

Understanding nanoplastics toxicity and their interaction with engineered cationic nanopolymers in microalgae by physiological and proteomic approaches

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Proteomic analysis

In-Gel Digestion (Stacking gel)

The protein extracts from three independent replicates of *Anabaena* exposed to PS-NPs, G7 and their binary mixture for 72h plus the control non-exposed cyanobacterial cells were suspended in a volume up to 50 μ l of sample buffer, and then applied onto 1.2 cm wide wells of a conventional SDS-PAGE gel (0.75 mm thick, 4% stacking, and 10% resolving). The run was stopped as soon as the front entered 3 mm into the resolving gel, so that the whole proteome became concentrated in the stacking/resolving gel interface. The unseparated protein bands were visualized by Coomassie staining, excised, cut into cubes (2 x 2 mm), and placed in 0.5 ml microcentrifuge tubes.¹ The gel pieces were destained in acetonitrile:water (ACN:H₂O, 1:1), reduced and alkylated (disulfide bonds from cysteinyl residues were reduced with 10 mM DTT for 1 h at 56 °C, and then thiol groups were alkylated with 10 mM iodoacetamide for 30 min at room temperature in darkness) and digested *in situ* with sequencing-grade trypsin (Promega, Madison, WI) as described by Shevchenko et al.² with minor modifications. The gel pieces were dehydrated by removing all liquid using sufficient ACN. Acetonitrile was pipetted out and the gel pieces were dried in a speedvac. The dried gel pieces were re-hydrated in 100 mM Tris-HCl pH 8, 10mM CaCl₂ with 60 ng/ μ l trypsin at 5:1 protein:enzyme (w/w) ratio. The tubes were kept on ice for 2 h and incubated at 37 °C for 12 h. Digestion was stopped by the addition of 1% trifluoroacetic acid (TFA). Whole supernatants were dried and desalted onto OMIX Pipette tips C18 (Agilent Technologies) prior to mass spectrometric analysis.

TMT labeling and high pH fractionation

The resultant peptide mixture from desalted protein tryptic digest (50 μ g) was labeled using chemicals from the TMT six plex Isobaric Mass Tagging Kit (Thermo Fisher Scientific, MA, USA) (Reagents 126 for the Control sample, 128 for the 65 sample, 130 for the 45 sample and 131 for the Mix sample) essentially as described by manufacturer. Briefly, peptides were dissolved in 50 μ L of 100 mM triethylammonium bicarbonate (TEAB), adjusted to pH 8. For labeling, each TMT reagent was dissolved in 41 μ L of ACN and added to the respective peptide mixture and then incubated at room temperature for one hour. Labelling was stopped by the addition of 8 μ L 5% hydroxylamine. Whole supernatants were

dried and the four samples were mixed to obtain the “4plex-labeled mixture”. The mixture was analyzed by RP-LC-MS/MS to check the efficiency of the labelling.³

Fractionation

The sample was then fractionated using the Pierce High pH Reversed-Phase Peptide Fractionation Kit (Thermo Fisher Scientific, MA, USA), as described with minor modifications. The sample was re-hydrated in 0.1% TFA and then loaded onto an equilibrated, high-pH, reversed-phase fractionation spin column. A step gradient of increasing ACN concentrations (5-80%) in a volatile high-pH (Triethylamine (0.1%)) is then applied to the columns to elute bound peptides into nine different fractions collected by centrifugation. The fractions obtained from high-pH, reversed-phase 4plex-labeled mixture were dried and stored until analysis by mass spectrometry for quantification.

Quantitative analysis by reverse phase-liquid chromatography RP-LC-MS/MS

The fractions were resuspended in 10 µl of 0.1% formic acid and analyzed by RP-LC-MS/MS in an Easy-nLC II system coupled to an ion trap LTQ-Orbitrap-Velos-Pro hybrid mass spectrometer (Thermo Scientific). The peptides were concentrated (on-line) by reverse phase chromatography using a 0.1mm × 20 mm C18 RP precolumn (Proxeon), and then separated using a 0.075mm x 250 mm C18 RP column (Proxeon) operating at 0.3 µl/min. Peptides were eluted using a 90-min dual gradient. The gradient profile was set as follows: 5–25% solvent B for 68 min, 25–40% solvent B for 22min, 40–100% solvent B for 2 min and 100% solvent B for 18 min (Solvent A: 0,1% formic acid in water, solvent B: 0,1% formic acid, 80% ACN in water). ESI ionization was done using a Nano-bore emitters Stainless Steel ID 30 µm (Proxeon) interface at 2.1 kV spray voltage with S-Lens of 60%.

The instrument method consisted of a data-dependent top-20 experiment with an Orbitrap MS1 scan at a resolution ($m/\Delta m$) of 30,000 followed by either twenty high energy collision dissociation (HCD) MS/MS mass-analyzed in the Orbitrap at 7,500 ($\Delta m/m$) resolution. MS2 experiments were performed using HCD to generate high resolution and high mass accuracy MS2 spectra.

The minimum MS signal for triggering MS/MS was set to 500. The lock mass option was enabled for both MS and MS/MS mode and the polydimethylcyclosiloxane ions (protonated $(\text{Si}(\text{CH}_3)_2\text{O})_6$; m/z 445.120025) were used for internal recalibration of the mass spectra.

Peptides were detected in survey scans from 400 to 1600 amu (1 µscan) using an isolation width of 1.3 u (in mass-to-charge ratio units), normalized collision energy of 40% for HCD fragmentation, and dynamic exclusion applied during 60 seconds periods. Charge-state screening was enabled to reject unassigned and singly charged protonated ions.⁴

Quantitative data analysis

Peptide identification from raw data (a single search was performed with all nine raws from the fractionation) was carried out using PEAKS Studio X+ search engine (Bioinformatics Solutions Inc., Waterloo, Ontario, Canada). Database searches were performed against uniprot-*Nostoc (Anabaena)* sp. PCC 7120 (6070 entries; UniProt release 12/2019) (decoy-fusion database). The following constraints were used for the searches: tryptic cleavage after Arg and Lys (semi-specific), up to two missed cleavage sites, and tolerances of 20 ppm for precursor ions and 0.05 Da for MS/MS fragment ions and the searches

were performed allowing optional Met oxidation and Cys carbamidomethylation and fixed TMT 6plex reagent labeling at the N-terminus and lysine residues. False discovery rates (FDR) for peptide spectrum matches (PSM) was limited to 0.01. Only those proteins with at least two distinct peptides and at least one unique peptide being discovered from LC/MS/MS analyses were considered reliably identified and sent to be quantified.

Quantitation of TMT labeled peptides was performed with PEAKS Studio X+ search engine, selected “Reporter Ion Quantification TMT” under the “Quantifications” options. Auto normalization mode was used that calculates a global ratio from the total intensity of all labels in all quantifiable peptides. The -10LgP, Quality and Reporter Ion Intensity (1.7e4) were used for Spectrum filter and Significance (20, PEAKSQ method) was used for peptide and protein abundance calculation. For the Protein quantification, protein groups for peptide uniqueness were considered, using only unique peptides for protein quantification and the modified peptides were excluded.^{3,5}

Table S1: Data displayed by STRING MCL clustering (inflation parameter = 3)

Cluster number	cluster color	Gene count	Protein name	Protein identifier
1	Red	12	FusA	103690.1713
1	Red	12	SecA	103690.1713
1	Red	12	Rps7	103690.1713
1	Red	12	Rps4	103690.1713
1	Red	12	Rps5	103690.1713
1	Red	12	RpsN	103690.1713
1	Red	12	Hpf	103690.1713
1	Red	12	DapB	103690.1713
1	Red	12	RpoC2	103690.1714
1	Red	12	Rpl1	103690.1713
1	Red	12	RplN	103690.1713
1	Red	12	RpoB	103690.1714
2	Lime Green	9	DnaK2	103690.1713
2	Lime Green	9	ClpP3	103690.1713
2	Lime Green	9	Alr0286	103690.1714
2	Lime Green	9	GroL2	103690.1713
2	Lime Green	9	ClpB2	103690.1713
2	Lime Green	9	Alr1809	103690.1713
2	Lime Green	9	Alr2323	103690.1713
2	Lime Green	9	GroL1	103690.1713
2	Lime Green	9	17132093	103690.1713
3	Cyan	5	Alr4642	103690.1713
3	Cyan	5	All0737	103690.1713
3	Cyan	5	All1541	103690.1714

3	Cyan	5	Alr4641	103690.1713
3	Cyan	5	Alr4745	103690.1713
4	Medium Purple	5	PecA	103690.1713
4	Medium Purple	5	CpcG3	103690.1713
4	Medium Purple	5	PecC	103690.1713
4	Medium Purple	5	ApcE	103690.1713
4	Medium Purple	5	PecB	103690.1713
5	Medium Purple (2)	4	NdhI	103690.1714
5	Medium Purple (2)	4	PsbB	103690.1714
5	Medium Purple (2)	4	Alr1129	103690.1713
5	Medium Purple (2)	4	All0107	103690.1714
6	Orchid	2	Alr0668	103690.1713
6	Orchid	2	Alr0669	103690.1713
7	Purple	2	All1267	103690.1713
7	Purple	2	Alr0782	103690.1713
8	Pink	2	All0667	103690.1713
8	Pink	2	All0666	103690.1713
9	Pale Violet Red	2	PepA	103690.1714
9	Pale Violet Red	2	Ndk	103690.1713
10	Brown	2	Alr3411	103690.1713
10	Brown	2	Alr1548	103690.1714
11	Dark Golden Rod	2	Alr4029	103690.1713
11	Dark Golden Rod	2	Alr4028	103690.1713
12	Yellow	2	Alr2117	103690.1713
12	Yellow	2	All3054	103690.1713
13	Olive	2	Alr0490	103690.1713
13	Olive	2	All2127	103690.1713
14	Green Yellow	1	All4499	103690.1713
15	Green	1	Alr2269	103690.1713
16	Light Green	1	GlnA	103690.1713

Table S2: Particle hydrodynamic size, based on volume distribution, determined by DLS and ζ -potential measured by ELS in pure water and in culture medium (AA/8 + N) with their 95% confidence intervals.

	Size (nm)		ζ -Potential (mV)
	Pure water (pH 6.5)	AA/8 + N (pH 7.4)	AA/8 + N (pH 7.4)
Without nanoparticles	--	1.8 \pm 1.1	-19.4 \pm 1.6
PS-NPs	23.8 \pm 0.6	24.9 \pm 1.1	-19.8 \pm 0.7
G7*	7.6 \pm 0.3*	10.1 \pm 1.1*	20.8 \pm 1.1*
Mix	27.3 \pm 3.3	527.1 \pm 69.4	-17.0 \pm 0.9

* In agreement with Tamayo-Belda *et al.* after filtration through a 100 nm filter.⁵⁵

Table S3: Effective concentrations of polystyrene nanoplastics (PS-NPs) both individually and in mixture with PAMAM dendrimers of generation 7 (Mix) that induced 10%, 50% and 90% of growth inhibition, chlorophyll *a* and phycocyanin concentration decrease and the model type fitted on *Anabaena* sp. PCC7120 for 72 h.

Measured parameter	Model Fitted (PS-NPs / Mix)	Effective concentration	PS-NPs (mg/mL)	Mix (Constant ratio dilutions)
Growth (mg of dry weight/mL)	W1.3 / W1.4	EC ₁₀	46.12 \pm 2.08	0.59 \pm 0.06
		EC ₅₀	64.40 \pm 0.90	1.39 \pm 0.06
		EC ₉₀	81.26 \pm 3.29	3.25 \pm 0.13
Chlorophyll <i>a</i> (mg/mL)	LL.2 / W1.3	EC ₁₀	40.51 \pm 1.21	0.56 \pm 0.09
		EC ₅₀	59.35 \pm 0.65	1.22 \pm 0.07
		EC ₉₀	75.71 \pm 1.25	1.99 \pm 0.16
Phycocyanin (mg/mL)	LL.5 / W2.3	EC ₁₀	40.03 \pm 2.36	0.94 \pm 0.19
		EC ₅₀	59.47 \pm 1.17	1.47 \pm 0.18
		EC ₉₀	76.53 \pm 2.15	2.31 \pm 0.43

Table S4: Surface and volume related properties of polystyrene nanoplastics (PS-NPs), PAMAM dendrimers of generation 7 (G7) and their mixture (Mix) in AA/8+N.

Particle/Combo	PS-NPs	G7	Mix
Radius (nm)	12	4	264
Surface area (nm ²)	1.81E+03	2.01E+02	8.76E+05
Volume (nm ³)	7.24E+03	2.68E+02	7.71E+07
Surf. area/Volume	0.250	0.750	0.011
Concentration (µg mL ⁻¹)	64.4	3.9	64.4 (PS-NPs) 3.92 (G7)
Concentration (particle number mL ⁻¹)	6.89E+12	1.96E+13	7.15E+08
Total Surface area (nm ² mL ⁻¹)	1.25E+16	3.94E+15	6.27E+14
Total Volume (nm ³ mL ⁻¹)	4.99E+16	5.25E+15	5.51E+16
Total Surf. area/Volume	0.250	0.750	0.011

Table S5: Protein description data from Uniprot

Category	Gene	Accession	Length	Protein names & description
Oxidative stress	all0737*	Q8YYV6	483	Thioredoxin reductase (EC 1.8.1.9); Biological process: cell redox homeostasis [GO:0045454]; removal of superoxide radicals [GO:0019430]; Cellular component: cell [GO:0005623]; cytoplasm [GO:0005737]; Associated terms: cell [GO:0005623]; cytoplasm [GO:0005737]; thioredoxin-disulfide reductase activity [GO:0004791]; cell redox homeostasis [GO:0045454]; removal of superoxide radicals [GO:0019430]; Molecular function: thioredoxin-disulfide reductase activity [GO:0004791]; Domain features: DOMAIN 339-483; note="Thioredoxin"; evidence="ECO:0000259 PROSITE:PS51352"; Keywords: FAD; Flavoprotein; Oxidoreductase; Redox-active center; Protein families: Class-II pyridine nucleotide-disulfide oxidoreductase family
	all1541*	Q8YWR3	251	Peroxiredoxin 2 family protein/glutaredoxin Biological process: cell redox homeostasis [GO:0045454]; Cellular component: cell [GO:0005623]; Associated terms: cell [GO:0005623]; electron transfer activity [GO:0009055]; protein disulfide oxidoreductase activity [GO:0015035]; cell redox homeostasis [GO:0045454]; Molecular function: electron transfer activity [GO:0009055]; protein disulfide oxidoreductase activity [GO:0015035]; Domain features: DOMAIN 4-168; note="Thioredoxin"; evidence="ECO:0000259 PROSITE:PS51352"

alr0672*	Q8YZ15	433	Alr0672 protein; Molecular function: peroxidase activity; ⁶ Domain features: DOMAIN 273-418; note="acidPPc"; evidence="ECO:0000259 Pfam:PF01569"
alr4641*	Q8YNC5	203	Peroxiredoxin ; Biological process: cell redox homeostasis [GO:0045454]; Cellular component: cell [GO:0005623]; Associated terms: cell [GO:0005623]; peroxiredoxin activity [GO:0051920]; cell redox homeostasis [GO:0045454]; Molecular function: peroxiredoxin activity [GO:0051920]; Domain features: DOMAIN 11-169; note="Thioredoxin"; evidence="ECO:0000259 PROSITE:PS51352"
alr4642	Q8YNC4	213	Alr4642 protein ; Biological process: cell redox homeostasis [GO:0045454]; Cellular component: cell [GO:0005623]; Associated terms: cell [GO:0005623]; antioxidant activity [GO:0016209]; oxidoreductase activity [GO:0016491]; cell redox homeostasis [GO:0045454]; Molecular function: antioxidant activity [GO:0016209]; oxidoreductase activity [GO:0016491]; Domain features: DOMAIN 63-213; note="Thioredoxin"; evidence="ECO:0000259 PROSITE:PS51352"
alr4745	Q8YN25	475	Dihydrolipoyl dehydrogenase (EC 1.8.1.4) ; Biological process: cell redox homeostasis [GO:0045454]; Cellular component: cell [GO:0005623]; Associated terms: cell [GO:0005623]; dihydrolipoyl dehydrogenase activity [GO:0004148]; electron transfer activity [GO:0009055]; flavin adenine dinucleotide binding [GO:0050660]; cell redox homeostasis [GO:0045454]; Molecular function: dihydrolipoyl dehydrogenase activity [GO:0004148]; electron transfer activity [GO:0009055]; flavin adenine dinucleotide binding [GO:0050660]; Domain features: DOMAIN 7-338; note="Pyr_redox_2"; evidence="ECO:0000259 Pfam:PF07992"; DOMAIN 357-469; note="Pyr_redox_dim"; evidence="ECO:0000259 Pfam:PF02852"; Keywords: FAD; Flavoprotein; NAD; Nucleotide-binding; Oxidoreductase; Redox-active center; Protein families: Class-I pyridine nucleotide-disulfide oxidoreductase family
alr7524	Q8ZSI6	193	Alr7524 protein; {ECO:0000250}; Associated terms: peroxiredoxin activity [GO:0051920]; Molecular function: peroxiredoxin activity [GO:0051920]; Domain features: DOMAIN 57-123; note="CMD"; evidence="ECO:0000259 Pfam:PF02627"; Keywords: Plasmid
dpsA*	Q8YQL3	184	Nutrient stress-induced DNA-binding protein; Function: Involved in protection of chromosomal DNA from damage under nutrient-limited and oxidative stress conditions.

				Binds heme (By similarity); Biological process: cellular iron ion homeostasis [GO:0006879]; Cellular component: cell [GO:0005623]; Associated terms: cell [GO:0005623]; DNA binding [GO:0003677]; ferric iron binding [GO:0008199]; oxidoreductase activity, oxidizing metal ions [GO:0016722]; cellular iron ion homeostasis [GO:0006879]; Molecular function: DNA binding [GO:0003677]; ferric iron binding [GO:0008199]; oxidoreductase activity, oxidizing metal ions [GO:0016722]; Keywords: DNA-binding; Heme; Iron; Metal-binding; Protein families: Dps family
Stress response	alr0286	Q8Z017	150	Small heat shock protein; Domain features: DOMAIN 33-146; note="SHSP"; evidence="ECO:0000259 PROSITE:PS01031" Keywords: Stress response; Protein families: Small heat shock protein (HSP20) family
	alr1809	Q8YW07	155	Heat shock protein, class I; Domain features: DOMAIN 43-155; note="SHSP"; evidence="ECO:0000259 PROSITE:PS01031" Keywords: Stress response; Protein families: Small heat shock protein (HSP20) family
	alr2323	Q8YUL8	658	Heat shock protein ; Biological process: protein folding [GO:0006457]; Associated terms: ATP binding [GO:0005524]; unfolded protein binding [GO:0051082]; protein folding [GO:0006457]; Molecular function: ATP binding [GO:0005524]; unfolded protein binding [GO:0051082]; Domain features: DOMAIN 25-178; note="HATPase_c"; evidence="ECO:0000259 SMART:SM00387" Keywords: Stress response
	clpB	Q8YST5	839	Endopeptidase Clp ATP-binding chain; Subcellular location: Cytoplasm {ECO:0000305}; Biological process: protein metabolic process [GO:0019538]; Associated terms: ATP binding [GO:0005524]; protein metabolic process [GO:0019538]; Molecular function: ATP binding [GO:0005524]; Domain features: DOMAIN 432-467; note="UVR"; evidence="ECO:0000259 PROSITE:PS50151" Keywords: ATP-binding; Chaperone; Coiled coil; Nucleotide-binding; Repeat; Protein families: ClpA/ClpB family
	clpB2	Q8YM56	872	Chaperone protein ClpB 2; Function: Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from heat-induced damage, in cooperation with DnaK, DnaJ and GrpE. Acts before DnaK, in the processing of protein aggregates. Protein binding stimulates the ATPase activity; ATP hydrolysis unfolds the

				denatured protein aggregates, which probably helps expose new hydrophobic binding sites on the surface of ClpB-bound aggregates, contributing to the solubilization and refolding of denatured protein aggregates by DnaK (By similarity). {ECO:0000250}; Subcellular location: Cytoplasm {ECO:0000255 HAMAP-Rule:MF_00444}; Biological process: protein metabolic process [GO:0019538]; protein refolding [GO:0042026]; response to heat [GO:0009408]; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; ATP binding [GO:0005524]; protein metabolic process [GO:0019538]; protein refolding [GO:0042026]; response to heat [GO:0009408]; Molecular function: ATP binding [GO:0005524]; Domain features: DOMAIN 6-148; note="Clp R"; evidence="ECO:0000255 PROSITE-ProRule:PRU01251" Keywords: ATP-binding; Chaperone; Coiled coil; Cytoplasm; Nucleotide-binding; Repeat; Stress response; Protein families: ClpA/ClpB family
clpP3	Q8YP43	197		Probable ATP-dependent Clp protease proteolytic subunit 3 (EC 3.4.21.92) (Endopeptidase Clp 3) involved in the efficient protein homeostasis; ⁷ Function: Cleaves peptides in various proteins in a process that requires ATP hydrolysis. Has a chymotrypsin-like activity. Plays a major role in the degradation of misfolded proteins. {ECO:0000255 HAMAP-Rule:MF_00444}; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; serine-type endopeptidase activity [GO:0004252]; Molecular function: serine-type endopeptidase activity [GO:0004252]; Keywords: Cytoplasm; Hydrolase; Protease; Serine protease; Protein families: Peptidase S14 family
dnaK2	Q8YW74	633		Chaperone protein dnaK2 (HSP70-2) (Heat shock 70 kDa protein 2) (Heat shock protein 70-2); Function: Acts as a chaperone. {ECO:0000250}; Subcellular location: Cytoplasm {ECO:0000255 HAMAP-Rule:MF_00600}; Biological process: protein folding [GO:0006457]; Associated terms: ATP binding [GO:0005524]; unfolded protein binding [GO:0051082]; protein folding [GO:0006457]; Molecular function: ATP binding [GO:0005524]; unfolded protein binding [GO:0051082]; Keywords: ATP-binding; Chaperone; Nucleotide-binding; Phosphoprotein; Stress response; Protein families: Heat shock protein 70 family
groL1	Q8YQZ8	544		60 kDa chaperonin 1 (GroEL protein 1) (Protein Cpn60 1); Function: Prevents misfolding and promotes the refolding

				and proper assembly of unfolded polypeptides generated under stress conditions. {ECO:0000255 HAMAP-Rule:MF_00600}; Subcellular location: Cytoplasm {ECO:0000255 HAMAP-Rule:MF_00600}; Biological process: protein refolding [GO:0042026]; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; ATP binding [GO:0005524]; unfolded protein binding [GO:0051082]; protein refolding [GO:0042026]; Molecular function: ATP binding [GO:0005524]; unfolded protein binding [GO:0051082]; Keywords: ATP-binding; Chaperone; Cytoplasm; Nucleotide-binding; Protein families: Chaperonin (HSP60) family
	groL2	Q8YVS8	560	60 kDa chaperonin 2 (GroEL protein 2) (Protein Cpn60 2); Function: Prevents misfolding and promotes the refolding and proper assembly of unfolded polypeptides generated under stress conditions. {ECO:0000255 HAMAP-Rule:MF_00600}; Biological process: protein refolding [GO:0042026]; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; ATP binding [GO:0005524]; unfolded protein binding [GO:0051082]; protein refolding [GO:0042026]; Molecular function: ATP binding [GO:0005524]; unfolded protein binding [GO:0051082]; Keywords: ATP-binding; Chaperone; Cytoplasm; Nucleotide-binding; Protein families: Chaperonin (HSP60) family
Surface location	alr1540*	Q8YWR4	128	Alr1540 protein; Transmembrane; Domain features: DOMAIN 22-77; note="PG_binding_1"; evidence="ECO:0000259 Pfam:PF01471"
	all0767	Q8YYS9	185	All0767 protein; Cellular component: integral component of membrane [GO:0016021]; Associated terms: integral component of membrane [GO:0016021]; Keywords: Membrane; Transmembrane; Transmembrane helix
	all2358	Q8YUI8	326	Phosphonate ABC transport phosphonate binding component; Transmembrane; Biological process: transmembrane transport [GO:0055085]; Cellular component: ATP-binding cassette (ABC) transporter complex [GO:0043190]; Associated terms: ATP-binding cassette (ABC) transporter complex [GO:0043190]; transmembrane transport [GO:0055085]
	all3054	Q8YSN0	1038	All3054 protein; Transmembrane; ; Cellular component: integral component of membrane [GO:0016021]; Associated terms: integral component of membrane [GO:0016021]; Domain features: DOMAIN 54-281; note="PBP_domain";

			evidence="ECO:0000259 Pfam:PF12849" Keywords: Membrane; Transmembrane; Transmembrane helix
all7121*	Q8YL17	694	All7121 protein; Cellular component: integral component of membrane [GO:0016021]; Associated terms: integral component of membrane [GO:0016021]; electron transfer activity [GO:0009055]; heme binding [GO:0020037]; metal ion binding [GO:0046872]; Molecular function: electron transfer activity [GO:0009055]; heme binding [GO:0020037]; metal ion binding [GO:0046872]; Domain features: DOMAIN 163-351; note="Cytochrome c"; evidence="ECO:0000259 PROSITE:PS51007"; DOMAIN 473-649; note="Cytochrome c"; evidence="ECO:0000259 PROSITE:PS51007" Keywords: Heme; Iron; Membrane; Metal-binding; Plasmid; Transmembrane; Transmembrane helix
alr0140	Q8Z0F7	552	Periplasmic oligopeptide-binding protein of oligopeptide ABC transporter; Subcellular location: Cell outer membrane {ECO:0000256 RuleBase:RU003357, ECO:0000256 SAAS:SAAS01009251}; Biological process: transmembrane transport [GO:0055085]; Cellular component: ATP-binding cassette (ABC) transporter complex [GO:0043190]; Associated terms: ATP-binding cassette (ABC) transporter complex [GO:0043190]; transmembrane transport [GO:0055085]; Domain features: DOMAIN 96-459; note="SBP_bac_5"; evidence="ECO:0000259 Pfam:PF00496"
alr0397*	Q8YZR0	867	Alr0397 protein; Cellular component: cell outer membrane [GO:0009279]; Associated terms: cell outer membrane [GO:0009279]; siderophore uptake transmembrane transporter activity [GO:0015344]; signaling receptor activity [GO:0038023]; Molecular function: siderophore uptake transmembrane transporter activity [GO:0015344]; signaling receptor activity [GO:0038023]; Domain features: DOMAIN 71-167; note="AMIN"; evidence="ECO:0000259 Pfam:PF11741"; DOMAIN 199-301; note="Plug"; evidence="ECO:0000259 Pfam:PF07715"; DOMAIN 400-865; note="TonB_dep_Rec"; evidence="ECO:0000259 Pfam:PF00593" Keywords: Cell outer membrane; Membrane; Receptor; TonB box; Protein families: TonB-dependent receptor family
alr0474*	Q8YZI6	596	Alr0474 protein
alr0564	Q8YZB5	397	Alr0564 protein ; Biological process: peptidoglycan turnover [GO:0009254]; Cellular component: outer membrane [GO:0019867]; Associated terms: outer

			membrane [GO:0019867]; hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553]; peptidoglycan turnover [GO:0009254]; Molecular function: hydrolase activity, hydrolyzing O-glycosyl compounds [GO:0004553]; Domain features: DOMAIN 154-295; note="MltA"; evidence="ECO:0000259 SMART:SM00925" Keywords: Signal
all4499	Q8YNR3	546	All4499 protein ; Biological process: carbohydrate transport [GO:0008643]; Cellular component: integral component of membrane [GO:0016021]; Associated terms: integral component of membrane [GO:0016021]; porin activity [GO:0015288]; carbohydrate transport [GO:0008643]; Molecular function: porin activity [GO:0015288]; Domain features: DOMAIN 55-119; note="SLH"; evidence="ECO:0000259 PROSITE:PS51272" Keywords: Coiled coil; Signal; Protein families: OprB family
alr3411	Q8YRN3	190	Alr3411 protein; Identify in the outer membrane fraction. ⁸
alr0880	Q8YYH0	702	Oligopeptidase A; Transmembrane; Associated terms: metal ion binding [GO:0046872]; metalloendopeptidase activity [GO:0004222]; Molecular function: metal ion binding [GO:0046872]; metalloendopeptidase activity [GO:0004222]; Domain features: DOMAIN 235-696; note="Peptidase_M3"; evidence="ECO:0000259 Pfam:PF01432" Keywords: Coiled coil; Hydrolase; Metal-binding; Metalloprotease; Protease; Zinc; Protein families: Peptidase M3 family
alr2117	Q8YV64	603	Alr2117 protein; Cellular component: integral component of membrane [GO:0016021]; Associated terms: integral component of membrane [GO:0016021]; Keywords: Coiled coil; Membrane; Transmembrane; Transmembrane helix
alr2269	Q8YUR6	833	Alr2269 protein; Cellular component: outer membrane [GO:0019867]; Associated terms: outer membrane [GO:0019867]; Domain features: DOMAIN 315-378; note="POTRA_2"; evidence="ECO:0000259 Pfam:PF08479"; DOMAIN 405-466; note="POTRA"; evidence="ECO:0000259 Pfam:PF07244"; DOMAIN 493-833; note="Bac_surface_Ag"; evidence="ECO:0000259 Pfam:PF01103" Keywords: 3D-structure; Signal
alr3345	Q8YRU8	340	Alr3345 protein; Cellular component: outer membrane-bounded periplasmic space [GO:0030288]; Associated terms: outer membrane-bounded periplasmic space

				[GO:0030288]
	alr4028 *	Q8YQ12	287	Alr4028 protein; Domain features: DOMAIN 93-201; note="Plug"; evidence="ECO:0000259 Pfam:PF07715" Keywords:
	alr4029 *	Q8YQ11	258	Alr4029 protein; Domain features: DOMAIN 2-255; note="TonB_dep_Rec"; evidence="ECO:0000259 Pfam:PF00593" Keywords: Receptor
	alr4280 *	Q8YPB8	436	Alr4280 protein; Transmembrane; Domain features: DOMAIN 74-127; note="Biotin_lipoyl_2"; evidence="ECO:0000259 Pfam:PF13533" Keywords: Coiled coil
	alr4821 *	Q8YMV5	352	Alr4821 protein; Cellular component: integral component of membrane [GO:0016021]; Associated terms: integral component of membrane [GO:0016021]; Keywords: Coiled coil; Membrane; Transmembrane; Transmembrane helix
	alr7346	Q8YKF2	262	Alr7346 protein; Subcellular location: Periplasm. Note=Periplasmic or loosely attached to the cytoplasmic or the outer membrane; Domain features: DOMAIN 6-258; note="DUF3598"; evidence="ECO:0000259 Pfam:PF12204" Keywords: Plasmid
	nucA	P38446	274	Nuclease (EC 3.1.30.-) (Endonuclease); Pathway: Carbohydrate metabolism; tricarboxylic acid cycle; isocitrate from oxaloacetate: step 2/2. {ECO:0000256 PIRNR:PIRNR036687}; Function: Catalyzes the degradation of both RNA and DNA; has the potential to act as an endonuclease; Cellular component: periplasmic space [GO:0042597]; Associated terms: periplasmic space [GO:0042597]; endonuclease activity [GO:0004519]; metal ion binding [GO:0046872]; nucleic acid binding [GO:0003676]; Molecular function: endonuclease activity [GO:0004519]; metal ion binding [GO:0046872]; nucleic acid binding [GO:0003676]; Keywords: 3D-structure; Endonuclease; Hydrolase; Magnesium; Manganese; Metal-binding; Nuclease; Periplasm; Plasmid; Signal; Protein families: DNA/RNA non-specific endonuclease family
Carbon metaboli sm and	all1267	Q8YXE6	876	Aconitate hydratase B (EC 4.2.1.3) (EC 4.2.1.99) (2-methylisocitrate dehydratase) ; Biological process: tricarboxylic acid cycle [GO:0006099]; Cellular component: cytosol [GO:0005829]; Associated terms: cytosol [GO:0005829]; 2-methylisocitrate dehydratase activity [GO:0047456]; 4 iron, 4 sulfur cluster binding [GO:0051539]; aconitate hydratase activity [GO:0003994];

			citrate dehydratase activity [GO:0047780]; metal ion binding [GO:0046872]; tricarboxylic acid cycle [GO:0006099]; Molecular function: 2-methylisocitrate dehydratase activity [GO:0047456]; 4 iron, 4 sulfur cluster binding [GO:0051539]; aconitate hydratase activity [GO:0003994]; citrate dehydratase activity [GO:0047780]; metal ion binding [GO:0046872]; Domain features: DOMAIN 4-175; note="Aconitase_B_N"; evidence="ECO:0000259 Pfam:PF11791"; DOMAIN 187-390; note="Aconitase_2_N"; evidence="ECO:0000259 Pfam:PF06434"; DOMAIN 479-825; note="Aconitase"; evidence="ECO:0000259 Pfam:PF00330" Keywords: 4Fe-4S; Iron; Iron-sulfur; Lyase; Metal-binding; Tricarboxylic acid cycle; Protein families: Aconitase/IPM isomerase family
all2127*	Q8YV54	452	All2127 protein; Associated terms: 4 iron, 4 sulfur cluster binding [GO:0051539]; catalytic activity [GO:0003824]; metal ion binding [GO:0046872]; Molecular function: 4 iron, 4 sulfur cluster binding [GO:0051539]; catalytic activity [GO:0003824]; metal ion binding [GO:0046872]; Domain features: DOMAIN 96-239; note="Radical_SAM"; evidence="ECO:0000259 Pfam:PF04055" Keywords: 4Fe-4S; Iron; Iron-sulfur; Metal-binding; S-adenosyl-L-methionine
all2396	Q8YUF4	454	All2396 protein; Keywords:
all4388	Q8YP14	493	All4388 protein; Cellular component: membrane [GO:0016020]; Associated terms: membrane [GO:0016020]; polysaccharide transmembrane transporter activity [GO:0015159]; Molecular function: polysaccharide transmembrane transporter activity [GO:0015159]; Domain features: DOMAIN 380-433; note="SLBB"; evidence="ECO:0000259 Pfam:PF10531" Keywords: Signal
all5089	Q8YM51	478	Phosphoglucomutase/phosphomannomutase ; Biological process: carbohydrate metabolic process [GO:0005975]; Associated terms: intramolecular transferase activity, phosphotransferases [GO:0016868]; magnesium ion binding [GO:0000287]; carbohydrate metabolic process [GO:0005975]; Molecular function: intramolecular transferase activity, phosphotransferases [GO:0016868]; magnesium ion binding [GO:0000287]; Domain features: DOMAIN 8-141; note="PGM_PMM_I"; evidence="ECO:0000259 Pfam:PF02878"; DOMAIN 162-268; note="PGM_PMM_II";

			evidence="ECO:0000259 Pfam:PF02879"; DOMAIN 277-382; note="PGM_PMM_III"; evidence="ECO:0000259 Pfam:PF02880"; DOMAIN 418-468; note="PGM_PMM_IV"; evidence="ECO:0000259 Pfam:PF00408" Keywords: Isomerase; Magnesium; Metal-binding; Protein families: Phosphohexose mutase family
all5295*	Q8YLK3	334	All5295 protein; Associated terms: catalytic activity [GO:0003824]; coenzyme binding [GO:0050662]; Molecular function: catalytic activity [GO:0003824]; coenzyme binding [GO:0050662]; Domain features: DOMAIN 7-234; note="Epimerase"; evidence="ECO:0000259 Pfam:PF01370"
all7222	Q8YKR9	348	All7222 protein; Domain features: DOMAIN 94-198; note="CbiA"; evidence="ECO:0000259 Pfam:PF01656" Keywords: Plasmid
alr0658	Q8YZ29	461	UDP-glucose 6-dehydrogenase (EC 1.1.1.22) ; Biological process: polysaccharide biosynthetic process [GO:0000271]; D binding [GO:0051287]; UDP-glucose 6-dehydrogenase activity [GO:0003979]; polysaccharide biosynthetic process [GO:0000271]; Molecular function: NAD binding [GO:0051287]; UDP-glucose 6-dehydrogenase activity [GO:0003979]; Domain features: DOMAIN 344-446; note="UDPG_MGDP_dh_C"; evidence="ECO:0000259 SMART:SM00984" Keywords: NAD; Oxidoreductase; Protein families: UDP-glucose/GDP-mannose dehydrogenase family
alr0663*	Q8YZ24	632	Alr0663 protein ; Biological process: carbohydrate metabolic process [GO:0005975]; Associated terms: catalytic activity [GO:0003824]; carbohydrate metabolic process [GO:0005975]; Molecular function: catalytic activity [GO:0003824]; Domain features: DOMAIN 55-504; note="Amy"; evidence="ECO:0000259 SMART:SM00642"
alr0782	Q8YYR4	235	Ribulose-phosphate 3-epimerase (EC 5.1.3.1) ; Biological process: carbohydrate metabolic process [GO:0005975]; pentose-phosphate shunt [GO:0006098]; Associated terms: metal ion binding [GO:0046872]; ribulose-phosphate 3-epimerase activity [GO:0004750]; carbohydrate metabolic process [GO:0005975]; pentose-phosphate shunt [GO:0006098]; Molecular function: metal ion binding [GO:0046872]; ribulose-phosphate 3-epimerase activity [GO:0004750]; Keywords: Carbohydrate metabolism; Cobalt; Isomerase; Manganese; Metal-binding; Zinc; Protein families: Ribulose-phosphate 3-epimerase family
alr2090	Q8YV91	602	Alr2090 protein; Domain features: DOMAIN 406-469;

			note="SLH"; evidence="ECO:0000259 PROSITE:PS51272"; DOMAIN 470-529; note="SLH"; evidence="ECO:0000259 PROSITE:PS51272"; DOMAIN 531-595; note="SLH"; evidence="ECO:0000259 PROSITE:PS51272"
alr3338	Q8YRV4	449	Phosphoglycerate mutase; Associated terms: catalytic activity [GO:0003824]; Molecular function: catalytic activity [GO:0003824]; Keywords: Protein families: Phosphoglycerate mutase family
alr3729	Q8YQT8	138	Alr3729 protein; Biological process: polyketide metabolic process [GO:0030638]; Associated terms: polyketide metabolic process [GO:0030638]
alr4380 *	Q8YP22	326	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24) ; Biological process: porphyrin-containing compound biosynthetic process [GO:0006779]; Associated terms: metal ion binding [GO:0046872]; porphobilinogen synthase activity [GO:0004655]; porphyrin-containing compound biosynthetic process [GO:0006779]; Molecular function: metal ion binding [GO:0046872]; porphobilinogen synthase activity [GO:0004655]; Keywords: Lyase; Magnesium; Metal-binding; Porphyrin biosynthesis; Zinc; Protein families: ALAD family
alr4566 *	Q8YNJ9	384	NADH-dependent butanol dehydrogenase; Associated terms: metal ion binding [GO:0046872]; oxidoreductase activity [GO:0016491]; Molecular function: metal ion binding [GO:0046872]; oxidoreductase activity [GO:0016491]; Domain features: DOMAIN 9-362; note="Fe-ADH"; evidence="ECO:0000259 Pfam:PF00465"
alr7200 *	Q8YKU1	539	Alr7200 protein; Associated terms: ATP binding [GO:0005524]; Molecular function: ATP binding [GO:0005524]; Domain features: DOMAIN 279-408; note="AAA"; evidence="ECO:0000259 SMART:SM00382" Keywords: Plasmid
ccmK*	Q8YYI1	114	Carbon dioxide concentrating mechanism protein; Subcellular location: Cell inner membrane {ECO:0000255 HAMAP-Rule:MF_01701}; Peripheral membrane protein {ECO:0000255 HAMAP-Rule:MF_01701}; Domain features: DOMAIN 3-81; note="BMC"; evidence="ECO:0000259 SMART:SM00877"
cysA*	Q8ZOH0	338	Sulfate/thiosulfate import ATP-binding protein CysA (EC 7.3.2.3) (Sulfate-transporting ATPase); Function: Part of the ABC transporter complex CysAWTP involved in

				sulfate/thiosulfate import. Responsible for energy coupling to the transport system. {ECO:0000255 HAMAP-Rule:MF_01701}; Cellular component: ATP-binding cassette (ABC) transporter complex [GO:0043190]; Associated terms: ATP-binding cassette (ABC) transporter complex [GO:0043190]; ATP binding [GO:0005524]; ATPase activity [GO:0016887]; ATPase-coupled sulfate transmembrane transporter activity [GO:0015419]; ATPase-coupled thiosulfate transmembrane transporter activity [GO:0102025]; Molecular function: ATPase activity [GO:0016887]; ATPase-coupled sulfate transmembrane transporter activity [GO:0015419]; ATPase-coupled thiosulfate transmembrane transporter activity [GO:0102025]; ATP binding [GO:0005524]; Domain features: DOMAIN 3-233; note="ABC transporter"; evidence="ECO:0000255 HAMAP-Rule:MF_01701" Keywords: ATP-binding; Cell inner membrane; Cell membrane; Membrane; Nucleotide-binding; Sulfate transport; Translocase; Transport; Protein families: ABC transporter superfamily, Sulfate/tungstate importer (TC 3.A.1.6) family
Organo-nitrogen metabolism	all0666*	Q8YZ21	348	All0666 protein; Cross-reference (InterPro): DUF1822 (This entry includes a group of bacterial proteins, including EipB from Brucella. EipB is a periplasmic protein that functions as part of a system required for cell envelope homeostasis)
	all0667*	Q8YZ20	481	All0667 protein; Protein-protein interaction databases (String): Three gene neighborhood (all0666, tplA, alr0841)
	all2425	Q8YUC7	255	All2425 protein; Domain features: DOMAIN 128-243; note="Peptidase_M15_3"; evidence="ECO:0000259 Pfam:PF08291"
	all2500	Q8YU55	428	Carboxyl-terminal protease; Associated terms: serine-type peptidase activity [GO:0008236]; Molecular function: serine-type peptidase activity [GO:0008236]; Domain features: DOMAIN 106-190; note="PDZ"; evidence="ECO:0000259 PROSITE:PS50106" Keywords: Coiled coil; Hydrolase; Protease; Serine protease; Protein families: Peptidase S41A family
	all4737*	Q8YN33	223	All4737 protein; Associated terms: cofactor binding [GO:0048037]; Molecular function: cofactor binding [GO:0048037]; Family and domain databases (InterPro): FMN-binding split barrel, Pyridoxamine 5'-phosphate oxidase-related.
	all4999	Q8YMD5	597	N-acetylmuramoyl-L-alanine amidase ; Biological process: peptidoglycan catabolic process [GO:0009253]; Associated

			terms: N-acetylmuramoyl-L-alanine amidase activity [GO:0008745]; peptidoglycan catabolic process [GO:0009253]; Molecular function: N-acetylmuramoyl-L-alanine amidase activity [GO:0008745]; Domain features: DOMAIN 237-295; note="SH3b"; evidence="ECO:0000259 SMART:SM00287"; DOMAIN 478-590; note="MurNAc-LAA"; evidence="ECO:0000259 SMART:SM00646"
all7011	Q8YLC4	323	All7011 protein; Associated terms: ATP binding [GO:0005524]; metal ion binding [GO:0046872]; Molecular function: ATP binding [GO:0005524]; metal ion binding [GO:0046872]; Domain features: DOMAIN 129-320; note="ATP-grasp"; evidence="ECO:0000259 PROSITE:PS50975" Keywords: ATP-binding; Nucleotide-binding; Plasmid
alr0668 *	Q8YZ19	198	Alr0668 protein; Isolated within the heterocyst fraction. ⁹
alr0669 *	Q8YZ18	295	Alr0669 protein; Domain features: DOMAIN 26-76; note="PG_binding_1"; evidence="ECO:0000259 Pfam:PF01471"; Family and domain databases (InterPro): PGBD superfamily (This superfamily represents peptidoglycan binding domain (PGBD). PGBD may have a general peptidoglycan binding function. It has a core structure consisting of a closed, three-helical bundle with a left-handed twist. It is found at the N or C terminus of a variety of enzymes involved in bacterial cell wall degradation)
alr2927 *	Q8YT00	132	Alr2927 protein; Domain features: DOMAIN 48-112; note="PPC"; evidence="ECO:0000259 Pfam:PF04151"
alr3301 *	Q8YRZ1	277	Alr3301 protein; Keywords: Coiled coil; Associated to heterocyst differentiation, ¹⁰ and to nitrogen deprivation. ¹¹
alr3804 *	Q8YQL7	383	Deoxyhypusine synthase-like protein (EC 2.5.-.-) ; Biological process: peptidyl-lysine modification to peptidyl-hypusine [GO:0008612]; Associated terms: transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765]; peptidyl-lysine modification to peptidyl-hypusine [GO:0008612]; Molecular function: transferase activity, transferring alkyl or aryl (other than methyl) groups [GO:0016765]; Keywords: Transferase; Protein families: Deoxyhypusine synthase family
asl0662 *	Q8YZ25	59	Asl0662 protein; Related to heterocyst and nitrogen starvation. ¹¹
cynS	P58703	146	Cyanate hydratase (Cyanase) (EC 4.2.1.104) (Cyanate hydrolase) (Cyanate lyase); Function: Catalyzes the reaction of cyanate with bicarbonate to produce ammonia

				and carbon dioxide. {ECO:0000255 HAMAP-Rule:MF_00535}; Subcellular location: Cytoplasm {ECO:0000255 HAMAP-Rule:MF_00102}; Biological process: cyanate metabolic process [GO:0009439]; Associated terms: cyanate hydratase activity [GO:0008824]; DNA binding [GO:0003677]; cyanate metabolic process [GO:0009439]; Molecular function: cyanate hydratase activity [GO:0008824]; DNA binding [GO:0003677]; Keywords: Lyase; Protein families: Cyanase family
dapB	Q8YU19	278		4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8); Function: Catalyzes the conversion of 4-hydroxy-tetrahydrodipicolinate (HTPA) to tetrahydrodipicolinate. {ECO:0000255 HAMAP-Rule:MF_00102}; Subcellular location: Cytoplasm {ECO:0000250 UniProtKB:P9WN39}; Biological process: diaminopimelate biosynthetic process [GO:0019877]; lysine biosynthetic process via diaminopimelate [GO:0009089]; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; 4-hydroxy-tetrahydrodipicolinate reductase [GO:0008839]; NAD binding [GO:0051287]; NADP binding [GO:0050661]; oxidoreductase activity, acting on CH or CH2 groups, NAD or NADP as acceptor [GO:0016726]; diaminopimelate biosynthetic process [GO:0019877]; lysine biosynthetic process via diaminopimelate [GO:0009089]; Molecular function: 4-hydroxy-tetrahydrodipicolinate reductase [GO:0008839]; NAD binding [GO:0051287]; NADP binding [GO:0050661]; oxidoreductase activity, acting on CH or CH2 groups, NAD or NADP as acceptor [GO:0016726]; Keywords: Amino-acid biosynthesis; Cytoplasm; Diaminopimelate biosynthesis; Lysine biosynthesis; NAD; NADP; Oxidoreductase; Protein families: DapB family
glnA*	P00964	474		Glutamine synthetase (GS) (EC 6.3.1.2) (Glutamate--ammonia ligase) (Glutamine synthetase I beta) (GSI beta); Function: Involved in nitrogen metabolism via ammonium assimilation. Catalyzes the ATP-dependent biosynthesis of glutamine from glutamate and ammonia. {ECO:0000250 UniProtKB:P77961}; Biological process: glutamine biosynthetic process [GO:0006542]; heterocyst differentiation [GO:0043158]; nitrogen fixation [GO:0009399]; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; ATP binding [GO:0005524]; glutamate-ammonia ligase activity [GO:0004356]; metal ion binding

				[GO:0046872]; glutamine biosynthetic process [GO:0006542]; heterocyst differentiation [GO:0043158]; nitrogen fixation [GO:0009399]; Molecular function: ATP binding [GO:0005524]; glutamate-ammonia ligase activity [GO:0004356]; metal ion binding [GO:0046872]; Keywords: ATP-binding; Cytoplasm; Direct protein sequencing; Heterocyst; Ligase; Magnesium; Metal-binding; Nitrogen fixation; Nucleotide-binding; Phosphoprotein; Protein families: Glutamine synthetase family
leuC	Q8YX02	467		3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) (Alpha-IPM isomerase) (IPMI) (Isopropylmalate isomerase); Function: Catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate. {ECO:0000255 HAMAP-Rule:MF_01026}; Subcellular location: Cytoplasm {ECO:0000255 HAMAP-Rule:MF_00451}; Biological process: leucine biosynthetic process [GO:0009098]; Associated terms: 3-isopropylmalate dehydratase activity [GO:0003861]; 4 iron, 4 sulfur cluster binding [GO:0051539]; metal ion binding [GO:0046872]; leucine biosynthetic process [GO:0009098]; Molecular function: 3-isopropylmalate dehydratase activity [GO:0003861]; 4 iron, 4 sulfur cluster binding [GO:0051539]; metal ion binding [GO:0046872]; Keywords: 4Fe-4S; Amino-acid biosynthesis; Branched-chain amino acid biosynthesis; Iron; Iron-sulfur; Leucine biosynthesis; Lyase; Metal-binding; Protein families: Aconitase/IPM isomerase family, LeuC type 1 subfamily
ndk	Q8YRP2	149		Nucleoside diphosphate kinase (NDK) (NDP kinase) (EC 2.7.4.6) (Nucleoside-2-P kinase); Function: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate. {ECO:0000255 HAMAP-Rule:MF_00451}; Subcellular location: Cytoplasm {ECO:0000255 HAMAP-Rule:MF_00181}; Biological process: CTP biosynthetic process [GO:0006241]; GTP biosynthetic process [GO:0006183]; UTP biosynthetic process [GO:0006228]; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; ATP binding [GO:0005524]; metal ion binding [GO:0046872]; nucleoside diphosphate kinase activity [GO:0004550]; CTP biosynthetic process [GO:0006241]; GTP biosynthetic process [GO:0006183]; UTP biosynthetic process

				[GO:0006228]; Molecular function: ATP binding [GO:0005524]; metal ion binding [GO:0046872]; nucleoside diphosphate kinase activity [GO:0004550]; Keywords: ATP-binding; Cytoplasm; Kinase; Magnesium; Metal-binding; Nucleotide metabolism; Nucleotide-binding; Phosphoprotein; Transferase; Protein families: NDK family
	pepA	Q8Z064	491	Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (EC 3.4.11.10) (Leucyl aminopeptidase); Function: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides. {ECO:0000255 HAMAP-Rule:MF_00181}; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; aminopeptidase activity [GO:0004177]; manganese ion binding [GO:0030145]; metalloexopeptidase activity [GO:0008235]; Molecular function: aminopeptidase activity [GO:0004177]; manganese ion binding [GO:0030145]; metalloexopeptidase activity [GO:0008235]; Keywords: Aminopeptidase; Cytoplasm; Hydrolase; Manganese; Metal-binding; Protease; Protein families: Peptidase M17 family
Nucleic acid metabolism	alr4692 *	Q8YN78	155	Transcriptional regulator; Associated terms: DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; Molecular function: DNA binding [GO:0003677]; DNA-binding transcription factor activity [GO:0003700]; Domain features: DOMAIN 20-152; note="HTH marR-type"; evidence="ECO:0000259 PROSITE:PS50995" Keywords: DNA-binding; Transcription; Transcription regulation
	alr7083 *	Q8YL52	372	Chromosome partitioning protein, ParB family; Associated terms: DNA binding [GO:0003677]; Molecular function: DNA binding [GO:0003677]; Domain features: DOMAIN 61-147; note="ParB"; evidence="ECO:0000259 SMART:SM00470" Keywords: Coiled coil; Plasmid; Protein families: ParB family
	alr7311 *	Q8YKI6	404	Alr7311 protein; Subcellular location: Cytoplasm {ECO:0000255 HAMAP-Rule:MF_00054}; Biological process: DNA-templated transcription, initiation [GO:0006352]; Associated terms: DNA-binding transcription factor activity [GO:0003700]; DNA-templated transcription, initiation [GO:0006352]; Molecular function: DNA-binding transcription factor activity [GO:0003700]; Domain features: DOMAIN 308-

			351; note="Sigma70_r4"; evidence="ECO:0000259 Pfam:PF04545" Keywords: Plasmid
fusA	Q8YP62	692	Elongation factor G (EF-G); Function: Catalyzes the GTP-dependent ribosomal translocation step during translation elongation. During this step, the ribosome changes from the pre-translocational (PRE) to the post-translocational (POST) state as the newly formed A-site-bound peptidyl-tRNA and P-site-bound deacylated tRNA move to the P and E sites, respectively. Catalyzes the coordinated movement of the two tRNA molecules, the mRNA and conformational changes in the ribosome. {ECO:0000255 HAMAP-Rule:MF_00054}; Subcellular location: Cytoplasm {ECO:0000256 HAMAP-Rule:MF_00839}; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; GTP binding [GO:0005525]; GTPase activity [GO:0003924]; translation elongation factor activity [GO:0003746]; Molecular function: GTPase activity [GO:0003924]; GTP binding [GO:0005525]; translation elongation factor activity [GO:0003746]; Domain features: DOMAIN 8-282; note="tr-type G" Keywords: Cytoplasm; Elongation factor; GTP-binding; Nucleotide-binding; Protein biosynthesis; Protein families: TRAFAC class translation factor GTPase superfamily, Classic translation factor GTPase family, EF-G/EF-2 subfamily
hpf	Q8YSA5	213	Ribosome hibernation promoting factor (HPF); Function: Required for dimerization of active 70S ribosomes into 100S ribosomes in stationary phase; 100S ribosomes are translationally inactive and sometimes present during exponential growth. {ECO:0000256 HAMAP-Rule:MF_00839}; Protein L1 is also a translational repressor protein, it controls the translation of the L11 operon by binding to its mRNA. {ECO:0000255 HAMAP-Rule:MF_01318}; ; Biological process: primary metabolic process [GO:0044238]; regulation of translation [GO:0006417]; Cellular component: cytoplasm [GO:0005737]; Associated terms: cytoplasm [GO:0005737]; primary metabolic process [GO:0044238]; regulation of translation [GO:0006417]; Domain features: DOMAIN 130-184; note="Ribosom_S30AE_C"; evidence="ECO:0000259 Pfam:PF16321" Keywords: Coiled coil; Cytoplasm; Translation regulation; Protein families: HPF/YfiA ribosome-associated protein family, Long HPF subfamily
rpl1	Q8YLJ7	238	50S ribosomal protein L1; Function: Binds directly to 23S

				<p>rRNA. The L1 stalk is quite mobile in the ribosome, and is involved in E site tRNA release. {ECO:0000255 HAMAP-Rule:MF_01318}; Biological process: regulation of translation [GO:0006417]; translation [GO:0006412]; Cellular component: large ribosomal subunit [GO:0015934]; Associated terms: large ribosomal subunit [GO:0015934]; rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; tRNA binding [GO:0000049]; regulation of translation [GO:0006417]; translation [GO:0006412]; Molecular function: rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; tRNA binding [GO:0000049]; Keywords: RNA-binding; Repressor; Ribonucleoprotein; Ribosomal protein; Translation regulation; rRNA-binding; tRNA-binding; Protein families: Universal ribosomal protein uL1 family</p>
rplN	Q8YPI9	122	<p>50S ribosomal protein L14; Function: Binds to 23S rRNA. Forms part of two intersubunit bridges in the 70S ribosome. {ECO:0000255 HAMAP-Rule:MF_01367}; Biological process: translation [GO:0006412]; Cellular component: large ribosomal subunit [GO:0015934]; Associated terms: large ribosomal subunit [GO:0015934]; rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; translation [GO:0006412]; Molecular function: rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; Keywords: RNA-binding; Ribonucleoprotein; Ribosomal protein; rRNA-binding; Protein families: Universal ribosomal protein uL14 family</p>	
rpoB	P22703	1131	<p>DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta); Function: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. {ECO:0000255 HAMAP-Rule:MF_01321}; Biological process: transcription, DNA-templated [GO:0006351]; Associated terms: DNA binding [GO:0003677]; DNA-directed 5'-3' RNA polymerase activity [GO:0003899]; ribonucleoside binding [GO:0032549]; transcription, DNA-templated [GO:0006351]; Molecular function: DNA binding [GO:0003677]; DNA-directed 5'-3' RNA polymerase activity [GO:0003899]; ribonucleoside binding [GO:0032549]; Keywords: DNA-directed RNA polymerase; Nucleotidyltransferase; Transcription; Transferase; Protein families: RNA polymerase beta chain</p>	

			family
rpoC2	P22705	1355	DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta'); Function: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. {ECO:0000255 HAMAP-Rule:MF_01324}; With S5 and S12 plays an important role in translational accuracy. {ECO:0000255 HAMAP-Rule:MF_01306}; ; Biological process: transcription, DNA-templated [GO:0006351]; Associated terms: DNA binding [GO:0003677]; DNA-directed 5'-3' RNA polymerase activity [GO:0003899]; zinc ion binding [GO:0008270]; transcription, DNA-templated [GO:0006351]; Molecular function: DNA binding [GO:0003677]; DNA-directed 5'-3' RNA polymerase activity [GO:0003899]; zinc ion binding [GO:0008270]; Keywords: DNA-directed RNA polymerase; Metal-binding; Nucleotidyltransferase; Transcription; Transferase; Zinc; Protein families: RNA polymerase beta' chain family, RpoC2 subfamily
rpsD	Q8YT10	202	30S ribosomal protein S4; Function: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the body of the 30S subunit. {ECO:0000255 HAMAP-Rule:MF_01306}; Located at the back of the 30S subunit body where it stabilizes the conformation of the head with respect to the body. {ECO:0000255 HAMAP-Rule:MF_01307}; ; Biological process: translation [GO:0006412]; Cellular component: small ribosomal subunit [GO:0015935]; Associated terms: small ribosomal subunit [GO:0015935]; rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; translation [GO:0006412]; Molecular function: rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; Domain features: DOMAIN 90-152; note="S4 RNA-binding"; evidence="ECO:0000255 HAMAP-Rule:MF_01306" Keywords: RNA-binding; Ribonucleoprotein; Ribosomal protein; rRNA-binding; Protein families: Universal ribosomal protein uS4 family
rpsE	Q8YPJ5	174	30S ribosomal protein S5; Function: With S4 and S12 plays an important role in translational accuracy. {ECO:0000255 HAMAP-Rule:MF_01307}; Biological process: translation [GO:0006412]; Cellular component: small ribosomal subunit [GO:0015935]; Associated terms: small ribosomal subunit [GO:0015935]; rRNA binding [GO:0019843]; structural constituent of ribosome

			<p>[GO:0003735]; translation [GO:0006412]; Molecular function: rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; Domain features: DOMAIN 18-81; note="S5 DRBM"; evidence="ECO:0000255 HAMAP-Rule:MF_01307"</p> <p>Keywords: RNA-binding; Ribonucleoprotein; Ribosomal protein; rRNA-binding; Protein families: Universal ribosomal protein uS5 family</p>
rpsG	Q8YP61	156	<p>30S ribosomal protein S7; Function: One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates assembly of the head domain of the 30S subunit. Is located at the subunit interface close to the decoding center, probably blocks exit of the E-site tRNA. {ECO:0000255 HAMAP-Rule:MF_00480; Biological process: translation [GO:0006412]; Cellular component: small ribosomal subunit [GO:0015935]; Associated terms: small ribosomal subunit [GO:0015935]; rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; tRNA binding [GO:0000049]; translation [GO:0006412]; Molecular function: rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; tRNA binding [GO:0000049]; Keywords: RNA-binding; Ribonucleoprotein; Ribosomal protein; rRNA-binding; tRNA-binding; Protein families: Universal ribosomal protein uS7 family</p>
rpsN	Q8YQ66	100	<p>30S ribosomal protein S14; Function: Binds 16S rRNA, required for the assembly of 30S particles and may also be responsible for determining the conformation of the 16S rRNA at the A site. {ECO:0000255 HAMAP-Rule:MF_00537}; Probably participates in protein translocation into and across both the cytoplasmic and thylakoid membranes in cyanobacterial cells. {ECO:0000255 HAMAP-Rule:MF_01382}; Subcellular location: Cell inner membrane {ECO:0000255 HAMAP-Rule:MF_01382}; Peripheral membrane protein {ECO:0000255 HAMAP-Rule:MF_01382}; Cytoplasmic side {ECO:0000255 HAMAP-Rule:MF_01382}. Cellular thylakoid membrane {ECO:0000255 HAMAP-Rule:MF_01382}; Peripheral membrane protein {ECO:0000255 HAMAP-Rule:MF_01382}; Cytoplasmic side {ECO:0000255 HAMAP-Rule:MF_01382}. Cytoplasm {ECO:0000255 HAMAP-Rule:MF_01382}; Biological process: translation [GO:0006412]; Cellular component: ribosome [GO:0005840]; Associated terms: ribosome [GO:0005840]; rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735];</p>

				translation [GO:0006412]; Molecular function: rRNA binding [GO:0019843]; structural constituent of ribosome [GO:0003735]; Keywords: RNA-binding; Ribonucleoprotein; Ribosomal protein; rRNA-binding; Protein families: Universal ribosomal protein uS14 family
	secA	Q8YMS8	930	Protein translocase subunit SecA; Function: Part of the Sec protein translocase complex. Interacts with the SecYEG preprotein conducting channel. Has a central role in coupling the hydrolysis of ATP to the transfer of proteins into and across the cell membrane, serving as an ATP-driven molecular motor driving the stepwise translocation of polypeptide chains across the membrane. {ECO:0000255 HAMAP-Rule:MF_01382}; Biological process: intracellular protein transmembrane transport [GO:0065002]; protein import [GO:0017038]; protein targeting [GO:0006605]; Cellular component: cytoplasm [GO:0005737]; plasma membrane [GO:0005886]; thylakoid membrane [GO:0042651]; Associated terms: cytoplasm [GO:0005737]; plasma membrane [GO:0005886]; thylakoid membrane [GO:0042651]; ATP binding [GO:0005524]; intracellular protein transmembrane transport [GO:0065002]; protein import [GO:0017038]; protein targeting [GO:0006605]; Molecular function: ATP binding [GO:0005524]; Keywords: ATP-binding; Cell inner membrane; Cell membrane; Cytoplasm; Membrane; Nucleotide-binding; Protein transport; Thylakoid; Translocation; Transport; Protein families: SecA family
Photosynthesis	all7255	Q8YKN8	499	Zeta-carotene desaturase; Transmembrane; Biological process: carotenoid biosynthetic process [GO:0016117]; Associated terms: oxidoreductase activity [GO:0016491]; carotenoid biosynthetic process [GO:0016117]; Molecular function: oxidoreductase activity [GO:0016491]; Domain features: DOMAIN 13-474; note="Amino_oxidase"; evidence="ECO:0000259 Pfam:PF01593" Keywords: Carotenoid biosynthesis; Oxidoreductase; Plasmid; Protein families: Carotenoid/retinoid oxidoreductase family
	all7348*	Q8YKF0	460	All7348 protein; Subcellular location: Cellular thylakoid membrane {ECO:0000250}; Peripheral membrane protein {ECO:0000250}; Cytoplasmic side {ECO:0000250}. Note=Anchors the phycobilisome perpendicularly to the cytoplasmic surface of the thylakoid membrane. {ECO:0000250}; Cellular component: integral component of membrane [GO:0016021]; Associated terms: integral component of membrane [GO:0016021]; 2 iron, 2 sulfur cluster binding [GO:0051537]; chlorophyllide a oxygenase

			[overall] activity [GO:0010277]; Molecular function: 2 iron, 2 sulfur cluster binding [GO:0051537]; chlorophyllide a oxygenase [overall] activity [GO:0010277]; Domain features: DOMAIN 11-122; note="Rieske"; evidence="ECO:0000259 PROSITE:PS51296" Keywords: Membrane; Plasmid; Transmembrane; Transmembrane helix
apcE*	P80559	1132	Phycobiliprotein ApcE (Anchor polypeptide) (PBS-anchor protein) (Phycobilisome linker polypeptide); Function: This protein is postulated to act both as terminal energy acceptor (by its phycobin-like domains) and as a linker polypeptide (by its repeats and arms) that stabilizes the phycobilisome core architecture. Has intrinsic bilin lyase activity (By similarity). {ECO:0000250}; Linker polypeptides determine the state of aggregation and the location of the disk-shaped phycobiliprotein units within the phycobilisome and modulate their spectroscopic properties in order to mediate a directed and optimal energy transfer. {ECO:0000250}; Subcellular location: Cellular thylakoid membrane {ECO:0000250}; Peripheral membrane protein {ECO:0000250}; Cytoplasmic side {ECO:0000250}; Biological process: oxidation-reduction process [GO:0055114]; photosynthesis [GO:0015979]; protein-chromophore linkage [GO:0018298]; Cellular component: phycobilisome [GO:0030089]; Associated terms: phycobilisome [GO:0030089]; lyase activity [GO:0016829]; oxidation-reduction process [GO:0055114]; photosynthesis [GO:0015979]; protein-chromophore linkage [GO:0018298]; Molecular function: lyase activity [GO:0016829]; Domain features: DOMAIN 253-433; note="PBS-linker 1"; evidence="ECO:0000255 PROSITE-ProRule:PRU00775"; DOMAIN 514-692; note="PBS-linker 2"; evidence="ECO:0000255 PROSITE-ProRule:PRU00775"; DOMAIN 709-887; note="PBS-linker 3"; evidence="ECO:0000255 PROSITE-ProRule:PRU00775"; DOMAIN 940-1121; note="PBS-linker 4"; evidence="ECO:0000255 PROSITE-ProRule:PRU00775" Keywords: 3D-structure; Bile pigment; Chromophore; Direct protein sequencing; Electron transport; Lyase; Membrane; Photosynthesis; Phycobilisome; Repeat; Thylakoid; Transport; Protein families: Phycobilisome linker protein family
cpcG3	P29988	237	Phycobilisome rod-core linker polypeptide CpcG3 (L-RC 27.2); Function: Rod-core linker protein required for attachment of phycocyanin to allophycocyanin in cores of

				<p>phycobilisomes. {ECO:0000250}; Subcellular location: Cellular thylakoid membrane {ECO:0000255 HAMAP-Rule:MF_01351}; Peripheral membrane protein {ECO:0000255 HAMAP-Rule:MF_01351}; Biological process: photosynthesis [GO:0015979]; Cellular component: phycobilisome [GO:0030089]; Associated terms: phycobilisome [GO:0030089]; photosynthesis [GO:0015979]; Domain features: DOMAIN 11-191; note="PBS-linker"; evidence="ECO:0000255 PROSITE-ProRule:PRU00775" Keywords: Membrane; Photosynthesis; Phycobilisome; Thylakoid; Protein families: Phycobilisome linker protein family</p>
ndhI	Q9WWM 6	194		<p>NAD(P)H-quinone oxidoreductase subunit I (EC 7.1.1.-) (NAD(P)H dehydrogenase I subunit I) (NDH-1 subunit I) (NDH-I); Function: NDH-1 shuttles electrons from an unknown electron donor, via FMN and iron-sulfur (Fe-S) centers, to quinones in the respiratory and/or the photosynthetic chain. The immediate electron acceptor for the enzyme in this species is believed to be plastoquinone. Couples the redox reaction to proton translocation, and thus conserves the redox energy in a proton gradient. {ECO:0000255 HAMAP-Rule:MF_01351}; Subcellular location: Cellular thylakoid membrane {ECO:0000250}; Peripheral membrane protein {ECO:0000250}; Cytoplasmic side {ECO:0000250}. Note=Forms the periphery of the phycobilisome rod. {ECO:0000250}; Biological process: photosynthesis, light reaction [GO:0019684]; Cellular component: thylakoid membrane [GO:0042651]; Associated terms: thylakoid membrane [GO:0042651]; 4 iron, 4 sulfur cluster binding [GO:0051539]; iron ion binding [GO:0005506]; NADH dehydrogenase (ubiquinone) activity [GO:0008137]; quinone binding [GO:0048038]; photosynthesis, light reaction [GO:0019684]; Molecular function: 4 iron, 4 sulfur cluster binding [GO:0051539]; iron ion binding [GO:0005506]; NADH dehydrogenase (ubiquinone) activity [GO:0008137]; quinone binding [GO:0048038]; Domain features: DOMAIN 55-84; note="4Fe-4S ferredoxin-type 1"; evidence="ECO:0000255 HAMAP-Rule:MF_01351"; DOMAIN 95-124; note="4Fe-4S ferredoxin-type 2"; evidence="ECO:0000255 HAMAP-Rule:MF_01351" Keywords: 4Fe-4S; Iron; Iron-sulfur; Membrane; Metal-binding; NAD; NADP; Plastoquinone; Quinone; Repeat; Thylakoid; Translocase; Protein families: Complex I 23 kDa subunit family</p>
pecA*	P35796	162		<p>Phycocerythrocyanin alpha chain; Function: Light-</p>

			<p>harvesting photosynthetic bile pigment-protein from the phycobiliprotein complex; Subcellular location: Cellular thylakoid membrane {ECO:0000250}; Peripheral membrane protein {ECO:0000250}; Cytoplasmic side {ECO:0000250}. Note=Forms the periphery of the phycobilisome rod. {ECO:0000250}; Biological process: oxidation-reduction process [GO:0055114]; photosynthesis [GO:0015979]; protein-chromophore linkage [GO:0018298]; Cellular component: phycobilisome [GO:0030089]; Associated terms: phycobilisome [GO:0030089]; oxidation-reduction process [GO:0055114]; photosynthesis [GO:0015979]; protein-chromophore linkage [GO:0018298]; Keywords: Bile pigment; Chromophore; Electron transport; Membrane; Photosynthesis; Phycobilisome; Thylakoid; Transport; Protein families: Phycobiliprotein family</p>
pecB	P35797	172	<p>Phycocerythrocyanin subunit beta; Function: Light-harvesting photosynthetic bile pigment-protein from the phycobiliprotein complex; Subcellular location: Cellular thylakoid membrane; Peripheral membrane protein; Cytoplasmic side. Note=This protein occurs in the rod, it is associated with phycoerythrocyanin; Biological process: oxidation-reduction process [GO:0055114]; photosynthesis [GO:0015979]; protein-chromophore linkage [GO:0018298]; Cellular component: phycobilisome [GO:0030089]; Associated terms: phycobilisome [GO:0030089]; oxidation-reduction process [GO:0055114]; photosynthesis [GO:0015979]; protein-chromophore linkage [GO:0018298]; Keywords: Bile pigment; Chromophore; Electron transport; Membrane; Photosynthesis; Phycobilisome; Thylakoid; Transport; Protein families: Phycobiliprotein family</p>
pecC	P31329	278	<p>Phycobilisome 34.5 kDa linker polypeptide, phycoerythrocyanin-associated, rod; Function: Rod linker protein, associated with phycoerythrocyanin. Linker polypeptides determine the state of aggregation and the location of the disk-shaped phycobiliprotein units within the phycobilisome and modulate their spectroscopic properties in order to mediate a directed and optimal energy transfer; Subcellular location: Cellular thylakoid membrane {ECO:0000250}; Multi-pass membrane protein {ECO:0000250}; Transmembrane; Biological process: photosynthesis [GO:0015979]; Cellular component: phycobilisome [GO:0030089]; Associated terms: phycobilisome [GO:0030089]; photosynthesis [GO:0015979]; Domain features: DOMAIN 2-178;</p>

			note="PBS-linker"; evidence="ECO:0000255 PROSITE-ProRule:PRU00775"; DOMAIN 226-278; note="CpcD-like"; evidence="ECO:0000255 PROSITE-ProRule:PRU00771" Keywords: Direct protein sequencing; Membrane; Photosynthesis; Phycobilisome; Thylakoid; Protein families: Phycobilisome linker protein family
alr1129	Q8YXT2	325	Alr1129 protein; Domain features: DOMAIN 5-76; note="PRC"; evidence="ECO:0000259 Pfam:PF05239"; DOMAIN 85-163; note="PRC"; evidence="ECO:0000259 Pfam:PF05239"
psaL	P58577	172	Photosystem I reaction center subunit XI (PSI subunit V) (PSI-L); Subcellular location: Cellular thylakoid membrane {ECO:0000255 HAMAP-Rule:MF_01495}; Multi-pass membrane protein {ECO:0000255 HAMAP-Rule:MF_01495}; Transmembrane; Biological process: photosynthesis [GO:0015979]; Cellular component: integral component of membrane [GO:0016021]; photosystem I reaction center [GO:0009538]; thylakoid membrane [GO:0042651]; Associated terms: integral component of membrane [GO:0016021]; photosystem I reaction center [GO:0009538]; thylakoid membrane [GO:0042651]; photosynthesis [GO:0015979]; Keywords: 3D-structure; Membrane; Photosynthesis; Photosystem I; Thylakoid; Transmembrane; Transmembrane helix; Protein families: PsaL family
psbB	P20093	509	Photosystem II CP47 reaction center protein (PSII 47 kDa protein) (Protein CP-47); Function: One of the components of the core complex of photosystem II (PSII). It binds chlorophyll and helps catalyze the primary light-induced photochemical processes of PSII. PSII is a light-driven water: plastoquinone oxidoreductase, using light energy to abstract electrons from H(2)O, generating O(2) and a proton gradient subsequently used for ATP formation. {ECO:0000255 HAMAP-Rule:MF_01495}; Biological process: photosynthetic electron transport in photosystem II [GO:0009772]; protein-chromophore linkage [GO:0018298]; Cellular component: integral component of membrane [GO:0016021]; photosystem II [GO:0009523]; thylakoid membrane [GO:0042651]; Associated terms: integral component of membrane [GO:0016021]; photosystem II [GO:0009523]; thylakoid membrane [GO:0042651]; chlorophyll binding [GO:0016168]; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity [GO:0045156]; photosynthetic electron transport in

				photosystem II [GO:0009772]; protein-chromophore linkage [GO:0018298]; Molecular function: chlorophyll binding [GO:0016168]; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity [GO:0045156]; Keywords: Chlorophyll; Chromophore; Membrane; Photosynthesis; Photosystem II; Thylakoid; Transmembrane; Transmembrane helix; Protein families: PsbB/PsbC family, PsbB subfamily
No clustered Signal domine proteins	all0050*	Q8Z0P0	345	All0050 protein; Keywords: Signal
	all1755	Q8YW61	132	All1755 protein; Keywords: Signal
	all1783*	Q8YW33	201	All1783 protein; Keywords: Signal
	all4130	Q8YPR2	301	Binding protein of ABC transporter component; Domain features: DOMAIN 36-269; note="PBPb"; evidence="ECO:0000259 SMART:SM00062" Keywords: Signal
	alr0490	Q8YZH0	225	Alr0490 protein; Keywords: Signal
	alr1548	Q8YWQ6	312	Alr1548 protein; Domain features: DOMAIN 214-281; note="TPR_REGION"; evidence="ECO:0000259 PROSITE:PS50293" Keywords: Coiled coil; Signal
	alr3932	Q8YQA1	231	Alr3932 protein; Keywords: Signal
	alr7326	Q8YKH2	173	Alr7326 protein; Keywords: Plasmid; Signal
	alr7345	Q8YKF3	303	Alr7345 protein; Associated terms: methyltransferase activity [GO:0008168]; Molecular function: methyltransferase activity [GO:0008168]; Domain features: DOMAIN 142-201; note="Methyltransf_11"; evidence="ECO:0000259 Pfam:PF08241" Keywords: Plasmid; Signal
	all2086	Q8YV95	564	All2086 protein
	all2262	Q8YUS2	142	All2262 protein; Keywords: Coiled coil
	all2480	Q8YU74	283	Beta-lactamase; Associated terms: penicillin binding [GO:0008658]; Molecular function: penicillin binding [GO:0008658]; Domain features: DOMAIN 64-274; note="Transpeptidase"; evidence="ECO:0000259 Pfam:PF00905" Keywords: 3D-structure
	all2965*	Q8YSW4	162	All2965 protein
	alr0436	Q8YZM1	470	Alr0436 protein
	alr4359	Q8YP41	418	Alr4359 protein; Domain features: DOMAIN 43-215; note="VWFA"; evidence="ECO:0000259 PROSITE:PS50234"
alr7233	Q8YKR0	341	Alr7233 protein; Keywords: Plasmid	
alr7300	Q8YKJ5	269	Alr7300 protein; Keywords: Plasmid	

	alr7312 *	Q8YKI5	383	Alr7312 protein; Keywords: Plasmid
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Figure 1B specific information:

FTIR peaks specific information

The FTIR spectra present the characteristic bands of PS: C–H stretching vibration (3070 cm^{-1} and 3028 cm^{-1}), C–H₂ stretching vibration (2924 cm^{-1} and 2854 cm^{-1}) and stretching (1646 cm^{-1} , 1556 cm^{-1} , 1456 cm^{-1}) of the benzene ring;¹² G7: N–H stretching of primary and secondary amine groups stretching (3408 cm^{-1} and 3292 cm^{-1}), C–H stretching (2934 cm^{-1} and 2866 cm^{-1}), C = O stretching of primary amide (1650 cm^{-1}) H–C–H asymmetric, N–H bending/C–N stretching secondary amide (1562 cm^{-1}), H–C–H scissor (1452 cm^{-1}), H–C–H asymmetric (1368 cm^{-1}) and C–O stretching vibration (1060 cm^{-1}).¹³ The suspension containing both nanopolymers shows the characteristic peaks from each one: from PS the C–H stretching vibration (3086 cm^{-1} and 3031 cm^{-1}), C–H₂ stretching vibration (2924 cm^{-1} and 2856 cm^{-1}) and stretching of the benzene ring (1646 cm^{-1} , 1556 cm^{-1} , 1456 cm^{-1}) and from the G7, N–H stretching of primary and secondary amine groups stretching (3408 cm^{-1} and 3288 cm^{-1}), C–H₂ stretching vibration shared with PS, C = O stretching of primary amide, N–H bending/C–N stretching secondary amide and H–C–H scissor (which three peaks overlapped with those corresponding to the benzene ring), H–C–H asymmetric (1368 cm^{-1}) and C–O stretching vibration (1030 cm^{-1}). Thus, the chemical surface of the aggregates rather than being homogeneous appear to present an irregular surface presenting region with characteristics corresponding to G7 and others corresponding to PS-NPs, which surface net charge prevails over the G7 positive charge due to its higher concentration and dimensions.

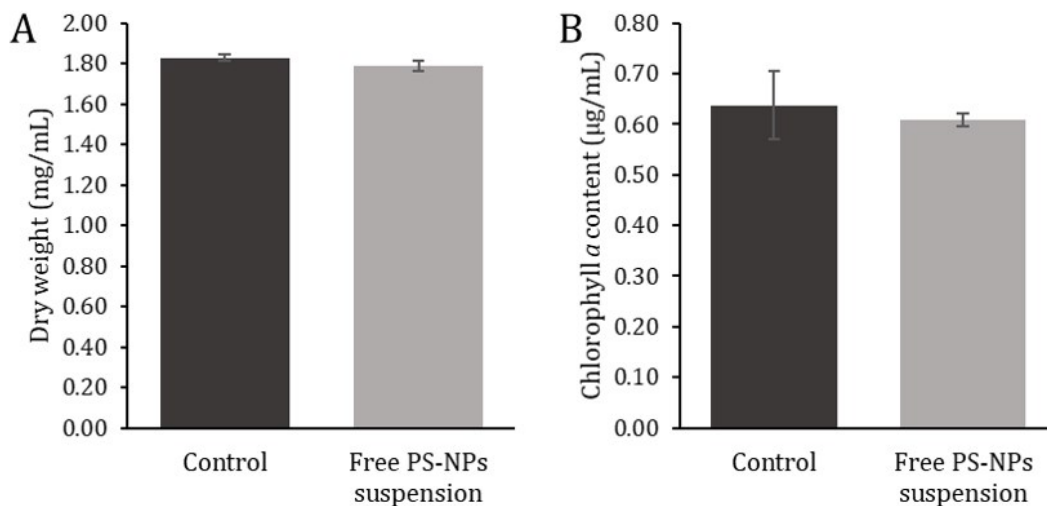


Figure S1: Effect of free PS-NPs suspension on *Anabaena* sp. PCC7120 growth for 72 h at $\sim 65 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ on a rotary shaker in AA/8 + N in terms of growth inhibition (A) and chlorophyll *a* content (B). Different letters indicate treatments that are significantly different (Tukey's HSD, $p < 0.05$).

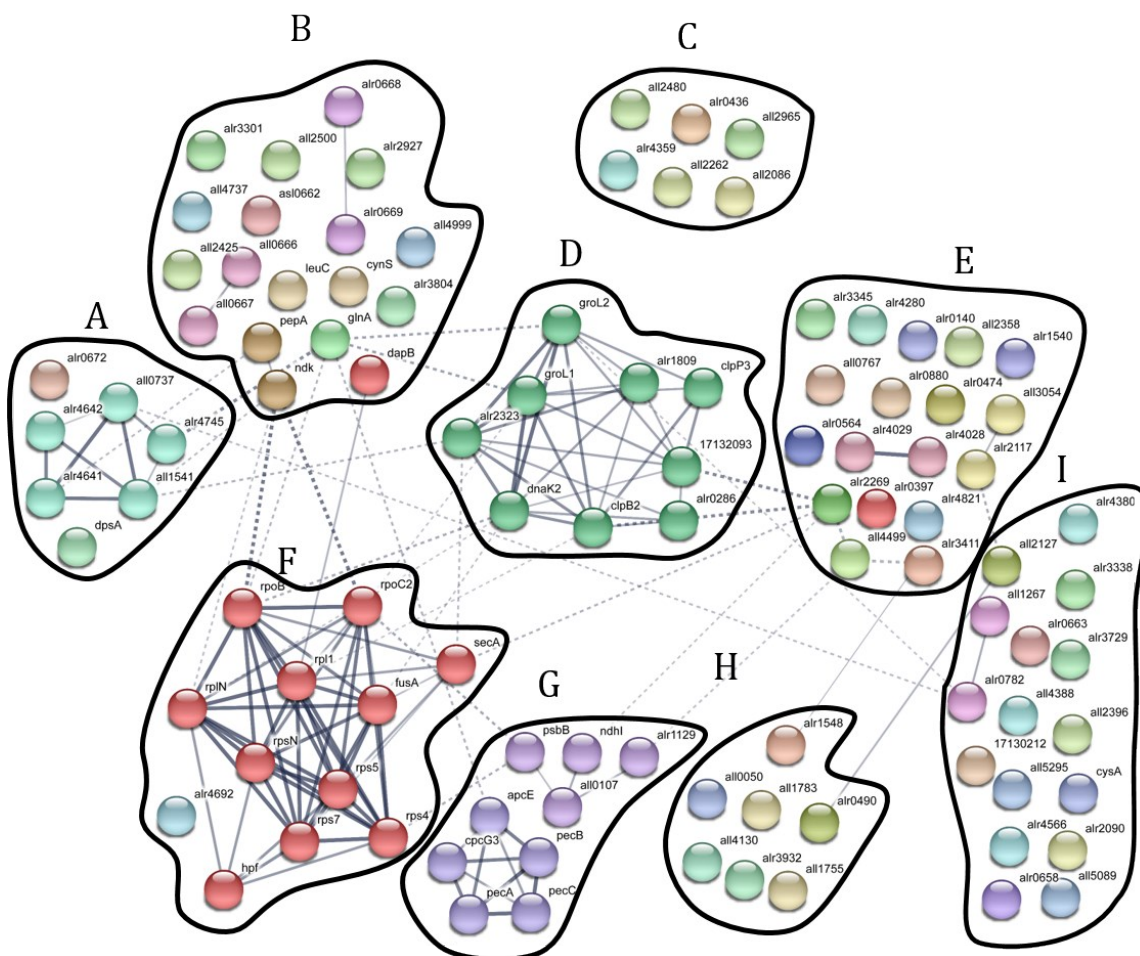


Figure S2: Protein-protein interaction network from STRING software clustered by MCL algorithm (inflation parameter = 3) complemented with Uniprot protein information. Proteins were allocated into 9 categories: Oxidative stress (A), Organo-nitrogen metabolism (B), No clustered proteins (C), Stress response (D), Surface location (E), Nucleic acid metabolism (F), Photosynthesis (G), Signal domain (H) and Carbon metabolism and energy (I).

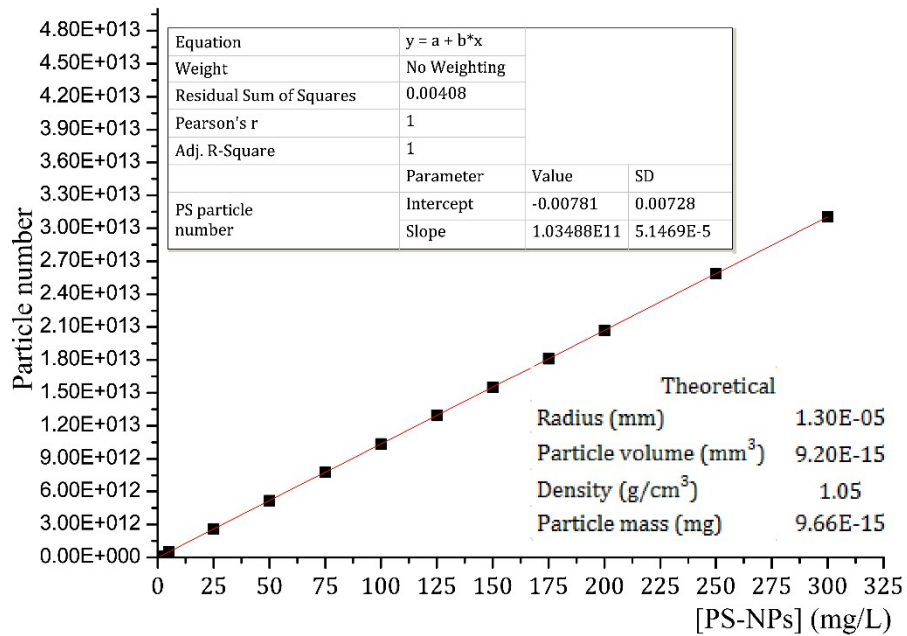


Figure S3: Theoretical linear regression between PS-NPs particle number and concentration as well as the correspondent related parameters.

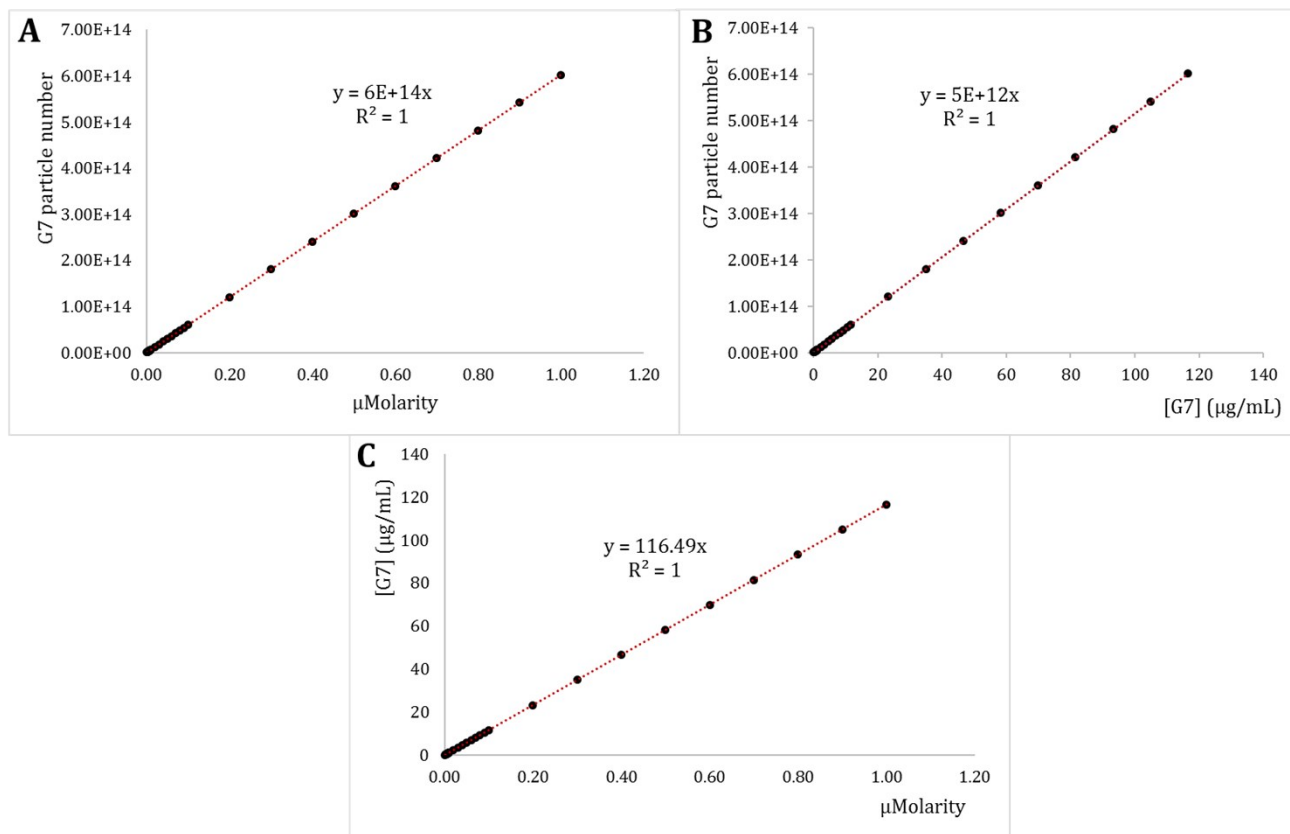


Figure S4: Theoretical linear regressions between G7 particle number and concentration (in term of μM or mg/L) as well as the corresponding related parameters.

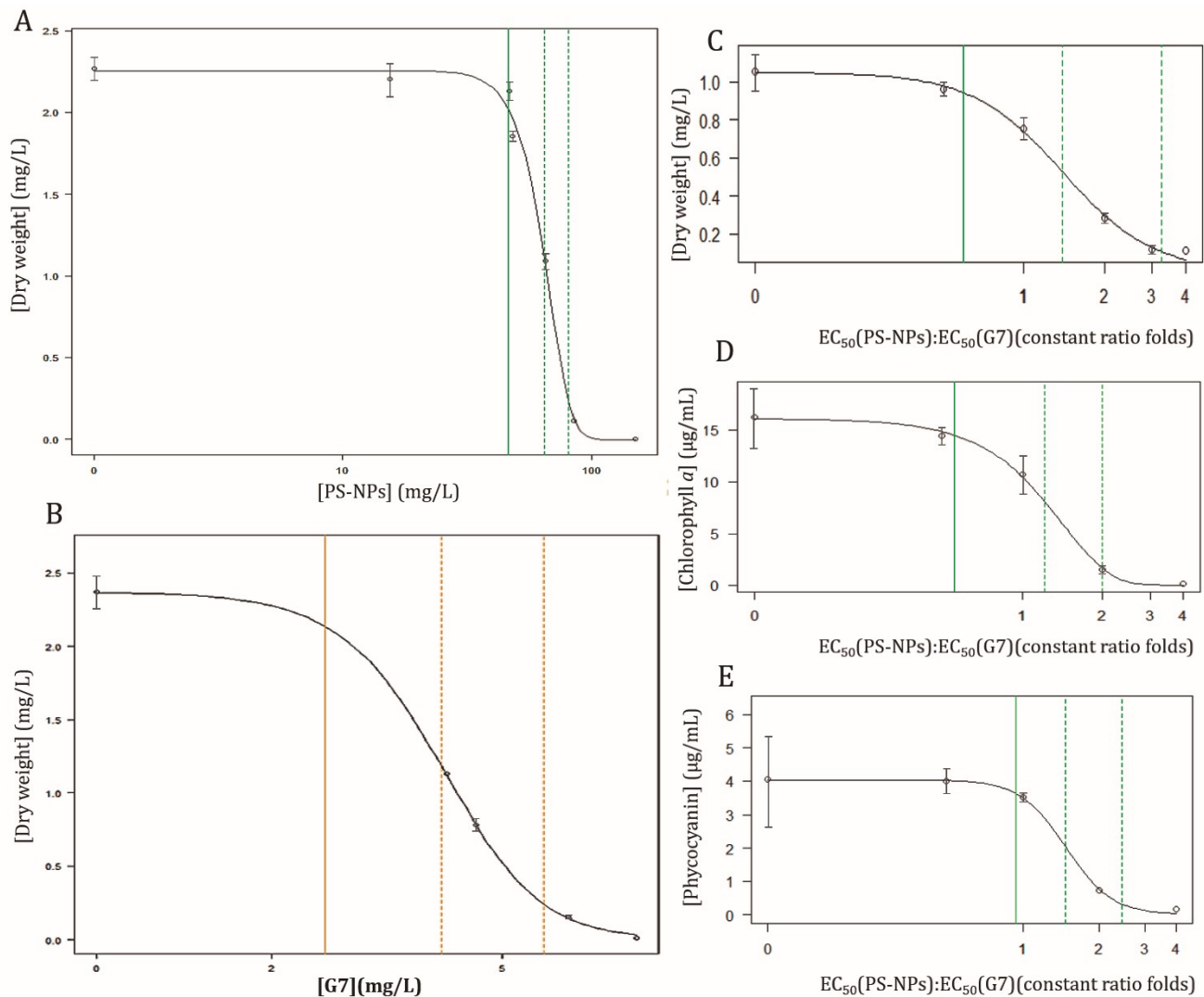


Figure S5: Individual dose-response curves (DRC) for growth inhibition of *Anabaena* exposed to PS-NPs (A) and G7 (B) for 72 h. Binary mixture DRC for growth inhibition (C), for chlorophyll *a* concentration (D) and for phycocyanin concentration decrease (E).

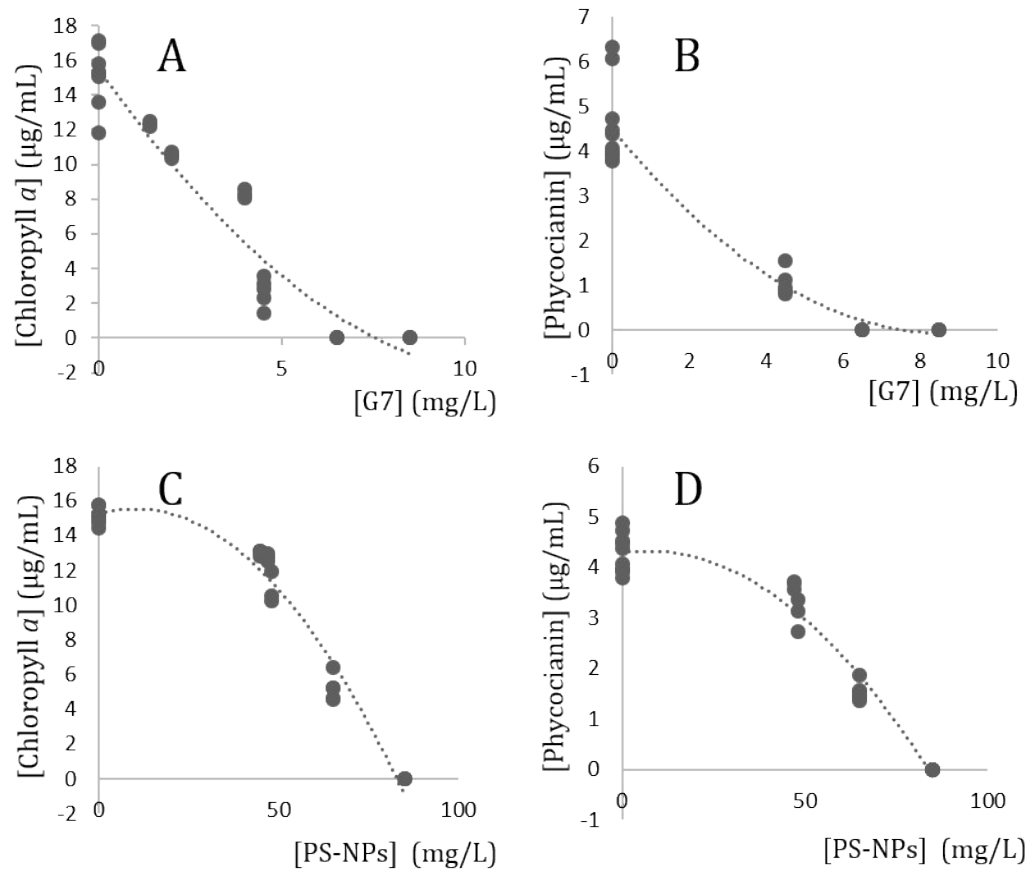


Figure S6: Dose-response curves (DRC) of *Anabaena* sp. PCC 7120 exposed to G7 PAMAM dendrimers (A, B), PS-NPs (C, D) and their mixture in the ratio 1:1 (EC₅₀ for growth inhibition) (E, F) in terms of chlorophyll *a* (A, C) and phycocyanin content (B, D).

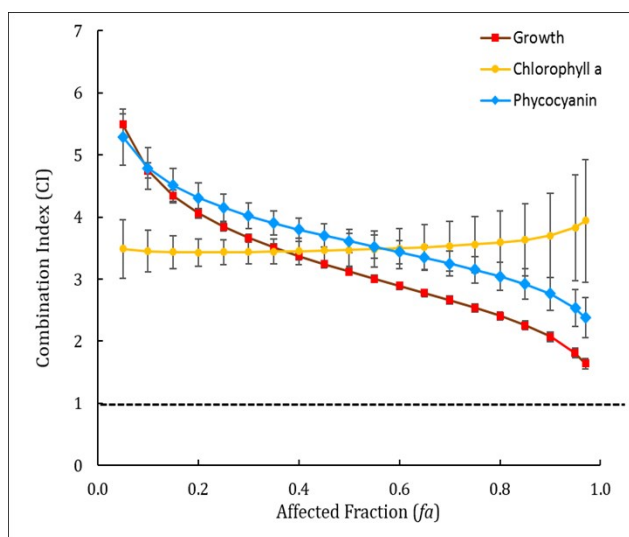


Figure S7: Combination index plot for binary combinations of PS-NPs and G7 in a constant ratio corresponding to the EC₅₀ of both nanoparticles for growth inhibition; CI values are plotted as a function

of the growth inhibition, decrease in chlorophyll a concentration and decrease in phycocyanin concentration (through all effect levels, fa). CI > 1 indicates antagonism and the dashed line additivity (CI = 1)

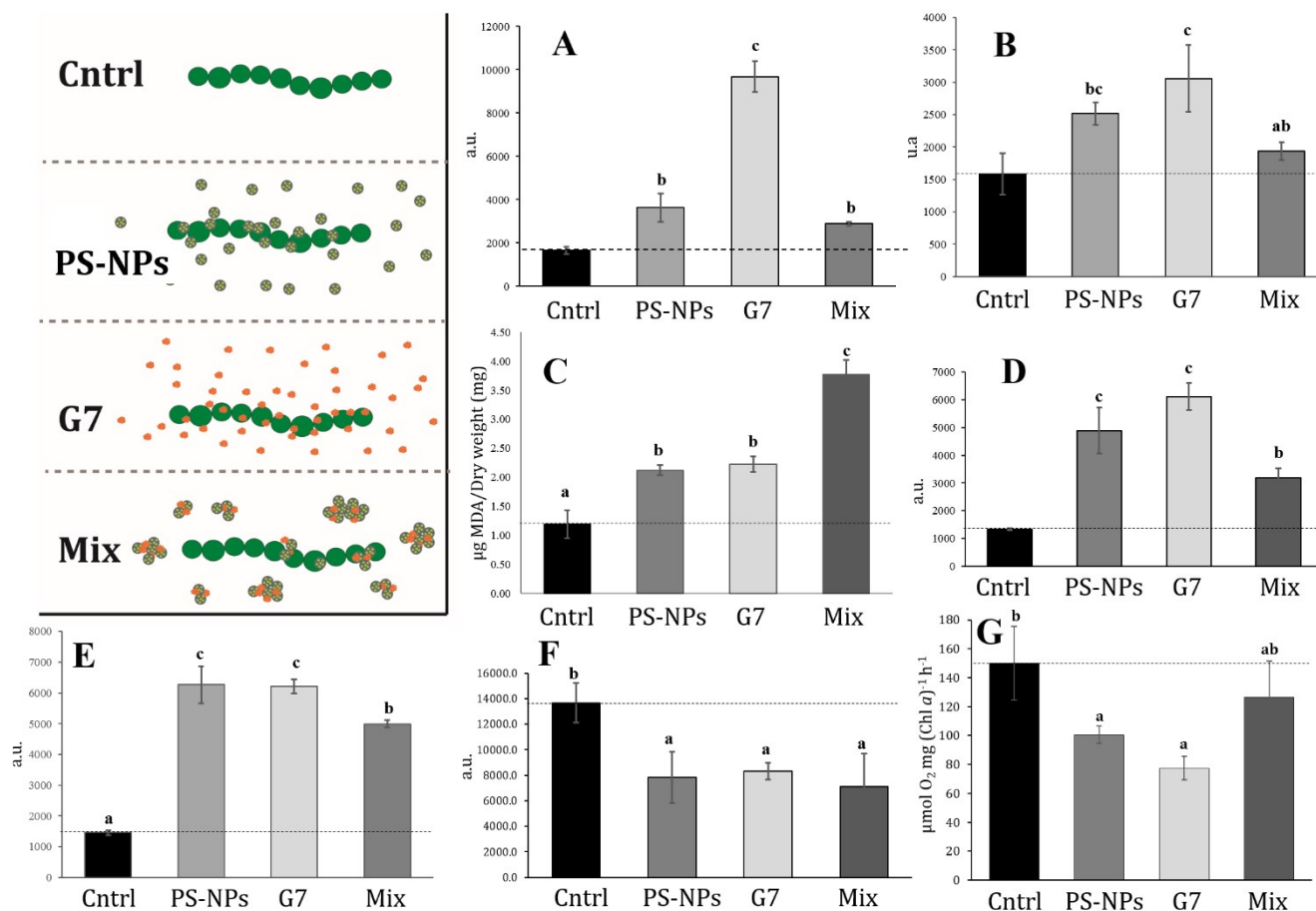


Figure S8: Physiological response of *Anabaena* sp. PCC7120 after its exposure to PAMAM dendrimer of generation 7 (G7) and polystyrene nanoparticles (PS-NPs), their mixture (Mix) and non-exposed cultures (Cntrl). Measurements were conducted by fluorimetry using a set of fluorochromes to evaluate: intracellular ROS formation by using 2 different fluorochromes [H_2DCF DA for general ROS formation (A), DHR 123 for H_2O_2 formation (B)], lipid peroxidation (C) by quantification of TBARS, membrane integrity by propidium iodide (D), cytoplasmic membrane potential (E) by DiBAC₄(3)), intracellular pH (F) by using BCECF AM and photosynthesis (G). Different letters indicate treatments that are significantly different (Tukey's HSD, $p < 0.05$).

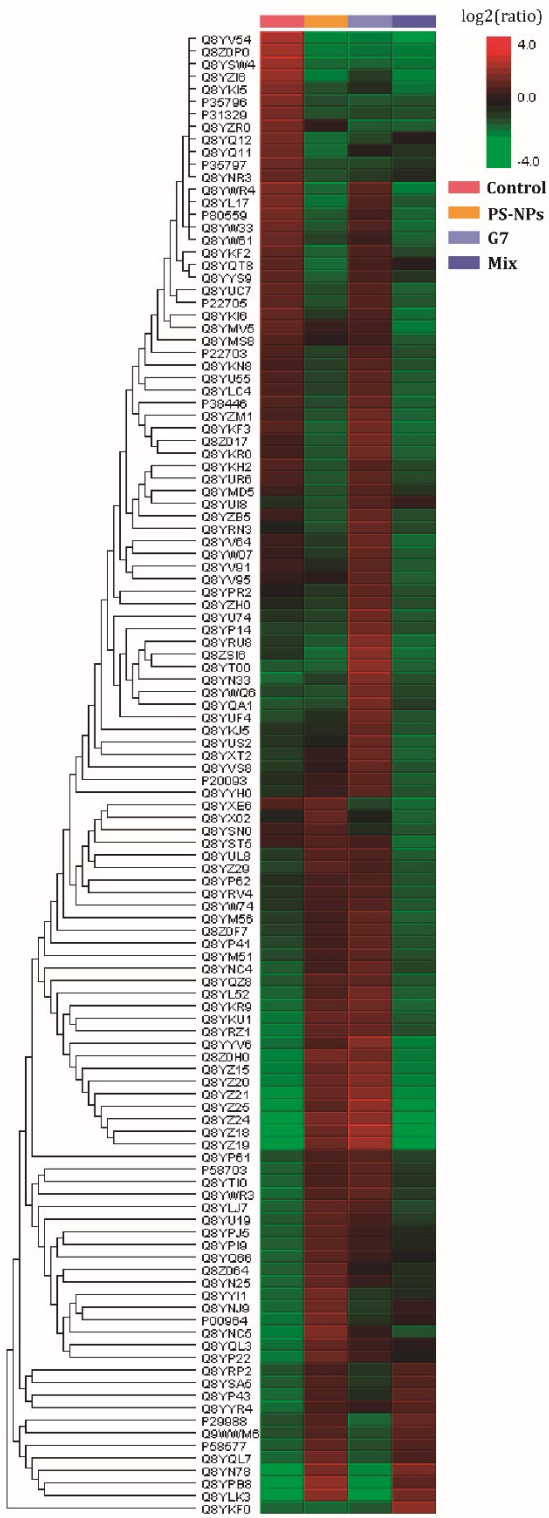
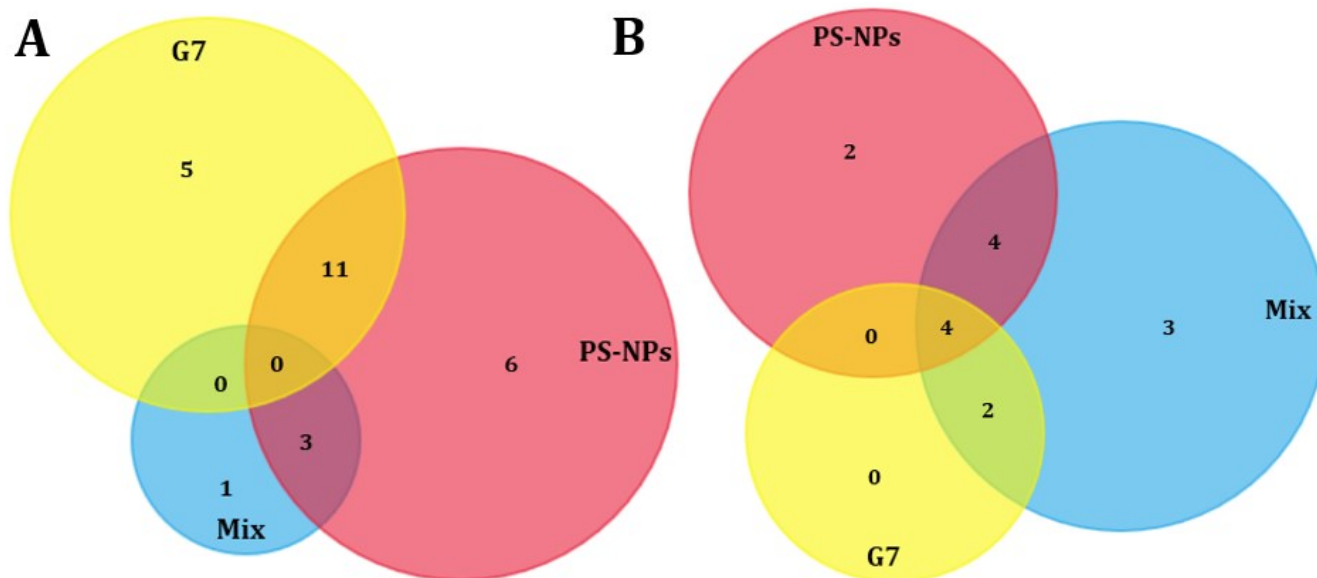


Figure S9: Heatmap with phylogenetic tree representing the proteomic response of *Anabaena* sp. PCC7120 in which at least one treatment induced significant change (FC <0.83 or >1.2, p <0.01) with respect to the control (p<0.01) after its exposure to PAMAM dendrimer of generation 7 (G7), polystyrene nanoparticles (PS-NPs) and the combination of both nanoparticles (Mix).



Upregulated (A)						
PS-NPs	G7	Mix	PS-NPs & G7	PS-NPs & Mix	G7 & Mix	PS-NPs, G7 & Mix
GlnA	All7222	All7348	Alr0663	All5295	-	-
CcmK	Alr7083	-	Alr0672	Alr4692	-	-
Alr4641	All0737	-	Alr0668	Alr4280	-	-
Alr4566	Alr2927	-	Alr0669	-	-	-
DpsA	All4737	-	Alr4380	-	-	-
Alr3804	-	-	Alr3301	-	-	-
-	-	-	Asl0662	-	-	-
-	-	-	Alr7200	-	-	-
-	-	-	All0667	-	-	-
-	-	-	CysA	-	-	-
-	-	-	All0666	-	-	-
Downregulated (B)						
PS-NPs	G7	Mix	PS-NPs & G7	PS-NPs & Mix	G7 & Mix	PS-NPs, G7 & Mix
Alr4029	-	All1783	-	ApcE	PecA	All0050
Alr4028	-	Alr7311	-	All7121	Alr0397	All2965
-	-	Alr4821	-	Alr7312	-	Alr0474
				Alr1540		All2127

Figure S10: Venn diagram of DEPs upregulated (A) and downregulated (B) upon the exposure of *Anabaena* sp. PCC7120 for 72 h to PS-NPs, G7 and their combined exposure (Mix) (FC <0.5 or >2, p <0.01). The table shows the DEPs clustered based on the Venn diagram distribution.

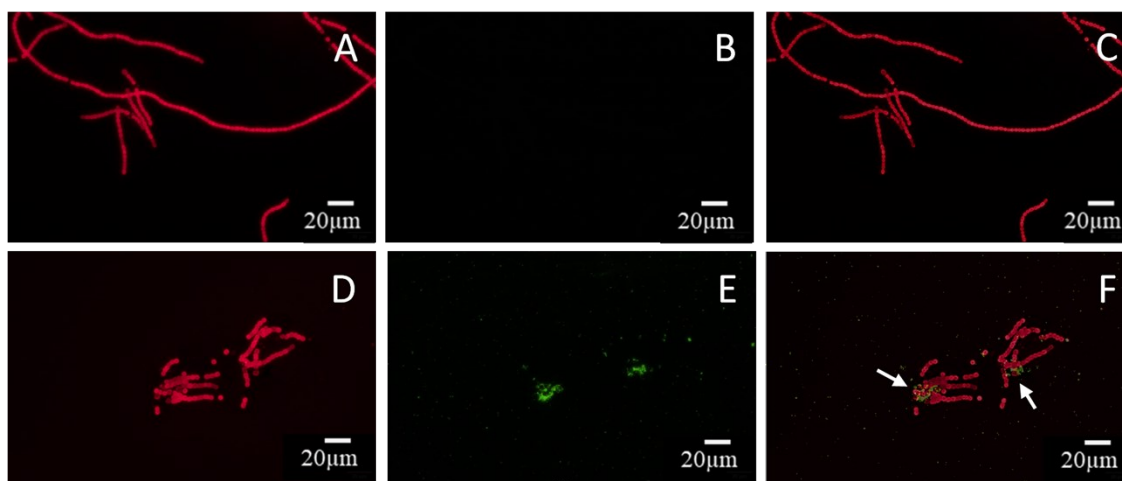


Figure S11: Fluorescence microscopy images (left to right): chlorophyll a fluorescence (red), PS-NPs fluorescence (green), and red/green fluorescence overlay. Images show *Anabaena* sp. PCC7120 cells after six days -control- (A, B, C) and *Anabaena* sp. PCC7120 cells after six days of exposure to the mixture PS-NPs + G7 (D, E, F). White arrows in the overlay images indicate heteroaggregates of PS-NPs and G7 adhered to sites of filament fragmentation.

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