zhan X. (2016) Proteomic analysis of plasma membrane proteins in wheat roots exposed to phenanthrene. *Environment Science and Pollution Research* **23**, 10863-10871.

Shen Y., Li J., Gu R., Yue L., Zhan X. & Xing B. (2017) Phenanthrene-triggered Chlorosis is caused by elevated Chlorophyll degradation and leaf moisture. *Environmental Pollution* **220**, 1311-1321.

Shen Y., Li J., Gu R., Yue L., Zhan X. & Xing B. (2017) Phenanthrene-triggered Chlorosis is caused by elevated Chlorophyll degradation and leaf moisture. *Environmental Pollution* **220**, 1311-1321.

Song H., Wang Y.S., Sun C.C., Wang Y.T., Peng Y.L. & Cheng H. (2012) Effects of pyrene on antioxidant systems and lipid peroxidation level in mangrove plants, *Bruguiera gymnorrhiza*. *Ecotoxicology* **21**, 1625-1632.

Song H., Wang Y.s., Sun C.c., Wu M.l., Peng Y.l., Deng C. & Li Q. (2011) Effects of polycyclic aromatic hydrocarbons exposure on antioxidant system activities and proline content in *Kandelia candel*. *Oceanological and Hydrobiological Studies* **40**, 9-18.

Sun H., Liu F., Sun L., Liu J., Wang M., Chen X., Xu X., Ma R., Feng K. & Jiang R. (2016) Proteomic analysis of amino acid metabolism differences between wild and cultivated *Panax ginseng*. *Journal of Ginseng Research* **40**, 113-120.

Thomas G. & Donald R.O. (1984) Detection of oxygen-evolving Photosystem II centers inactive in plastoquinone reduction. *Biochimica et Biophysica Acta - Bioenergetics* **852**, 320-330.

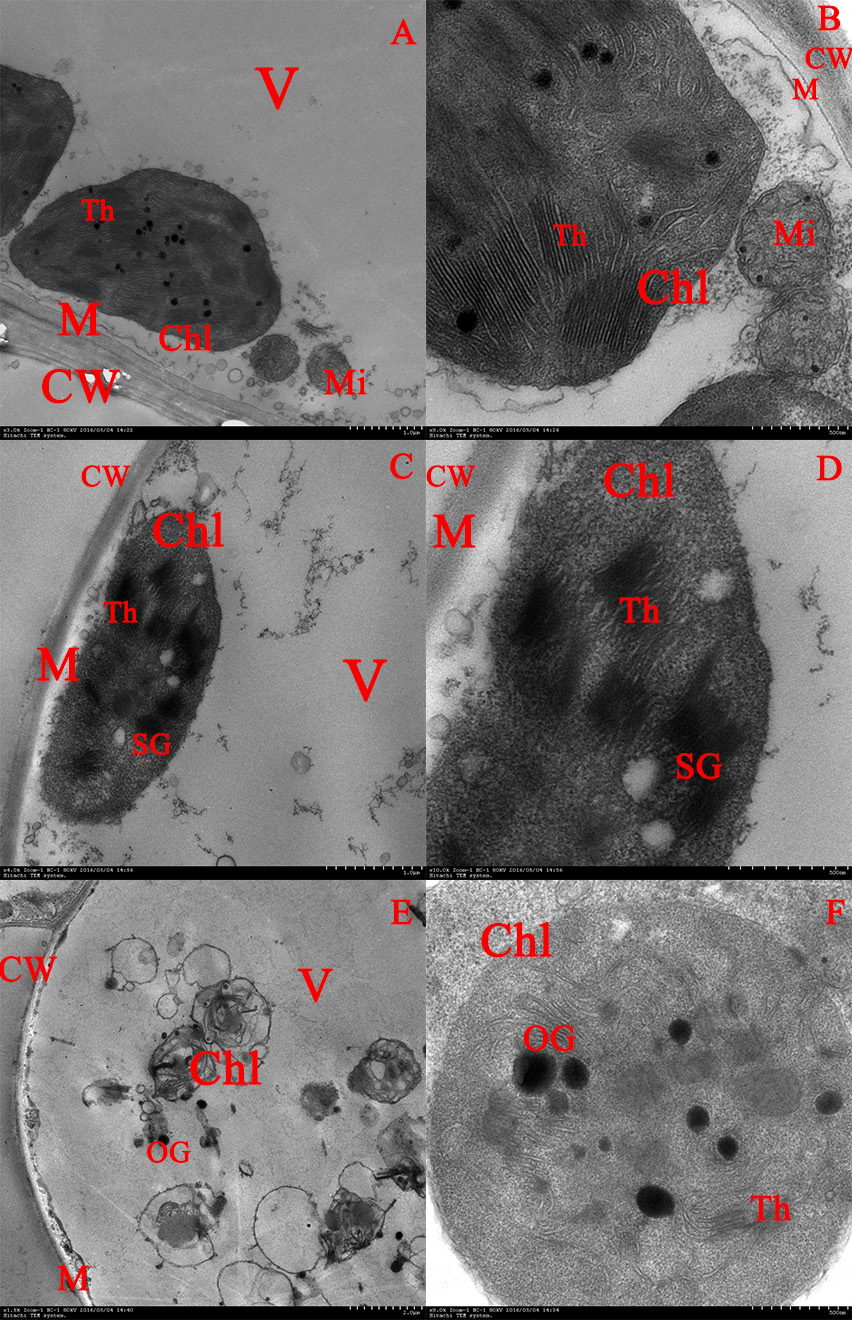
Weisman D., Alkio M. & Colón-Carmona A. (2010) Transcriptional responses to polycyclic aromatic hydrocarbon-induced stress in *Arabidopsis thaliana* reveal the involvement of hormone and defense signaling pathways. *BMC Plant Biology* **10**, 59.

Xu S., Wang T., Li X. & Wang Y. (2016) SIRT2 activates G6PD to enhance NADPH production and promote leukaemia cell proliferation. *Scientific Reports* **6**, 32734.

Zhan X., Yi X., Yue L., Fan X., Xu G. & Xing B. (2015) Cytoplasmic pH-Stat during Phenanthrene Uptake by Wheat Roots: A Mechanistic Consideration. *Environmental Science and Technology* **49**, 6037-6044.

Zhang K., Shen Y., Zhou X., Fang Y., Liu Y. & Ma L. (2016) Photosynthetic electron-transfer reactions in the gametophyte of *Pteris multifida* reveal the presence of allelopathic interference from the invasive plant species *Bidens pilosa*. *Journal of Photochemistry and Photobiology Biology* **158**, 81-88.

**Transmission electron microscope (TEM) images of wheat leaf cells under phenanthrene treatment for 9 days**



**Figure S5.** Transmission electron microscope (TEM) images of wheat leaf cells under phenanthrene treatment for 9 days. Control samples: A (×2 k), B (×8 k); 0.5 mg L-1 phenanthrene treatment: C (×2 k), D (×8 k); 1.0 mg L-1 phenanthrene treatment: E (×1.5 k), F (×8 k). Chl, chloroplast; Th, Thylakoid; CW, cell wall; Mi, mitochondria; M, cell membrane; OG, osmilphilic granule; SG, starch grain; V, vacuole.