

Table 2. Quantification of selected protein complexes in *Synechocystis* cells.

Protein abundances were estimated as molecules per cell, as inferred from mass spectrometry, immunoblotting and spectrophotometric analysis. The stoichiometries of protein complexes were based on Uniprot (www.uniprot.org, (**UniProt Consortium, 2018**)) and RCSB (www.rcsb.org, (**Berman, 2000**)) databases. Protein abundances are not precise estimates but indicate ranges. The range in the second column reflects the minimal and maximal protein amounts estimated across all light intensities studied in this work. Estimation of protein abundances is detailed in **Table 2—Source data 1**, a list of all proteins is provided in **Table 2—Source data 2**. The experimental conditions of (**Moal and Lagoutte, 2012**) are comparable to the conditions used in this study with the exception of high light used here and distinct *Synechocystis* substrains (**Figure 2—source data 2**).

Protein complex	Molecules per cell	Method	Stoichiometry	Reference
Elongation factor	179000–274000	Proteomics	TufA	This study
Phosphoglycerate kinase	45000–73000	Proteomics	Pgk	This study
Ribosome small subunit	36000–66000	Proteomics	Rps1A,1B,B,C,D,E,F,G,H,I,J,K,L,M,N,O,P,Q,R,S,T,U	This study
Phycobilisome (phycocyanin)	12000–23000	Proteomics	((CpcA,B) ₁₈ ,C1,C2,D,G) ₆	This study
	26000–66000	Spectrophotometry		This study
Photosystem I	31000–63000	Proteomics	(PsaA,B,C,D,E,F,I,J,K,L,M,X) ₃	This study
	96000	Spectroscopy		Keren et al., 2004
	540000	Spectroscopy		Moal and Lagoutte, 2012
Ribosome large subunit	33000–54000	Proteomics	RplA,B,C,D,E,F,I,J,K,L,M,N,O,P,Q,R,S,T,U,V,W,X,Y, RpmA, B,C,E,F,G,H,I,J	This study
Transketolase	31000–50000	Proteomics	TktA ₂	This study
PII signal transducing protein	36000–46000	Proteomics	GlnB ₃	This study
Photosystem II	23000–46000	Proteomics	(PsbA1,A2,B,C,D,E,F,H,I,J,K,L,M,N,O,T,U,V,X,Y,Z, Ycf12) ₂	This study
	17000–29000	Immunoblotting		This study
	100000	Spectroscopy		Moal and Lagoutte, 2012
RuBisCO	26000–43000	Proteomics	(Rbcl, RbcS) ₈	This study
	39000–63000	Immunoblotting		This study
Ferredoxin-NADP reductase (FNR)	33000–42000	Proteomics	PetH	This study
	140000	Immunoblotting		Moal and Lagoutte, 2012
D-fructose 1,6-bisphosphatase class 2	29000–36000	Proteomics	Slr20944	This study
Phycobilisome (allophycocyanin)	19000–38000	Proteomics	(ApcA,B) ₃₄ ,C ₆ ,D ₂ ,E ₆ ,F ₂	This study
	9000–19000	Spectrophotometry		This study
G3P dehydrogenase	21000–32000	Proteomics	Gap2 ₄	This study
Plastocyanin	15000–29000	Proteomics	PetE	This study
Superoxide dismutase [Fe]	14000–25000	Proteomics	SodB ₂	This study
Orange carotenoid protein	15000–24000	Proteomics	Slr1963 ₂	This study
RNA polymerase	8000–15000	Proteomics	RpoA ₂ ,B,C1,C2,D,E,F	This study
Cytochrome b6/f	8000–15000	Proteomics	(PetA,B,C2,D,G,L,M,N) ₂	This study
Chaperonine GroEL	7000–13000	Proteomics	GroL1 ₁₄	This study
Ribosome recycling factor	6000–7000	Proteomics	Frr	This study
Phosphoglycerate dehydrogenase	3000–5000	Proteomics	SerA ₄	This study
Pyruvate dehydrogenase	3000–4000	Proteomics	(PdhA, PdhB) ₂	This study
Glutamine synthetase	2000–4000	Proteomics	GlnA ₁₂	This study
Isocitrate dehydrogenase	2000–3000	Proteomics	Icd ₂	This study

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Table 2 continued

Protein complex	Molecules per cell	Method	Stoichiometry	Reference
Glycogen synthase	2000–3000	Proteomics	GlgA1	This study
DNA polymerase III	1000–2000	Proteomics	DnaN ₂	This study
Pyruvate kinase	1000–2000	Proteomics	Pyk2 ₄	This study
Acetyl-coenzyme A carboxylase	1000	Proteomics	AccB, AccC, AccA ₂ , ACCD ₂	This study
Carbonic anhydrase	400–700	Proteomics	IcfA ₆	This study
Acetyl-coenzyme A reductase	300–600	Proteomics	PhaB ₄	This study
Circadian clock proteins KaiA/ KaiB/KaiC	200–500	Proteomics	KaiA ₂ /KaiB ₄ /KaiC ₆	This study

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The following source data is available for Table 2:

Source data 1. Calculations of selected protein complex copies in *Synechocystis* cells.

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Source data 2. List of all proteins quantified by proteomics measurements in *Synechocystis* cells.

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