

Šebela, M.; Raus, M.; Ondřej, V.; Hašler, P. The influence of metabolic inhibitors, antibiotics and microgravity on intact cell MALDI-TOF mass spectra of the cyanobacterium *Synechococcus* sp. UPOC S4.

Supplementary file 1

Assigning of peaks from intact cell MALDI-TOF mass spectra of *Synechococcus* sp. UPOC S4 to amino acid sequences from the UniProt database. This assignment was achieved using pFilter accessible at <https://software.cr-hana.upol.cz/pfilter/>. The term “MISSING IN CONTROL” refers to those peaks, which appeared in a sample spectrum but were not present in the respective control spectrum. The term “MISSING IN SAMPLE” refers to a comparison in the opposite direction.

ANTIMYCIN A

1 and 2 μM, 1 week

MISSING IN CONTROL: 20 peaks, uncharacterized proteins plus m/z 3443.74 PSBT_SYNR3 Photosystem II reaction center protein T; m/z 6370.62 Q05WR3_9SYNE Possible high light inducible protein; m/z 6370.62 A4CU05_SYNPV Uncharacterized protein - Amidinotransferase super family; m/z 7706.62 Q0IBT9_SYNS3 Possible SAP domain - Nif11 domain; m/z 8677.30 A5GQ62_SYNR3 Uncharacterized protein - hercynine metabolism small protein; m/z 8677.30 1 uM K9RU07_SYNP3 Ferredoxin; m/z 8677.30 1 uM A0A1J0PAE3_9SYNE Acyl carrier protein; m/z 8677.30 1 uM A3YVC4_9SYNE Uncharacterized protein - Cell division protein SepF; m/z 8692.09 YiaG super family, DNA-binding transcriptional regulator YiaG; m/z 9067.28 2 uM K9RQM6_SYNP3 Putative redox protein, regulator of disulfide bond formation; m/z 9067.28 2 uM Q0IBQ1_SYNS3 Nif11 domain-containing protein; m/z 9128.53 2 uM NDHO_SYNPW NAD(P)H-quinone oxidoreductase subunit O; m/z 12240.03 Y026_SYNS3 Nucleoid-associated protein sync_0026; m/z 12576.10 Photosystem II reaction center Psb28 protein

MISSING IN SAMPLE: 2 peaks, only uncharacterized proteins

5 and 10 μM, 1 week

MISSING IN CONTROL: 18 peaks (at 5 μM), 25 peaks (at 10 μM), uncharacterized proteins plus m/z 3444.71 A0A4P7ZVD3_9SYNE Photosystem II reaction center protein T; m/z 3638.09 10 uM Translocase; m/z 4361.43 Q05XIO_9SYNE Cytochrome b6-f complex subunit 7; m/z 4361.43 A3YYM8_9SYNE Photosystem II protein Y; m/z 4380.59 RL36_SYNS9 50S ribosomal protein L36

MISSING IN SAMPLE: 2 peaks (5 and 10 μM) including m/z 8708.98 K9SS39_9SYNE Photosystem I reaction center subunit PsaK

1 and 2 μM , 3 weeks

MISSING IN CONTROL: 3 peaks including m/z 6153.17 2 μM Q3B0Y5_SYNS9 General secretion pathway protein E; m/z 6153.17 2 μM Q0IAS5_SYNS3 Ferrochelatase; m/z 6153.17 2 μM Q3B0V3_SYNS9 High light-inducible protein-like; m/z 6153.17 Q3B0V3_SYNS9 High light-inducible protein-like

MISSING IN SAMPLE: 31 peaks, uncharacterized proteins plus m/z 4429.12 A0A1J0PAG3_9SYNE Photosystem II reaction center protein I; m/z 4858.50 Q3AY61_SYNS9 Possible high light inducible protein; m/z 6115.87 A3YXR5_9SYNE PCP_red domain-containing protein; m/z 6680.04 K9SUE7_9SYNE Copper chaperone; m/z 6939.69 B1XKM3_SYNP2 Conserved hypothetical membrane protein; m/z 7084.66 B1XKL5_SYNP2 Chaperone protein domain protein; m/z 7193.64 K9RSN2_SYNP3 Photosystem II reaction center protein K; m/z 8324.51 B1XPV2_SYNP2 30S ribosomal protein S18; m/z 9130.66 Q05QL5_9SYNE Possible SAP domain; m/z 9142.47 NDHL_SYNPW NAD(P)H-quinone oxidoreductase subunit L; m/z 9142.47 A0A2P7EBS2_9SYNE GMC oxidoreductase (Fragment); m/z 10314.88 K9STH7_9SYNE Transposase; m/z 10314.88 YIDD_SYNS9 Putative membrane protein insertion efficiency factor; m/z 10764.46 A0A164CRS2_9SYNE Uncharacterized protein - DnaJ super family, DnaJ-class molecular chaperone with C-terminal Zn finger domain; m/z 12206.4 A3YUU8_9SYNE Uncharacterized protein - PRK07375, Na⁺/H⁺ antiporter subunit C; m/z 12243.8 B1XPW9_SYNP2 Arsenical resistance operon repressor, ArsR family; m/z 12420.08 A0A1J0P969_9SYNE Uncharacterized protein - MopB_CT superfamily, Molybdopterin-Binding, C-terminal (MopB_CT) domain; m/z 12420.08 K9SUE0_9SYNE Cupin_7 domain-containing protein

5 and 10 μM , 3 weeks

MISSING IN CONTROL: no peak was missing

MISSING IN SAMPLE: numerous peaks disappeared

AZIDE

2 and 5 μM , 2 weeks

MISSING IN CONTROL: 11 peaks, uncharacterized proteins plus m/z 5064.10 A5GIA9_SYNPW Cytochrome b559 subunit beta; m/z 5224.27 PSBK_SYNPW Photosystem II reaction center protein K; m/z 7047.75 A0A2P7EC83_9SYNE Photosystem II reaction center protein J; m/z 7051.62 NBLA_SYNE7 Phycobilisome degradation protein NblA

MISSING IN SAMPLE: no difference

10 μ M, 2 weeks

MISSING IN CONTROL: 39 peaks, uncharacterized proteins plus m/z 3872.48 A3Z0W3_9SYNE Uncharacterized protein - PIN_SF super family; m/z 3889.18 A3YUT5_9SYNE Photosystem II reaction center protein M; m/z 4080.56 K9SR44_9SYNE Photosystem II reaction center protein T; m/z 4100.92 A0A0G8AWI1_9SYNE Cytochrome b6-f complex subunit 5; m/z 4112.87 A0A164BUR5_9SYNE Photosystem I reaction center subunit VIII; m/z 4297.12 A0A164B792_9SYNE Photosystem II protein Y; m/z 4764.83 PSBF_SYNP2 Cytochrome b559 subunit beta; m/z 4907.10 A3YZK2_9SYNE Possible high light inducible protein; m/z 4907.10 A0A2P7EAR9_9SYNE DNA polymerase subunit beta (Fragment); m/z 4997.24 A0A2P7EAR9_9SYNE DNA polymerase subunit beta (Fragment); m/z 6454.65 A5GI63_SYNPW Uncharacterized protein - NdhS, NAD(P)H dehydrogenase subunit S; m/z 10259.9 Q3AZP3_SYNS9 Possible acyl carrier protein; m/z 10259.9 A5GU92_SYNR3 Predicted enzyme of the cupin superfamily; m/z 10259.93 B4WQD9_SYNS7 YCII-related domain superfamily; m/z 10316.30 A0A4V1DHG1_9SYNE YCII domain-containing protein

MISSING IN SAMPLE: 24 peaks, uncharacterized proteins plus m/z 4896.64 K9SYJ1_9SYNE Photosystem II reaction center protein Ycf12; m/z 5983.25 Q05TX4_9SYNE Uncharacterized protein - G3P_acyltransf super family; m/z 6165.01 A4CU28_SYNPV Putative hydroxylase; m/z 6917.87 B4WLS7_SYNS7 Uncharacterized protein - Cys_rich_CPXG; m/z 6935.76 A0A0G8ARK5_9SYNE Photosystem II reaction center protein J; m/z 8343.64 A5GNK4_SYNPW CP12 domain-containing protein; m/z 8724.39 A0A2P7EFI8_9SYNE Protein translocase subunit SecE; m/z 8724.39 A5GT09_SYNR3 Predicted periplasmic or secreted lipoprotein; m/z 8764.02 Q3AYN7_SYNS9 Possible high light inducible protein; m/z 8764.02 Q05TX2_9SYNE Antitoxin; m/z 9780.29 50S ribosomal protein L27; m/z 12403.77 B4WSH1_SYNS7 Photosystem II reaction center Psb28 protein

2 and 5 μ M, 3 weeks

MISSING IN CONTROL: 14 peaks, uncharacterized proteins plus m/z 4719.88 K9SUR2_9SYNE Cytochrome b559 subunit beta; m/z 5121.15 A0A1J0PBS6_9SYNE High light inducible protein; m/z 5121.15 A3Z318_9SYNE Glutaredoxin-related protein (Fragment); m/z 7308.65 A0A4P7ZUJ9_9SYNE Photosystem II reaction center protein H; m/z 9351.08 A0A164CHG7_9SYNE Molybdopterin synthase sulfur carrier subunit

MISSING IN SAMPLE: 15 peaks, uncharacterized proteins plus m/z 5272.37 A5GN15_SYNPW Conserved hypothetical membrane protein; m/z 6579.14 Q0I6T3_SYNS3 Putative inner membrane protein; m/z 7572.62 Q0I6F2_SYNS3 Putative transcriptional regulator; m/z 7861.06 B1XKL4_SYNP2 Ferredoxin-thioredoxin reductase variable chain; m/z 7963.73 NDHO_SYNJ B NAD(P)H-quinone oxidoreductase subunit O; m/z 7963.73 A0A1J0PC15_9SYNE Thiamine biosynthesis protein ThiS; m/z 7963.73 Q2JK49_SYNJ B CAB/ELIP/HLIP family protein; m/z 8712.62 A5GPD7_SYNPW Protein translocase subunit SecE

10 μ M, 3 weeks

MISSING IN CONTROL: 33 peaks, uncharacterized proteins plus m/z 3164.66 Cytochrome b6-f complex subunit 8; m/z 3594.45 PETN_SYNPW Cytochrome b6-f complex subunit 8; m/z 3812.22 PSBM_SYNR3 Photosystem II reaction center protein M; m/z 3873.99 K9RVZ0_SYNP3 Photosystem II reaction center protein M; m/z 4082.61 K9SR44_9SYNE Photosystem II reaction center protein T; m/z 4226.23 B4WM03_SYNS7 Photosystem II reaction center protein I; m/z 4297.63 A0A164B792_9SYNE Photosystem II protein Y; m/z 4655.46 A3YYU1_9SYNE Uncharacterized protein HTH_55 super family, RctB helix turn helix domain; m/z 4844.49 Q0I7S6_SYNS3 Photosystem II protein Y; m/z 4912.08 B4WQE6_SYNS7 DDE_Tnp_IS240 domain-containing protein; m/z 4959.73 K9RS61_SYNP3 Photosystem I reaction center subunit IX; m/z 5105.81 PSBF_SYNS9 Cytochrome b559 subunit beta; m/z 5121.46 A0A1J0PBS6_9SYNE High light inducible protein; m/z 5121.46 K9SQX4_9SYNE Uncharacterized protein - ExoD super family, Exopolysaccharide synthesis; m/z 5121.46 A3Z318_9SYNE Glutaredoxin-related protein (Fragment); m/z 5344.85 K9RT21_SYNP3 Uncharacterized protein HicB, Predicted nuclease of the RNase H fold; m/z 6891.09 K9RTR4_SYNP3 50S ribosomal protein L32

MISSING IN SAMPLE: 44 peaks, uncharacterized proteins plus m/z 4896.62 K9SYJ1_9SYNE Photosystem II reaction center protein Ycf12; m/z 5272.37 A5GN15_SYNPW Conserved hypothetical membrane protein;

m/z 5997.26 B1XIS0_SYNP2 Conserved hypothetical membrane protein; m/z 6165.65 A4CU28_SYNPV Putative hydroxylase; m/z 6294.48 A0A4P7ZXQ6_9SYNE RHH_5 domain-containing protein; m/z 6408.12 K9SVD1_9SYNE Sec-independent protein translocase protein TatA; m/z 6579.14 Q0I6T3_SYNS3 Putative inner membrane protein; m/z 6788.29 A0A4V1DI31_9SYNE High light inducible protein; m/z 6937.00 B1XKM3_SYNP2 Conserved hypothetical membrane protein; m/z 7629.61 RL33_SYNS9 50S ribosomal protein L33; m/z 7663.31 A0A164C6F4_9SYNE Photosystem I reaction center subunit IV; m/z 7663.31 K9RVM2_SYNP3 Uncharacterized protein NdhS, NAD(P)H dehydrogenase subunit S; m/z 7963.73 Q2JK49_SYNJB CAB/ELIP/HLIP family protein; m/z 7963.73 A0A1J0PC15_9SYNE Thiamine biosynthesis protein ThiS; m/z 7963.73 NDHO_SYNJB NAD(P)H-quinone oxidoreductase subunit O; m/z 9741.52 A4CXC4_SYNPV NAD(P)H-quinone oxidoreductase subunit; m/z 9741.52 A3Z2T2_9SYNE Putative multidrug efflux ABC transporter (Fragment); m/z 9794.99 RL31_SYNS3 50S ribosomal protein L31; m/z 11513.60 Q0ID52_SYNS3 Uncharacterized yci family conserved protein

BROMOPYRUVIC ACID

1 – 5 μ M, 1 week

MISSING IN CONTROL: no significant changes

MISSING IN SAMPLE: no significant changes

2 and 5 μ M, 2 weeks

MISSING IN CONTROL: 10 peaks, uncharacterized proteins plus m/z 3057.24 PSAM_SYNJB Photosystem I reaction center subunit XII; m/z 4041.47 PSBJ_SYNJB Photosystem II reaction center protein J; m/z 4406.08 A0A164CVM2_9SYNE Photosystem I reaction center subunit IX; m/z 7396.07 2 μ M A5GUT0_SYNR3 Sulfur transfer protein involved in thiamine biosynthesis; m/z 8875.83 2 μ M A0A1J0PE26_9SYNE Exodeoxyribonuclease 7 small subunit; m/z 8875.83 2 μ M Q05RG5_9SYNE Putative carboxysome peptide B; m/z 9040.23 B4WH35_SYNS7 50S ribosomal protein L28; m/z 10198.26 2 μ M RS15_SYNS9 30S ribosomal protein S15; m/z 10198.26 2 μ M A0A0G8AXA2_9SYNE Cell division topological specificity factor; m/z 13984.01 2 μ M K9SSQ4_9SYNE ATP synthase epsilon chain; m/z 13984.01 2 μ M B1X133_SYNP2 Glyoxalase_6 domain-containing protein; m/z 14373.91 2 μ M A0A1J0P8I1_9SYNE DNA-binding protein; m/z 14373.91 2 μ M A3Z2U0_9SYNE Heat shock protein DnaJ-like

MISSING IN SAMPLE: 20 peaks, uncharacterized proteins plus m/z 3286.32 PETM_SYNR3 Cytochrome b6-f complex subunit 7; m/z 3854.36 Q05SW8_9SYNE Branched-chain amino acid aminotransferase; m/z 5299.83 A3Z2N9_9SYNE Glutamate 5-kinase, ProB-related; m/z 5854.00 Q0IDS1_SYNS3 Uncharacterized protein - NTase_sub_bind super family, Nucleotidyltransferase substrate binding protein like; m/z 6180.11 RL32_SYNS9 50S ribosomal protein L32; m/z 6571.67 A0A164B4C6_9SYNE Cytochrome b6-f complex subunit 5; m/z 6571.67 K9SQK4_9SYNE Uncharacterized protein - COG3415 super family, transposase [Mobilome: prophages, transposons]; m/z 7312.37 A0A162BKL1_9SYNE Nif11 domain-containing protein; m/z 8206.35 Q3AUQ7_SYNS9 Sec-independent protein translocase protein TatA; m/z 8206.35 A0A4P7ZTGO_9SYNE Sulfur carrier protein ThiS

10 μ M, 1 and 2 weeks

MISSING IN CONTROL: 28 peaks after 1 week of incubation (almost all these signals were missing after 2 weeks), uncharacterized proteins plus m/z 3517.27 PETN_SYNR3 Cytochrome b6-f complex subunit 8; m/z 4455.44 K9STJ1_9SYNE Uncharacterized protein - PLN00180 super family, NDF6 (NDH-dependent flow 6); m/z 7130.37 A3Z2C8_9SYNE Sigma factor SigF; m/z 7307.50 A0A4P7ZUJ9_9SYNE Photosystem II reaction center protein H; m/z 7307.50 Q05W71_9SYNE Possible high light inducible protein; m/z 8025.83 K9RWY0_SYNP3 Ferredoxin; m/z 9037.00 A5GUA2_SYNR3 Uncharacterized protein - Aquarius_N super family, Intron-binding protein aquarius N-terminus; m/z 9188.29 A0A0G8AXP1_9SYNE Uncharacterized protein - small_w_EgtBD super family, hercynine metabolism small protein; m/z 9802.61 Q3AZD0_SYNS9 Bacterial nucleoid protein Hbs - histone-like DNA-binding protein HU

MISSING IN SAMPLE: 40 peaks, uncharacterized proteins plus m/z 3765.29 K9SW16_9SYNE Cytochrome B6-F complex subunit 5; m/z 3815.77 K9RXC9_SYNP3 Photosystem II reaction center protein T; m/z 3815.77 A0A1J0P8S9_9SYNE Photosystem II reaction center protein Ycf12; m/z 4432.62 PSAJ_SYNR3 Photosystem I reaction center subunit IX; m/z 5399.39 A0A164CW13_9SYNE Uncharacterized protein - Phytase-like super family; m/z 5540.67 A3YXF2_9SYNE Photosystem II reaction center protein K; m/z 5997.66 B1XIS0_SYNP2 Conserved hypothetical membrane protein; m/z 6070.47 B4WRS1_SYNS7 Uncharacterized protein - GST_C_family super family, -terminal, alpha helical domain of the Glutathione S-transferase family; m/z 6165.62 A4CU28_SYNPV Putative hydroxylase; m/z 6331.58 B4WKF5_SYNS7 Uncharacterized protein - PRK07208 super family; m/z 6346.23 Q0I967_SYNS3 Uncharacterized protein - NADB_Rossmann super family; m/z 6426.47 A0A164CQ37_9SYNE Uncharacterized protein - NdhS, NAD(P)H dehydrogenase subunit S; m/z 6683.20 - Q3B0S1_SYNS9 Photosystem II reaction center protein

Z; m/z 7517.90 A5GKZ1_SYNPW Zn-ribbon protein; m/z 7517.90 A5GRA1_SYNR3 Uncharacterized conserved membrane protein - Pmp3, Proteolipid membrane potential modulator; m/z 7629.62 RL33_SYNS9 50S ribosomal protein L33; m/z 7664.05 A0A164C6F4_9SYNE Photosystem I reaction center subunit IV; m/z 7664.05 K9RVM2_SYNP3 Uncharacterized protein - NdhS, NAD(P)H dehydrogenase subunit S; m/z 7664.05 Q05RA3_9SYNE Nif11 domain-containing protein; m/z 7962.73 NDHO_SYNJB NAD(P)H-quinone oxidoreductase subunit O; m/z 8206.35 Q3AUQ7_SYNS9 Sec-independent protein translocase protein TatA; m/z 8206.35 A0A4P7ZTGO_9SYNE Sulfur carrier protein ThiS; m/z 8762.98 K9SS07_9SYNE DNA-directed RNA polymerase subunit omega; m/z 8762.98 A5GS68_SYNR3 Carboxysome peptide B; m/z 9721.41 Q3AZ30_SYNS9 Bacterial translation initiation factor 1 (BIF-1); m/z 9721.41 Q05XK8_9SYNE Translation initiation factor IF-1; m/z 9738.37 A0A4P7ZUR7_9SYNE CopG family transcriptional regulator; m/z 9738.37 A5GMC7_SYNPW Uncharacterized conserved membrane protein - kdpB super family, K⁺-transporting ATPase, B subunit; m/z 9795.32 RL31_SYNS3 50S ribosomal protein L31

2 μM, 3 weeks

MISSING IN CONTROL: 1 peak, m/z 8769.86 A4CWR9_SYNPV UPF0033 domain-containing protein - SirA_YedF_YeeD, irA, YedF, and YeeD. Two-layered alpha/beta sandwich domain

MISSING IN SAMPLE: 8 peaks, uncharacterized proteins plus m/z 5273.20 A5GN15_SYNPW Conserved hypothetical membrane protein; m/z 5914.73 A4CT42_SYNPV PCP_red domain-containing protein

5 μM, 3 weeks

MISSING IN CONTROL: 2 peaks including m/z 7106.65 A0A4P7ZUN2_9SYNE RHH_5 domain-containing protein; m/z 7913.07 ATPL_SYNS9 ATP synthase subunit c

MISSING IN SAMPLE: numerous peaks were missing

10 μM, 3 weeks

MISSING IN CONTROL: no differential peaks

MISSING IN SAMPLE: almost all peaks were missing

DEOXYGLUCOSE

1 and 2 μ M, 1 week

MISSING IN CONTROL: 9 peaks (at 1 μ M), 8 peaks (at 2 μ M), uncharacterized proteins

MISSING IN SAMPLE: 4 peaks, uncharacterized proteins

5 and 10 μ M, 1 week

MISSING IN CONTROL: 24 peaks (at 5 μ M), 5 peaks (at 10 μ M), uncharacterized proteins plus

5 μ M – m/z 5237.24 Q05TE9_9SYNE Phycocyanobilin:ferredoxin oxidoreductase, m/z 5269.97 K9SW43_9SYNE 50S ribosomal protein L34, m/z 5950.52 valyl-tRNA synthetase, m/z 6093.95 A4CU00_SYNPV Nif11 domain-containing protein, m/z 6278.87 A4CWX9_SYNPV Cyanate hydratase, m/z 6662.88 Q05UL3_9SYNE Photosystem II reaction center protein Z,

10 μ M – m/z 5251.95 Q0I8E4_SYNS3 Lhc-like protein LhI4

MISSING IN SAMPLE: 6 peaks, uncharacterized proteins plus m/z 8872.91 A4CUL1_SYNPV 50S ribosomal protein L28, m/z 12413.95 B4WJM2_SYNS7 2Fe-2S ferredoxin-type domain-containing protein

1 and 2 μ M, 2 weeks

MISSING IN CONTROL: 11 peaks (at 1 μ M), 17 peaks (at 2 μ M), uncharacterized proteins plus

1 μ M – m/z 5803.10 Q3AZA1_SYNS9 Putative high light inducible protein, m/z 5982.24 A0A4P7ZY82_9SYNE Cytochrome B6, m/z 10309.6 K9SZ84_9SYNE Putative transcriptional regulator

2 μ M – m/z 3812.30 PSBM_SYNR3 Photosystem II reaction center protein M, m/z 6664.24 PSBZ_SYNJB Photosystem II reaction center protein Z, m/z 6863.59 A3Z082_9SYNE Uncharacterized protein NAD(P)⁺-dependent aldehyde dehydrogenase superfamily / Q0I7D7_SYNS3 Possible high light inducible protein-related protein,

MISSING IN SAMPLE: 11 peaks (at 1 μ M), 12 peaks (at 2 μ M), uncharacterized proteins plus

1 μ M – m/z 11019.56 A0A163ZQG7_9SYNE Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit

2 μ M – m/z 5034.03 A5GQF3_SYNR3 Cytochrome b559 subunit beta/ Q0I7Z7_SYNS3 Lhc-like protein LhI4

1 and 2 μM – m/z 4765.27 PSBF_SYNP2 Cytochrome b559 subunit beta, m/z 11736.72 A4CRP3_SYNPV Thioredoxin

5 and 10 μM , 2 weeks

MISSING IN CONTROL: 24 peaks (at 5 μM), 13 peaks (at 10 μM), uncharacterized proteins plus

5 μM – m/z 5952.43 valyl-tRNA synthetase, m/z 6095.30 A4CU00_SYNPV Nif11 domain-containing protein, /z 6536.36 K9RPF0_SYNP3 CsbD domain-containing protein, m/z 7048.71 K9SP56_9SYNE Photosystem II reaction center protein H, m/z 7922.45 A3YYG0_9SYNE Putative high light inducible protein, m/z 9012.96 Q05TX6_9SYNE Antitoxin, m/z 10301.43 A5GT93_SYNR3 CP12 domain-containing protein

10 μM – m/z 5616.59 A0A1J0PA22_9SYNE UPF0391 membrane protein, m/z 6191.88 Q05Q08_9SYNE Possible transcriptional regulator, luxR family protein, m/z 6535.72 K9RPF0_SYNP3 CsbD domain-containing protein, m/z 7944.18 A0A1J0PCN5_9SYNE Ferredoxin / B4WSJ5_SYNS7 Photosystem I reaction center subunit IV, m/z 9012.75 Q05TX6_9SYNE Antitoxin

MISSING IN SAMPLE: 8 peaks (at 5 μM), 11 peaks (at 10 μM), uncharacterized proteins plus

10 μM – m/z 3571.58 PSAM_SYNS9 Photosystem I reaction center subunit XII, m/z 7614.12 PSAE_SYNS9 Photosystem I reaction center subunit IV, m/z 9936.31 A0A2P7EFU2_9SYNE 4a-hydroxytetrahydrobiopterin dehydratase,

5 and 10 μM m/z 11736.71 A4CRP3_SYNPV Thioredoxin, m/z 11844.24 Q3AZL8_SYNS9 Ferredoxin (2Fe-2S), m/z 12246.92 K9RQQ2_SYNP3 Putative transcriptional regulator

1 and 2 μM , 3 weeks

MISSING IN CONTROL: 12 peaks (at 1 μM), 7 peaks (at 2 μM), uncharacterized proteins plus

1 μM – m/z 6666.63 A0A4P7ZTH0_9SYNE Photosystem II reaction center protein Z, m/z 6997.93 A0A4P7ZW72_9SYNE Photosystem II reaction center protein J, m/z 9013.65 Q05TX6_9SYNE Antitoxin,

2 μM – m/z 7504.47 7504.47 B4WG39_SYNS7 Uncharacterized protein, EamA-like transporter family, m/z 7704.62 A0A4P7ZRH5_9SYNE Ferredoxin, m/z 7757.42 A5GV83_SYNR3 Phycobilisome 7.8 kDa linker

polypeptide, allophycocyanin-associated, core, m/z 11393.16 A0A164B4A7_9SYNE Cytochrome c6, m/z 11693.06 A5GV69_SYNR3 Ferredoxin

MISSING IN SAMPLE: 7 peaks (at 2 μ M), uncharacterized proteins plus

2 μ M – m/z 6500.13 Q3AZH3_SYNS9 Nif11 domain-containing protein, m/z 7107.07 A0A4P7ZUN2_9SYNE RHH_5 domain-containing protein, m/z 7807.31 A0A4P7ZQK1_9SYNE Nif11-like leader peptide family natural product, m/z 9136.27 A5GI41_SYNPW Uncharacterized protein, hercynine metabolism small protein

5 and 10 μ M, 3 weeks

MISSING IN CONTROL: 14 peaks (at 5 μ M), 12 peaks (at 10 μ M), uncharacterized proteins plus

5 μ M – m/z 3766.14 K9SW16_9SYNE Cytochrome B6-F complex subunit 5, m/z 4003.62 P95823_SYNE7 Photosystem I Psal protein, m/z 6923.78 A0A4P7ZUJ6_9SYNE CopG family transcriptional regulator, m/z 7813.96 Q0I950_SYNS3 Possible high light inducible protein-related protein / A3YVN2_9SYNE Phycobilisome 7.8 kDa linker polypeptide, allophycocyanin-associated, core, m/z 9072.32 Q05VL8_9SYNE Glutaredoxin, m/z 9745.22 A3YZ34_9SYNE 4a-hydroxytetrahydrobiopterin dehydratase, m/z 12023.8 Q3B072_SYNS9 NAD(P)H-quinone oxidoreductase subunit 4L, m/z 12670.7 Q31QE9_SYNE7 Transcriptional regulator, ArsR family

10 μ M – m/z 6115.11 Chlorophyll A-B binding protein, m/z 9270.74 A5GV49_SYNR3 Ferredoxin-thioredoxin reductase, variable chain, m/z 10978.92 A0A1J0P9G7_9SYNE Addiction module antitoxin RelB, m/z 11395.45 K9STF0_9SYNE NIL domain-containing protein

5 and 10 μ M – m/z 10518.35 Q3AWV1_SYNS9 4a-hydroxytetrahydrobiopterin dehydratase / A0A1J0PD95_9SYNE Carbon dioxide-concentrating protein CcmK

MISSING IN SAMPLE: 4 peaks (at 5 μ M), 18 peaks (at 10 μ M), uncharacterized proteins plus

10 μ M – m/z 5934.89 K9S0C9_SYNP3 Chlorophyll A-B binding protein, m/z 6151.76 Q3B0V3_SYNS9 High light-inducible protein-like, m/z 6500.13 Q3AZH3_SYNS9 Nif11 domain-containing protein, m/z 6521.36 K9SWP9_9SYNE CsbD domain-containing protein, m/z 6537.38 A0A4P7ZVT8_9SYNE Ribbon-helix-helix protein, CopG family, m/z 7321.16 A0A164A3E5_9SYNE Uncharacterized protein, DNA topoisomerase 4 subunit A, m/z 7807.31 A0A4P7ZQK1_9SYNE Nif11-like leader peptide family natural product, m/z 10164.11 A0A4P7ZXV3_9SYNE Cell division protein SepF

5 and 10 μ M – m/z 5863.19 A5GPZ9_SYNR3 HLIP family protein

FLUOROACETIC ACID

1 and 2 μ M, 1 week

MISSING IN CONTROL: 22 peaks, uncharacterized proteins plus

1 μ M – m/z 5681.35 A5GNH0_SYNPW High light inducible protein / A3YU00_9SYNE Nif11 domain-containing protein, m/z 6102.46 B1XIJ1_SYNP2 High light inducible protein hli5, m/z 6192.62 Q05Q08_9SYNE Possible transcriptional regulator, luxR family protein, m/z 6580.72 Q0I6T3_SYNS3 Putative inner membrane protein, m/z 7176.82 A5GNP5_SYNPW High light inducible protein, m/z 7306.04 Q2JP93_SYNJB Molybdenum-pterin binding domain protein, m/z 7779.32 A4CXM7_SYNPV Possible high light inducible protein, m/z 9776.22 A5GR75_SYNR3 DNA-binding protein HU / Q05SB4_9SYNE Nif11 domain-containing protein

2 μ M – m/z 5252.61 Q0I8E4_SYNS3 Lhc-like protein Lhl4, m/z 5737.61 A3Z2H0_9SYNE Aspartate aminotransferase, m/z 6861.19 Q0I8E5_SYNS3 Putative high light inducible protein, m/z 7613.70 PSAE_SYNS9 Photosystem I reaction center subunit IV / B4WUC4_SYNS7 DDE_Tnp_Tn3 domain-containing protein,

MISSING IN SAMPLE: 3 peaks, including m/z 9852.53 A4CVP3_SYNPV Ferredoxin, m/z 10318.99 A4CY55_SYNPV Guanosine-3',5'-bis(Diphosphate) 3'-diphosphatase, (PpGpp)ase

5 and 10 μ M, 1 week

MISSING IN CONTROL: 14 peaks (at 5 μ M), 4 peaks (at 10 μ M), uncharacterized proteins plus

5 μ M – m/z 3764.24 K9SW16_9SYNE Cytochrome B6-F complex subunit 5, m/z 3813.14 PSBM_SYNR3 Photosystem II reaction center protein M, m/z 5269.73 K9SW43_9SYNE 50S ribosomal protein L34, m/z 6094.18 A4CU00_SYNPV Nif11 domain-containing protein, m/z 7614.35 PSAE_SYNS9 Photosystem I reaction center subunit IV, m/z 7688.95 A0A4P7ZS73_9SYNE Ribbon-helix-helix protein, CopG family, m/z 7948.45, B1XKY2_SYNP2 Ferredoxin / A0A4P7ZRM0_9SYNE Acetyltransferase / B4WFM6_SYNS7 Uncharacterized protein, VapB_antitoxin Bacterial antitoxin of type II TA system, VapB, m/z 7963.88 NDHO_SYNJB NAD(P)H-quinone oxidoreductase subunit O, m/z 8713.04 A5GPD7_SYNPW Protein translocase subunit SecE

10 μ M – m/z 6094.18 A4CU00_SYNPV Nif11 domain-containing protein,

MISSING IN SAMPLE: 1 peak, uncharacterized protein

1 and 2 μ M, 2 weeks

MISSING IN CONTROL: 16 peaks, uncharacterized proteins plus

1 μ M – m/z 4546.04 Q05VL7_9SYNE Peptide chain release factor 2, m/z 4741.64 YCF12_SYNP2 Photosystem II reaction center protein Ycf12, m/z 5080.38 K9RSW9_SYNP3 Cytochrome b559 subunit beta, m/z 7436.99 A5GJR2_SYNPW Nif11 domain-containing protein, m/z 8036.83 B4WIY0_SYNS7 Ferredoxin, m/z 9135.30 NDHO_SYNS9 NAD(P)H-quinone oxidoreductase subunit O, m/z 9146.39 Q3AVY9_SYNS9 Glutaredoxin, m/z 11133.56 A4CWI1_SYNPV Ribonucleotide reductase (Class II) / Q31RE9_SYNE7 Ferredoxin (2Fe-2S), m/z 11817.36 A0A1J0P8W2_9SYNE Glutaredoxin

2 μ M – m/z 3765.64 K9SW16_9SYNE Cytochrome B6-F complex subunit 5, m/z 7649.37 K9SXJ5_9SYNE Photosystem I reaction center subunit IV / A0A1J0PD21_9SYNE High light inducible protein,

MISSING IN SAMPLE: 14 peaks (at 1 μ M) and 15 (at 2 μ M) peaks uncharacterized plus m/z 3566.49 A0A164C392_9SYNE Cytochrome b6-f complex subunit 8, m/z 4432.41 PSAJ_SYNR3 Photosystem I reaction center subunit IX, m/z 5914.05 A4CT42_SYNPV PCP_red domain-containing protein, m/z 5935.05 K9S0C9_SYNP3 Chlorophyll A-B binding protein, m/z 6138.62 A0A4P7ZV86_9SYNE Protochlorophyllide oxidoreductase, m/z 6925.29 K9RZ10_SYNP3 30S ribosomal protein S21, m/z 7963.74 NDHO_SYNJB NAD(P)H-quinone oxidoreductase subunit O, m/z 9012.54 Q05TX6_9SYNE Antitoxin

5 and 10 μ M, 2 weeks

MISSING IN CONTROL: 12 peaks, uncharacterized proteins plus

m/z 3829.00 Q05Q15_9SYNE Photosystem II reaction center protein M, m/z 4858.86 Q3AY61_SYNS9 Possible high light inducible protein, m/z 4913.48 B4WQE6_SYNS7 DDE_Tnp_IS240 domain-containing protein, m/z 5616.87 A0A1J0PA22_9SYNE UPF0391 membrane protein BM449_05130, m/z 7647.45 Q3AX15_SYNS9 ThiS, thiamine-biosynthesis, m/z 8712.51 A5GPD7_SYNPW Protein translocase subunit SecE, m/z 8749.87 A0A1J0PE01_9SYNE Cell division protein SepF / A5GLQ2_SYNPW High light inducible protein

MISSING IN SAMPLE: 10 peaks, uncharacterized proteins plus m/z 5935.05 K9S0C9_SYNP3 Chlorophyll A-B binding protein, m/z 6370.75 Q05WR3_9SYNE Possible high light inducible protein, m/z 6815.15 B4WSG7_SYNS7 Proto-chlorophyllide reductase 57 kD subunit superfamily / A0A1J0PC22_9SYNE Uncharacterized protein, SH3 super family Src Homology 3 domain superfamily

1 and 2 μ M, 3 weeks

MISSING IN CONTROL: 19 peaks (1 μ M), 13 peaks (2 μ M), uncharacterized proteins

1 μ M – m/z 3873.32 A3Z0W3_9SYNE Uncharacterized protein, PIN (PiIT N terminus) domain: Superfamily, m/z 3874.73 K9RVZ0_SYNP3 Photosystem II reaction center protein M, m/z 4020.79 A0A4P7ZWX4_9SYNE Photosystem I reaction center subunit VIII, m/z 7558.06 PSBH_SYNJB Photosystem II reaction center protein H, m/z 7575.47 RL35_SYNS9 50S ribosomal protein L35, m/z 8714.28 A5GPD7_SYNPW Protein translocase subunit SecE, m/z 9072.51 RL28_SYNP2 50S ribosomal protein L28, m/z 9345.85 RS17_SYNE7 30S ribosomal protein S17, m/z 9665.51 Q05UN9_9SYNE 50S ribosomal protein L35 / B4WLZ0_SYNS7 Putative membrane protein insertion efficiency factor

2 μ M – m/z 5121.12 A0A1J0PBS6_9SYNE High light inducible protein, m/z 5342.65 K9RZM0_SYNP3 Uncharacterized protein, ParE_toxin super family ParE toxin of type II toxin-antitoxin system, m/z 7645.26 A4CYF4_SYNPV Translocase / Q3AWH3_SYNS9 Salt-stress induced hydrophobic peptide, m/z 8680.94 A0A4P7ZTBO_9SYNE Uncharacterized protein, MazE_antitoxin super family Antidote-toxin recognition MazE, bacterial antitoxin

MISSING IN SAMPLE: 9 peaks (at 1 μ M), 15 peaks (at 2 μ M), uncharacterized proteins plus

1 μ M – m/z 11653.08 A0A1J0P988_9SYNE Thioredoxin

2 μ M – m/z 7305.72 Q2JP93_SYNJB Molybdenum-pterin binding domain protein / A0A1J0PAN2_9SYNE Photosystem II reaction center protein H, m/z 7650.50 K9SXJ5_9SYNE Photosystem I reaction center subunit IV / A0A1J0PD21_9SYNE High light inducible protein, m/z 8314.67 A0A4P7ZV37_9SYNE Ferrous iron transport protein A / A0A164D6F8_9SYNE Nif11 domain-containing protein / Q05SV1_9SYNE 30S ribosomal protein S18, m/z 8676.68 K9RU07_SYNP3 Ferredoxin / A5GQ62_SYNR3 Uncharacterized protein, hercynine metabolism small protein / B4WHG5_SYNS7 Translation initiation factor IF-1, m/z 9013.85 A0A164CD71_9SYNE Nif11 domain-containing / Q05TX6_9SYNE Antitoxin, m/z 9197.47 A0A4P7ZUZ9_9SYNE 50S ribosomal protein L31, m/z 12244.15 B1XPW9_SYNP2 Arsenical resistance operon repressor, ArsR family / A0A162BKT8_9SYNE Nucleoid-associated protein MITS9508_00776

5 and 10 μ M, 3 weeks

MISSING IN CONTROL: 5 peaks (at 5 μ M), 5 peaks (at 10 μ M), uncharacterized proteins plus

5 μ M – m/z 5727.78 Q05WU3_9SYNE Glutamate-1-semialdehyde aminotransferase, m/z 6991.74 A3YV23_9SYNE PINc domain-containing protein, m/z 7647.17 Q3AX15_SYNS9 ThiS, thiamine-biosynthesis,

10 μ M – m/z 6705.21 Q0IE04_SYNS3 Photosystem II reaction center protein Z, m/z 6993.79 A5GK98_SYNPW High light inducible protein / A4CTP9_SYNPV Possible high light inducible protein, m/z 10252.36 A5GRL7_SYNR3 Thioredoxin family protein

MISSING IN SAMPLE: 17 peaks (at 5 μ M), 10 peaks (at 10 μ M), uncharacterized proteins plus

5 μ M – m/z 7650.50 RL29_SYNE7 50S ribosomal protein L29 / K9SXJ5_9SYNE Photosystem I reaction center subunit IV / A0A1J0PD21_9SYNE High light inducible protein, m/z 8314.67 A0A4P7ZV37_9SYNE Ferrous iron transport protein / A0A164D6F8_9SYNE Nif11 domain-containing protein, m/z 9013.85 A0A164CD71_9SYNE Nif11 domain-containing protein / Q05TX6_9SYNE Antitoxin, m/z 10876.87 Q05YD5_9SYNE Possible SAP domain

10 μ M – m/z 6562.92 B4WTQ9_SYNS7 Ribulose biphosphate carboxylase, small subunit, m/z 7961.80 A4CUE3_SYNPV Ribulose-phosphate 3-epimerase, m/z 9197.47 A0A4P7ZUZ9_9SYNE 50S ribosomal protein L31, m/z 10303.74 B4WHE8_SYNS7 50S ribosomal protein L23,

5 and 10 μ M – m/z 10316.80 A0A4V1DHG1_9SYNE YCII domain-containing protein

MALONIC ACID

1 and 2 μ M, 1 week

MISSING IN CONTROL: 12 peaks, uncharacterized proteins plus

1 μ M – m/z 5711.06 B4WGD5_SYNS7 Uncharacterized protein, transcriptional regulators CsoR (copper-sensitive operon repressor), m/z 6920.21 B4WJ98_SYNS7 Uncharacterized protein, NdhS NAD(P)H dehydrogenase subunit S, m/z 7687.92 A0A4P7ZS73_9SYNE Ribbon-helix-helix protein, CopG family, m/z 9012.88 Q05TX6_9SYNE Antitoxin

MISSING IN SAMPLE: 7 peaks, uncharacterized proteins

5 and 10 μ M, 1 week

MISSING IN CONTROL: 6 peaks (at 5 μ M), 4 peaks (at 10 μ M), uncharacterized proteins plus

5 μ M – m/z 7791.75 B4WI75_SYNS7 Phycobilisome 7.8 kDa linker polypeptide, allophycocyanin-associated, core, m/z 7813.17 Q0I950_SYNS3 Possible high light inducible protein-related protein, m/z 9014.15 Q05TX6_9SYNE Antitoxin / A0A164CD71_9SYNE Nif11 domain-containing protein, m/z 9829.93 B1XMV8_SYNP2 ThiS family domain protein / A0A4P7ZS91_9SYNE RHH_5 domain-containing protein

10 μ M – m/z 7815.15 A3YVN2_9SYNE Phycobilisome 7.8 kDa linker polypeptide, allophycocyanin-associated, core, m/z 11988.34 Q0I8E6_SYNS3 Predicted SH3-like domain containing protein

MISSING IN SAMPLE: 4 peaks, uncharacterized proteins including m/z 8161.94 A5GLI5_SYNPW BoIA-like protein

1 and 2 μ M, 2 weeks

MISSING IN CONTROL: 5 peaks (1 μ M), 16 peaks (2 μ M), uncharacterized proteins plus

1 μ M – m/z 6990.71 A3YV23_9SYNE PINc domain-containing protein

2 μ M – m/z 5066.96 B4WR12_SYNS7 Photosystem II reaction center protein K, m/z 5950.75 K9RVM7_SYNP3 Uncharacterized protein, valS super family valyl-tRNA synthetase, m/z 6094.58 A4CU00_SYNPV Nif11 domain-containing protein, m/z 6520.90 K9SWP9_9SYNE CsbD domain-containing protein, m/z 6663.28 PSBZ_SYNJB Photosystem II reaction center protein Z, m/z 6807.83 B1XLD7_SYNP2 Copper-binding metallochaperone, m/z 6864.22 Q0I7D7_SYNS3 Possible high light inducible protein-related protein / A3Z082_9SYNE Uncharacterized protein, NAD(P)⁺-dependent aldehyde dehydrogenase superfamily, m/z 7556.01 K9RTG0_SYNP3 Chlorophyll A-B binding protein

MISSING IN SAMPLE: 9 peaks (1 μ M), 16 peaks (at 2 μ M) uncharacterized proteins plus

1 μ M – m/z 7650.77 K9SXJ5_9SYNE Photosystem I reaction center subunit IV / A0A1J0PD21_9SYNE High light inducible protein, m/z 8677.70 K9RU07_SYNP3 Ferredoxin / A5GQ62_SYNR3 Uncharacterized protein, hercynine metabolism small protein,

2 μ M – m/z 4859.99 Q3AY61_SYNS9 Possible high light inducible protein, m/z 6663.28 PSBZ_SYNJB Photosystem II reaction center protein Z, m/z 7703.70 A0A1J0PDL8_9SYNE Hydrogenase maturation

protein HypC / A0A4P7ZWN5_9SYNE CpcD/allophycocyanin linker domain-containing protein, m/z 8726.16 A5GT09_SYNR3 Predicted periplasmic or secreted lipoprotein, m/z 8764.94 Q3AYN7_SYNS9 Possible high light inducible protein / Q05TX2_9SYNE Antitoxin, m/z 9106.97 Q05VW9_9SYNE NAD(P)H-quinone oxidoreductase subunit O / A4CT67_SYNPV Cytochrome b559 subunit alpha / PSBE_SYNS3 Cytochrome b559 subunit alpha, m/z 10724.58 K9RPF6_SYNP3 Glutaredoxin-like domain (DUF836), m/z 12207.91 A5GNE6_SYNPW Nitrogen regulatory protein P-II, m/z 12244.67 A0A4P7ZSN5_9SYNE Hydrogenase maturation factor HypA / B1XPW9_SYNP2 Arsenical resistance operon repressor, ArsR family

1 and 2 μM – m/z 5983.37 A0A4P7ZY82_9SYNE Cytochrome B6

5 a 10 μM , 2 weeks

MISSING IN CONTROL: 7 peaks (at 5 μM), 10 peaks (at 10 μM), uncharacterized proteins plus

5 μM – m/z 3812.79 PSBM_SYNR3 Photosystem II reaction center protein M, m/z 4003.56 P95823_SYNE7 Photosystem I PsaI protein, m/z 7742.47 Q2JIJ4_SYNJB CP12 domain protein,

10 μM – m/z 5738.36 A3Z2H0_9SYNE Aspartate aminotransferase, m/z 6538.58 A0A4P7ZVT8_9SYNE Ribbon-helix-helix protein, CopG family

MISSING IN SAMPLE: 7 peaks (at 5 μM), 7 peaks (at 10 μM) uncharacterized peaks plus

5 μM – m/z 5710.14 B4WGD5_SYNS7 Uncharacterized protein, transcriptional regulators CsoR (copper-sensitive operon repressor), m/z 6920.59 B4WJ98_SYNS7 Uncharacterized protein, NAD(P)H dehydrogenase subunit S, m/z 7500.21 K9SWT6_9SYNE Putative transcriptional regulator, m/z 8764.94 Q3AYN7_SYNS9 Possible high light inducible protein / Q05TX2_9SYNE Antitoxin

10 μM – m/z 6354.00 A4CX12_SYNPV N-carbamoyl-L-amino acid amidohydrolase, m/z 6468.62 A8HTL9_SYNP2 NblA, m/z 7686.81 A0A164BQV3_9SYNE Phycobilisome 7.8 kDa linker polypeptide, allophycocyanin-associated, core

1 a 2 μM , 3 weeks

MISSING IN CONTROL: 15 peaks (at 1 μM), 8 peaks (at 2 μM), uncharacterized proteins plus

1 μM – m/z 6115.37 K9SXX0_9SYNE Chlorophyll A-B binding protein, m/z 6364.76 K9RMW4_SYNP3 Chlorophyll A-B binding protein, m/z 6652.21 A3Z1I4_9SYNE RNA-binding S4, m/z 6663.78 PSBZ_SYNJB Photosystem II reaction center protein Z, m/z 6991.38 A3YV23_9SYNE PINc domain-containing protein,

2 μM – m/z 5738.27 A3Z2H0_9SYNE Aspartate aminotransferase, m/z 6992.10 A3YV23_9SYNE PINc domain-containing protein, m/z 7967.98 B4WU84_SYNS7 Nif11 domain-containing protein

MISSING IN SAMPLE: 16 peaks (at 1 μM), 13 peaks (at 2 μM), uncharacterized proteins plus

1 μM – m/z 5548.95 B4WNV1_SYNS7 Uncharacterized protein, light-harvesting-like protein 3, m/z 6500.13 Q3AZH3_SYNS9 Nif11 domain-containing protein, m/z 7107.07 A0A4P7ZUN2_9SYNE RHH_5 domain-containing protein

2 μM – m/z 8313.43 A0A164D6F8_9SYNE Nif11 domain-containing protein, m/z 9136.27 A5GI41_SYNPW Uncharacterized protein, hercynine metabolism small protein

1 and 2 μM – m/z 5147.61 A3YXX8_9SYNE Uncharacterized protein, Pyruvate phosphate dikinase, m/z 5863.19 A5GPZ9_SYNR3 HLIP family protein, m/z 5934.89 K9S0C9_SYNP3 Chlorophyll A-B binding protein, m/z 8329.81 A3YV18_9SYNE Antitoxin, m/z 10164.11 A0A4P7ZXV3_9SYNE Cell division protein SepF, m/z 11526.27 A4CYB5_SYNPV SUI1 domain-containing protein, m/z 12250.37 K9SS56_9SYNE Carbon dioxide concentrating mechanism/carboxysome shell protein

5 and 10 μM , 3 weeks

MISSING IN CONTROL: 8 peaks (at 5 μM), 11 peaks (at 10 μM), uncharacterized proteins plus

5 μM – m/z 5199.17 PSBK_SYNR3 Photosystem II reaction center protein K, m/z 7519.27 A5GRA1_SYNR3 Uncharacterized conserved membrane protein, m/z 7557.35 K9RTG0_SYNP3 Chlorophyll A-B binding protein

10 μM – m/z 6366.36 K9RMW4_SYNP3 Chlorophyll A-B binding protein, m/z 6666.77 A0A4P7ZTH0_9SYNE Photosystem II reaction center protein Z, m/z 7506.62 A5GN33_SYNPW Hypothetical membrane protein, m/z 7560.45 B4WGY3_SYNS7 DDE_5 domain-containing protein / PSBH_SYNJB Photosystem II reaction center protein H, m/z 8706.92 B4WLDO_SYNS7 NAD(P)H-quinone oxidoreductase subunit L,

MISSING IN SAMPLE: 12 peaks (at 5 μM), 7 peaks (at 10 μM), uncharacterized proteins plus

5 μ M – m/z 5147.61 A3YXX8_9SYNE Uncharacterized protein, Pyruvate phosphate dikinase, m/z 5371.61 Q05WR3_9SYNE Possible high light inducible protein, m/z 5548.95 B4WNV1_SYNS7 Uncharacterized protein, light-harvesting-like protein 3, m/z 5934.89 K9S0C9_SYNP3 Chlorophyll A-B binding protein, m/z 6194.72 A0A4V1DHJ0_9SYNE 50S ribosomal protein L32, m/z 6772.71 A5GVH5_SYNR3 High light inducible protein, m/z 8313.43 A0A164BYD7_9SYNE Nif11 domain-containing protein, m/z 8329.81 A3YV18_9SYNE Antitoxin, m/z 9175.03 PSBE_SYNR3 Cytochrome b559 subunit alpha

10 μ M – m/z 11526.27 A4CYB5_SYNPV SUI1 domain-containing protein

5 and 10 μ M, m/z 5863.19 A5GPZ9_SYNR3 HLIP family protein, m/z 6500.13 Q3AZH3_SYNS9 Nif11 domain-containing protein, m/z 10164.11 A0A4P7ZXV3_9SYNE Cell division protein SepF

CHLORAMPHENICOL

1 μ M, 1 week

MISSING IN CONTROL: no difference

MISSING IN SAMPLE: just a few peaks, uncharacterized proteins

2 μ M, 1 week

MISSING IN CONTROL: no difference

MISSING IN SAMPLE: 1 peak, uncharacterized protein

5 μ M, 1 week

MISSING IN CONTROL: 2 peaks, including m/z 12629.31 K9SRF7_9SYNE Anti-sigma factor antagonist

MISSING IN SAMPLE: 13 peaks, uncharacterized proteins plus m/z 6520.99 K9SWP9_9SYNE CsbD domain-containing protein; m/z 6864.31 Q0I7D7_SYNS3 Possible high light inducible protein-related protein; m/z 6864.31 A3Z082_9SYNE Uncharacterized protein - NAD(P)⁺-dependent aldehyde dehydrogenase superfamily; m/z 7304.64 Q2JP93_SYNJB Molybdenum-pterin binding domain protein; m/z Q2JP93_SYNJB Molybdenum-pterin binding domain protein; m/z 7831.99 A0A0G8ATC7_9SYNE Stress-induced morphogen; m/z 8456.47 A3Z2M6_9SYNE YCII-related domain protein (Fragment); m/z 8456.47 Q3AYE7_SYNS9 Nif11 domain-containing protein

10 μ M, 1 week

MISSING IN CONTROL: 3 peaks, uncharacterized proteins

MISSING IN SAMPLE: m/z 8831.72 A0A1J0PC10_9SYNE SpoVT-AbrB domain-containing protein

1 μ M, 2 weeks

MISSING IN CONTROL: 2 peaks, uncharacterized proteins including m/z 11811.76 Q3AYG2_SYNS9 Cytochrome c6 (Soluble cytochrome f) (Cytochrome c553)

MISSING IN SAMPLE: 5 peaks, uncharacterized proteins plus m/z 6863.31 A3Z082_9SYNE Uncharacterized protein - ALDH-SF super family; m/z 6863.31 Q0I7D7_SYNS3 Possible high light inducible protein-related protein; A0A4P7ZW69_9SYNE Ribbon-helix-helix protein, CopG family; m/z 8207.29 K9SQD3_9SYNE 30S ribosomal protein S18

2 μ M, 2 weeks

MISSING IN CONTROL: 2 peaks, uncharacterized proteins including m/z 11812.34 A0A1J0PDR2_9SYNE Nucleoid-associated protein BM449 or A5GNU2_SYNPW RHH_5 domain-containing protein

MISSING IN SAMPLE: 13 peaks, uncharacterized proteins plus m/z 3764.80 K9SW16_9SYNE Cytochrome B6-F complex subunit 5; m/z 4859.77 Q3AY61_SYNS9 Possible high light inducible protein; m/z 4976.41 B4WKQ1_SYNS7 Protein PsbN; m/z 5710.98 B4WGD5_SYNS7 Uncharacterized protein - CsoR-like_DUF156 super family, Transcriptional regulators CsoR; m/z 6920.06 B4WJ98_SYNS7 Uncharacterized protein - NdhS NAD(P)H dehydrogenase subunit S; m/z 7176.96 A5GNP5_SYNPW High light inducible protein; m/z 7304.60 Q2JP93_SYNJB Molybdenum-pterin binding domain protein; m/z 7829.83 A5GII8_SYNPW Uncharacterized membrane protein; m/z 8207.29 K9SQD3_9SYNE 30S ribosomal protein S18; m/z 8315.07 A0A4P7ZV37_9SYNE Ferrous iron transport protein; m/z 8710.03 A0A163YG82_9SYNE CDP-6-deoxy-delta-3,4-glucoseen reductase; m/z 10765.39 A0A164CRS2_9SYNE Uncharacterized protein - DnaJ super family DnaJ-class molecular chaperone with C-terminal Zn finger domain

5 μ M, 2 weeks

MISSING IN CONTROL: 2 peaks, uncharacterized proteins

MISSING IN SAMPLE: 16 peaks, uncharacterized proteins plus m/z 4976.41 B4WKQ1_SYNS7 Protein PsbN; m/z 6095.00 A5GLD4_SYNPW Uncharacterized protein - Nucleotide-Binding Domain of the sugar kinase/HSP70/actin superfamily; m/z 6095.00 A4CU00_SYNPV Nif11 domain-containing protein; m/z 7176.96 A5GNP5_SYNPW High light inducible protein; m/z 7304.60 Q2JP93_SYNJB Molybdenum-pterin binding domain protein; m/z 9830.71 B1XMV8_SYNP2 ThiS family domain protein m/z 9830.71 A0A4P7ZS91_9SYNE RHH_5 domain-containing protein

10 μ M, 2 weeks

MISSING IN CONTROL: no difference

MISSING IN SAMPLE: outside exceptions, a majority of peaks disappeared

1 μ M, 3 weeks

MISSING IN CONTROL: 8 peaks, uncharacterized proteins plus m/z 5710.86 B4WGD5_SYNS7 Uncharacterized protein - CsoR-like_DUF156 super family, Transcriptional regulators CsoR; m/z 8207.71 K9SQD3_9SYNE 30S ribosomal protein S18

MISSING IN SAMPLE: 3 peaks including m/z 5239.89 A0A4V1DHX4_9SYNE Photosystem II reaction center protein K

2 μ M, 3 weeks

MISSING IN CONTROL: 9 peaks, m/z 5464.06 Q2JLF4_SYNJB Carbohydrate uptake ABC transporter-2 (CUT2) family, ATP-binding protein, truncation; m/z 5711.25 B4WGD5_SYNS7 CsoR-like_DUF156 super family cl00846 Transcriptional regulators; 7518.94 A4CXY5_SYNPV Salt-stress induced hydrophobic peptide; m/z 9755.82 A5GR99_SYNR3 Uncharacterized protein - chp_P_marinus_1 super family; m/z 9799.89 A3YUF7_9SYNE Glutaredoxin

MISSING IN SAMPLE: 4 peaks including m/z 4620.39 B4WU16_SYNS7 Y1_Tnp domain-containing protein

5 μ M, 3 weeks

MISSING IN CONTROL: 13 peaks, uncharacterized proteins plus m/z 5453.98 Q2JLF4_SYNJB Carbohydrate uptake ABC transporter-2 (CUT2) family, ATP-binding protein, truncation; m/z 8205.88 Q3AUQ7_SYNS9 Sec-independent protein translocase protein TatA; m/z 8710.47 A0A163YG82_9SYNE CDP-6-deoxy-delta-3,4-glucoseen reductase

MISSING IN SAMPLE: 6 peaks, uncharacterized proteins plus m/z 4620.39 B4WU16_SYNS7 Y1_Tnp domain-containing protein plus a few other uncharacterized proteins

10 μ M, 3 weeks

MISSING IN CONTROL: no differential peaks

MISSING IN SAMPLE: numerous peaks disappeared

STREPTOMYCIN

1 and 2 μ M, 1 week

MISSING IN CONTROL: no difference

MISSING IN SAMPLE: just a few peaks, uncharacterized proteins

5 μ M, 1 week

MISSING IN CONTROL: 1 peak, m/z 3872.91 A3ZOW3_9SYNE Uncharacterized protein - PIN_SF super family

MISSING IN SAMPLE: 9 peaks, uncharacterized proteins plus m/z 8109.22 A5GU94_SYNR3 BolA-like protein; m/z 8459.60 RPOZ_SYNS3 DNA-directed RNA polymerase subunit omega; m/z 9830.43 B1XMV8_SYNP2 ThiS family domain protein – sulfur carrier; m/z 12246.22 K9RQQ2_SYNP3 Putative transcriptional regulator

10 μ M, 1 week

MISSING IN CONTROL: 4 peaks, including m/z 3889.17 A3YUT5_9SYNE Photosystem II reaction center protein M; m/z 12578.68 A0A4P7ZVA0_9SYNE AIR synthase; m/z 12578.68 Q2JL23_SYNJB Iron-sulfur cluster assembly accessory protein

MISSING IN SAMPLE: 20 peaks, uncharacterized proteins plus m/z 4859.41 Q3AY61_SYNS9 Possible high light inducible protein; m/z 6407.77 K9SVD1_9SYNE Sec-independent protein translocase protein TatA; m/z 6993.12 A5GK98_SYNPW High light inducible protein; m/z 6993.12 A4CTP9_SYNPV Possible high light inducible protein; m/z 7177.29 A5GNP5_SYNPW High light inducible protein; m/z 8459.60 RPOZ_SYNS3 DNA-directed RNA polymerase subunit omega; m/z 9013.46 Q05TX6_9SYNE Antitoxin; m/z 9830.43 B1XMV8_SYNP2 ThiS family domain protein – sulfur carrier; m/z 9830.43 A0A4P7ZS91_9SYNE RHH_5 domain-containing protein – transcription regulator; m/z 12246.22 K9RQQ2_SYNP3 Putative transcriptional regulator

1 μ M, 2 weeks

MISSING IN CONTROL: 14 peaks, uncharacterized proteins plus m/z 3765.63 K9SW16_9SYNE Cytochrome B6-F complex subunit 5; m/z 3874.20 K9RVZ0_SYNP3 Photosystem II reaction center protein M; m/z 3874.20 A3Z0W3_9SYNE Uncharacterized protein - PIN_SF super family; m/z 5170.29 Q05UQ6_9SYNE Uncharacterized protein - Medium chain reductase/dehydrogenase (MDR)/zinc-dependent alcohol dehydrogenase-like family; m/z 7532.87 A0A4P7ZV92_9SYNE RHH_5 domain-containing protein; m/z 8711.49 A5GPD7_SYNPW Protein translocase subunit SecE; m/z 10373.54 A3YYK3_9SYNE RNA-binding protein RbpD; m/z 12024.07 Q3B072_SYNS9 NAD(P)H-quinone oxidoreductase subunit 4L; m/z 12578.41 A0A4P7ZVA0_9SYNE AIR synthase

MISSING IN SAMPLE: 28 peaks, uncharacterized proteins plus m/z 4505.66 PSBL_SYNS3 Photosystem II reaction center protein L; m/z 5382.88 A4CRN4_SYNPV 50S ribosomal protein L34; m/z 5842.06 B4WII5_SYNS7 Photosystem I reaction center subunit VIII; m/z 5983.44 Q05TX4_9SYNE Uncharacterized protein - Glycerol-3-phosphate acyltransferase; m/z 6166.07 A4CU28_SYNPV Putative hydroxylase; m/z 6345.55 Q0I967_SYNS3 Uncharacterized protein - NADB_Rossmann super family; m/z 7627.56 RL35_SYNJB 50S ribosomal protein L35; m/z 7662.95 K9RVM2_SYNP3 Uncharacterized protein - NAD(P)H dehydrogenase subunit S; m/z 7963.08 NDHO_SYNJB NAD(P)H-quinone oxidoreductase subunit O; m/z 8230.69 Q31RI2_SYNE7 Uncharacterized protein - Unstab_antitox; m/z 9012.75 Q05TX6_9SYNE

Antitoxin; m/z 11684.22 K9SYX4_9SYNE UPF0060 membrane protein; m/z 14172.83 CRCB2_SYNS9
Putative fluoride ion transporter CrcB 2

2, 5 and 10 μ M, 2 weeks

MISSING IN CONTROL: up to 20 peaks, uncharacterized proteins plus m/z 3765.63 K9SW16_9SYNE
Cytochrome B6-F complex subunit 5; m/z 3874.26 K9RVZ0_SYNP3 Photosystem II reaction center protein
M; m/z 3909.27 PSBM_SYNE7 Photosystem II reaction center protein M; m/z 4082.06 K9SR44_9SYNE
Photosystem II reaction center protein T; m/z 5402.01 K9SQ74_9SYNE Uncharacterized protein -
Flavin_utilizing_monooxygenases super family; m/z 7519.17 A4CXY5_SYNPV Salt-stress induced
hydrophobic peptide; m/z 7532.70 A0A4P7ZV92_9SYNE RHH_5 domain-containing protein; m/z 8711.30
A0A163YG82_9SYNE CDP-6-deoxy-delta-3,4-glucose reductase; m/z 8711.30 A5GPD7_SYNPW Protein
translocase subunit SecE; m/z 8711.30 K9SS39_9SYNE Photosystem I reaction center subunit Psak; m/z
10414.77 A0A4P7ZVNO_9SYNE Galactose oxidase; m/z 12576.59 K9SR95_9SYNE Photosystem II reaction
center Psb28 protein

MISSING IN SAMPLE: up to 36 peaks, uncharacterized proteins plus m/z 6070.03 B4WRS1_SYNS7
Uncharacterized protein - GST_C_family super family; m/z 6166.07 A4CU28_SYNPV Putative hydroxylase;
m/z 6278.80 A4CWX9_SYNPV Cyanate hydratase; m/z 6345.55 Q0I967_SYNS3 Uncharacterized protein -
NADB_Rossmann super family; m/z 6408.23 K9SVD1_9SYNE Sec-independent protein translocase
protein TatA; m/z 6663.46 A5GNQ1_SYNPW Uncharacterized conserved membrane protein; m/z
7305.54 A4CQV2_SYNPV Uncharacterized protein - TNFRSF super family; m/z 7629.66 RL33_SYNS9 50S
ribosomal protein L33; m/z 7662.95 K9RVM2_SYNP3 Uncharacterized protein NAD(P)H dehydrogenase
subunit S; m/z 7948.06 B4WFM6_SYNS7 Uncharacterized protein - VapB_antitoxin; m/z 7948.06
A0A4P7ZRM0_9SYNE Acetyltransferase; m/z 7948.06 B1XKY2_SYNP2 Ferredoxin; m/z 7963.08
NDHO_SYNJB NAD(P)H-quinone oxidoreductase subunit O; m/z 8230.69 Q31RI2_SYNE7 Uncharacterized
protein - Unstab_antitox; m/z 9012.75 Q05TX6_9SYNE Antitoxin; m/z 9829.88 A0A4P7ZS91_9SYNE
RHH_5 domain-containing protein - transcription regulator; m/z 9829.88 B1XMV8_SYNP2 ThiS family
domain protein; m/z 11513.81 Q0ID52_SYNS3 Uncharacterized yciI family conserved protein; m/z
11684.22 K9SYX4_9SYNE UPF0060 membrane protein; m/z 14172.83 CRCB2_SYNS9 Putative fluoride ion
transporter CrcB; m/z 14172.83 A5GUG5_SYNR3 Ferric uptake regulator family protein

1, 2, 5 and 10 μ M, 3 weeks

MISSING IN CONTROL: up to 20 peaks, uncharacterized proteins plus m/z 3872.70 A3Z0W3_9SYNE Uncharacterized protein - PIN_SF super family; m/z 4764.66 PSBF_SYNP2 Cytochrome b559 subunit beta; m/z 5149.93 A3YYY5_9SYNE Bacterial metallothionein; m/z 5402.09 5 μ M K9SQ74_9SYNE Uncharacterized protein - Flavin_utilizing_monooxygenases super family; m/z 5698.26 5 μ M Q0I7M0_SYNS3 Possible high light inducible protein; m/z 5752.98 5 μ M A0A4P7ZT99_9SYNE High light inducible protein; m/z 9255.16 5 μ M RPOZ_SYNS9 DNA-directed RNA polymerase subunit omega; m/z 12576.08 K9SR95_9SYNE Photosystem II reaction center Psb28 protein

MISSING IN SAMPLE: up to 24 peaks were missing

MICROGRAVITY

2 and 3 weeks

MISSING IN CONTROL: 35 peaks, uncharacterized proteins plus m/z 3873.25 A3Z0W3_9SYNE Uncharacterized protein - PIN_SF super family; m/z 4043.25 PSBJ_SYNJ B Photosystem II reaction center protein J; m/z 4080.94 K9SR44_9SYNE Photosystem II reaction center protein T; m/z 4619.92 B4WU16_SYNS7 Y1_Tnp domain-containing protein; m/z 4989.10 Q05RZ3_9SYNE Possible high light inducible protein; m/z 5120.49 A3Z318_9SYNE Glutaredoxin-related protein (Fragment); m/z 5120.49 A0A1J0PBS6_9SYNE High light inducible protein; m/z 5372.84 RL34_SYNS3 50S ribosomal protein L34; m/z 9146.22 Q3AVY9_SYNS9 Glutaredoxin; m/z 12023.02 A0A162CTQ0_9SYNE MazG nucleotide pyrophosphohydrolase domain protein

MISSING IN SAMPLE: 44 peaks, uncharacterized proteins plus m/z 3574.29 PSAM_SYNPW Photosystem I reaction center subunit XII; m/z 3626.34 PETN_SYNS9 Cytochrome b6-f complex subunit 8; m/z 3911.25 A0A1J0PC67_9SYNE Photosystem II reaction center protein M; m/z 4333.13 A3YY19_9SYNE Photosystem I reaction center subunit IX; m/z 4431.18 PSAJ_SYNR3 Photosystem I reaction center subunit IX; m/z 4962.98 A3YVC3_9SYNE Possible high light inducible polypeptide HliC; m/z B4WKQ1_SYNS7 Protein PsbN; 4977.06 m/z 4994.44 A3YTM9_9SYNE Cytochrome b559 subunit beta; m/z 5099.57 A3YW30_9SYNE Possible high light inducible protein; m/z 5539.90 A3YXF2_9SYNE Photosystem II reaction center protein K; m/z 5757.04 Q05WF0_9SYNE High light inducible protein hli2; m/z 6297.80 B1XMX1_SYNP2 Uncharacterized protein - NdhS, NAD(P)H dehydrogenase subunit S; m/z 6346.55 Q0I967_SYNS3 Uncharacterized protein - NADB_Rossmann super family; m/z 6427.62 Q05UF0_9SYNE

Uncharacterized protein - NdhS, NAD(P)H dehydrogenase subunit S; m/z 6469.68 Q0I6B3_SYNS3 Valyl-tRNA synthetase; m/z 7087.99 A3Z0W8_9SYNE Uncharacterized protein - VapB_antitoxin; m/z 7948.26 B1XKY2_SYNP2 Ferredoxin; m/z 7948.26 A0A4P7ZRM0_9SYNE Acetyltransferase; m/z 7948.26 B4WFM6_SYNS7 Uncharacterized protein - VapB_antitoxin; m/z 8330.00 A3YV18_9SYNE Antitoxin; m/z 8502.86 B4WVY0_SYNS7 HTH cro/C1-type domain-containing protein - HTH_XRE, Helix-turn-helix XRE-family like proteins; m/z 8502.86 Q05UH5_9SYNE Uncharacterized protein - small_w_EgtBD, hercynine metabolism small protein; m/z 8578.39 Q3AUX7_SYNS9 Transcriptional regulator, LuxR family; m/z 9795.57 RL31_SYNS3 50S ribosomal protein L31; m/z 10781.42 A4CVU0_SYNPV Putative nicotinamide nucleotide transhydrogenase, subunit alpha 2 (A2); m/z 10781.42 A5GM89_SYNPW NAD/NADP transhydrogenase subunit alpha part 2