

Supplementary materials

Application of spectroscopic methods for the identification of superoxide dismutases in cyanobacteria

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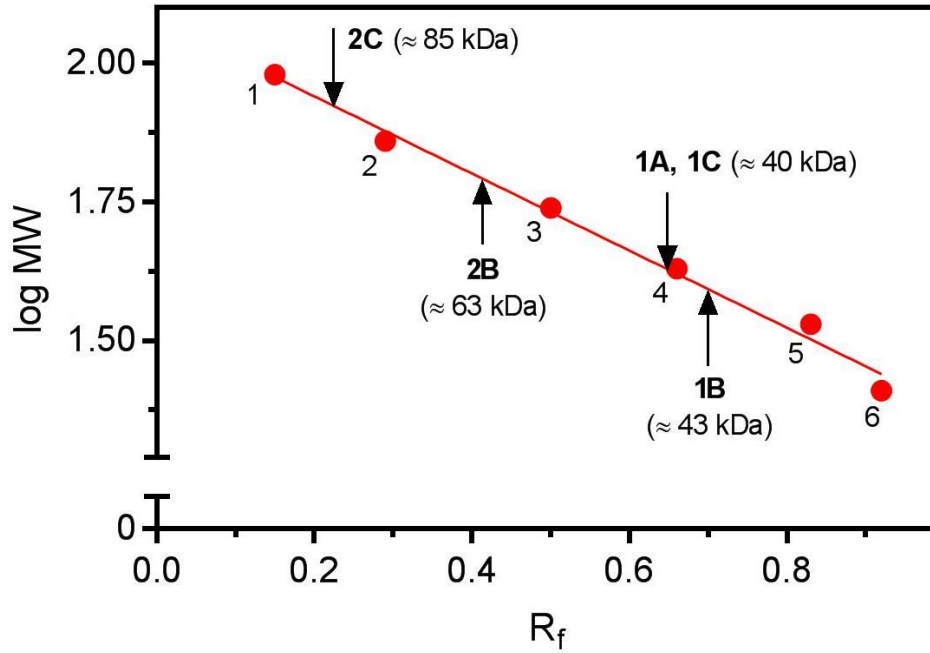


Figure S1. Determining the molecular weight (MW) of SODs from Figure 2. (the main text of the article). Arrows indicate the estimated MW (kDa) for each SOD band: 1A, 1B, 1C, 2B, and 2C. A standard curve of the log MW vs. R_f was generated using the PageRuler™ Prestained Protein Ladder (Thermo Scientific) from Figure 2 (the main text of the article). The strong relationship ($R^2 = 0.9904$, $y = -0.6952x + 2.08$, $P < 10^{-4}$) between the proteins' MW and the relative migration distance (R_f) demonstrates reliability in predicting MW. R_f is defined as the migration distance of the protein through the gel divided by the migration distance of the dye front. The numbers near calibration points represent marker proteins from the PageRuler™ Prestained Protein Ladder: 1. 95 kDa, 2. 72 kDa, 3. 55 kDa, 4. 43 kDa, 5. 34 kDa, 6. 26 kDa.

Table S1. Parameters, i.e., log MW and R_f values used for preparation the curve from Figure S1.

No.	MW [kDa]	log MW	R_f
1	95	1.98	0.15
2	72	1.86	0.29
3	55	1.74	0.50
4	43	1.63	0.66
5	34	1.53	0.83
6	26	1.41	0.92

Table S2. MW of SODs determined based on the curve from Figure S1.

SOD activity bands	R_f	log MW ^a	Estimated MW [kDa] ^b
1A (FeSOD1)	0.7	1.6	~ 40 (39.8)
1B (FeSOD1)	0.65	1.63	~ 43 (42.6)
1C (FeSOD1)	0.7	1.6	~ 40 (39.8)
2B (FeSOD2)	0.41	1.8	~ 63 (63.09)
2C (FeSOD2)	0.22	1.93	~ 85 (85.1)

^aValues calculated based on the equation of the curve from Fig. 1S, i.e. $y = -0.6952x + 2.08$

^bCalculated based on $MW = 10^y$

Notes S1.

Sequenced 16S rRNA fragments for *Geitlerinema* sp. ZHR1A and *G. violaceus* CCALA979

> *Geitlerinema* sp. ZHR1A, 16S rRNA (fragment) obtained using CYA 359F and CYA 781R

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> *Gloeobacter violaceus* CCALA 979, 16S rRNA (fragment) obtained using CYA 359F and CYA 781R

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Y: C/T

W: A/T

Notes S2.

All 16S rRNA sequences used for reconstruction of the phylogenetic tree

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> *Gloeobacter violaceus* CCLA 979, 16S rRNA (fragment) obtained using CYA 359F and CYA 781R
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> Geitlerinema sp. ZHRIa, 16S rRNA (fragment) obtained using CYA 359F and CYA 781R
TGTGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAATACCGCGTGAGGGACGAAGGCCTGTGGGTTGTAAACCTCTTTTCT
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>ENA|HE974210.1:257..1733:rRNA|HE974210.1:257..1733:rRNA.1 Microcystis aeruginosa PCC 9701
ribosomal RNA 16s ribosomal RNA
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>ENA|CP003607.1:2196585..2197955:rRNA|CP003607.1:2196585..2197955:rRNA.1 Oscillatoria
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>J01395.1:223-1714 Chlamydomonas reinhardtii 16S ribosomal RNA gene, complete sequence;
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>ENA|GU084820.1:229350..230840:rRNA|GU084820.1:229350..230840:rRNA.1 Volvox carteri f.
nagariensis 16S ribosomal RNA
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>ENA|AF170718|AF170718.1 Galdieria sulphuraria strain SAG 107.79 culture-collection SAG:107.79
16S small subunit ribosomal RNA gene, partial sequence; plastid.
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>ENA|AP012987.1:208682..210168:rRNA|AP012987.1:208682..210168:rRNA.1 Porphyridium purpureum
16S small subunit ribosomal RNA
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>X12742.1 Chlorella ellipsoidea chloroplast 16S rDNA
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>ENA|AJ400848.1:134008..135498:rRNA|AJ400848.1:134008..135498:rRNA.1 Spinacia oleracea
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>ENA|M82900|M82900.1 *Nicotiana plumbaginifolia* 16S rRNA gene.

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>ENA|AP000423.1:101012..102502:rRNA|AP000423.1:101012..102502:rRNA.1 *Arabidopsis thaliana*
(thale cress) 16S ribosomal RNA

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(tomato) 16S ribosomal RNA

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