Supplementary material

Single and combined exposures of micro(nano)plastics and azithromycin disturb photosynthetic carbon fixation of *Synechocystis* sp.

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Text S1 Chemicals

Methanol (HPLC grade) was obtained from Sinopharm Chemical Reagent Co., Ltd (China). 2',7'-dichloro fluorescin diacetate (DCFH-DA, analytical grade) and propidium iodide (PI) were purchased from AAT Bioquest Inc (USA) and Beyotime Biotechnology (China), respectively. Ultrapure water was acquired from a Milli-Q Gradient (USA).

Text S2 Determination of cell density and photosynthetic pigments

The growth inhibition rates of *Microcystis* strains exposed to MNPs or/and antibiotics for 96 h were calculated as follows:[1]

$$IR\ (\%) = \frac{\mathrm{N}_c - \mathrm{N}_t}{\mathrm{N}_c} \times 100$$

Where, N_c and N_t are cell density of the control cultures and treated cultures, respectively, and IR represents the growth inhibition rate.

5 mL cell suspension was centrifuged at 3500 g for 10 min, and cell pellets were obtained. Photosynthetic pigments (including chlorophyll a and carotenoids) of *Synechocystis* sp. were extracted with 5 mL methanol (HPLC grade). Cell suspensions were centrifuged (3500 g, 10 min) after keeping in darkness for 24 h at 4°C. The absorbance of the resulting supernatant was measured by an ultraviolet spectrophotometer (UV-2600, Shimadzu, Japan) at 652, 665, and 470 nm. The following equation was used for calculation of photosynthetic pigments content:[2]

$$\text{Chlorophyll a } (mg/L) = 16.52\mathrm{A}_{665} - 8.096\mathrm{A}_{652}$$

$$\text{Carotenoids a (mg/L)} = (1000\mathrm{A}_{470} - 1.91\mathrm{C}_{\mathrm{a}})/225$$

Where C_a is the concentration of chlorophyll a (mg/L).

Text S3 Oxidative stress and cell membrane integrity

5 mL of cell suspension was incubated with 50 μM 2',7′-dichlorodihydrofluorescein diacetate (DCFH-DA) in darkness at 25 °C for 30 min. The cells were sonicated by an ultrasonic cell crusher (JY92INN-II, Scientz Biotechnology Co., Ltd, China) (5 min; 200 W; 3 s/3 s (work/rest) cycle). After centrifugation at 3600 g for 10 min, the supernatant was used to determine the fluorescence intensity using a fluorescence spectrophotometer (Cary Eclipse, Varian, USA) at the excitation wavelength of 485 nm and the emission wavelength of 530 nm.[3] The intracellular ROS content was expressed as the ratio of cell number normalized-fluorescence intensity between exposure groups and the control group.

For testing the effects of MNPs and antibiotics on membrane integrity, 5 mL of cell suspension was centrifuged at 3500 g for 10 min, followed by washing three times with phosphate buffer saline (PBS). Thereafter, the cells were incubated with 50 μL propidium iodide (PI, 10 μmol/L) for 10 min, and then washed three times with the PBS. The fluorescence of PI-stained cells was recorded using confocal laser scanning microscopy under 488 nm laser excitation.

Text S4 Scanning electron microscopy

The heteroaggregation between *Synechocystis* sp. and MNPs (50 mg/L) was directly observed by using a scanning electron microscopy (SEM) (Quanta FEG 450, FEI, USA). SEM observations were performed on *Synechocystis* sp. exposed to MNPs for

96 h. Cells were fixed in 2.5% glutaraldehyde at 4 °C for 12 h.[4] After being washed three times by phosphate buffer (PH=7.4), the fixed cells were dehydrated by ascending alcohol series: 10 min each in 30%, 50%, 70%, 85%, 95%, and 100% alcohol.[5,6] Subsequently, the samples were dried by critical point dryer. After coating with gold, scanning electron micrographs were taken with a Quanta FEG 450 (FEI, USA).

Text S5 DLVO theory calculation

The interaction energies between *Synechocystis* sp. (~ 2 μm) and MNPs or MNPs and MNPs are calculated using DLVO theory. Sphere-plate geometry was used to predict the heteroaggregation between *Synechocystis* sp. and MNPs: *Synechocystis* sp. were regarded as plates while NPs (i.e., NP0.05 and NP0.5) were regarded as spheres in *Synechocystis* sp.-NPs coexistence system, and the cells were regarded as spheres while MP50 were regarded as plates in *Synechocystis* sp.-MP50 coexistence system. For the interaction between *Synechocystis* sp. and MP5 or MNPs and MNPs, sphere-sphere geometry was used in the DLVO calculation. The hydrodynamic particle sizes of MNPs (50 mg/L) in BG11 medium were measured by the Zetasizer Advance (Malvern Instruments Ltd., Worcestershire, UK) after the ultrasonic dispersion for 20 min. Correspondingly, the Zeta potentials of MNPs and *Synechocystis* sp. were determined by Zetasizer Advance. The calculation formula and parameters for DLVO calculation are provided in Table S4-S7.

Text S6 Proteomic analysis

Protein Extraction. The cyanobacterial culture suspension (40 mL) were harvested and centrifuged at 4000 *g* for 10 min at 4 °C. The cell pellets were mixed with lysis buffer (8 M urea, 10 mM dithiothreitol, 1% Protease Inhibitor Cocktail) and sonicated three times in an ice-water bath using a high intensity ultrasonic processor (Scientz). After centrifugation at 12000 *g* at 4 °C for 10 min, the supernatant was collected and used for the determination of the protein concentration using BCA protein assay kit (Beyotime Biotechnology, China).

Trypsin Digestion. The extracted proteins were conducted enzymatic hydrolysis using trypsin (Promega, USA).[7] Briefly, the protein solution was reduced with dithiothreitol (5 mM) for 30 min at 56 °C and alkylated with iodoacetamide (11 mM) for 15 min at room temperature in the dark. The protein sample was then diluted by adding TEAB (100 mM) to urea concentration less than 2 M. Then, trypsin was added at 1:50 trypsin-to-protein mass ratio for the first digestion overnight and 1:100 trypsin-to-protein mass ratio for a second 4 h-digestion. Finally, the peptides were desalted using C18 SPE column.

HPLC-MS/MS Analysis. Proteomics analysis was performed on an ultra-high performance liquid chromatography (EASY-nLC 1000 UPLC) coupled to tandem mass spectrometry (MS/MS) in Q ExactiveTM Plus (Thermo Fisher Scientific). Peptides were separated with a HPLC system on a home-made reversed-phase analytical column (15 cm length, 75 μm i.d.) using two mobile phases: (A) 0.1% formic acid and 2% acetonitrile in water) and (B) 0.1% formic acid and 90% acetonitrile in water. The tryptic peptides were dissolved in A, and directly loaded onto the analytical column. The column flow rate was set at 450 nL/min with the following gradient: 0-62 min: 4-23% B; 62-82 min: 23-35% B; 82-86 min: 35-80% B; 86-90 min: 80% B. Then, the peptides were subjected to NSI source and analyzed by MS/MS. The MS data was obtained under following conditions: the electrospray voltage was set as 2.0 kV; the full MS scan resolution was set to 60,000 for a scan range of 350-1600 m/z; peptides were detected by the Orbitrap at a resolution of 120,000. Peptides were further selected for MS/MS using a normalized collision energy (NCE) of 28% and the fragments were detected in the Orbitrap at a resolution of 30,000. Automatic gain control (AGC) target was set at 1E5, with an intensity threshold of 3.3E4 and a maximum injection time of 60 ms.

Protein identification. The MS/MS data were processed by Maxquant search engine (v.1.6.15.0). The MS/MS spectra were matched against the Universal Protein Resource (UniProt) database concatenated with reverse decoy database. False discovery rate (FDR) was adjusted to 0.01 and minimum score for modified peptides was set 40.

Text S7 Independent action (IA) model

The type of combined toxicity is judged by the independent action (IA) model:[8]

$$E(Cx_{mix}) = 1 - \prod_{i=1}^{n}(1 - E(C_{x_i}))$$

where $E(Cx_{mix})$ represents the growth inhibition rate (%) induced by n kinds pollutants in the mixture, and $E(Cx_i)$ is the growth inhibition rate (%) induced by the i-th pollutant at C_i concentration applied singly. If the experimental result is lower than the expected result that calculated by the IA model, the interaction between AZM and MNPs can be determined as antagonism. In contrast, the higher experimental result compared to the expected result suggests the synergistic toxicity, while the additive toxicity was determined when the expected result is equal to the experimental result.[5]

Table S1 Components of BG11 medium.

Compound	Concentration (mg/L)
$NaNO_3$	1500
K_2HPO_4	50
$MgSO_4 \cdot 7H_2O$	65
$CaCl_2 \cdot 2H_2O$	36
Citric acid	6
Ferric ammonium citrate	6
$EDTANa_2$	1
Na_2CO_3	20
H_2BO_3	2.86
$MnCl_2 \cdot 4H_2O$	1.86
$ZnSO_4 \cdot 7H_2O$	0.22
$Na_2MoO_4 \cdot 2H_2O$	0.39
$CuSO_4 \cdot 5H_2O$	0.08
$Co(NO_3)_2 \cdot 6H_2O$	0.05

Table S2 Photochemical parameters tested by OJIP-test.[9]

Parameters	Illustrations
V_j	Relative variable fluorescence intensity at the J-step
Fv/Fm	Maximum quantum yield for primary photochemistry
Quantum efficiencies or flux ratios	
φEo	Quantum yield for electron transport
φDo	Maximum quantum yield of non-photochemical deexcitation
Ψo	Probability that a trapped exciton moves an electron into the electron transport chain beyond QA
Specific fluxes or specific activities	
ABS/RC	Absorption flux per reaction center
TRo/RC	Trapped energy flux per reaction center
ETo/RC	Electron transport flux per reaction center
DIo/RC	Dissipated energy flux per reaction center
Performance indexes	
Pi_{ABS}	Performance index on absorption basis
Density of reaction centers	
RC/CS	Density of reaction centers (QA-reducing PSII reaction centers)

Table S3 The toxicity interactions of nano/microplastics (MNPs) at 50 mg/L and azithromycin (AZM) at 1 μg/L identified by the independent action (IA) model.

	EC (MNPs)	EC (AZM)	$EC_{expected}$	EC_{tested}	Combined toxicity
NP0.05+AZM	14.72	18.33	33.05	16.16	antagonism
NP0.5+AZM	19.74	18.33	38.07	20.16	antagonism

MP5+AZM	17.65	18.33	35.98	31.82	antagonism
MP50+AZM	15.61	18.33	33.94	32.54	antagonism

Table S4 DLVO equations for computing the total interaction energy.[10-13]

Interaction pairs	**Geometry**	**The total interaction energy:** $\Phi_{tot} = \Phi_{vdw} + \Phi_{edl}$
MNPs-MNPs	Particle-particle	van der Waals interaction energy (Φ_{vdw}): $\Phi_{vdw} = -\frac{A_{131}}{6}\left[\frac{2r^2}{h^2 + 4rh} + \frac{2r^2}{h^2 + 4rh + 4r^2} + \ln\left(\frac{h^2 + 4rh}{h^2 + 4rh +}\right.\right.$ Electrostatic interaction energy (Φ_{edl}): $\Phi_{edl} = 32\pi\varepsilon_r\varepsilon_0\left(\frac{k_BT}{ze}\right)^2\tanh\left(\frac{ze\psi_{P_1}}{4k_BT}\right)\tanh\left(\frac{ze\psi_{P_1}}{4k_BT}\right)\exp^{(-kh)}$
MP5-Cells		van der Waals interaction energy (Φ_{vdw}): $\Phi_{vdw} = -\frac{A_{132}}{6}\left[\frac{2r^2}{h^2 + 4rh} + \frac{2r^2}{h^2 + 4rh + 4r^2} + \ln\left(\frac{h^2 + 4rh}{h^2 + 4rh +}\right.\right.$ Electrostatic interaction energy (Φ_{edl}): $\Phi_{edl} = 32\pi\varepsilon_r\varepsilon_0\left(\frac{k_BT}{ze}\right)^2\tanh\left(\frac{ze\psi_{P_1}}{4k_BT}\right)\tanh\left(\frac{ze\psi_{P_2}}{4k_BT}\right)\exp^{(-kh)}$
NP0.05-Cells NP0.5-Cells Cells-MP50	Particle-plate	van der Waals interaction energy (Φ_{vdw}): $\Phi_{vdw} = -\frac{A_{132}}{6}\left[\frac{r}{h} + \frac{r}{h + 2r} + \ln\left(\frac{h}{h + 2r}\right)\right]$ Electrostatic interaction energy (Φ_{edl}): $\Phi_{edl} = 64\pi\varepsilon_r\varepsilon_0\left(\frac{k_BT}{ze}\right)^2\tanh\left(\frac{ze\psi_{P_1}}{4k_BT}\right)\tanh\left(\frac{ze\psi_{P_2}}{4k_BT}\right)\exp^{(-kh)}$

Table S5 Hamaker constants used in different interaction pairs.

Interaction pairs	Hamaker constant (J)
MNPs-MNPs	$A_{131} = \left(\sqrt{A_{11}} - \sqrt{A_{33}}\right)^2 = 7.71\times10^{-21}$
MNPs-Cells	$A_{132} = \left(\sqrt{A_{11}} - \sqrt{A_{33}}\right)\left(\sqrt{A_{22}} - \sqrt{A_{33}}\right)$ $= 1.59\times10^{-22}$

Note: The Hamaker constants of polystyrene MNPs (A_{33}), *Synechocystis* sp. (A_{22}), and water (A_{11}) were 7.85×10^{-20} J,[14] 7.75×10^{-20} J,[15] and 3.7×10^{-20} J,[10] respectively.

Table S6 Other key parameters used in DLVO calculations.[10, 11]

Parameters	**Description**
R	The radius of MNPs or *Synechocystis* sp.
H	The separation distance between MNPs and MNPs or *Synechocystis* sp.
ε_r	The dielectric constant of the medium (78.4 for water)
ε_0	The vacuum permittivity (8.854×10^{-12} C^2 N^{-1} m^{-2})
k_B	The Boltzmann constant (1.381×10^{-23} C^2 J K^{-1})
T	The temperature (298.15 K)
Z	The valence of electrolyte
E	The electron charge (1.60×10^{-19} C)
ψ_{p1}	Surface potentials of particle 1; calculated from measured zeta potentials (ξ_{p1}): $\psi p1 = \xi p1\left(1 + \frac{d}{r}\right)\exp^{(kd)}$
ψ_{p2}	Surface potentials of particle 2; calculated from measured zeta potentials (ξ_{p2}): $\psi p2 = \xi p2\left(1 + \frac{d}{r}\right)\exp^{(kd)}$
ξ_{p1}	Zeta potential of particle 1
ξ_{p2}	Zeta potential of particle 2
D	The distance between the surface of the charged particle and the slipping plane (5 Å)
K	The reciprocal of the Debye length $k^{-1} = \sqrt{\frac{\varepsilon_r \varepsilon_0 k_B T}{2 N_A I e^2}}$
N_A	The avogadro constant (6.02×10^{23} mol^{-1})
I	The solution ionic strength

Table S7 Summary of parameters of MNPs or *Synechocystis* sp. used in the DLVO equations.

	ζ (mV)	Hydrodynamic size (nm)
NP0.05	-28.41 ± 0.58	87.53 ± 1.45
NP0.5	-54.81 ± 1.35	642.41 ± 3.62
MP5	-36.42 ± 2.17	5270.23 ± 10.37
MP50	-24.6 ± 0.84	46700.45 ± 22.83
Synechocystis sp.	-26.08 ± 1.32	2920.45 ± 8.72

Table S8 Enriched GO terms in the AZM group.

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Ribosomal function	GO:0003735	structural constituent of ribosome	Upregulation: P74410 P73299 P48958 P74267 P73305 P36237
	GO:0006412	translation	Upregulation: P74410 P73299 P48958 P74267 P73305 P36237
Carbon fixation	GO:0015977	carbon fixation	Upregulation: Q55670 P73406
	GO:0031470	carboxysome	Upregulation: Q55670 P73406

Table S9 Enriched GO terms in the NP0.05 group.

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Photoreaction center	GO:0019684	photosynthesis light reaction	Downregulation: P26522 P26525 Upregulation: Q55013
	GO:0031676	plasma membrane-derived thylakoid membrane	Downregulation: Q01950 P26522 P32421 P26525 P72712 P09190 Q55013 P72673 P74063 Upregulation: Q57038 P37277 P72804 P74102
	GO:0008137	NADH dehydrogenase (ubiquinone) activity	Downregulation: P32421 P26523 P26525

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Carbon fixation	GO:0048038	quinone binding	Downregulation: P26522 P26525 P32421 P26523
	GO:0015977	carbon fixation	Downregulation: P73406 Q55550
	GO:0031470	carboxysome	Downregulation: P73406 Q55550
	GO:0015979	photosynthesis	Downregulation: Q55550 P72712 P37277 P74063 P72772 P51634 Q55087 P73202 Upregulation: P37277 P72712 Q01950 P73202
Chlorophyll biosynthetic	GO:0015995	chlorophyll biosynthetic process	Downregulation: P72772 P73020 P51634 Q55087
	GO:0016851	magnesium chelatase activity	Downregulation: P51634 P72772 P73020
Outside the clusters (GO terms without the edge)	GO:0008299	isoprenoid biosynthetic process	Downregulation: P72580 P72683 P74287
	GO:0009236	cobalamin biosynthetic process	Downregulation: P72694 P72862 P73644 Q55822
	GO:0005737	cytoplasm	Downregulation: P45450 P54123 P54899 P72749 P72796 P72848 P72856 P73077 P73127 P73390 P73410 P73460 P73534 P73562 P73658 P73755 P73820 P73950 P73951 P74287 P74330 P74739 P74750 P77962 P80505 Q55368 Q55443 Q55504 Q55653 Q55716 Q55750 Q55797 Q55822 Q55842 Q55880 Q55978 Q55982
	GO:0051287	NAD binding	Downregulation:

Cluster	GO.ID	Description of GO terms	Regulation of proteins
	GO:0005829	cytosol	P54899 P72661 P73496 P73574 P80505 Q55650 Q55982 Downregulation: P72776 P73138 P73242 P73248 P73335 P73336 P73471 P73534 P73761 P73769 P73887 P74008 P74089 P74299 P74330 P74395 P74457 P74578 P74667 P77962 Q55163 Q55336 Q55368 Q55803 Q55804 Q55822 Q55849 Upregulation: P20804 P73299

Table S10 Enriched GO terms in the MP50 group.

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Photosynthetic carbon fixation	GO:0031470	carboxysome	Downregulation: P54205 P54206 P72757 P72759 P72760 P72761 P73406 P73407 Q54735 Q55121 Q55550
	GO:0015977	carbon fixation	Downregulation: P72757 P72759 P72760 P72761 P73406 P73407 Q54735 Q55121 Q55550
	GO:0015979	photosynthesis	Downregulation: P12975 P26287 P26290 P29254 P29255 P72757 P72759 P72760 P72761 P73406 P73407 P73731 P74063 Q54735 Q55121 Q55332 Q55356 Q55544 Q55550 Q57038 Q59987
	GO:0043886	structural constituent of carboxysome	Downregulation: P72760 P72761 P73406 P73407 P72759
	GO:0009654	photosystem II oxygen evolving complex	Downregulation: Q55332 P10549 Q55356 P73731
	GO:0030096	plasma membrane-	Downregulation:

Cluster	GO.ID	Description of GO terms	Regulation of proteins
		derived thylakoid photosystem II	Q55332 P09193 P05429 P10549 Q55356
Proton-transporting ATP synthase	GO:0046933	proton-transporting ATP synthase activity	Downregulation: P26533 P17253 P27178 P27179 P26527 P27180
	GO:0045261	proton-transporting ATP synthase complex catalytic core F(1)	Downregulation: P26533 P17253 P27179 P26527 P27180
	GO:0045260	plasma membrane proton-transporting ATP synthase complex	Downregulation: P26533 P17253 P27179 P26527 P27180
	GO:0015986	ATP synthesis coupled proton transport	Downregulation: P26533 P17253 P27179 P27180
	GO:0005524	ATP binding	Downregulation: P17253 P20169 P22034 P22358 P26527 P26533 P27179 P28372 P49057 P51634 P52276 P52415 P53383 P72641 P72644 P72648 P72710 P72730 P72830 P72940 P72991 P73020 P73077 P73090 P73162 P73220 P73239 P73241 P73274 P73302 P73326 P73340 P73436 P73443 P73449 P73465 P73468 P73471 P73493 P73533 P73558 P73625 P73646 P73650 P73651 P73721 P73833 P73942 P74015 P74081 P74111 P74140 P74176 P74208 P74210 P74217 P74232 P74260 P74292 P74296 P74303 P74317 P74330 P74344 P74374 P74391 P74494 P74503 P74587 P74638 P74646 P74686 P74706 P74724 P74730 P74737 P77961 P77973 Q05971 Q55074 Q55160 Q55168 Q55187 Q55195 Q55196 Q55336 Q55404 Q55419 Q55422 Q55468 Q55478 Q55503 Q55510 Q55619 Q55653 Q55662 Q55690 Q55700 Q55709 Q55716 Q55729 Q55753 Q55778 Q55779 Q55842 Q55843 Q55849 Q55855

Cluster	GO.ID	Description of GO terms	Regulation of proteins
			Q55856 Q55898 Q57396 Q59997 Q59999
Ribosomal function	GO:0006412	translation	Upregulation: P48958 Downregulation: P73530 P73298 P74230 P73314 P48939 P73304 P23350 P73294 P73308
	GO:0003735	structural constituent of ribosome	Upregulation: P48958 Downregulation: P73530 P73298 P74230 P73314 P48939 P73304 P23350 P73294 P73317 P73308 P73306
	GO:0022627	cytosolic small ribosomal subunit	Downregulation: P73530 P73298 P73314 P73304
	GO:0022625	cytosolic large ribosomal subunit	Downregulation: P23350 P73294 P73317 P73308 P73306
	GO:0019843	rRNA binding	Downregulation: P74230 P73314 P48939 P73304 P73317 P73308 P73306
Ubiquinone and quinone	GO:0008137	NADH dehydrogenase (ubiquinone) activity	Downregulation: P32421 Q55429 P26523 P27724 P26525 P19125
	GO:0051287	NAD binding	Downregulation: P27724 P73960 P73574 P72642 Q55982 P73821 P49433 P80505 P73033 P73058 P72661 P54899
	GO:0048038	quinone binding	Downregulation: P32421 Q55429 P26523 P26522 P27724 P26525 P19125 P74338 P74069
	GO:0016655	oxidoreductase activity acting on NAD(P)H	Downregulation: P26522 P74338 P74069

Cluster	GO.ID	Description of GO terms	Regulation of proteins
		quinone or similar compound as acceptor	
	GO:0031676	plasma membrane-derived thylakoid membrane	Downregulation: P12975 P26287 P26290 P29254 P29255 P74063 Q55332 Q55356 Q55544 Q57038 P05429 P09193 P10549 P19125 P26522 P26525 P27724 P32421 P32422 P74069 P74102 P74338
Chlorophyll binding	GO:0016168	chlorophyll binding	Downregulation: P29254 P29255 P09193 P05429
	GO:0018298	protein-chromophore linkage	Downregulation: P74102 P29254 P29255 P09193 P05429 Q55544 Q01951 Q01952 P72870 P74551
AMP salvage	GO:0044209	AMP salvage	Downregulation: P73935 P73302 P72641
	GO:0005737	cytoplasm	Downregulation: P73562 P73511 P74561 P52981 P73997 P73848 P52997 P73951 P72785 Q55513 Q55982 P74709 P74618 P73162 P73326 P73133 P73935 P73302 P72641 P74721 P73546 P74122 P77973 P52276 Q55128 P74163 Q55503 P74592 P54416 Q59993 Q55662 P72697 P72856 Q55504 Q55710 P74587 P73456 P73340 Q59977 Q55822 Q05971 P73410 P72662 P74330 P73618 P74782 P74432 P74750 P73077 P73297 P28371 Q55119 P74739 P54225 Q55167 P72908 Q55855 Q55665 P77961 P74292 P73493 P80505 P73560 Q55716 P73965 P72931 Q55443 P73172 Q55527 Q55653 P73058 P73646 P74106 Q55805 P48054 P74383 P74287 Q55383 Q55729 P74344 Q55368 P54899 P54386 P74494 Q55497 P72848 P74707 P72622 P73789 P73728 Q55187 P73950 P72649 Q55797 P72644 Q55843 Q55842 Q55172 P73390

Cluster	GO.ID	Description of GO terms	Regulation of proteins
			P73389 P73660 P72808 P73971 P74342 Q55880 P74737 P54004 P74516 P74572 Q55863 P73534 P72656 Q55848 P73820 P72667 P73658 P74035 P74565 P77962 P73201 P72796
	GO:0006526	arginine biosynthetic process	Downregulation: P73326 P73133 P74122 P77973 P74587
Iron-sulfur binding	GO:0051539	4 iron 4 sulfur cluster binding	Downregulation: P53383 P28372 P26525 P32422 P29254 P29255 P73672 Q55643 P73667
	GO:0046872	metal ion binding	Downregulation: P53383 P28372 Q57038 P26290 P32422 P09193 P73426 P74141 P73997 Q55643 Q55982 P74709 Q55798 Q55592 P74081 Q55404 P72703 P20170 P74334 P72830 Q55415 P74217 Q55160 P73911 Q59997 Q05971 P74740 P74208 P73833 P73335 P73922 P73248 P74689 P74370 P74432 P74391 P73355 P74159 P74449 P73649 P27320 P55037 P55038 P54225 P73723 P77961 P73493 P73119 P73965 P72849 Q55902 P73058 P74024 P74022 P72933 P74158 P72827 Q55629 P72661 P74589 Q55729 Q55368 P74542 P74724 P74210 P74494 P74571 P72848 P73441 P73085 P74232 Q55898 P74025 P73270 P72934 Q55880 P73599 P74016 P74305
Thiamine pyrophosphate binding	GO:0030976	thiamine pyrophosphate binding	Downregulation: P73067 P73918 P73913
	GO:0003984	acetolactate synthase activity	Downregulation: P73918 P73913 Q55141
	GO:0000287	magnesium ion binding	Downregulation: P54205 P29254 P29255 P73067 P73960 P52997 P73667 P73162 P73918 P73913 P73617 Q55849 Q55504 P74646 P77972 Q55336 P72931 P80507 P74287 Q55482 P74503 P73443 Q55574 Q55187 P74296 P74643 P72644

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Methylerythritol biosynthesis	GO:0019288	isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway	P72659 P73849 P73436 Q55863 P73534 P74104 Q55848 P72796 Downregulation: P73067 P73426 P73672 Q55643
	GO:0016114	terpenoid biosynthetic process	Downregulation: P73067 P73426 P73672 Q55643
Membrane bounded	GO:0030288	outer membrane-bounded periplasmic space	Downregulation: Q55136 P75023 P73458 P72939 Q55763 P73589 P73693 P73732 P74223 P72802 P73736 P73037 P72704 P74016 P74305 P72780 P72707 Q55648 P74789 P73762 P74162 P72989 P73643 P73601 P73600 P73111 P73107 Q55972 Q55426 Q55386 P74233 P73344 P73592 P74673 P72765 P74500 P74506 P73222 P73091 P73681 P73001 P74598 P73595 P73594
	GO:0004175	endopeptidase activity	Downregulation: P75023 P73458
Amino acid biosynthesis	GO:0009082	branched-chain amino acid biosynthetic process	Downregulation: P48576 P74207 P73960
	GO:0009098	leucine biosynthetic process	Downregulation: P48576 P74207 P73960
Outside the clusters (GO terms without the edge)	GO:0005829	cytosol	Upregulation: P20804 Downregulation: P73525 P52981 P73067 P48576 P73960 P72642 P73527 P52208 Q46363 Q55141 P74008 P73302 P72641 P74384 P74308 P54261 P74468 P73617 P73257 P74163 Q55849 P73465 Q55074 Q55626 P74741 P74171

Cluster	GO.ID	Description of GO terms	Regulation of proteins
			P73911 P23353 Q55822 P74208 P74330 P73335 P77969 P74667 P73248 P74432 P50027 P72621 P27320 Q55336 P33779 P52983 P73043 Q55778 P49433 P74260 P73033 P73560 P74416 Q55690 P49057 Q55526 P72648 P73058 P80507 P73274 P73443 P73242 P73754 Q55786 Q55163 P73677 P74344 Q55368 P74724 Q55733 P72948 Q55942 Q55802 Q55890 P74314 P73404 P73761 P73176 P73090 P74643 P73471 Q55422 Q55172 P72659 P73942 Q55709 Q55624 Q55863 P73534 P73348 P74104 Q55766 P72666 Q55787 P72687 P74061 P73138 Q55900 P74089 P77962 P73137 P74591
	GO:0006189	‘de novo’ IMP biosynthetic process	Downregulation: P74384 P74741 Q55336 Q55135 Q55498 P74724 P74232 P73471 Q55422 P72644 Q55843 Q55842 Q55172
	GO:0000105	histidine biosynthetic process	Downregulation: P74561 Q55503 P74592 Q55626 P73058 P73807 P74106 Q55805 P48054 P74542
	GO:0000160	phosphorelay signal transduction system	Downregulation: P73078 Q55447 P73175 P73150 P73006 P74138 P74298 P73686 P73104 Q55448 P73005 P74294 P73724 P72790 P72843 Q79EE5P73928 Q55169 P72781
	GO:0019253	reductive pentose-phosphate cycle	Downregulation: P54205 P54206
	GO:0004089	carbonate dehydratase activity	Downregulation: Q54735 Q55136
	GO:0030170	pyridoxal phosphate binding	Downregulation: P73511 P73264 P73133 P73546 Q55128 Q55679 P73410 P72662 Q55484 P73043 Q55665 P74416 P73807 P72893 P74668 Q55793 P52056 P77962

Cluster	GO.ID	Description of GO terms	Regulation of proteins
	GO:0006633	fatty acid biosynthetic process	Downregulation: P73848 P73283 P73951 P74638 Q55120 Q55160
	GO:0009089	lysine biosynthetic process via diaminopimelate	Downregulation: P73562 P72642 Q55513 Q55484 P74667
	GO:0008236	serine-type peptidase activity	Downregulation: P75023 P73458
	GO:0042802	identical protein binding	Downregulation: Q54735 P73133 P74295 P72830 P73456 P74645 P74208 P73016 P73728 Q55168 P72780 P73348
	GO:0006096	glycolytic process	Downregulation: P72740 P77972 P74309 Q55855 P52983 P49433 P80505 Q55863 P73534
	GO:0005980	glycogen catabolic process	Downregulation: P73608 P73511
	GO:0005975	carbohydrate metabolic process	Downregulation: P52981 P74618 P74706 Q59977 Q55779 P73033 P74573 Q55383 P74589 P73585 P73757 P74643 Q55797 P73599 P74690 P74124 P73619 P74027 P74079 P73504 P73420 P73606 P72797 P74657
	GO:0019684	photosynthesis light reaction	Downregulation: P28372 P26522 P27724 P26525 P19125
	GO:0016616	oxidoreductase activity acting on the CH-OH group of donors NAD or NADP as acceptor	Downregulation: P73574 P73826 P74721

Table S11 Enriched GO terms in the AZM+NP0.05 group.

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Proton-transporting ATP synthase	GO:0045263	proton-transporting ATP synthase complex coupling factor F(o)	Upregulation: P27182 Downregulation: P27178 P27183
	GO:0046933	proton-transporting ATP synthase activity rotational mechanism	Upregulation: P27182 Downregulation: P27178 P27183
	GO:0048038	quinone binding	Downregulation: P26522 P26523
	GO:0031676	plasma membrane-derived thylakoid membrane	Upregulation: P27182 P21697 Downregulation: P09190 P26522 P27178 P27183
Isoprenoid biosynthesis	GO:0008299	isoprenoid biosynthetic process	Downregulation: P72580 P72683
	GO:0004659	prenyltransferase activity	Downregulation: P72580 P72683
Signal transduction and chemotaxis	GO:0007165	signal transduction	Upregulation: P75023 Downregulation: P37979 P73007 P73173 P74554
	GO:0006935	Chemotaxis	Downregulation:

			P37979 P73007 P73173
Outside the clusters (GO terms without the edge)	GO:0009055	electron transfer activity	Upregulation: P21697 P27320 Downregulation: P09190 P27319

Table S12 Enriched GO terms in the AZM+MP50 group.

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Photosynthetic carbon fixation	GO:0031470	carboxysome	Downregulation: P54205 P54206 P72757 P72758 P72759 P72760 P72761
	GO:0015977	carbon fixation	Downregulation: P72757 P72758 P72759 P72760 P72761 P73406 P73407 P74299 Q54735 Q55121 Q55550 Q55670 Q55875
	GO:0015979	photosynthesis	Downregulation: P12975 P19569 P26287 P26290 P29254 P29255 P29256 P37277 P51634 P72584 P72705 P72712 P72757 P72758 P72759 P72760 P72761
	GO:0043886	structural constituent of carboxysome	Downregulation: P72758 P72759 P72760 P72761 P73406 P73407
	GO:0030094	plasma membrane-derived photosystem I	Downregulation: P19569 P29254 P29255 P29256 P37277
	GO:0009538	photosystem I reaction center	Downregulation: P12975 P19569 P29256 P37277
Proton-transporting ATP synthase	GO:0046933	proton-transporting ATP synthase activity	Downregulation: P17253 P26527 P26533 P27179 P27180 P27181 P27182 P27183
	GO:0045261	proton-transporting ATP	Downregulation:

Cluster	GO.ID	Description of GO terms	Regulation of proteins
		synthase complex catalytic core F(1)	P17253 P26527 P26533 P27179 P27180
	GO:0045260	plasma membrane proton-transporting ATP synthase complex	Downregulation: P17253 P26527 P26533 P27179 P27180 P27181 P27183
	GO:0015986	ATP synthesis coupled proton transport	Downregulation: P17253 P26533 P27179 P27180 P27182
	GO:0005524	ATP binding	Downregulation: P17253 P20169 P22034 P22040 P22358 P26527 P26533 P27179 P28372 P37101 P45450 P49057 P49995 P51634 P52276 P52415 P53383 P72626 P72641 P72644 P72648 P72663 P72710 P72730 P72796 P72830 P72871 P72884 P72894 P72927 P72940 P72964 P72991 P73020 P73021 P73071 P73077 P73090 P73098 P73121 P73141 P73162 P73179 P73201 P73220 P73239 P73241 P73274 P73278 P73302 P73326 P73339 P73340 P73412 P73436 P73437 P73443 P73449 P73450 P73465 P73468 P73469 P73471 P73493 P73505 P73533 P73534 P73558 P73625 P73627 P73632 P73646 P73650 P73655 P73668 P73721 P73753 P73755 P73769 P73770 P73833 P73842 P73851 P73867 P73874 P73886 P73942 P73955 P74079 P74081 P74111 P74140 P74176 P74208 P74210 P74215 P74217 P74232 P74241 P74260 P74292 P74296 P74297 P74303 P74317 P74330 P74344 P74349 P74361 P74391 P74415 P74421 P74423 P74430 P74457 P74459 P74463 P74494 P74503 P74528 P74548 P74552 P74569 P74587 P74638 P74646 P74686 P74702 P74706 P74724 P74730 P74737 P74745 P74755 P77961 P77966 P77973 Q05971 Q05972 Q55074 Q55154 Q55160 Q55164 Q55168 Q55170 Q55174 Q55187 Q55195 Q55196 Q55247 Q55336 Q55404 Q55419

Cluster	GO.ID	Description of GO terms	Regulation of proteins
			Q55422 Q55435 Q55468 Q55469 Q55478 Q55486 Q55503 Q55505 Q55510 Q55522 Q55589 Q55593 Q55607 Q55614 Q55619 Q55622 Q55649 Q55653 Q55680 Q55690 Q55700 Q55709 Q55716 Q55729 Q55738 Q55750 Q55753 Q55756 Q55778 Q55779 Q55791 Q55794 Q55806 Q55807 Q55816 Q55842 Q55843 Q55848 Q55855 Q55856 Q55863 Q55898 Q55900 Q55905 Q57396 Q57417 Q59997 Q59998 Q59999 Q6YRQ2 Q6YRT3
	GO:0045263	proton-transporting ATP synthase complex coupling factor F(o)	Downregulation: P27181 P27182 P27183
Ribosomal function	GO:0006412	translation	Downregulation: P23349 P23350 P36236 P36239 P42352 P48939 P48944 P72687 P72851 P73293 P73294 P73296 P73298 P73303 P73304 P73305 P73307 P73308 P73309 P73310 P73311 P73313 P73314 P73315 P73318 P73320 P73336
	GO:0003735	structural constituent of ribosome	Downregulation: P23349 P23350 P36236 P36239 P42352 P48939 P48944 P72851 P73293 P73294 P73296 P73298 P73303 P73304 P73305 P73306 P73307 P73308 P73309 P73310 P73311 P73313 P73314 P73315 P73317 P73318 P73320 P73336
	GO:0022627	cytosolic small ribosomal subunit	Downregulation: P73293 P73298 P73304 P73311 P73314 P73530 P73636 P74071 P74142 P74229
	GO:0022625	cytosolic large ribosomal subunit	Downregulation: P23350 P36236 P36239 P42352 P73294 P73296 P73303 P73305 P73306 P73308 P73313 P73315 P73317 P73318
	GO:0019843	rRNA binding	Downregulation:

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Ubiquinone and quinone	GO:0008137	NADH dehydrogenase (ubiquinone) activity	P36236 P42352 P48939 P48944 P72656 P73303 P73304 P73306 P73307 P73308 P73309 P73311 P73313 P73314 P73315 P73317 P73318 P73320 Downregulation: P19050 P19125 P26523 P26525 P27724 P32421
	GO:0051287	NAD binding	Downregulation: P27724 P49433 P54899 P72642 P72661 P72834 P72946 P73033 P73058 P73496 P73574 P73821 P73960 P73990 P74586 P80046 P80505 Q55512 Q55650 Q55702 Q55982
	GO:0048038	quinone binding	Downregulation: P19050 P19125 P26522 P26523 P26525 P27724 P32421
	GO:0031676	plasma membrane-derived thylakoid membrane	Downregulation: P05429 P09190 P09192 P09193 P10549 P12975 P16033 P17253 P19050 P19125 P21697 P26287 P26290 P26522 P26525 P26527 P26533 P27179 P27180 P27181 P27182 P27183 P27589 P27724 P29254 P29255 P32421 P32422
Iron-sulfur binding	GO:0051539	4 iron 4 sulfur cluster binding	Downregulation: P19050 P26525 P28372 P29254 P29255 P32422 P42349 P52965 P53383 P54384
	GO:0046872	metal ion binding	Downregulation: P09193 P20170 P26290 P27320 P28372 P32422 P42349 P53383 P53579 P54225 P54384 P55037 P55038 P72587 P72588 P72631 P72656 P72661 P72703 P72756 P72793 P72827 P72830 P72848 P72849 P72854 P72894 P72927 P72934 P72946 P72988 P73058 P73085 P73119 P73159 P73248 P73270 P73282 P73335 P73355 P73374 P73426 P73441 P73493 P73510 P73529 P73599 P73600 P73623 P73632 P73639 P73649 P73714 P73723

Cluster	GO.ID	Description of GO terms	Regulation of proteins
			P73806 P73810 P73811 P73833 P73839 P73842 P73911 P73922 P73925 P73947 P73955 P73965 P73997 P74016 P74022 P74024 P74025 P74061 P74081 P74100 P74114 P74117 P74141 P74158 P74159 P74208 P74210 P74217 P74232 P74305 P74334 P74370 P74391 P74415 P74430 P74432 P74449 P74494 P74533 P74542 P74571 P74576 P74578 P74582 P74589 P74689 P74709 P74718 P74724 P74732 P74740 P77961 P77966 P77968
Photosynthetic electron transfer	GO:0009772	photosynthetic electron transport in photosystem II	Downregulation: P05429 P09192 P09193 P16033
	GO:0009523	photosystem II	Downregulation: P05429 P09190 P09192 P09193 P10549 P16033
	GO:0045156	electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity	Downregulation: P05429 P09192 P09193 P16033
	GO:0030096	plasma membrane-derived thylakoid photosystem II	Downregulation: P05429 P09190 P09192 P09193 P10549 P16033
	GO:0010242	oxygen evolving activity	Downregulation: P09192 P10549 P16033
	GO:0005506	iron ion binding	Downregulation: P09190 P09192 P16033 P19050 P24602 P26287 P26525
	GO:0016168	chlorophyll binding	Downregulation: P05429 P09192 P09193 P16033 P29254 P29255

Cluster	GO.ID	Description of GO terms	Regulation of proteins
Outside the clusters (GO terms without the edge)	GO:0018298	protein-chromophore linkage	Downregulation: P05429 P09192 P09193
	GO:0030089	phycobilisome	Downregulation: P72652 P72742 P72807 P72870 P73202 P73203 P73204 P74102 P74448 P74527 P74551 P74625 Q01951 Q01952 Q54714 Q54715 Q55138 Q55318 Q55544
	GO:0005829	cytosol	Downregulation: P0DJF8 P20804 P23353 P24602 P27320 P29107 P33779 P36265 P48576 P49057 P49433 P50027 P52208 P52981 P52983 P54261 P72588 P72621 P72633 P72641 P72642 P72646 P72648 P72659 P72687 P72688 P72720 P72753 P72776 P72828 P72861 P72871 P72874 P72927 P72946 P72948 P73007 P73033 P73039 P73043 P73057 P73058 P73067 P73071 P73090 P73137 P73138 P73168 P73176 P73196 P73242 P73248 P73257 P73263 P73274 P73282 P73287 P73302 P73335 P73336 P73339 P73348 P73404 P73418 P73424 P73443 P73453 P73465 P73471 P73495 P73501 P73525 P73527 P73534 P73560 P73617 P73632 P73655 P73677 P73754 P73761 P73769 P73839 P73842 P73887 P73911 P73942 P73960 P73990 P74002 P74008 P74027 P74061 P74089 P74104 P74163 P74171 P74208 P74228 P74260 P74286 P74299 P74308 P74314 P74324 P74328 P74330 P74344 P74355 P74384 P74395 P74416 P74421 P74432 P74457 P74468 P74507 P74514 P74536 P74569 P74578 P74582 P74591 P74643 P74667 P74702 P74724 P74741 P74753 P77960 P77962 P77969 P80507 Q46363 Q55074 Q55141 Q55163 Q55172 Q55247 Q55336 Q55361 Q55368 Q55422 Q55522 Q55526 Q55593 Q55624 Q55625 Q55626 Q55690 Q55692 Q55709 Q55733 Q55766 Q55778 Q55786 Q55787 Q55802 Q55806 Q55822 Q55863 Q55890

Cluster	GO.ID	Description of GO terms	Regulation of proteins
			Q55894 Q55900 Q55942 Q55959
	GO:0006189	‘de novo’ IMP biosynthetic process	Downregulation: P72644 P73471 P74232 P74384 P74601 P74724 P74741 Q55135 Q55172 Q55336 Q55422 Q55498 Q55621 Q55842 Q55843
	GO:0000105	histidine biosynthetic process	Downregulation: P48054 P72946 P73058 P73806 P73807 P74106 P74542 P74561 P74592 P74755 Q55503 Q55626 Q55805
	GO:0030288	outer membrane-bounded periplasmic space	Downregulation: P72704 P72707 P72765 P72780 P72802 P72939 P72989 P73037 P73091 P73107 P73111 P73222 P73344 P73458 P73510 P73581 P73589 P73592 P73594 P73595 P73596 P73597 P73600 P73601 P73643 P73693 P73732 P73736 P73762 P73837 P74016 P74162 P74164 P74182 P74223 P74233 P74251 P74305 P74390 P74474 P74500 P74506 P74598 P74615 P74673 P74789 P75023 Q55136 Q55146 Q55386 Q55426 Q55557 Q55558 Q55648
	GO:0009635	response to herbicide	Downregulation: P16033 P20169 P29273
	GO:0006537	glutamate biosynthetic process	Downregulation: P54386 P55037 P72762
	GO:0005978	glycogen biosynthetic process	Downregulation: P52415 P52981 P72623
	GO:0019253	reductive pentose-phosphate cycle	Downregulation: P37101 P54205 P54206
	GO:0006457	protein folding	Downregulation: P22034 P22358 P72704 P73098 P73462 P73789 P74702 Q05972 Q55154 Q55510 Q59978

Cluster	GO.ID	Description of GO terms	Regulation of proteins
	GO:0042802	identical protein binding	Downregulation: P72780 P72830 P73016 P73091 P73133 P73348 P73456 P73728 P73906 P74182 P74208 P74295 P74645 Q54735 Q55168
	GO:0006096	glycolytic process	Downregulation: P49433 P52983 P72740 P73534 P74309 P74421 P74507 P77972 P80505 Q55664 Q55855 Q55863 Q59994
	GO:0005980	glycogen catabolic process	Downregulation: P72691 P73511 P73546 P73608
	GO:0005975	carbohydrate metabolic process	Downregulation: P52981 P72720 P72797 P73033 P73420 P73504 P73585 P73597 P73599 P73606 P73619 P73757 P74027 P74079 P74124 P74340 P74573 P74589 P74618 P74643 P74657 P74690 P74706 Q55383 Q55517 Q55779 Q55797 Q59977
	GO:0042619	poly-hydroxybutyrate biosynthetic process	Downregulation: P73389 P73390 P73545 P73825 P73826
	GO:0009098	leucine biosynthetic process	Downregulation: P48576 P54384 P54691 P73960 P74207 P74269
	GO:0020037	heme binding	Downregulation: P09190 P24602 P26287
	GO:0005737	cytoplasm	Downregulation: P28371 P37101 P45450 P48054 P49995 P52231 P52232 P52276 P52981 P52997 P54123 P54224 P54225 P54386 P54416 P54899 P54902 P72586 P72622 P72641 P72644 P72649 P72656 P72662 P72667 P72689 P72697 P72753 P72785 P72794 P72796 P72797 P72808 P72848 P72856 P72861 P72894 P72924 P72931 P72946 P72955 P72965 P73058 P73061 P73077

Cluster	GO.ID	Description of GO terms	Regulation of proteins
			P73125 P73133 P73141 P73162 P73172 P73201 P73263 P73290 P73297 P73302 P73326 P73340 P73376 P73389 P73390 P73410 P73412 P73456 P73460 P73462 P73481 P73492 P73493 P73504 P73505 P73511 P73534 P73546 P73560 P73562 P73618 P73646 P73658 P73660 P73668 P73722 P73728 P73755 P73789 P73796 P73820 P73839 P73842 P73848 P73851 P73885 P73886 P73925 P73930 P73935 P73950 P73951 P73955 P73965 P73971 P73997 P74035 P74070 P74106 P74122 P74144 P74163 P74193 P74227 P74258 P74268 P74287 P74292 P74301 P74324 P74330 P74342 P74344 P74361 P74383 P74415 P74423 P74430 P74432 P74456 P74459 P74467 P74476 P74494 P74516 P74527 P74528 P74536 P74561 P74562 P74565 P74572 P74587 P74590 P74592 P74618 P74707 P74709 P74721 P74737 P74739 P74750 P74755 P74782 P77961 P77962 P77966 P77973 P80046 P80505 Q05971 Q55119 Q55128 Q55129 Q55139 Q55167 Q55170 Q55172 Q55187 Q55368 Q55383 Q55435 Q55443 Q55459 Q55469 Q55486 Q55503 Q55504 Q55505 Q55511 Q55513 Q55527 Q55593 Q55595 Q55653 Q55662 Q55665 Q55667 Q55670 Q55673 Q55694 Q55716 Q55729 Q55738 Q55746 Q55750 Q55756 Q55759 Q55797 Q55801 Q55805 Q55822 Q55842 Q55843 Q55848 Q55850 Q55855 Q55861 Q55863 Q55875 Q55880 Q55978 Q55982 Q55989 Q59975 Q59977 Q59978 Q59989 Q59992 Q59993
	GO:0009055	electron transfer activity	Downregulation: P09190 P21697 P26287 P27319 P27320 P29254 P29255 P32422
	GO:0019684	photosynthesis	Downregulation: P19050 P19125 P26522 P26525 P27724 P28372
	GO:0050661	NADP binding	Downregulation: P28463 P29107 P49433 P52208 P52986 P54902 P72642

Cluster	GO.ID	Description of GO terms	Regulation of proteins
	GO:0000287	magnesium ion binding	Downregulation: P29107 P29254 P29255 P52997 P54205 P72644 P72659 P72753 P72796 P72871 P72931 P72965 P73067 P73162 P73290 P73436 P73443 P73534 P73617 P73667 P73849 P73867 P73913 P73918 P73960 P74027 P74104 P74177 P74285 P74287 P74296 P74299 P74324 P74503 P74643 P74646 P77972 P80046 P80507 Q55187 Q55336 Q55469 Q55504 Q55557 Q55574 Q55621 Q55801 Q55848 Q55863
	GO:0009097	isoleucine biosynthetic process	Downregulation: P29107 P52986 P54691 P73375 P73913 P73918 P74269 P74689 Q55141 Q55512

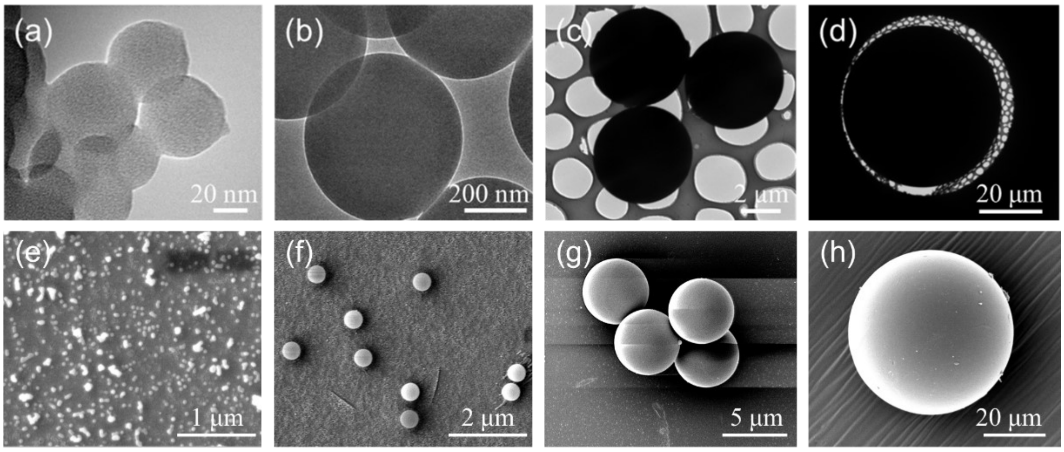

Fig. S1. Transmission electron microscopy (TEM) and scanning electron microscope (SEM) images of micro(nano)plastics (MNPs) (NP0.05 (a) and (e), NP0.5 (b) and (f), MP5 (c) and (g), MP50 (d) and (h)).

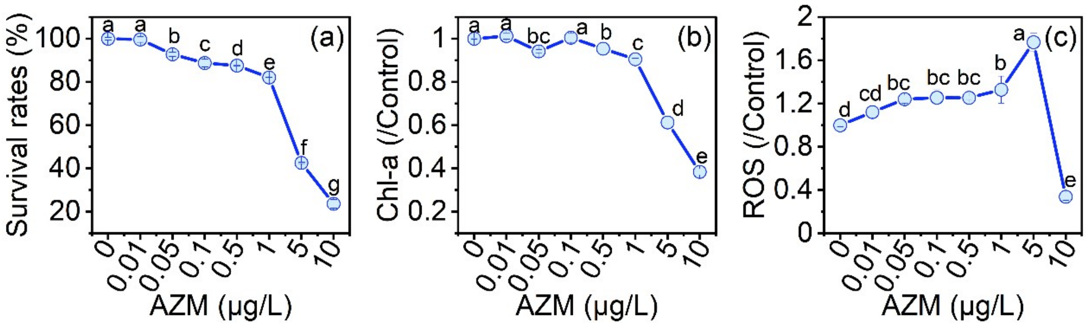

Fig. S2. Response of *Synechocystis* sp. to azithromycin (AZM) exposure at 0 - 10 μg/L (survival rates (a), chlorophyll a (chl-a) contents (b), and ROS generation (c)), letters indicate significant differences between treatments, one-way ANOVA: $p < 0.05$.

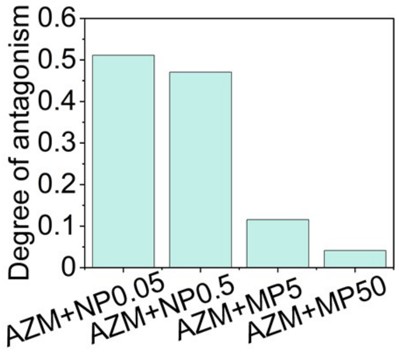

Fig. S3. Degree of antagonistic effects between MNPs and AZM, calculated by (1-$EC_{tested}/EC_{expected}$).

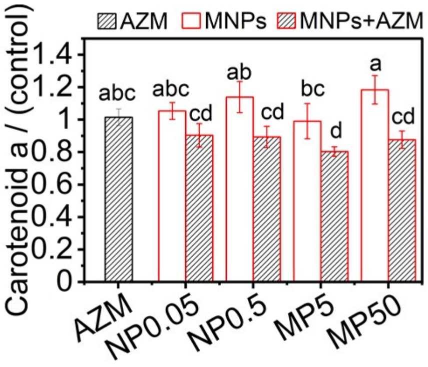

Fig. S4. Changes in the carotenoid a of *Synechocystis* sp. after 96 h cultivation in different exposure groups (different letters indicate significant differences between groups, one-way ANOVA: $p < 0.05$).

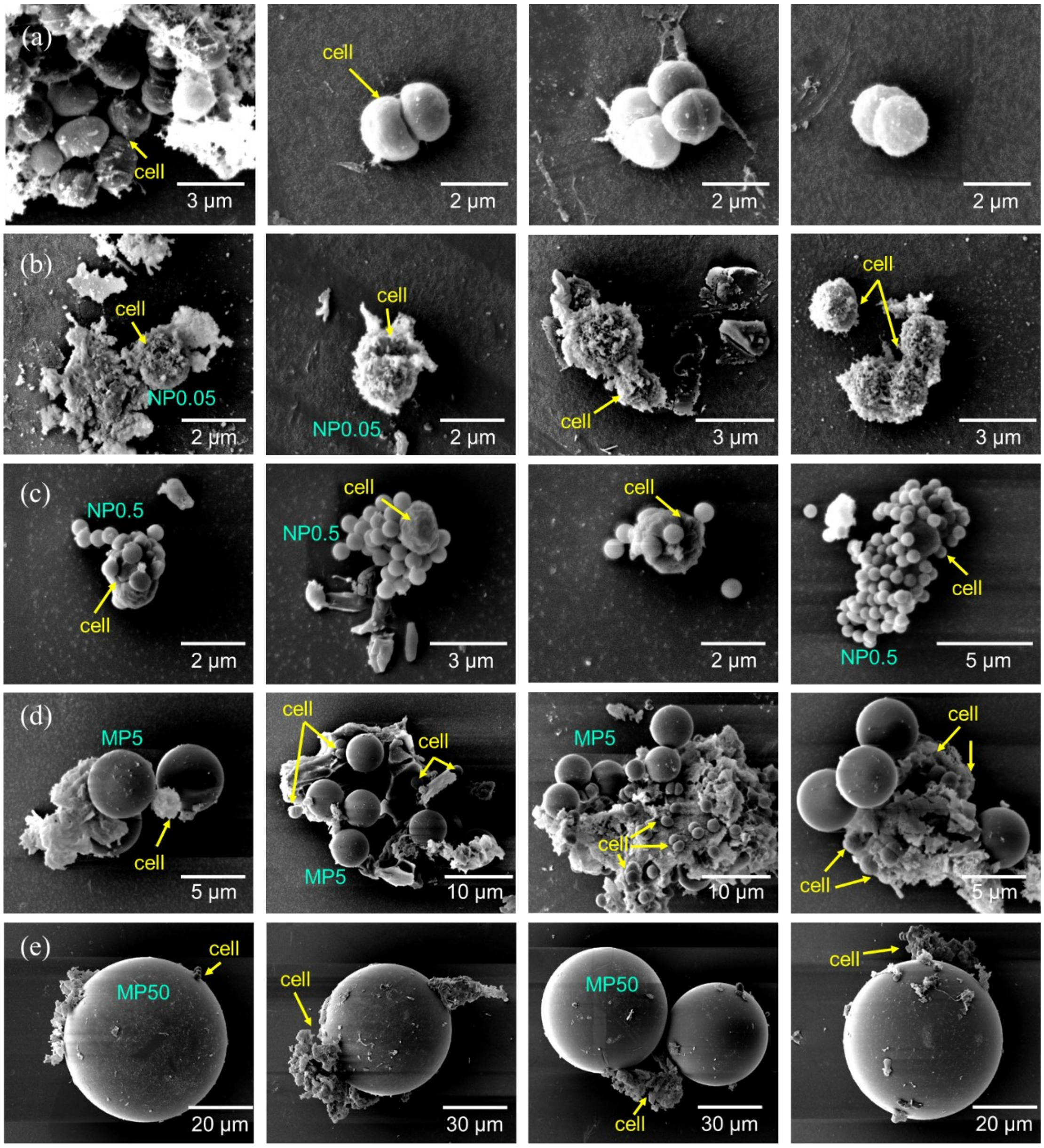

Fig. S5. Scanning electron microscope (SEM) images of *Synechocystis* sp. (a), and *Synechocystis* sp. exposed to micro(nano)plastics (MNPs) ((b) NP0.05, (c) NP0.5, (d) MP5, and (e) MP50).

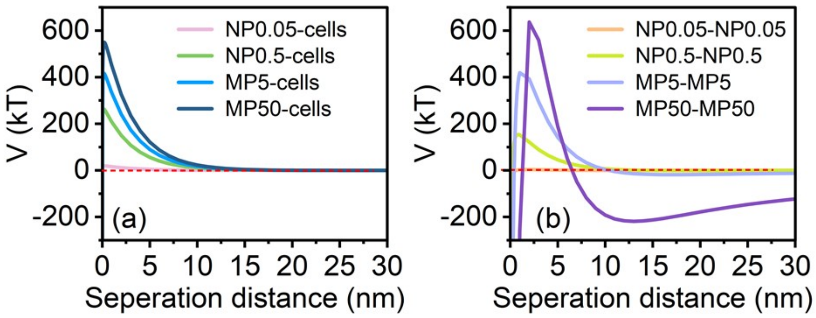

Fig. S6. Surface interaction energies between MNPs and *Synechocystis* sp. (a) or MNPs and MNPs (b) calculated by DLVO theory.

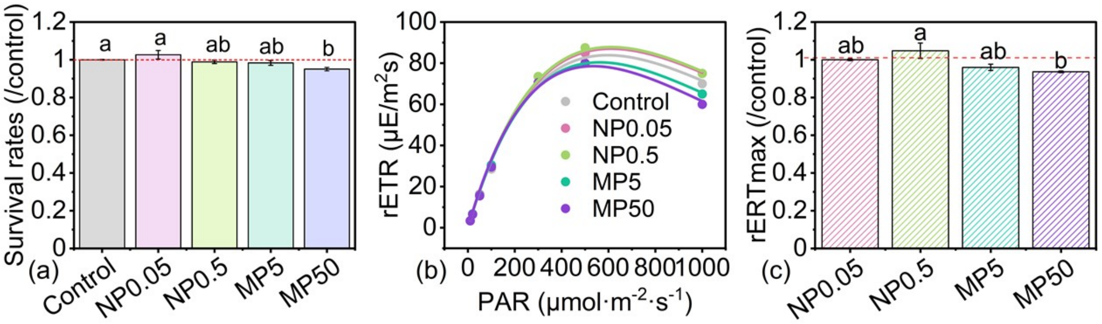

Fig. S7. Shading effects of MNPs on survival rates (a), rapid light curves (RLCs) (b), and the maximum relative electron transport rate (rETRmax) (c) of *Synechocystis* sp. after 96 hours cultivation (Different letters indicate significant differences between groups, one-way ANOVA: $p < 0.05$).

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