



Supplementary Information for

The crystal structures of *Arabidopsis* and *Chlamydomonas* phosphoribulokinase fill the last gap in the redox structural proteome of the Calvin-Benson cycle

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Supplementary Information

SI Materials and Methods

Activity Assay and Determination of pH and Temperature Dependence

Phosphoribulokinase activity was measured spectrophotometrically (Cary 60 UV-Vis; Agilent) at 25°C in 1 ml cuvette containing 50 mM Tris-HCl (pH 7.5), 10 mM MgCl₂, 20 mM KCl, 2 mM ATP, 2.5 mM phosphoenolpyruvate, 0.2 mM NADH, 5 U ml⁻¹ pyruvate kinase, 6 U ml⁻¹ lactate dehydrogenase and enzyme preparation. Following 1 min of blank acquisition, the reaction was started by the addition 0.5 mM ribulose-5-phosphate.

Temperature dependence was evaluated on aliquots of *AtPRK* and *CrPRK* desalted in PBS buffer and incubated for 20 min at temperatures ranging from 20°C to 60°C. Following incubation, the activity was assayed at 25°C as described above. Activities were measured on two independent protein purifications and are expressed as percentage of the highest measured activity.

The pH dependence of purified enzymes was determined in Britton-Robinson buffer for pH values ranging from 5.0 to 8.5. For pH values ranging from 9.0 to 10.0, 100 mM Glycine buffer was used. To ascertain that pH and buffer composition do not block pyruvate kinase and lactate dehydrogenase activity, their activity was controlled measuring the rate of NADH oxidation in a coupling assay performed at 25°C in 1 ml cuvette containing the above mentioned buffers and 10 mM MgCl₂, 20 mM KCl, 2 mM ADP, 0.2 mM NADH, 10 U ml⁻¹ pyruvate kinase, 12 U ml⁻¹ lactate dehydrogenase. Following 1 min of blank acquisition, the reaction was started by the addition 2.5 mM phosphoenolpyruvate and monitored spectrophotometrically at 340 nm.

Once the functionality of pyruvate kinase and lactate dehydrogenase was verified, to ascertain that their activity did not limit the measurements of PRK activity, the concentration of both enzymes was increased (i.e. from 5 to 15 U ml⁻¹ for pyruvate kinase and 6 to 18 U ml⁻¹ for lactate dehydrogenase) up to concentrations that did not increase PRK activity further.

Determined the experimental conditions, PRK activity was measured on a Cary 60 UV-Vis spectrophotometer (Agilent) at 25°C in 1 ml cuvette containing the above mentioned buffer at

different pH values, 10 mM MgCl₂, 20 mM KCl, 2 mM ATP, 2.5 mM phosphoenolpyruvate, 0.2 mM NADH, 10 U ml⁻¹ pyruvate kinase, 12 U ml⁻¹ lactate dehydrogenase and enzyme preparation. Following 1 min of blank acquisition, the reaction was started by the addition 0.5 mM ribulose-5-phosphate. Activities were measured on two independent protein purifications and are expressed as percentage of the highest measured activity.

Crystallization and Data Collection.

Aliquots of 2 µl for both proteins were mixed to an equal volume of reservoir, and the prepared drop was equilibrated against 900 (*CrPRK*) and 750 (*AtPRK*) µl of reservoir.

CrPRK crystals were obtained in different conditions of the Extension Kit from Hampton Research (solutions 22: 12% w/v PEG 20K, 0.1 M MES, pH 6.5; 26: 30% w/v PEG MME 5K, 0.1 M MES, pH 6.5, 0.2 M ammonium sulfate; 30: 10% w/v PEG 6K, 5% v/v MPD, 0.1 M HEPES, pH 7.5) and Structure screen 1 from Molecular Dimension (MD1-01-CF, solutions 35: 30% w/v PEG 4K, 0.1 M Tris-HCl, pH 8.5, 0.2 M lithium sulfate; and 50: 15% w/v PEG 8K, 0.5 M lithium sulfate). The conditions were optimized and the best diffracting crystal grew in about 10 days, from 22% w/v PEG MME 5K, 0.1 M MES, pH 6.5, 0.2 M ammonium sulfate. *CrPRK* crystal appeared as needle-like, in the majority of the cases forming a cluster. Aggregates were manually separated and the thicker individuals fished.

AtPRK crystals showed a bipiramidal morphology and grew in three to five weeks from a reservoir solution containing 1.4 – 1.7 M sodium malonate, pH 5.0. The best diffracting crystal of *AtPRK* was obtained in 1.5 M sodium malonate, pH 5.0.

Crystals were mounted from the crystallization drop into cryo-loops, briefly soaked in a cryoprotectant solution containing 30% w/v PEG MME and 20% v/v PEG 200 for *CrPRK* and 1.7 M sodium malonate, pH 5.0, and 30% v/v glycerol for *AtPRK*, then frozen in liquid nitrogen. Diffraction images were recorded at 100 K at the Elettra synchrotron radiation source (Trieste, beam line XRD1) for *CrPRK* and at the European Synchrotron Radiation Facility (Grenoble, beam line ID14-4) for *AtPRK*. Data collection parameters are reported in Table S4.

The data at a resolution of 2.6 Å for *CrPRK* and 2.5 Å for *AtPRK* were processed using XDS (1) and scaled with SCALA (2). The correct space group was determined with POINTLESS (2) and confirmed in the structure solution stage. Data collection statistics are reported in Table S5.

Structure Solution and Refinement.

CrPRK structure was solved by molecular replacement using the program PHASER (3) from PHENIX (4) starting from the coordinates of PRK from *Methanospirillum hungatei* (PDB code 5B3F) (5) deprived of sulfate ions and water molecules. The protein chain was traced by Autobuilt from PHENIX (4) and Buccaneer (6) from CCP4 package. The refinement was performed with REFMAC 5.8.0135 (7) selecting 5% of reflections for R_{free} . The manual rebuilding was performed with Coot (8). The residual electron density map showed the position of a sulfate ion for each monomer coming from the crystallization solution, which was added to the model. Water molecules were automatically added and, after a visual inspection, confirmed in the model if the relative electron density value in the $(2F_o - F_c)$ maps exceeded $0.19 \text{ e}^{-\text{\AA}^3}$ (1.0σ) and if they fell into an appropriate hydrogen bonding environment. The last refinement cycle was performed with PHENIX (4). The final model of *CrPRK* lacks six residues at the C-terminal end of both chains.

The structure of *CrPRK* without sulfate ions and waters, was used as initial model to solve the *AtPRK* structure by molecular replacement using MOLREP (9). The refinement was performed as described for *CrPRK*. The final model of *AtPRK* lacks three residues at the N-terminal domain and seven and ten residues at the C-terminal domain of chain A and B, respectively.

The refinement statistics of both structures are reported in Table S5. All structure figures were prepared using PyMOL (The PyMOL Molecular Graphics System, Schrödinger, LLC).

Small Angle X-ray Scattering Data Collection.

Data collection parameters are reported in Table S4. A Size Exclusion Chromatography SEC-SAXS experiment was performed using a HPLC system (Shimadzu) directly connected to the measurement capillary. A volume of $100 \mu\text{l}$ of reduced *CrPRK* (6.1 mg ml^{-1}) was loaded onto a Superdex 200 10/300 GL column (GE Healthcare) pre-equilibrated in 50 mM Tris-HCl, 150 mM

KCl, pH 7.5. The sample was eluted at a flow rate of 0.5 ml min⁻¹ and SAXS frames obtained by 1 s exposure were collected continuously. The automatic pipeline for SEC-SAXS data analysis implemented at BM29 was used to assess the quality of the collected data (10).

Small Angle X-ray Scattering Data Analysis.

Afterwards, a classification of the collected frames as buffer (0-14 ml) or protein frames (14-17.75 ml) was performed on the basis of the SAXS intensity trace (Fig. S13). Statistical test implemented in CorrMap (11) aided by visual inspection, was used to choose the superimposable buffer intensity profiles. The averaging of the buffer profiles, the subtraction of the averaged buffer intensity from the protein data and an automatic analysis of the subtracted protein profiles was performed with a Matlab script. The script used the tools of the ATSAS package (12) to automatically obtain from the subtracted intensity I(q): (i) the I(0) and the gyration radius (R_g) via the Guinier approximation (13) $I(q) = I(0) \cdot \exp[-(qR_g)^2/3]$; (ii) the pair-distance [p(r)] function, from which the maximum particle dimension (D_{max}) was estimated, in addition to an independent calculation of I(0) and R_g . Estimates of the MW were also determined both from the Porod invariant (14) as 0.6 times the Porod volume (V_p) for roughly globular particles (12) and by the invariant volume-of-correlation length (V_c), through a power-law relationship between V_c , R_g and MW that has been parametrized (15). The protein frames giving constant R_g values were scaled to the intensity of the elution maximum and averaged in order to obtain a single representative scattering profile with good signal to noise ratio, presented in the results and used for modelling.

Modeling from SAXS Data

The sequence and the homodimeric state of CrPRK were given as inputs in GASBOR and a 2-fold symmetry was imposed in the calculations. A series of 10 models was generated. The similarity of the structures obtained by repeated calculations was checked by DAMAVER (16) in which the superposition is performed by the SUPCOMB code (17).

All programs used for SAXS data analysis and reconstruction, belong to the ATSAS package 2.7 (12). The graphical representations of the obtained three-dimensional models were built by using

PyMOL (The PyMOL Molecular Graphics System, Schrödinger, LLC).

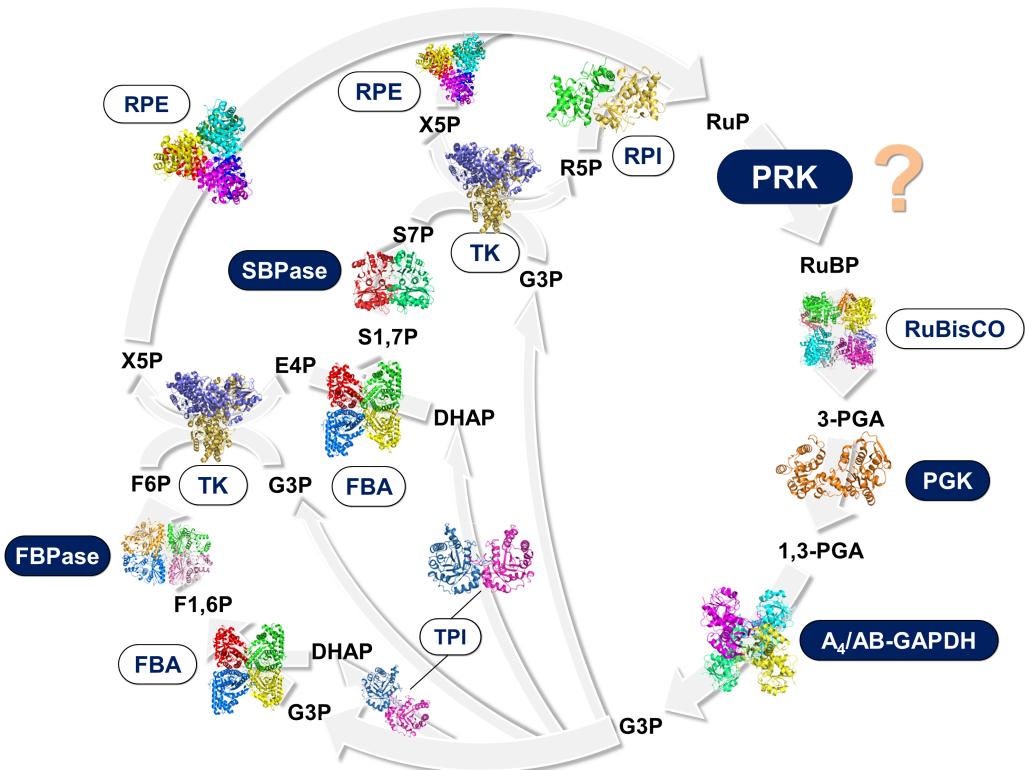


Fig. S1. Schematic representation of the CB cycle. The crystal structure of six chloroplast enzymes from different organisms: RuBisCO, ribulose-1,5-bisphosphate Carboxylase/Oxygenase from *Spinacia oleracea* (PDB ID code 1AUS) (18); GAPDH, glyceraldehyde-3-phosphatedehydrogenase from *Arabidopsis thaliana* (PDB ID code 3K2B) (19); TPI, triose phosphate isomerase from *Chlamydomonas reinhardtii* (PDB ID code 4MKN) (20); FBPase, fructose-1,6-bisphosphatase from *Pisum sativum* (PDB ID code 1DCU) (21); TK, transketolase from *Chlamydomonas reinhardtii* (PDB ID code 5ND5) (22); SBPase, sedoheptulose-1,7-bisphosphatase from *Physcomitrella patens* (PDB ID code 5IZ3) (23); RPE, ribulose-5-phosphate 3-epimerase from *Solanum tuberosa* (PDB ID code 1RPX) (24), is shown. For the remaining three enzymes, the crystal structure of the most homologous enzymes from non-photosynthetic organisms is reported: PGK, phosphoglycerate kinase from *Bacillus stearothermophilus* (PDB ID code 1PHP) (25) approximately 60% homologous to *Chlamydomonas reinhardtii* PGK1 (sequence accession number A8JC04); FBA, fructose-1,6-bisphosphatealdolase from *Toxoplasma gondii* (PDB ID code

5TJS) (26) approximately 55% homologous to *Arabidopsis thaliana* FBA1 (sequence accession number Q9SJU4); RPI, ribose-5-phosphateisomerase from *Toxoplasma gondii* (PDB ID code 4NML) approximately 50% homologous to *Spinacia oleracia* RPI (sequence accession number Q8RU73).

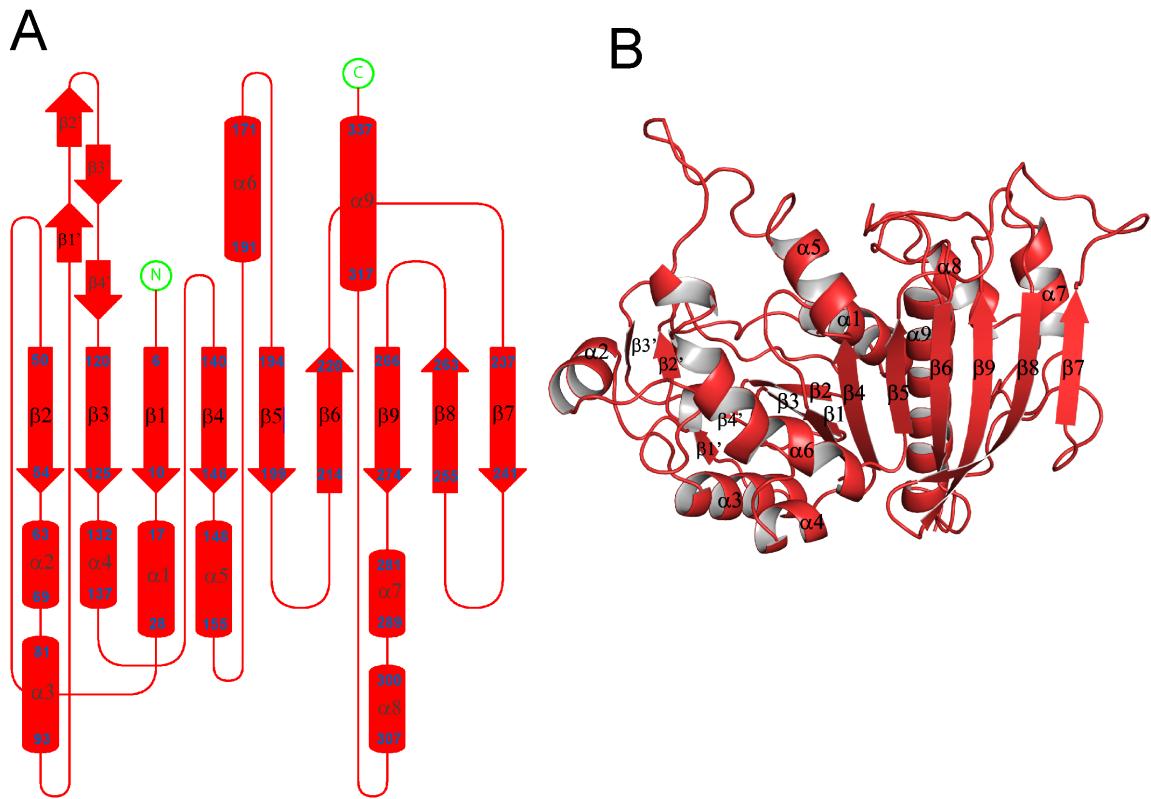


Fig. S2. Crystal structure of AtPRK's monomer. (A) Topology diagram of AtPRK. Similarly to CrPRK (Fig. 2A), the monomer is composed by a mixed β -sheet of nine strands, by nine α -helices and four additional small β -strands indicated by β' . (B) Cartoon representation of the monomer structure of AtPRK. Similarly to CrPRK (Fig. 2B) the central β -sheet is sandwiched between helices α_3 , α_4 and α_6 and helices α_1 , α_7 , α_8 and α_9 . The right end of the monomer consists of stand β_7 involved in the dimer interface, while the four additional β -strands (β_1' to β_4') form the left external end of the dimer.

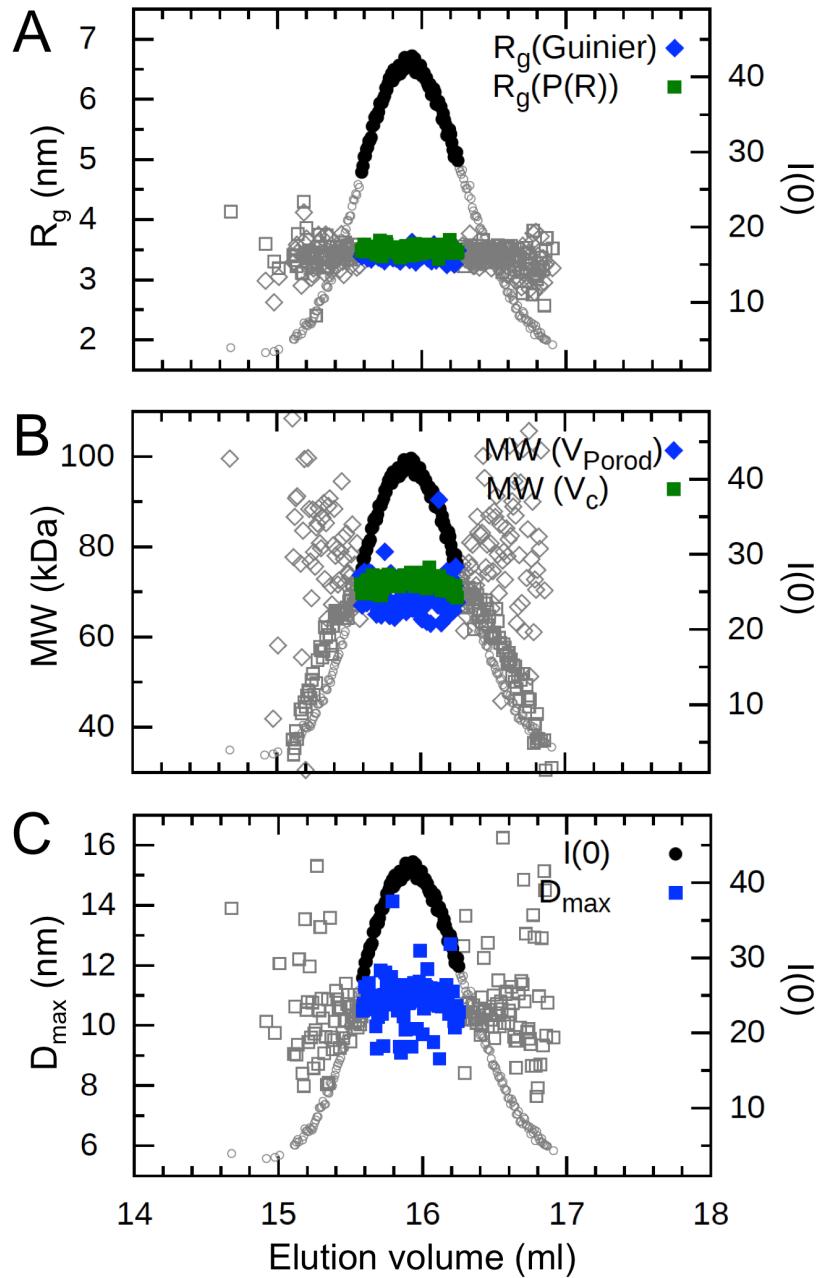


Fig. S3. Parameters determined by SEC-SAXS analysis of CrPRK. (A) $I(0)$ trace (dots) and R_g determined by the Guinier approximation (diamonds) and R_g calculated from the $P(r)$ function (squares). (B) $I(0)$ trace (dots) and MW estimated from the Porod volume (diamonds) and from the volume-of-correlation (squares). (C) $I(0)$ trace (dots) and D_{max} estimated from the $P(r)$ function (squares). The frames used in the average to obtain the representative scattering profile, are highlighted in black compared to the grey neglected frames.

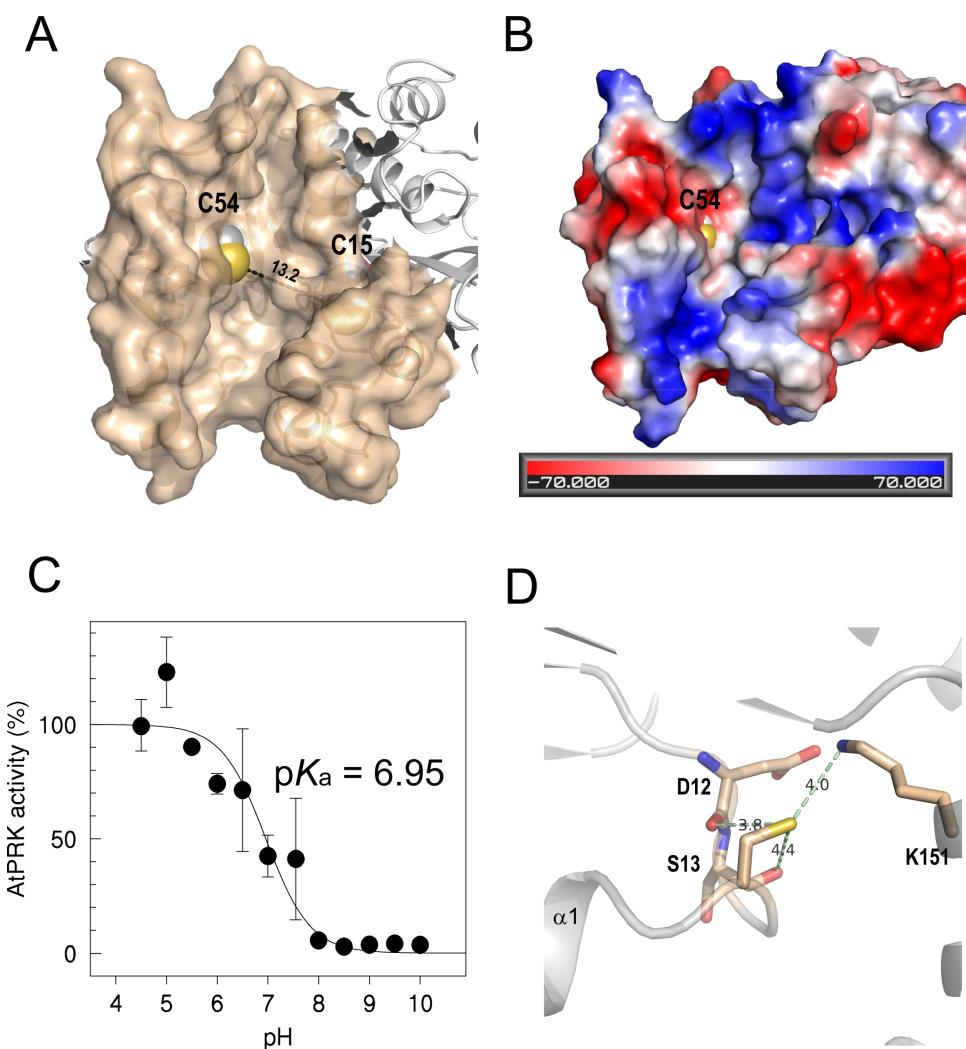
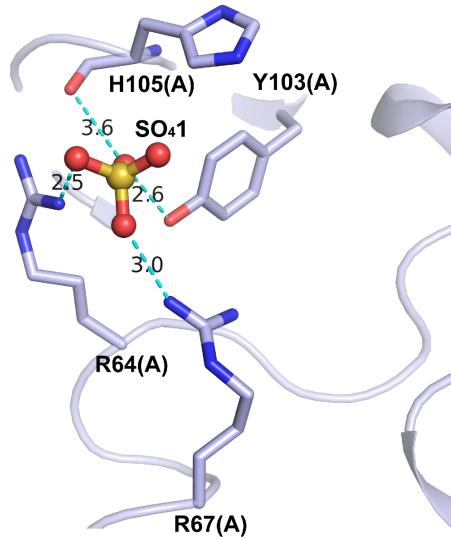


Fig. S4. Active site and TRX-dependent regulation of AtPRK. (A) The catalytic cavity is shown. The distance between the regulatory cysteines is higher than 13 Å. (B) Catalytic cavity electrostatic surface potential. The bottom of the catalytic cavity is marked by a positive potential. The negative potential region observed on the left side of the cavity, is suggested to be involved in the correct positioning of TRX close to regulatory cysteines. (C) The pK_a of Cys15 was determined by measuring the IAM-mediated inactivation as a function of pH. (D) Molecular environment of Cys15 considering a sphere of 5 Å centered on its thiol group. The hydrogen bonds between the thiol group and the neighboring residues and the corresponding distances, are shown.

A



B

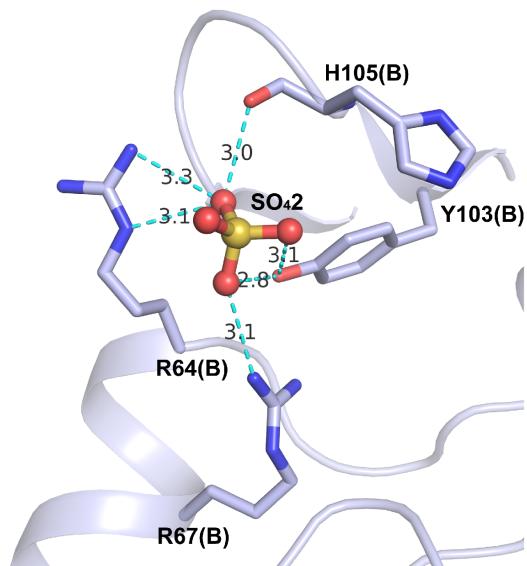
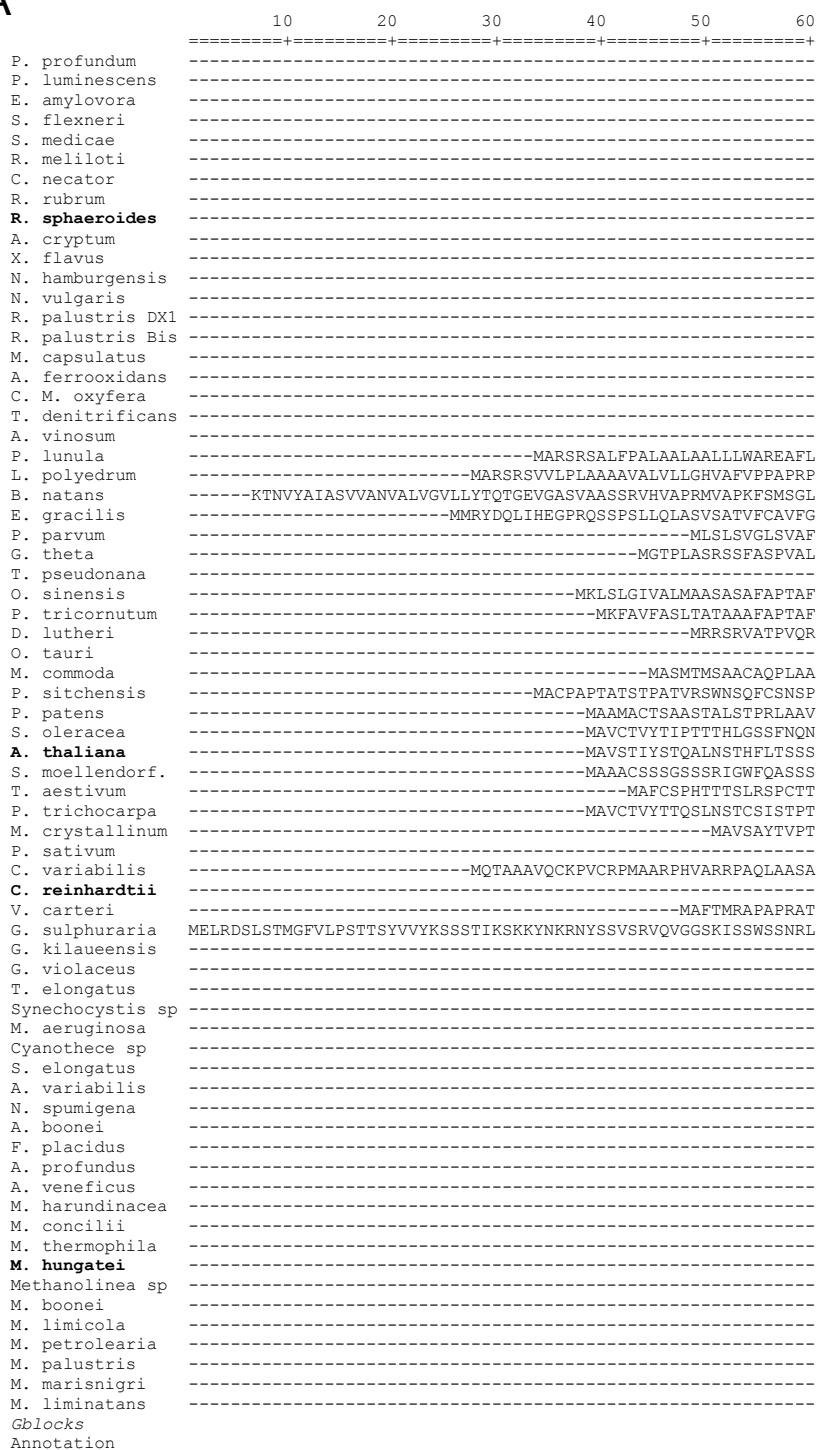
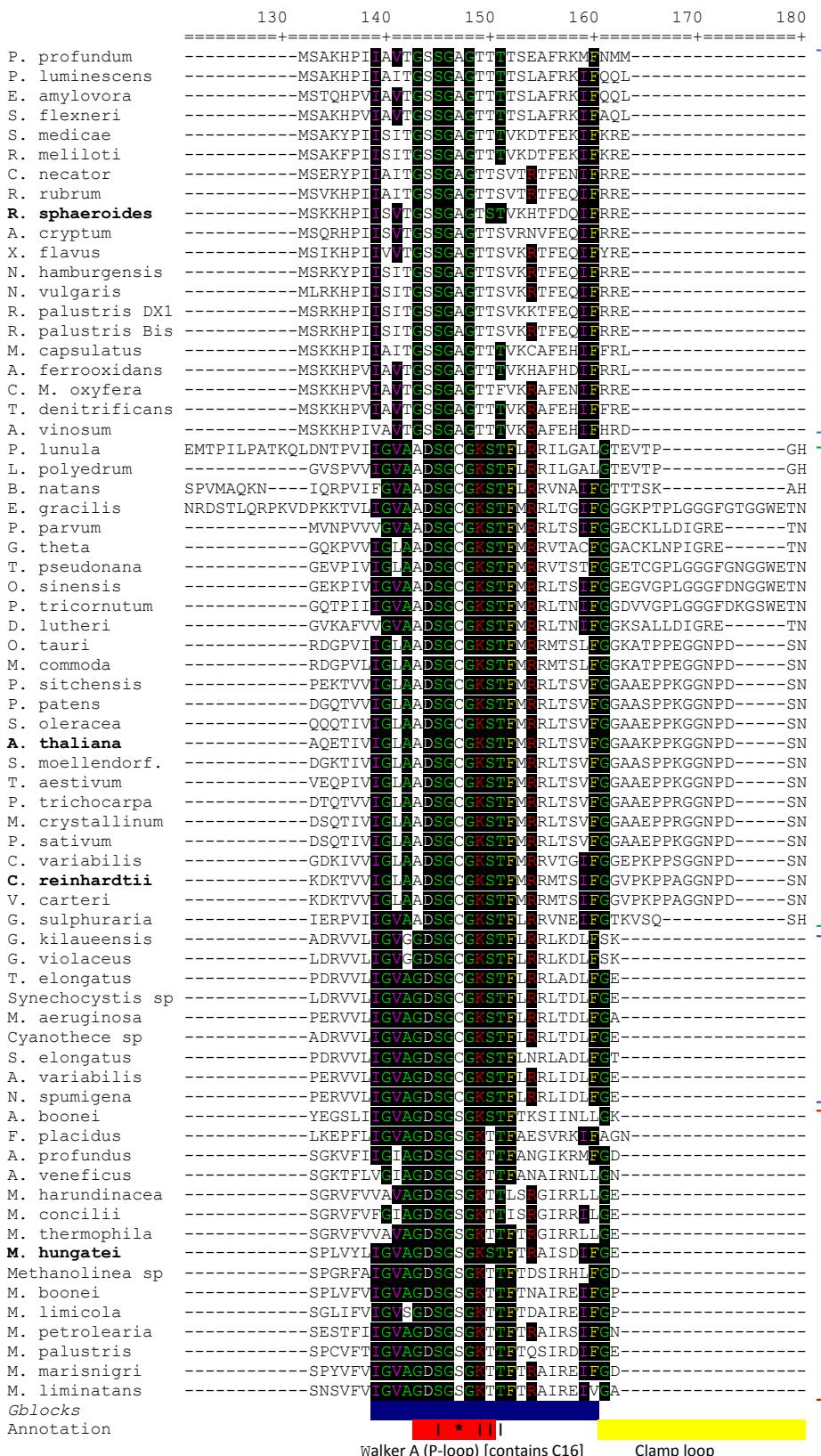
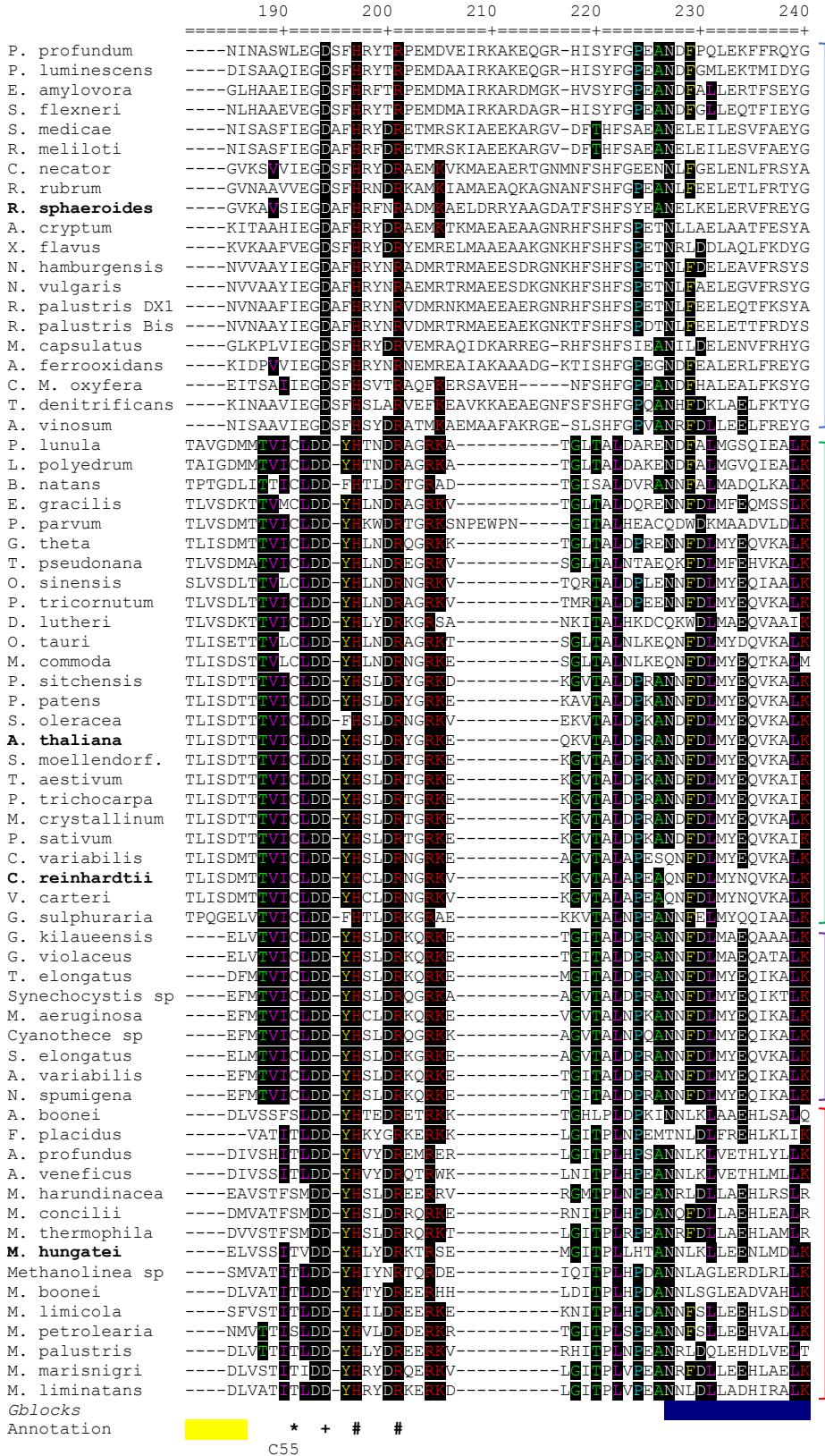


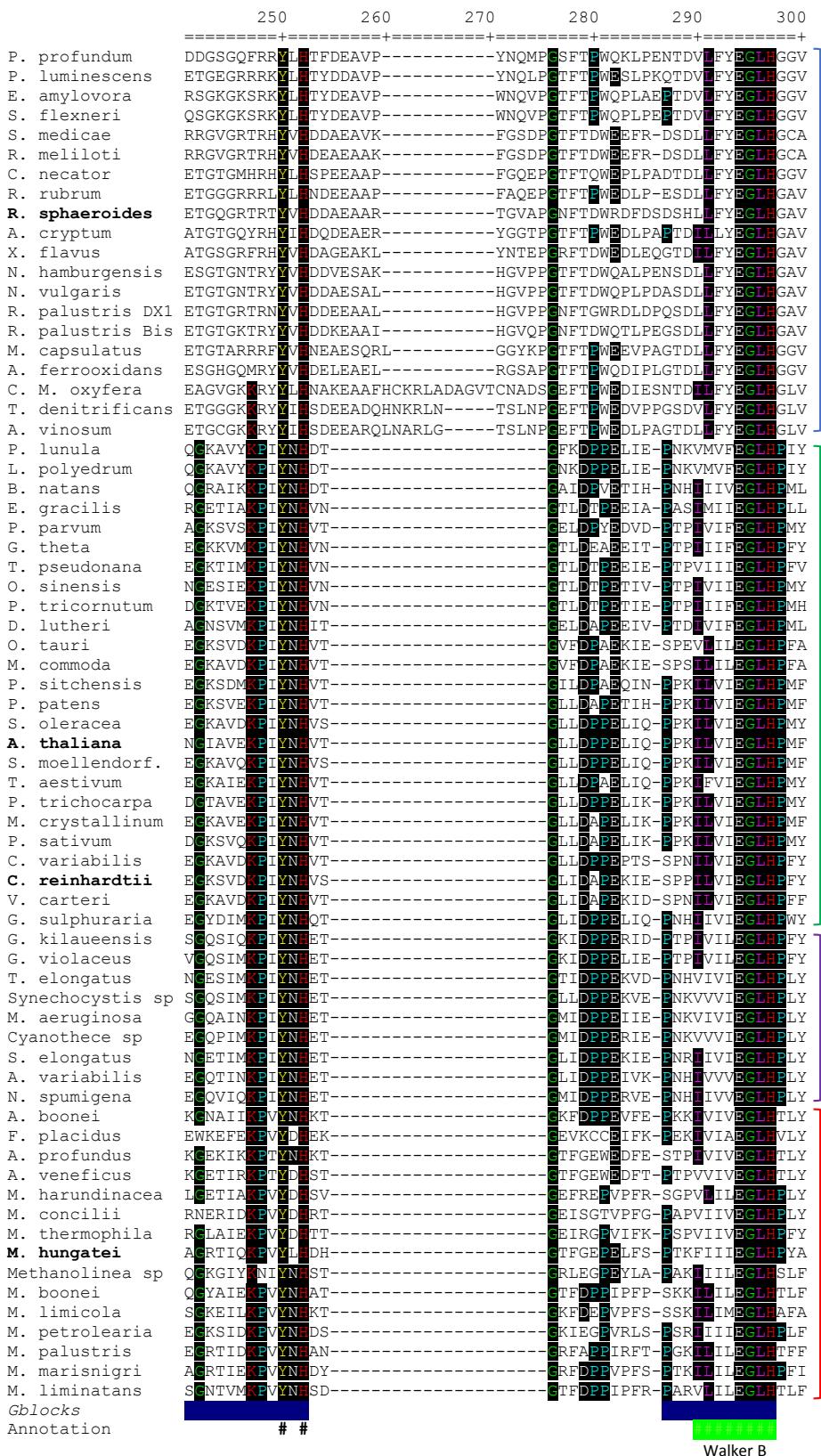
Fig. S5. Binding site of the sulfate ion in CrPRK. The interactions between a sulfate ion coming from the crystallization solution, and protein residues in (A) subunit A and (B) subunit B, are represented. Salt-bridges are formed with Arg64 and Arg67, and hydrogen bonds with Tyr103 and His105.

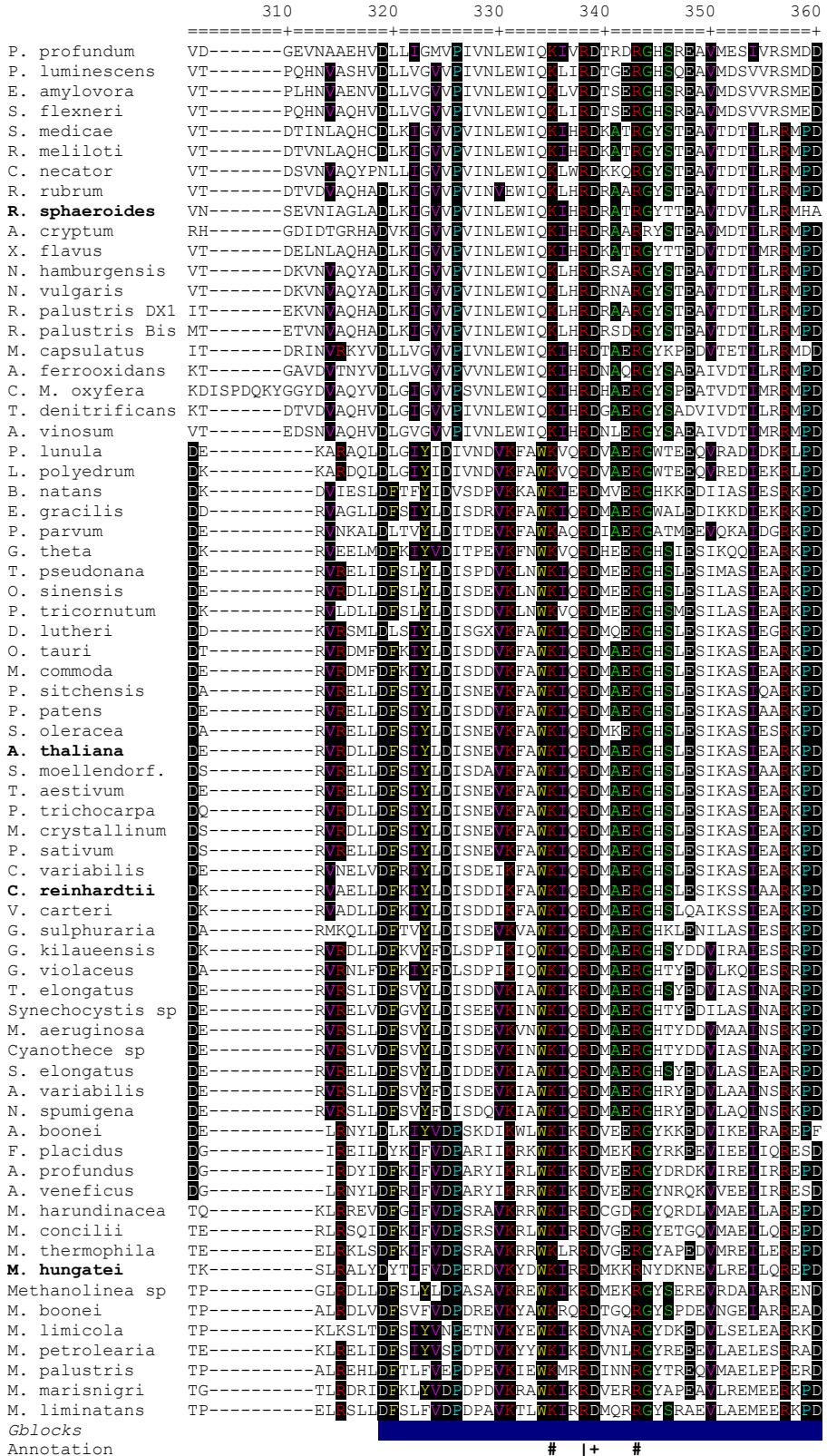
A

	70	80	90	100	110	120
P. profundum	=====	=====	=====	=====	=====	=====
P. luminescens	-----	-----	-----	-----	-----	-----
E. amylovora	-----	-----	-----	-----	-----	-----
S. flexneri	-----	-----	-----	-----	-----	-----
S. medicae	-----	-----	-----	-----	-----	-----
R. meliloti	-----	-----	-----	-----	-----	-----
C. necator	-----	-----	-----	-----	-----	-----
R. rubrum	-----	-----	-----	-----	-----	-----
R. sphaeroides	-----	-----	-----	-----	-----	-----
A. cryptum	-----	-----	-----	-----	-----	-----
X. flavus	-----	-----	-----	-----	-----	-----
N. hamburgensis	-----	-----	-----	-----	-----	-----
N. vulgaris	-----	-----	-----	-----	-----	-----
R. palustris DX1	-----	-----	-----	-----	-----	-----
R. palustris Bis	-----	-----	-----	-----	-----	-----
M. capsulatus	-----	-----	-----	-----	-----	-----
A. ferrooxidans	-----	-----	-----	-----	-----	-----
C. M. oxyfera	-----	-----	-----	-----	-----	-----
T. denitrificans	-----	-----	-----	-----	-----	-----
A. vinosum	-----	-----	-----	-----	-----	-----
P. lunula	LPRSSPQAPRASSARVPKVVALRAAADSQPTGLVWPSPEAEAKLREVDGIKLYPTHAWTE					
L. polyedrum	RAARALTAMRGAANSVPTGLVWPSPEAEAKLREEDGIKMYPTHAWTDDMMPIVPATKE					
B. natans	RPAQEAREVAAHGKGVYSTVALIDAPVATSEDSMTWSAKNEVDAGMGQVHIEAAISNEV					
E. gracilis	IGYTFSGGLVENYATTRPVQTQPAALILPKAVRYAGVSQGPQVESREARTALHAATGTV					
P. parvum	SPA-----PSVVSQSRVAPRATVVE--					
G. theta	-----RVTNDEMDVAIQQISMSSLAS--					
T. pseudonana	-----MKFLVASLIASASFINTPTLRGNSALAALKD--					
O. sinensis	-----MPANTLRAAAPAPSALNMALKE--					
P. tricornutum	VPS-----NLRGVAPSASSLNMALKE--					
D. lutheri	VPQ-----TACTVLMATKT--					
O. tauri	-----MSASLGFSITSVRAAPVRAVTRDAVKPRATRARVVTAK--					
M. commoda	RKFQGS-----RVSGKSVVRAAKRNVTVKAE--					
P. sitchensis	LAS-----FSLAHTTRRRPRLALVVCSVG--					
P. patens	KPARSARPVH-----LTSAFHGQSVASVSQVAGFESSGVKYRSAGRRAVVVCKAA--					
S. olerecea	NKQVFFNYKR-----SSSNNTLFTTRPSYVITCS--					
A. thaliana	SSKQVF-----LYRRQPQTNRNFNTLITC--					
S. moellendorf.	SSNIGILQHHPWRGSHASSLFSFPKLGARIGSSGGSGGTSSSNRVRVLVCCAAGG--					
T. aestivum	IPNSGFRQNQ-----VIFFTTRSSRRSNTRHGARTFQVSCA--					
P. trichocarpa	KTHLGFNQRH-----VVVFYSTMKKTTKRASSAVITCSA--					
M. crystallinum	TSHLGFNQKK-----QLFFCNKSAYKRVSFSSRPCVITCLAG--					
P. sativum	-----AG--					
C. variabilis	APIARPTFSS-----TLNQRTLKAGRVASRVVVVKAEG--					
C. reinhardtii	-----MAFTMRAPAPRATAQSRTANRARRSLVVRAD--					
V. carteri	-----AQSRVTASRASRRVLVVKQAQ--					
G. sulphuraria	LFQGKEINTTRKTTKYWIITVSSQTALEEFVNCGAKGVHESAGISRSKSKVLRNKG--					
G. kilaueensis	-----MVK--					
G. violaceus	-----MVST--					
T. elongatus	-----MSK--					
Synechocystis sp	-----MSSK--					
M. aeruginosa	-----MTTQ--					
Cyanothece sp	-----MANK--					
S. elongatus	-----MTTQ--					
A. variabilis	-----MSK--					
N. spumigena	-----MTTK--					
A. boonei	-----MLGEFRRRLEE--					
F. placidus	-----MILEK--					
A. profundus	-----MLKEKLKIK--					
A. veneficus	-----MTSNLKERLKE--					
M. harundinacea	-----MAERLKG--					
M. concili	-----MRSLKDRIRE--					
M. thermophila	-----MRLLEKIRE--					
M. hungatei	-----MSQOPENFREVIRH--					
Methanolinea sp	-----MTSKPGFKEIJKS--					
M. boonei	-----MPRTPPFKEIJIAR--					
M. limicola	-----MSCIDEYLSESGKCRNRFGSGDEYCFSSSGKGGINLKKIEN--					
M. petrolearia	-----MDYSHETNLKNFRHAVDS--					
M. palustris	-----MMQTEGKTGEKPDLCPGTGGGLNFKDRIAS--					
M. marisnigri	-----MPPSDFKRVIAE--					
M. liminatans	-----MDTPVFRDLISG--					
Gblocks						
Annotation						









	370	380	390	400	410	420
P. profundum	YLN ^Y I ^T P ^C FSRTHINFORV ^P T		VDT ^S ---	NPFSAKG ^T PSLD--	ES ^F VVI	
P. luminescens	YIN ^Y I ^T P ^C FSRTHINFORV ^P T		VDT ^S ---	NPFSAKAI ^T PSLD--	ES ^E IVI	
E. amylovora	YINF ^I T ^C FSRTHINEQRV ^P T		VDT ^S ---	NPFAA ^G PSLD--	ES ^E VVV	
S. flexneri	YIN ^Y I ^T P ^C FSRTHLNEQRV ^P T		VDT ^S ---	NPFAAKG ^T PSLD--	ES ^E VVI	
S. medicae	YVH ^Y I ^C POFSLTDINEQRV ^P I		VDT ^S ---	NPFIA ^W PTPA--	ESILVI	
R. meliloti	YVN ^Y I ^C POFSLTDINEQRV ^P I		VDT ^S ---	NPFIA ^W PTPA--	ESILVI	
C. necator	YVN ^Y I ^C POFSRTHVNFRQRV ^P C		VDT ^S ---	NPFIS ^E ELPAPD--	ESMVVI	
R. rubrum	YVH ^Y I ^C POFTRTDVNFRQRV ^P L		VDT ^S ---	NPFVA ^W HPSAD--	ES ^F VVI	
R. sphaeroides	YHV ^H I ^C POFSQTDINEQRV ^P V		VDT ^S ---	NPFIA ^W PTAD--	ESVVVI	
A. cryptum	YVH ^Y I ^C POFTETDINEQRV ^P T		VDT ^S ---	NPFIA ^W PTAD--	ESIVVI	
X. flavus	YVR ^Y I ^C POFTETDINEQRV ^P T		VDT ^S ---	NPFVA ^W PTPD--	ESMVVI	
N. hamburgensis	YVN ^Y I ^C POFAETDINEQRV ^P T		VDT ^S ---	NPFIA ^W PTPD--	ESMVVI	
N. vulgaris	YVN ^Y I ^C POFAETDINEQRV ^P T		VDT ^S ---	NPFIS ^E W ^I PTPD--	ESMVVI	
R. palustris DX1	YVH ^Y I ^C POFAETDINEQRV ^P T		VDT ^S ---	NPFIA ^W PTAD--	ESMVVI	
R. palustris Bis	YVH ^Y I ^C POGETDINFORV ^P T		VDT ^S ---	NPFIA ^W PTPD--	ESMVVI	
M. capsulatus	YVK ^V I ^C POFSQTDINEQRV ^P T		VDT ^S ---	NPFIA ^W PTPD--	ES ^E VII	
A. ferrooxidans	YIH ^I T ^C POFSRAHINFRQRV ^P L		VDT ^S ---	NPFIA ^W PTPD--	ESMVVI	
C. M. oxyfera	YINHLT ^C POFSRTHVNFRQRV ^P T		VDT ^S ---	NPFIA ^W PTPD--	ES ^E VVI	
T. denitrificans	YVN ^Y I ^T P ^C FSRTDINEQRV ^S T		VDT ^S ---	NPFIS ^E W ^I PTPD--	ES ^E VVI	
A. vinosum	YIR ^I T ^C POSLTDINEQRV ^P T		VDT ^S ---	NPFIA ^W PTPD--	ES ^E VII	
P. lunula	FSA ^Y VD ^C POKAN ^A DVILRYEP ^S		DQGL---	PYLK ^W KL ^I QKKG--	GAEPP	
L. polyedrum	FSA ^Y VD ^C KADAVILRYEP ^S		DQGL---	PYLK ^W KL ^I QKKG--	GAEPP	
B. natans	FEKFVE ^C POKAN ^A DV ^I SIE ^P KLDVA		--PGEET--	KYLNT ^W LIQKENQ-HGIRPV		
E. gracilis	FDK ^I VA ^C PORAK ^A ADM ^V I ^E VL ^P SRSLAPP		--KDETAPL-EYLR ^W LIQKTTT-KH ^E DPV			
P. parvum	FAAY ^V VE ^C POKAK ^A DI ^I IVQVL ^F SDL-I		--DDPTG--	KFLK ^W LIITKNNL-KHISPA		
G. theta	FDA ^Y ID ^C POKNK ^A DC ^V IQL ^P NL-VA		--NDK--	THLN ^W KL ^I QCKGV-DHYAPT		
T. pseudonana	FDA ^Y ID ^C POKKF ^A DY ^V EV ^P DL--		--DKEDK--	KTLK ^W PA ^I QKKGV-AD ^F PTP		
O. sinensis	FDA ^Y IA ^C POKEF ^A DL ^I EV ^L P ^Q QL--		--DEEDK--	KTLR ^W CIQKEGV-SD ^F SPC		
P. tricornutum	FDA ^Y ID ^C POKQI ^A DL ^I EV ^L P ^Q RL--		--DODDK--	KTLR ^W CIQKEGV-EN ^F DPC		
D. lutheri	FDAFVA ^C POQRAN ^A DI ^V EV ^L P ^Q QL-V		--NDAEG--	KFLR ^W FIQAGL-DLIKAP		
O. tauri	FDAFVD ^C POKEH ^A DV ^V EV ^L P ^Q IP--		--DNNEG--	KILR ^W VIIMKENV-EN ^F DAP		
M. commoda	FDEFVD ^C POKOY ^A DI ^V QVL ^P QL-IP--		--DNNEG--	KILR ^W VIIMKEGV-EN ^F DAP		
P. sitchensis	FDAF ^I D ^C POKQY ^A DV ^V QVL ^P QL-IP--		--EENEG--	KVLR ^W VIIMVMKEGV-NFFNPV		
P. patens	FDA ^Y ID ^C POKQY ^A DV ^V QVL ^P QL-IP--		--DDNEG--	KVLR ^W VIIMVMKEGV-PFFEPV		
S. oloracea	FDA ^Y ID ^C POQH ^A DV ^V EV ^L P ^Q EL-IP--		--DDEGG--	KVLR ^W VIIMQKEGV-KFFNPV		
A. thaliana	FDA ^Y ID ^C POKQY ^A DA ^V EV ^L P ^Q TL-IP--		--DDNEG--	KVLR ^W VIIMKEGV-KY ^F SPV		
S. moellendorff.	FDA ^Y ID ^C POKQY ^A DV ^V QVL ^P QL-IP--		--DNNEG--	KVLR ^W VIIMKEGV-DNF ^F EPV		
T. aestivum	FDA ^I D ^C POKQY ^A DA ^V EV ^L P ^Q QL-IP--		--DNEG--	KVLR ^W KL ^I MKEGI-KF ^F NPV		
P. trichocarpa	FDA ^Y ID ^C POKQY ^A DA ^V EV ^L P ^Q QL-IP--		--DNNEG--	KVLR ^W KL ^I MKEGV-EFF ^F SPV		
M. crystallinum	FDA ^Y ID ^C POKQY ^A DA ^V EV ^L P ^Q QL-IP--		--DNNEG--	KVLR ^W VIQKEGV-QY ^F SPV		
P. sativum	FEAY ^I D ^C POKQY ^A DA ^V EV ^L P ^Q QL-IP--		--DNNEG--	KILR ^W VIQKAGV-KY ^F SPV		
C. variabilis	FDA ^Y ID ^C POKKK ^A DM ^I QVL ^P QL-VP--		--DEKEG--	KILR ^W VIIMKDGV-KLFDPV		
C. reinhardtii	FDA ^Y ID ^C POKKD ^A DM ^I QVL ^P QL-VP--		--DDK-G--	QYLR ^W VIIMKEGS-KMFDPV		
V. carteri	FDA ^Y ID ^C POKKD ^A DM ^I QVL ^P QL-VP--		--DDK-G--	QYLR ^W VIIMKEGS-KMFDPV		
G. sulphuraria	FQQ ^Y ID ^C POKKD ^A VA ^V QVL ^P TRL-IP--		--DTEK--	KVLR ^W VIQREGI-QGFQSV		
G. kilaeensis	FSA ^Y ID ^C POKQH ^A DV ^V QVL ^P SELPEK--		--KDTG--	KKIKAAMVQVEGI-PNYDPP		
G. violaceus	FSA ^Y ID ^C POKQY ^A DV ^V QIL ^P SEL--		--PEKAGGI-	KRVKACMVQVDGI-PNYDAP		
T. elongatus	FMA ^Y ID ^C POKQY ^A DV ^V QIL ^P SQL-AK--		--EEKVG--	NILR ^W VIMLQREGK-PGE ^F EPV		
Synechocystis sp	FTA ^Y IE ^C POKQY ^A DV ^V QVL ^P RLI--		--EDKES--	KLLR ^W VIQKEGV-EFF ^F EPV		
M. aeruginosa	FSA ^Y ID ^C POKQY ^A DV ^V QVL ^P KLL--		--EDHES--	KLLR ^W VIQKEGV-EN ^F EPV		
Cyanothece sp	FSA ^Y IE ^C POREY ^A DV ^V QVL ^P NL-IE--		--NDKES--	KILR ^W VIQKEGI-EN ^F QPV		
S. elongatus	FKAY ^I E ^C PORGH ^A DI ^V VRMP ^P QL-IP--		--NTER--	KVLR ^W VIQREGR-DG ^F EPV		
A. variabilis	FKQY ^I E ^C POREF ^A DV ^V QVL ^P NL-IK--		--DDTDR--	KVLR ^W VIQREGK-EG ^F EPV		
N. sumigena	FEKF ^I E ^C POREF ^A DV ^V QVL ^P NL-IK--		--NTER--	KVLR ^W VIQREDK-EG ^F EPV		
A. boonei	YKRY ^I D ^C POKLY ^A DI ^V QIDISKFS--		--EDSYSVETILK ^W LDPLSGIEMPLSLS			
F. placidus	YKRY ^I D ^C POKLY ^A DI ^V QIY ^P SSLESTERISTLLGME--		--EMYR ^W VIQKEGV-FELDHV			
A. profundus	YKRY ^I D ^C POKLY ^A DI ^V QIY ^P SSIQSTERIKYLV ^S RE--		--EVYK ^W VIQKEGV-FELDHV			
A. veneficus	YKRY ^I D ^C POKLY ^A DI ^V QIY ^P SSIQSTERIKYLV ^S RE--		--YKQILD-HPLDEV			
M. harundinacea	YKLY ^I D ^C POVKA ^A EM ^V QIY ^P SSALQSVERITYLTEAPP--		--EGEKR--	NVYR ^W VIQKEGV-FELDHV		
M. concili	YKLY ^I D ^C POVKA ^A EM ^V QIY ^P SSALQSVERITYLTEAPP--		--LGWKK--	NIVYR ^W VIQKEGV-FELDHV		
M. thermophila	YKLY ^I D ^C POVKA ^A EM ^V QIY ^P SSALQSVERITYLTEAPP--		--NIYR ^W VIQKEGV-FELDHV			
M. hungatei	YRAY ^I A ^C PORDH ^A DA ^V QISYSYYGKE-----		--YATY ^W VIQKEGV-FELDHV			
Methanolinea sp	YRAY ^I A ^C PORDH ^A DA ^V QISYSYYGKE-----		--YATY ^W VIQKEGV-FELDHV			
M. boonei	YRAY ^I A ^C PORCNA ^A DA ^V IGIGYSKYGKD-----		--YENFVL ^W VIQKEGV-FELDHV			
M. limicola	YRAY ^I A ^C PORCNA ^A DA ^V IGIGYSKYGKD-----		--YENFVL ^W VIQKEGV-FELDHV			
M. petrolearia	YRAY ^I A ^C POSES ^A DA ^V IEISDSSFDSP-----		--YENFVL ^W VIQKEGV-FELDHV			
M. palustris	YRAY ^I A ^C POSES ^A DA ^V IEISDSSFDSP-----		--YENFVL ^W VIQKEGV-FELDHV			
M. marisnigri	YRAY ^I A ^C POCLF ^A DA ^V RIAFSKYGRD-----		--YERIYVA ^W VIQKEGV-FELDHV			
M. liminatans	YRAY ^I A ^C POCLF ^A DA ^V RIAFSKYGRD-----		--YERIYVA ^W VIQKEGV-FELDHV			
<i>Gblocks</i>						
Annotation						

	430	440	450	460	470	480
P. profundum	RFRG-----	IEN---VDF	YLLSMI QGSFMSRHTLVPGKMS-----			
P. luminescens	RFFD-----	LTQ---IDF	YLLAMLQGSFVSSINTIVVPGKMG-----			
E. amylovora	HFQG-----	LED---IDF	YLLSMLQGSFISHIKTLVVPGKMG-----			
S. flexneri	HFRN-----	LEG---IDF	WLLAMLQGSFISHINTLVPGKMG-----			
S. medicae	RFAK-----	PQS---IDF	YLLSMLHNSYMSRANIVVPGDKLD-----			
R. meliloti	RFAK-----	PQS---IDF	YLLSMLHNSYMSRANIVVPGDKLD-----			
C. necator	RFAN-----	PKG---IDF	YLLSMI HDSFMSRANTIVVPGKME-----			
R. rubrum	RFRD-----	PKG---IDF	YLLSMI LNDSFMSRPNTIVVPGKME-----			
R. sphaeroides	RFRN-----	PRG---IDF	YLLSMI HGWSMSRANIVVPGNKL-----			
A. cryptum	RFRD-----	PHG---IDF	YLLAMLHGFSMSRANIAVPGNKF-----			
X. flavus	RFRD-----	PHG---IDF	YLLSMI HNSFMSRANIVIPGNQD-----			
N. hamburgensis	RFKN-----	PRG---IDF	YLLSMI PNSFMSRANIVIHSKMD-----			
N. vulgaris	RFKN-----	PRG---IDF	YLLSMI PSSFMSRANIVIHSKLD-----			
R. palustris DX1	RFKN-----	PRG---IDFA	YLLSMI QGSFMSRANIVIHGAKLD-----			
R. palustris Bis	RFKS-----	PRG---IDFA	YLLSMI QGSFMSRANIVIHSKMD-----			
M. capsulatus	RFKE-----	PGKFN-VDF	YLLAMLQNSFMSRHNIVIPCGKMG-----			
A. ferrooxidans	RFRD-----	PKE---ENP	TLLQMLPGFSMSRSNTLVIPCTKMG-----			
C. M. oxyfera	RFVD-----	PKRFG-VDF	TLLVMINGFSISRRNTIVVPGKMV-----			
T. denitrificans	RFRN-----	PQG---VDF	YLLNMICNSFMSRRNTIVVPGKMG-----			
A. vinosum	RFKD-----	PKLQ---IDF	YLLSMI HDSFMSRRNIVVPGKMG-----			
P. lunula	SEKK-----	DLSLT-GSK	GATMKMYDDDWFGNPVTVVEMDEIDMDNA			
L. polyedrum	SEKK-----	DLTIT-GSK	GATIKMYDDWFNAVTVVEMDEIDMDNME			
B. natans	YMFEEGSTWDWPCAGPGAMA-CPY	--GTRVRYYNEMSGEKAHVLEVDGVFG--	ET			
E. gracilis	YIEKG-SSTWKPC-GDNLQ-CEY	--GLQLAYYTEEYMGCHPAEVLEMDSVIH	--NL			
P. parvum	YINDEG-ASTIWKP--PNKLT-TSA	--GVLFKSYQDEWFQGSVILEMDKID	--SL			
G. theta	YWDEG-SDIEWVPP-RNKLA-SSA	--GAGLKIYQTEKWAKDAAVIGMDKYD	--KI			
T. pseudonana	YIFDEG-SEI EWAPS-ADKLS-SPA	--GIKLSYKQEYFADAVAVVEMDQFD	--NI			
O. sinensis	YIFDEG-STIAWTPA--PSKLS-SSG	--GLTMAYGTEDYYGKPAQVVEMDQFD	--NI			
P. tricornutum	FIFDEG-SSIEWTPA--PTKLS-SPA	--GIKLAYYPPEFFGKDAQVILEMDNF	--NI			
D. lutheri	FIFDEG-STIEWTPC--GKLLT-CAY	--GIKFRYGTEMMGSEVTILEMDGRFD	--KL			
O. tauri	YIFDEG-STISWIIPC-GRKLT-CSY	--GIKFYYGPDTYYCKEVTVILEMDQFD	--KL			
M. commoda	YIFDEG-STISWIIPC-GRKLT-CSY	--GIKFYYGPDTFFGEEVILEMDQFD	--KL			
P. sitchensis	YIFDEG-STISWIIPC--GRKLT-CSY	--GIKFYYGPDIYYDNEVSVILEMDQFD	--RL			
P. patens	YIFDEG-STISWIIPC--GRKLT-CSY	--GIKFYYGPDTYYGNEVSVILEMDQFD	--KL			
S. oloracea	YIFDEG-STISWIIPC--GRKLT-CSY	--GIKFSYGPDTFYGNEVTVVEMDQFD	--RL			
A. thaliana	YIFDEG-STISWIIPC--GRKLT-CSY	--GIKFNYEPDSYFHDENVILEMDQFD	--RL			
S. moellendorf.	YIFDEG-STISWIIPC--GRKLT-CSY	--GIKFYYGPDTYYDNEVSVILEMDQFD	--KL			
T. aestivum	YIFDEG-STINWIIPC--GRKLT-CSY	--GIKFSYGPDTYFCQEVSILEMDQFD	--RL			
P. trichocarpa	YIFDEG-SSISWIIPC--GRKLT-CSY	--GIKFSYGPDXAYGHEVSVILEMDQFD	--RL			
M. crystallinum	YIFDEG-SSITWIIPC--GRKLT-CSY	--GIKFYYGPDTYFGNEVTVILEMDQFD	--RL			
P. sativum	YIFDEG-STISWIIPC--GRKLT-CSY	--GIKFYYGPETYKGNEVSVVEMDQFD	--RL			
C. variabilis	YIFDQG-STISWIIPC--GRKLT-CSF	--GIKMFYGPDTYYGEEVSVILEMDQFD	--KL			
C. reinhardtii	YIFDEG-STISWIIPC--GRKLT-CSF	--GIKMFYGPDTWYQEVSVILEMDQFD	--KL			
V. carteri	YIFDEG-STISWIIPC--GRKLT-CSF	--GIKMFYGPDTWYQEVSVILEMDQFD	--KL			
G. sulphuraria	YINDEG-STIDWIIPC--GRKLT-CSY	--GIKFHYGPDNWYNHDVSVILEDQNFE	--KL			
G. kilaueensis	YIFDRAISDVCW----KPNFP-NSD	--ELTCYGTDDYFGRPAVYLSIDEFA	--P			
G. violaceus	YIFDRAISDVWK---PNFPN-SDEE	--LTFCYGTQDYFGRPAVYLSIDEFA	--P			
T. elongatus	YIFDEG-STITWIIPC--GRKLT-CSY	--GIRLSYGPDEYYGHPVSVILEVDGRFE	--KL			
Synechocystis sp	YIFDEG-STIDWRPC--GRKLT-CTY	--GIKMYYGPDNFMGNEVSVILEVDGRFE	--NL			
M. aeruginosa	YIFDEG-STIDWRPC--GRKLT-CTY	--GIKMYYGPDNFMGNEVSVILEDQFD	--NL			
Cyanothece sp	YIFDEG-STIDWRPC--GRKLT-CAY	--GLKMYYGPDNIFGNEVSVILEIDQFD	--NL			
S. elongatus	YIFDEG-STIQWTPC--GRKLT-CSY	--GIRLAYGPDTYYGHEVSVILEVDQFE	--NL			
A. variabilis	YIFDEG-STINWTPC--GRKLT-CSY	--GMQLYYGSVYGRYVSVILEVDQFD	--NL			
N. spumigena	YIFDEG-STINWTPC--GRKLT-CSY	--GMQVYYGSVYGRYVSVILEVDQFD	--NL			
A. boonei	SIINT-----	--SQK	--MMISYRDDYYMKRVRITFDELIP			
F. placidus	TINVDL-----	--SRLIK-ASER	--DFAISFFSDYYYGKRAFIDIDFLN			
A. profundus	SENIDI-----	--SDLVK-ASER	--DFSIGFFSDYYYAEKAFFIDIDFLN			
A. veneficus	KDIDL-----	--SAFVR-ASER	--DFAIGFFSDYYYEKPAFFIDIDFLN			
M. harundinacea	DKIDL-----	--SAL	--EFSI-----			
M. concili	DKIDL-----	--FSL	--GEFSISFQRDDYYGKRVV			
M. thermophila	DKTIDL-----	--SKILR-RSEH	--EFSIEFQRDYYGKRVGIMTD			
M. hungatei	DKTIDL-----	--SRIMR-LTER	--EFSIEFQRDYYGKRVGIMTD			
Methanolinea sp	EGNIDL-----	--CDLFK-KSSH	--DFSLSCISHTPDSRNMRALVVDELM			
M. boonei	CGMDL-----	--VSLMS-SFDH	--NFMVEYRVVTEACRRMGR			
M. limicola	SISIDL-----	--TSLLA-FHES	--AFDUGIP			
M. petrolearia	CINFDL-----	--FAINS-LADR	--EFSIEFSTQRIECSFLRS			
M. palustris	NCNFDL-----	--NFRDFRTERG	--LTFDCEMN			
M. marisnigri	NCNFDL-----	--FAINS-LAER	--GEKIGALSLDEFQ			
M. liminatans	DSIDL-----	--NFLIEFSHEQRNERT	--ELN			
<i>Gblocks</i>	DSIDL-----	--FSLLS-LSDR	--DFMVEFTIEDVG			
Annotation	GESIDL-----	--FGLLS-LSER	--SEAMGA			
		--GEIFRLCER	--FLLEFGLSSLD			
		--GEIFRLCER	--GEIFRLCER			

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C243 C249

	490	500	510	520	530	540
P. profundum	-----	-----	-----	-----	-----	-----
P. luminescens	-----	-----	-----	LAME I IMT I PLVQLRLEGGKIS	-----	-----
E. amylovora	-----	-----	-----	-----	LAME I IMGPLVKRLIEGKKIG	-----
S. flexneri	-----	-----	-----	-----	LAME I IMLPLVQLMEGKKIE	-----
S. medicae	-----	-----	-----	-----	LAMQ I IFI I PLIH I KLLERKHRS	-----
R. meliloti	-----	-----	-----	-----	LAMQ I IFI I PLIH I KLLERKHRS	-----
C. necator	-----	-----	-----	-----	LAMQ I IFI I PFVLRMMERRKRAAQ	-----
R. rubrum	-----	-----	-----	-----	LSMQ I IFI I PFWIWRFMDKRARALGR	-----
R. sphaeroides	-----	-----	-----	-----	LAMQ I IFI I PLIDRVVRESKVA	-----
A. cryptum	-----	-----	-----	-----	LAMQ I IFI I PIIMOLMDRKRAQ	-----
X. flavus	-----	-----	-----	-----	LAMQ I IFI I PLIM I LMDRKRAG	-----
N. hamburgensis	-----	-----	-----	-----	LAMQ I IFI I PLILQLIDRKRA	-----
N. vulgaris	-----	-----	-----	-----	LAMQ I IFI I PLILQLIERKRA	-----
R. palustris DX1	-----	-----	-----	-----	LAMQ I IFI I PLIMQLIDRKRSVK	-----
R. palustris Bis	-----	-----	-----	-----	LAMQ I IFI I PLIMQLIERKRGAK	-----
M. capsulatus	-----	-----	-----	-----	LAME I IFRPILERMMADREKG	-----
A. ferrooxidans	-----	-----	-----	-----	YAME I ILGPRIERMLEDMHLTI	-----
C. M. oxyfera	-----	-----	-----	-----	LAME I ILAPIVHIMIENKLKA	-----
T. denitrificans	-----	-----	-----	-----	FAMP I ILAPLIQDMIANKKK	-----
A. vinosum	-----	-----	-----	-----	FAME I ILQPPIERMMMDARR	-----
P. lunula	DQLKEIEENLEGLAGS-PGELETEAMTKLRRSSPGS N GTG I IQ T VIAM K VREVYERLTAKV	-----	-----	-----	-----	-----
L. polyedrum	AQIKEIEDNLEGLPDKTPGELETEAMVLLKSSPGS N GTG I IQ T VIAM K VREVYERLTGK	-----	-----	-----	-----	-----
B. natans	EELFFIERLSNTNTKYFGELTKQMLKNAAPGSGDG S I IQ T VALVA K MRESYERFTGRT	-----	-----	-----	-----	-----
E. gracilis	KEGLYVEKFLHNTGAKEFGELTQELLKGQNPGSPGDNG T G FMQ T LAAL K IREIYERATGE	-----	-----	-----	-----	-----
P. parvum	EELIYVESQLCNTGTKYGYELTEQMVNKKASPGE S E FFQ T ICAF K IREAFAITA	-----	-----	-----	-----	-----
G. theta	DEMMYVEKQFASTGSKFVGEITKKMLEYEGQPGS G FFQ T ITAL K VREVYEGIAKV	-----	-----	-----	-----	-----
T. pseudonana	QELVYVESNLGNNTNSKFYGEVTQAMLSLADSPGS N GTG I MQ T LAFAFAIRELYNKSAAA	-----	-----	-----	-----	-----
O. sinensis	QELVYVESQLSNTSTKFYGELETQAMLKADAPGS N GTG I MQ T LAFAFAIRELYEKAAA	-----	-----	-----	-----	-----
P. tricornutum	QELVYVESALSNTKTFYGEMTQAMLLATAPGS N GTG I MQ T LAFAFAIRDIYEKTAAA	-----	-----	-----	-----	-----
D. lutheri	DELIYVESALTNTGAKFYGELETQQILKNDAVGSDNG T G FFQ T LCSF K IREAYEKATGK	-----	-----	-----	-----	-----
O. tauri	EELIYVESHLNSNTSSKFYGEITQQMLKYQNGPGS N GTG I FFQ T IVGL K VREVYERISGKE	-----	-----	-----	-----	-----
M. commoda	EELIYVESHLNSNTSTKFYGEITQQMLKADFPGS N GTG I FFQ T LCGL K VRELYERISKE	-----	-----	-----	-----	-----
P. sitchensis	EELIYVESHLSNISTKFYGEVTQQMLKHADFPGS N GTG I FFQ T IVGL K IRDVYEQLISQT	-----	-----	-----	-----	-----
P. patens	DELIYVESHLSNISTKFYGEITQQMLKHADFPGS N GTG I FFQ T ICGL K IRSVERILANQ	-----	-----	-----	-----	-----
S. oleracea	DELIYVESHLNSNLSTKFYGEVTQQMLKHQNFPGS N GTG I FFQ T IIGL K IRDLFEQLVASR	-----	-----	-----	-----	-----
A. thaliana	DELIYVESHLNSLNSTKFYGEVTQQMLKHADFPGS N GTG I FFQ T IVGL K IRDVFERITSQ	-----	-----	-----	-----	-----
S. moellendorf.	DELIYVESHLSNISTRFYGEITQQMLKHADFPGS N GTG I FFQ T IVGL K IRDVFERITSQ	-----	-----	-----	-----	-----
T. aestivum	DELIYVESHLNLSTKFYGEVTQQMLKHADFPGS N GTG I FFQ T IVGL K IRDLYEQQIAER	-----	-----	-----	-----	-----
P. trichocarpa	DELIYVESHLSNISTKFYGEVTQQMLKHADFPGS N GTG I FFQ T IVGL K IRDLYEQLIASR	-----	-----	-----	-----	-----
M. crystallinum	DELIYVESHLNLSTKFYGEVTQQMLKHQDFPGS N GTG I FFQ T IVGL K IRDLYEQLIASR	-----	-----	-----	-----	-----
P. sativum	DELIYVESHLNLSSKFYGEVTQQMLKHADFPGS N GTG I FFQ T IVGL K IRDLYEQLIASR	-----	-----	-----	-----	-----
C. variabilis	EELIYMESHLNSNTSAKFYGEITQQMLKNSSFPGS N GTG I FFQ T IVGL K CREVYERITQK	-----	-----	-----	-----	-----
C. reinhardtii	EELIYVESHLNSNTSAKFYGEITQQMLKNSGFPGS N GTG I FFQ T IVGL K VREVYERIVKKD	-----	-----	-----	-----	-----
V. carteri	EELIYVESHLNSNTSAKFYGEITQQMLKNSGFPGS N GTG I FFQ T IVGL K VREVYERIVKKD	-----	-----	-----	-----	-----
G. sulphuraria	EELIYIESHLNNNTSTKFYGEITQQLLRNSSAPGS N GTG I FFQ T IVGL K MRQIYEELTGKS	-----	-----	-----	-----	-----
G. kilaeensis	DDSPLEQKLRNTSETRFGE LASLILKH TDY PGSRD G FFQ T IVGL K FRSIYEALIAQS	-----	-----	-----	-----	-----
G. violaceus	EDSPEEKLRLNTSETTRYGE LASLILKH TDY PGSRD G FFQ T IVGL K FRSIYEALTAQL	-----	-----	-----	-----	-----
T. elongatus	DELIYVESHLNLSTKFYGEVTQMLKHADFPGS N GTG I FFQ T IVGL K MRATYERLTSRD	-----	-----	-----	-----	-----
Synechocystis sp	EEMVYVENHLSKTKGTKYGYEMTELLLHKHDYPGS N GTG I FFQ T IVGL K MRKVEQLTAE	-----	-----	-----	-----	-----
M. aeruginosa	EEMIYIESHLSKTKGTKYGYEMTELLLHKHDYPGS N GTG I FFQ T IVGL K MRKVEQLTAE	-----	-----	-----	-----	-----
Cyanothece sp	EEMIYIEQHLSRTGTKYGYEMTHLLQQHQHDYPGS N GTG I FFQ T IVGL K MRKVEQLTAE	-----	-----	-----	-----	-----
S. elongatus	EEMIYVEGHL SKTD TQY GE LTH LLL QHQHDYPGS N GTG I FFQ T IVGL K MRAAYERLTSQ	-----	-----	-----	-----	-----
A. variabilis	EEVIYIETHLSNTSTKFYGEQELTQLLQHREYPGS N GTG I FFQ T IVGL K MRAAYERLTAKE	-----	-----	-----	-----	-----
N. spumigena	DEVIYVETHLSKTKTYGEQEMTHLLQHREYPGS N GTG I FFQ T IVGL K MRAAYERLTTK	-----	-----	-----	-----	-----
A. boonei	-----HEADSLSERRIMEYTG FEN YILERSK VNG T QIAO LLVA WYF VEM MN NI FRI E-----	-----	-----	-----	-----	-----
F. placidus	-----VEIFESLL D ALR D ETG KV RW -----E ARE YV N SIE VAK L L C W NL V E I K M K G -----	-----	-----	-----	-----	-----
A. profundus	-----VDIFKSLFDLSRKEIGDG -----EIKVESEYVNAIEFSKLLVCW K LVEVLKHSR-----	-----	-----	-----	-----	-----
A. veneficus	-----VELFSTL LD IL RKE VG AD VE WK MT -----YVNAIEVAK L L CV WR FLE L K F RL EA E-----	-----	-----	-----	-----	-----
M. harundinacea	SMVEGVEAKL KSLAG -----STAPIC DRAGG DR VT S T GAQ L L SW RL LE K L Q L HLD KA-----	-----	-----	-----	-----	-----
M. concili	-----QSMISD L E K L G E S L G T D GM IS DR RE EY VN AIE T Q A O L I L T W N C V E K L D Y L L Q B E-----	-----	-----	-----	-----	-----
M. thermophila	TM IK D L E R K L C D F L G R D V P S V T E G -----C Q E D H G S Y V N A E M T Q L I L I W R F L E K I A N L A W -----	-----	-----	-----	-----	-----
M. hungatei	-----PDTIHK IER QIE F QT G I SPIN I F RG QEH IT G T IVRL I L S W Q I I N G R I A L S N H L -----	-----	-----	-----	-----	-----
Methanolinea sp	-----REMAGDL R R K IEE QT GT QP AD M F R G N A M V T A DM V R L I V S W R I I N H L A N L A -----	-----	-----	-----	-----	-----
M. boonei	-----YD T V R N L E S I E H Q T G I H P I E M F A G R K V V T P T N I V Q L L S W R I I N R R I F L Q D H R -----	-----	-----	-----	-----	-----
M. limicola	D V I R C L E N I E E Q T G -----V S P V S L F E G R D Y V T A T E M I Q L L S W R I I N R R I Q M E S -----	-----	-----	-----	-----	-----
M. petrolearia	-----HEV V S L L E K G I E M Q T G I G P V S V S D R S Y V T A T E M V E L I L S W R I I N R R M D M K Y G S -----	-----	-----	-----	-----	-----
M. palustris	-----T R M V K R L E T S I E E Q T Q V R P I S D F H D H D Y M T A T E V V Q L I L A W R I I H Q R V F L E R C L -----	-----	-----	-----	-----	-----
M. marisnigri	-----D A V A R K L E R N I E I Q T Q V E P I D L S Q D S D Y L T A G D M A Q L I L A W R I I N R R I F I E S A P -----	-----	-----	-----	-----	-----
M. liminatans	-----A S A I R R L A R T I G R E T R S E A V N L F A D R Q V T A G E I A E L I L A W R I L N R W H V L E A R -----	-----	-----	-----	-----	-----
<i>Gblocks</i>						
Annotation						

	550	560
P. profundum	-----	
P. luminescens	-----	
E. amylovora	-----	
S. flexneri	-----	
S. medicae	-----	
R. meliloti	-----	
C. necator	-----	
R. rubrum	-----	
R. sphaeroides	-----	
A. cryptum	-----	
X. flavus	-----	
N. hamburgensis	-----	
N. vulgaris	-----	
R. palustris DX1	-----	
R. palustris Bis	-----	
M. capsulatus	-----	
A. ferrooxidans	-----	
C. M. oxyfera	-----	
T. denitrificans	-----	
A. vinosum	-----	
P. lunula	GA-----	
L. polyedrum	-----	
B. natans	IQIPKWGLFLDDY-----	
E. gracilis	KA-----	
P. parvum	-----	
G. theta	VPAQAN-----	
T. pseudonana	KIAATKETAASA-----	
O. sinensis	KLAVIEA-----	
P. tricornutum	KAKAGVSAAAA-----	
D. lutheri	VDASAAA-----	
O. tauri	VVAKA-----	
M. commoda	VVTAA-----	
P. sitchensis	TGASLEAAKA-----	
P. patens	KNATLQSAKA-----	
S. oloracea	STATATAAKA-----	
A. thaliana	ATARAEAKA-----	
S. moellendorf.	GSPVGAAATSKV-----	
T. aestivum	AGVPAEAAKV-----	
P. trichocarpa	AKTPVEATKA-----	
M. crystallinum	TAAPAAATKA-----	
P. sativum	RAETPVGAAKA-----	
C. variabilis	-----	
C. reinhardtii	VVPV-----	
V. carteri	VVPA-----	
G. sulphuraria	IAPVLV-----	
G. kilaueensis	LAAAKV-----	
G. violaceus	LTASKAK-----	
T. elongatus	AATVTNR-----	
Synechocystis sp	KVPASV-----	
M. aeruginosa	AKVAASV-----	
Cyanothece sp	ESKVATQV-----	
S. elongatus	AAPVAASV-----	
A. variabilis	AKLAVQV-----	
N. spumigena	EAKLAVQV-----	
A. boonei	ENAREKNIY-----	
F. placidus	-----	
A. profundus	-----	
A. veneficus	L-----	
M. harundinacea	-----	
M. concilii	GY-----	
M. thermophila	-----	
M. hungatei	DQ-----	
Methanolinea sp	-----	
M. boonei	-----	
M. limicola	-----	
M. petrolearia	GVSS-----	
M. palustris	HQDHNK-----	
M. marisnigri	GAGGTGRTVTGNNGHGCGRR	
M. liminatans	SAHAKG-----	
<i>Gblocks</i>		
Annotation		

B

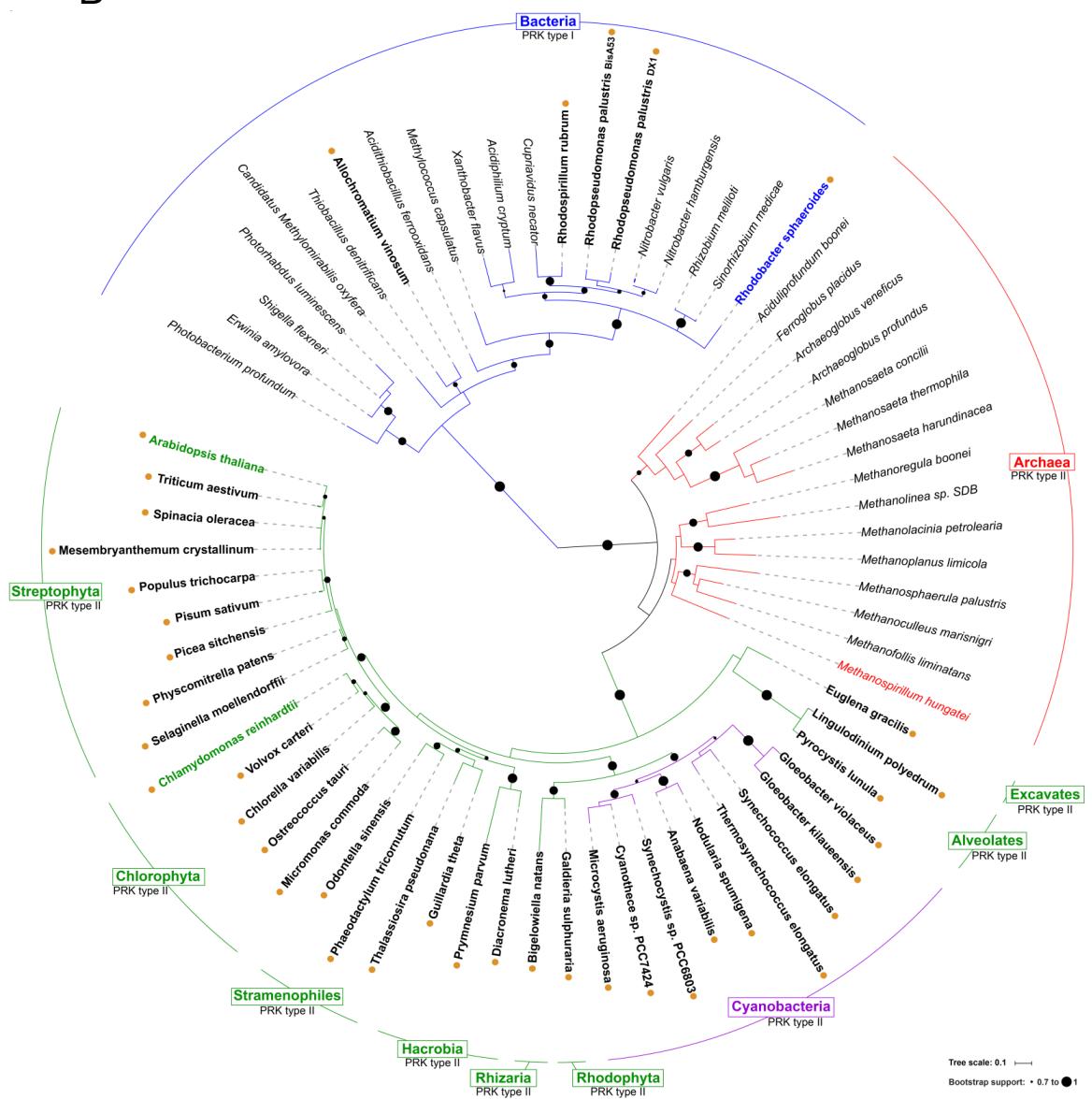


Fig. S6. Sequence alignment and phylogenetic analysis of 69 PRKs. (A) The sequences annotated as PRKs were retrieved from Uniprot and aligned using the phylogeny webserver suite (www.phylogeny.fr) (27). Blue areas in the “Gblocks” line define the conserved areas, later used by the software to determine the phylogeny. The alignment was performed by MUSCLE and curation by Gblocks. Annotations used are as follow: black boxes within the sequences indicate conservation of the residue in more than 70% of the sequences. Walker A (P-loop) and Walker B motives are represented by a red or green area, respectively, and the clamp loop is highlighted by a yellow area. Bars (!) or Hashtags (#) denote residues implicated in Ru5P or ATP binding, respectively. Plus sign (+) indicates two Aspartate residues shown to be crucial for catalysis by mutagenesis in *R. sphaeroides* (28). Star signs (*) indicate Cys residues implicated in disulfide bridges (Cys16 with Cys55; Cys243 with Cys249) (29), numbers below are for *C. reinhardtii* PRK. Blue and red bars on the right side indicate clusters of bacterial and archeal PRK, respectively, while the green one indicates the cluster of eukaryotic and the purple one is for the cyanobacterial PRKs. Species names in bold are indicating the 4 species with known structure. Uniprot accessions numbers and other details, for all protein sequences are reported in Table S6. (B) The phylogeny was built with PhyML and the tree with TreeDyn. The visual was obtained with iTOL (<http://itol.embl.de/>) (30). Bootstrap values superior to 0.7 are represented by black circles with a radius proportional to the value. Branch lengths are represented by straight lines at indicated scale, while dashes are presented for the sake of clarity. The clades are colored in function of their kingdom (Bacteria in blue, Archaea in red and Eukaryotes in green) except Cyanobacteria clade which is in purple. Photosynthetic species are in bold indicated by a yellow circle while the others are italicized. Species for which the PRK has a known structure, *i.e.* *R. sphaeroides* (31), *M. hungatei* (5), *C. reinhardtii* and *A. thaliana*, are represented in the color of their kingdom.

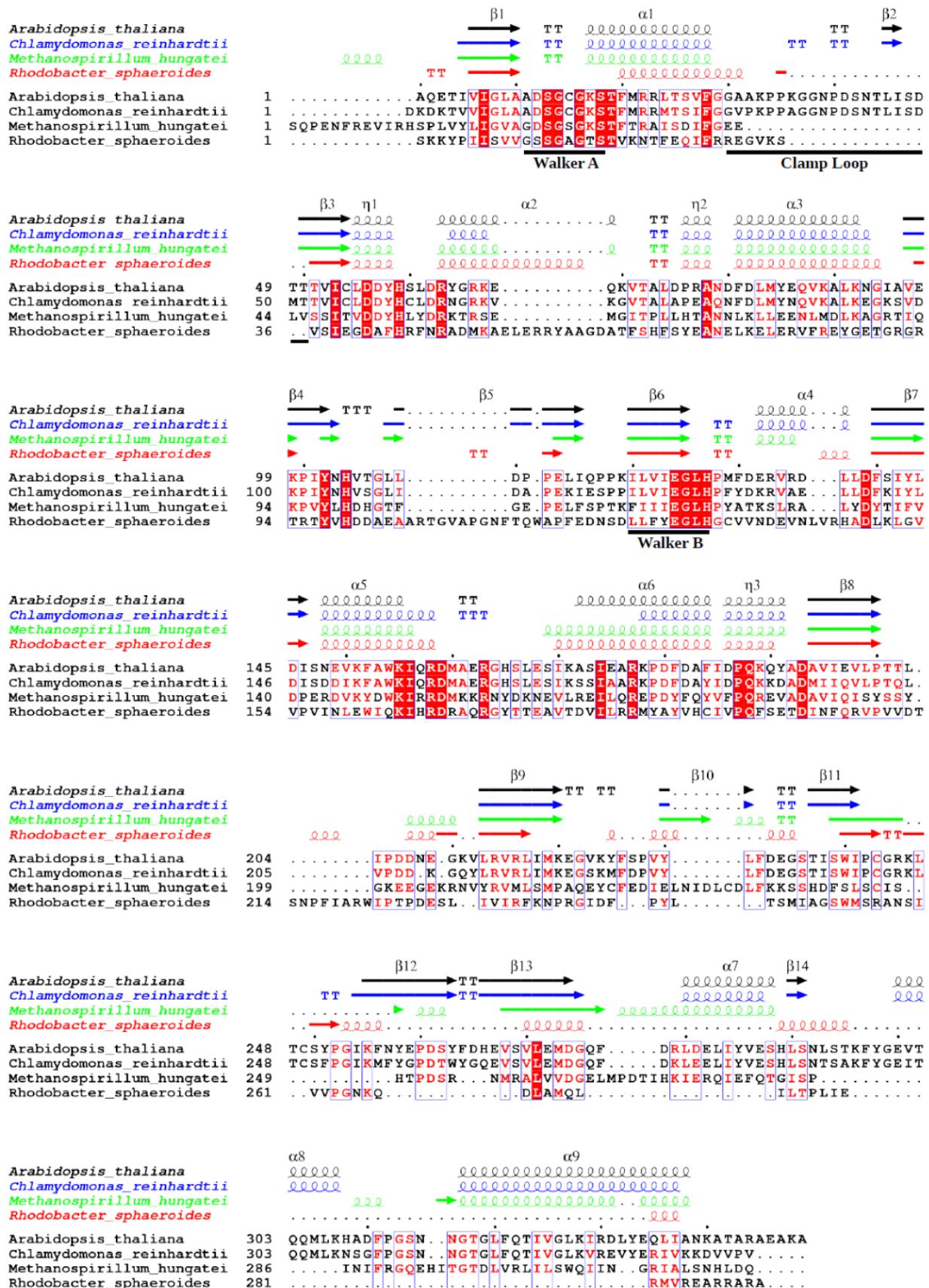


Fig. S7. Sequence and structural alignment of the four structurally known PRKs. The alignment was performed with Esprit (<http://escript.ibcp.fr>) (32) using the sequence and the structure of *AtPRK* (Uniprot accession code P25697 and PDB ID code 6H7H); *CrPRK* (Uniprot accession code P19824 and PDB ID code 6H7G); *RsPRK* (Uniprot accession code P12033 and PDB ID code 1A7J) (31), *MhPRK* (Uniprot accession code Q2FUB5 and PDB ID code 5B3F) (5). The sequence of both photosynthetic PRKs is much longer (349 and 344 residues for *AtPRK* and *CrPRK*, respectively) than bacterial (290 residues) and Archae (323 residues) PRKs. Sequence identities among considered PRKs are: 75% for *AtPRK* vs *CrPRK*; 35% for *AtPRK* vs *MhPRK*; 32% for *CrPRK* vs *MhPRK*; 22% for *AtPRK* vs *RsPRK*; 24% for *CrPRK* vs *RsPRK*. The sequence identities were calculated by Clustal Omega (33).

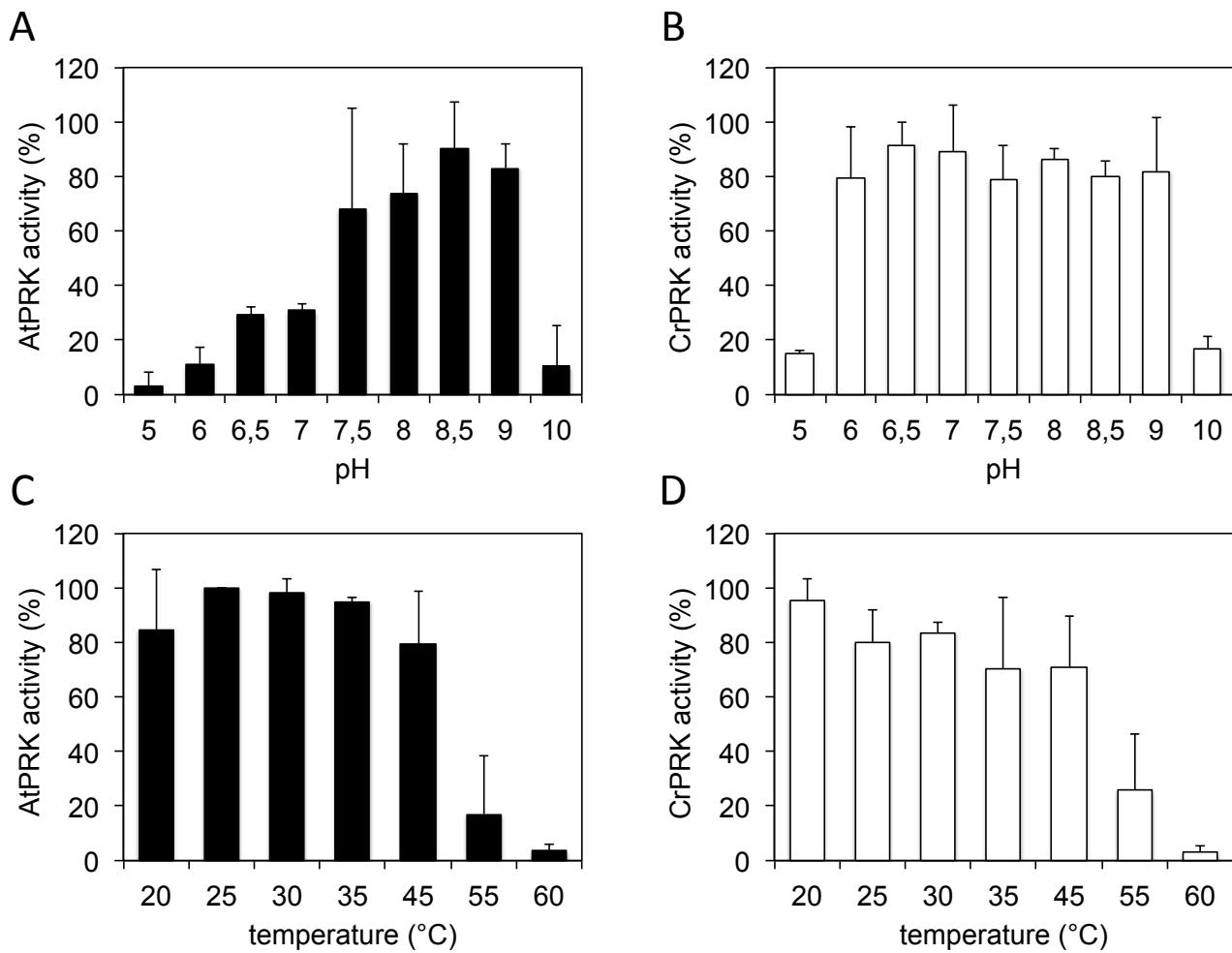


Fig. S8. pH and temperature dependence of photosynthetic PRKs. The enzyme activity of *AtPRK* (A and C) and of *CrPRK* (B and D) was evaluated at different pHs (upper panels) and temperatures (lower panels). Values are reported as means \pm SD ($n=3$).

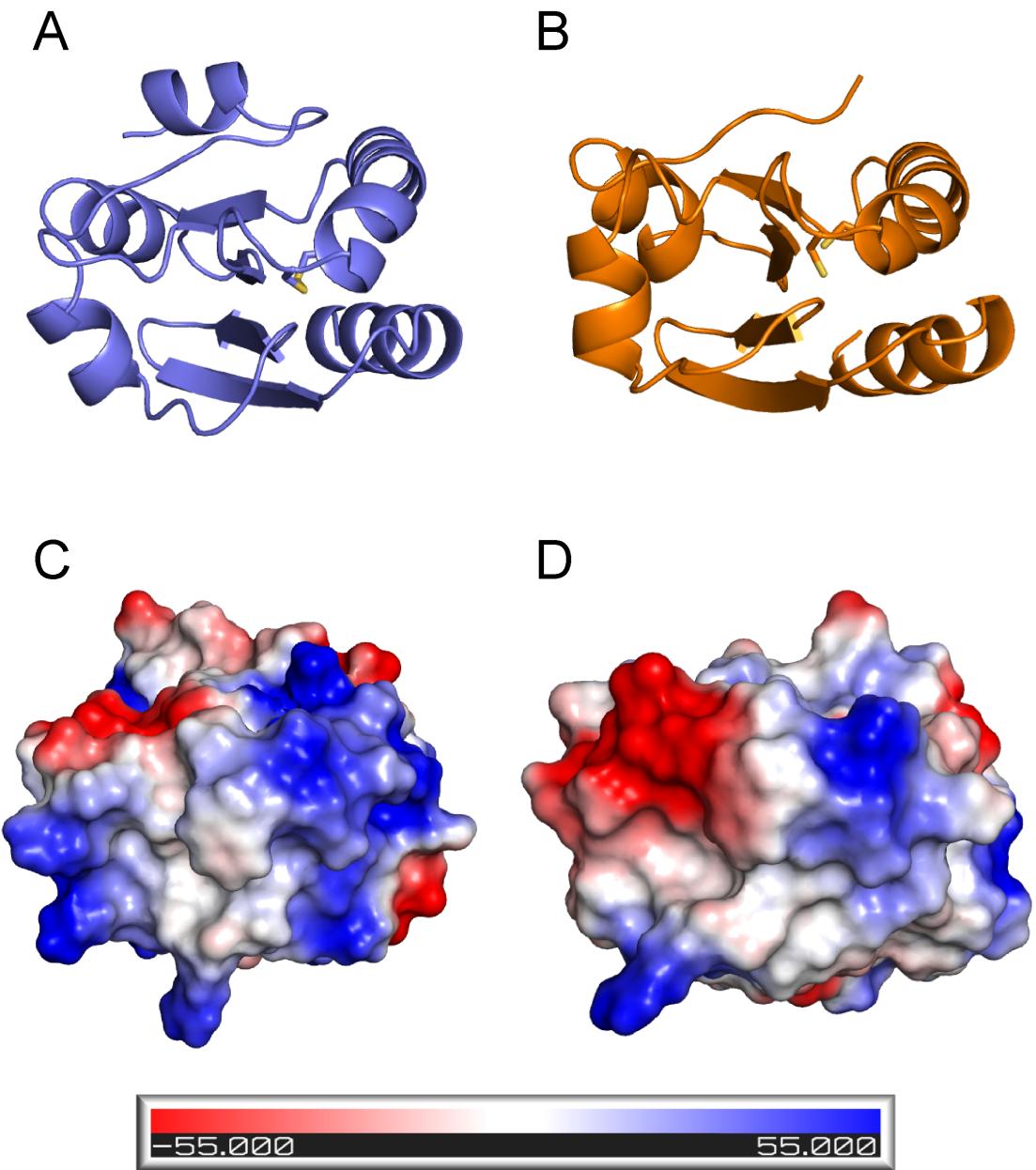
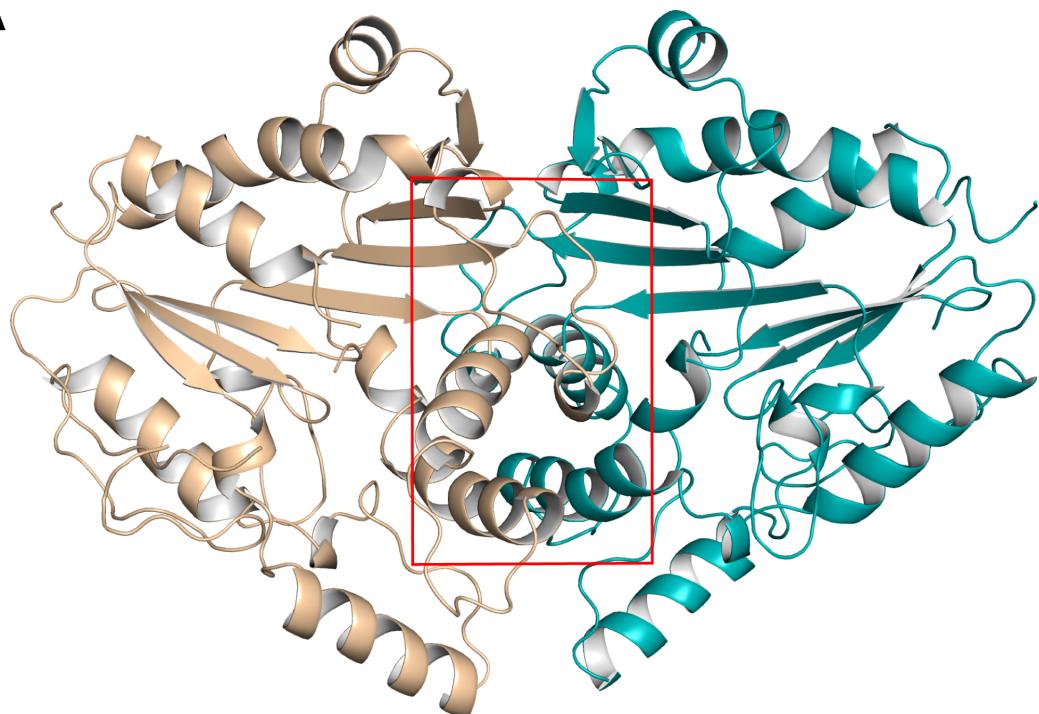


Fig. S9. Electrostatic surface potential of *A. thaliana* TRX-f1 and TRX-m2. Structure represented as ribbon (A, B) and electrostatic surface potential (C, D) of the homology model of *Arabidopsis thaliana* TRX-f1 (A, C) and TRX-m2 (B, D). The crystal structures of *Spinacia oleracea* TRX-f and TRX-m (PDB ID codes 1FAA and 1FB6) (34) were used as template to model *Arabidopsis thaliana* TRX-f1 and TRX-m2, respectively. The sequence identity of *Arabidopsis thaliana* TRXs with spinach enzymes is 59% and 75% for TRX-f1 and TRX-m2, respectively. The homology modelling was performed with Swiss-Model (35).

A



B

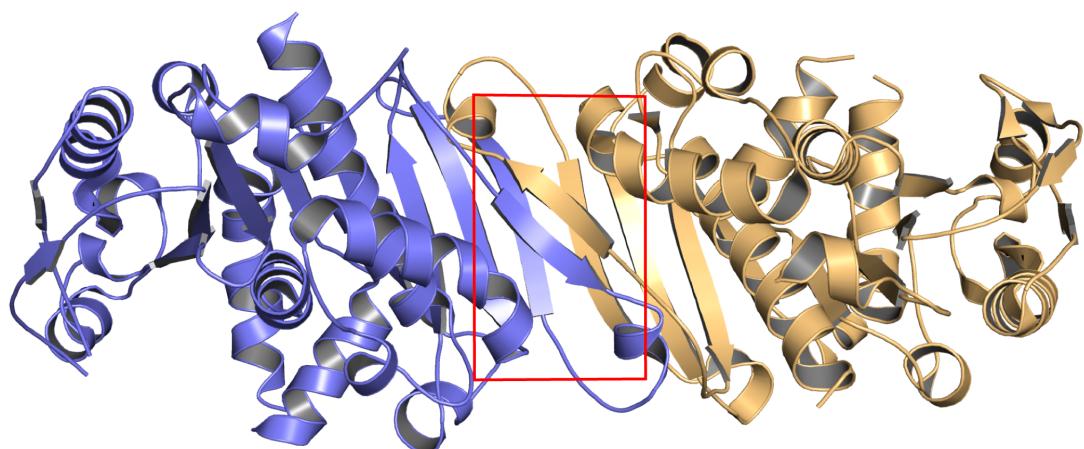


Fig. S10. Dimer interface of bacterial and Archaea PRKs. Dimer interface of (A), octameric *Rhodobacter sphaeroides* PRK (PDB ID code 1A7J) (31) and (B), dimeric *Methanospirillum hungatei* PRK (PDB ID code 5B3F) (5) is highlighted by a red box. The dimer interface of bacterial PRK is formed by three β -strands and one α -helix while in Archaea enzyme by two β -strands. The calculated dimer interface areas are 1667 and 1695 \AA^2 , respectively.

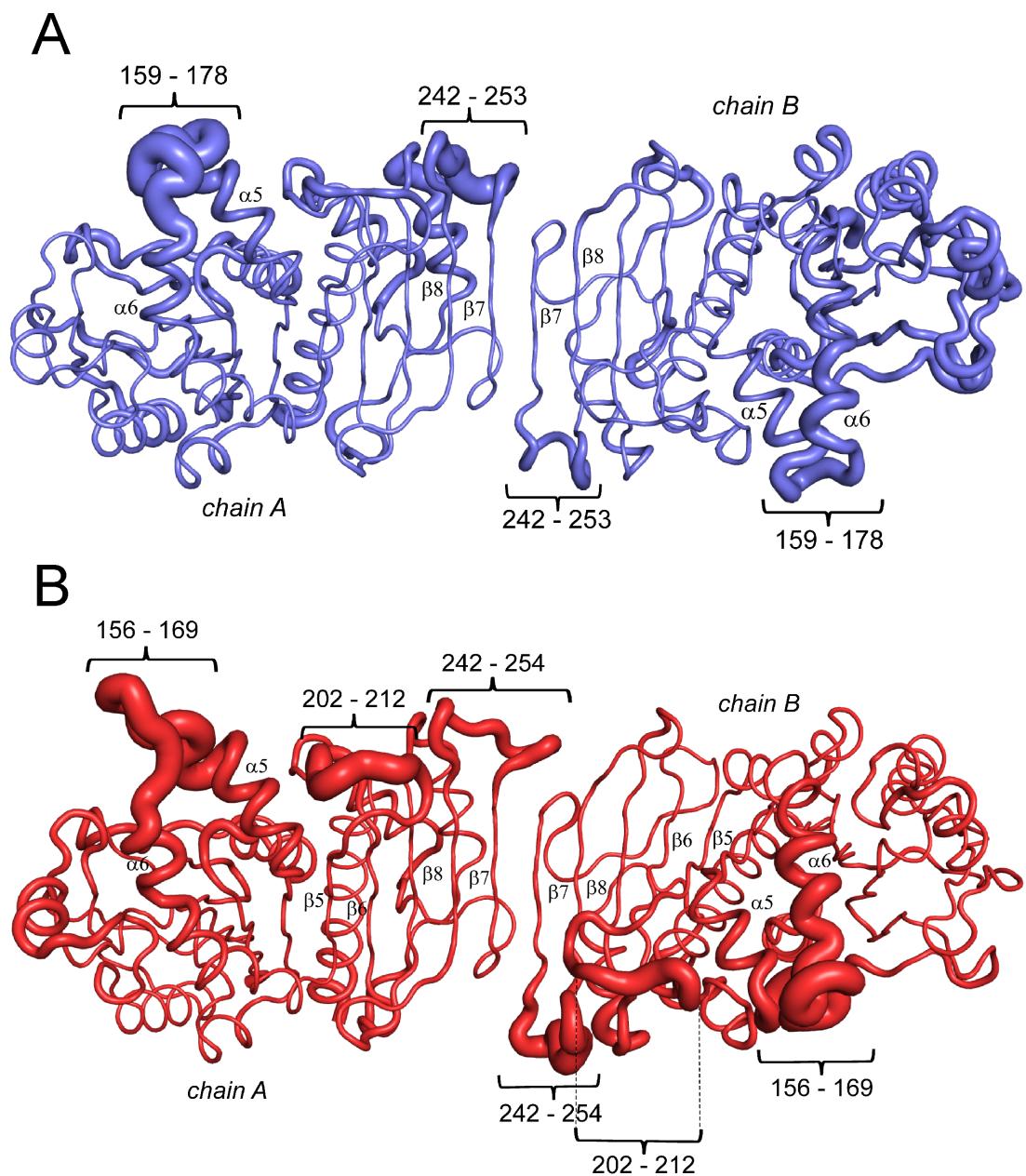


Fig. S11. Flexible and disordered regions in redox-sensitive PRKs. C_a trace of (A), CrPRK and (B), AtPRK. The trace thickness is proportional to the atomic B factor. AtPRK shows a higher number of flexible regions compared to CrPRK. The residues belonging to the flexible regions are reported.

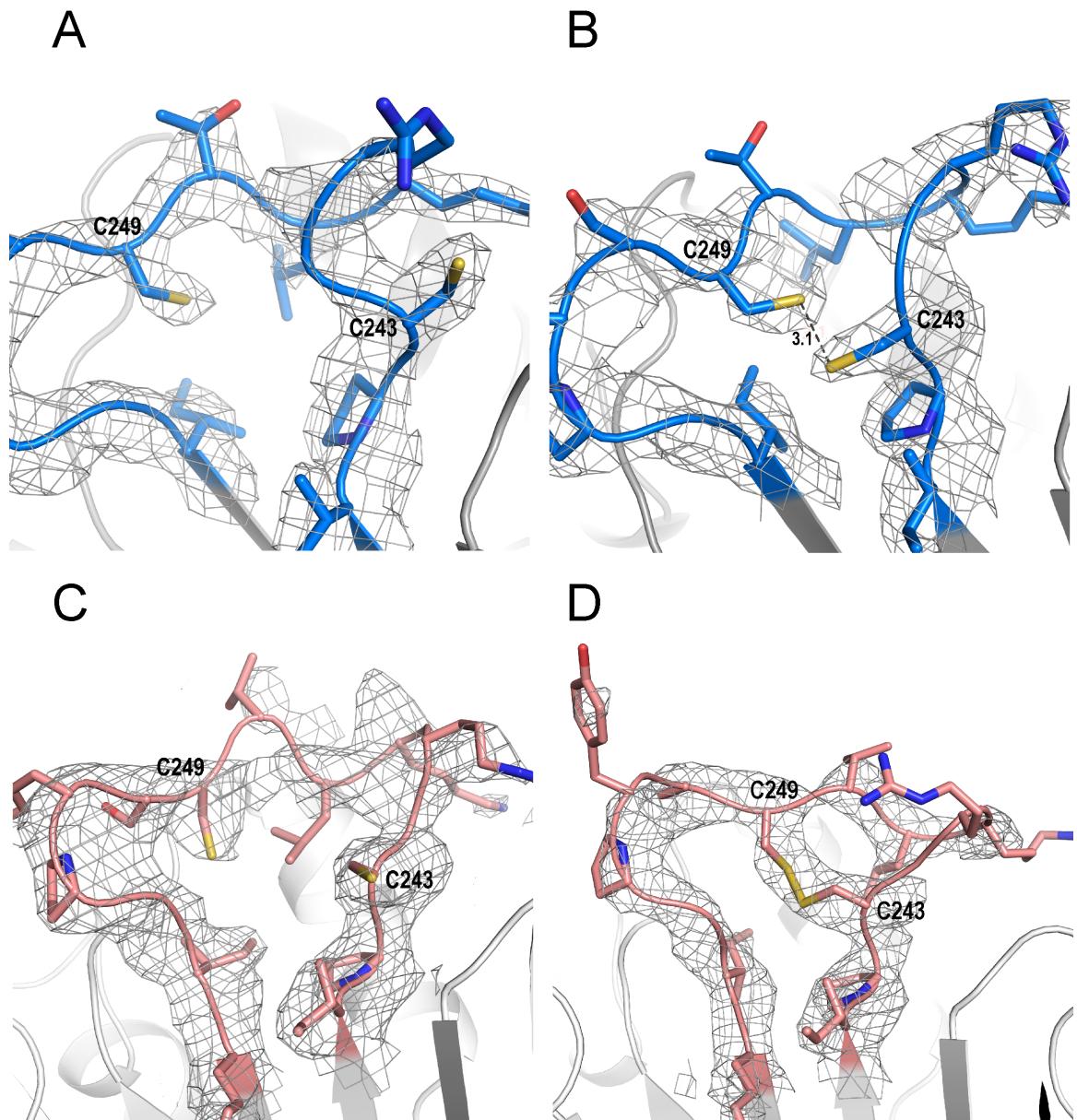


Fig. S12. Electron density of the C-terminal cysteine pair. $2F_o - F_c$ electron density map contoured at 1.2σ and associated with Cys243 and Cys249 in (A), CrPRK subunit A (B), CrPRK subunit B (C), AtPRK subunit A and (D), AtPRK subunit B. In CrPRK, both C-terminal cysteines are reduced even if in subunit B the thiol groups are only 3 Å apart. A disulfide bond is instead observed in subunits B of AtPRK, while the thiol groups of the other cysteine pair (subunit A) lie very distantly.

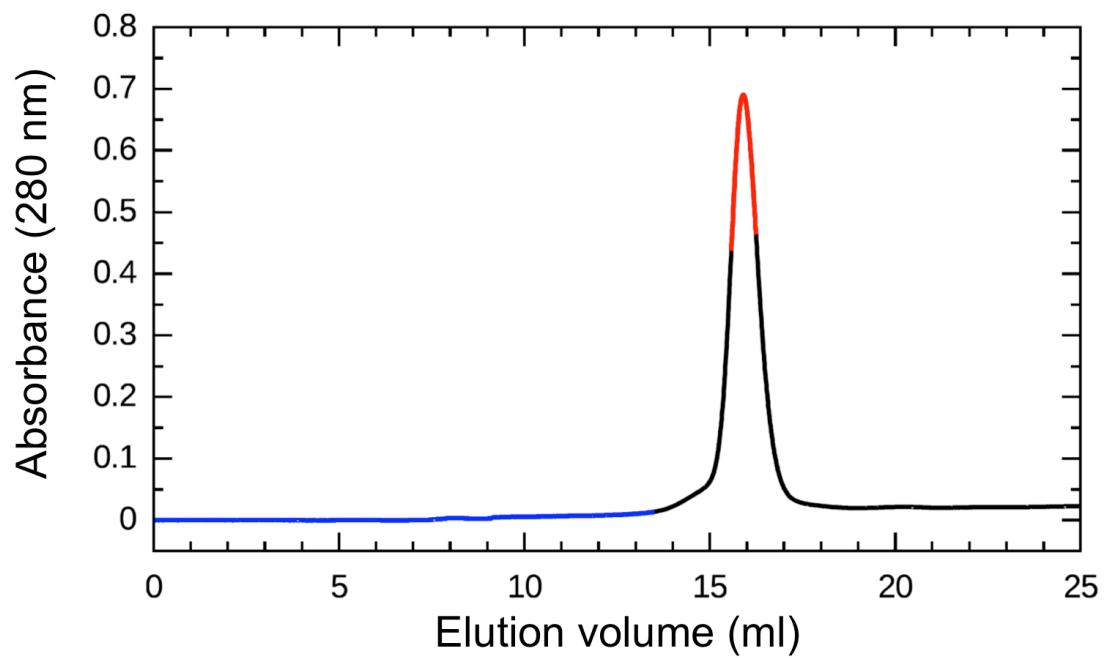


Fig. S13. UV trace of the chromatogram profile of CrPRK analyzed in SEC-SAXS mode.

Frames collected as buffer (from 0 to 14 ml) are highlighted in blue; frames collected as protein (from 14 to 17.5 ml) are highlighted in black; frames highlighted in red have been used for SAXS analysis.

Table S1. SEC-SAXS data analysis of reduced CrPRK.

Concentration (mg ml ⁻¹)	6.1 (injected)
Structural parameters	
q interval for Guinier linear fit (nm ⁻¹)	0.12-0.38
I(0) [from Guinier approximation]	42.0 ± 0.1
R _g (nm) [from Guinier approximation]	3.43 ± 0.01
q interval for Fourier inversion (nm ⁻¹)	0.12-3.5
I(0) [from P(R)]	42.4 ± 0.06
R _g (nm) [from P(R)]	3.55 ± 0.01
D _{max} (nm)	11.2±0.5
Porod volume estimate (nm ³)	115 ± 10
DAMMIN excluded volume (nm ³)	138 ± 1
Dry volume calculated from sequence (nm ³) (v=0.735 cm ³ g ⁻¹)	95
Molecular mass (kDa)	
From I(0)	70
From Vc	70
From Porod invariant	85
From Porod volume (x0.625)	72
From excluded volume (x0.5)	69
From sequence	77.8

Table S2. Accessibility values (ASA) for cysteine residues and a strictly conserved arginine.

Residue (Cr/At)	ASA (Å ²)*			
	CrPRK		AtPRK	
	A	B	A	B
Cys16/15	14.5	8.5	7.6	10.6
Cys55/54	10.6	10.6	6.3	9.5
Cys61	55.9	58.7	/	/
Cys243	26.6	37.8	53.4	14.8
Cys249	42.4	31.1	14.8	50.6
Arg64/63	51.4	88.7	82.6	88.2

*Radius of the probe solvent molecule 1.4 Å

Table S3. Secondary structure element content in the structurally known PRKs.

PRK	Quaternary structure	Helix content (%)	Sheet content (%)	Other (%)
<i>C. reinhardtii</i>	Dimer	31.2	21.9	46.9
<i>A. thaliana</i>	Dimer	32.3	21.9	45.8
<i>M. hungatei</i>	Dimer	50.0	22.2	27.8
<i>R. sphaeroides</i>	Octamer	41.2	16.9	41.9

Table S4. X-ray (CrPRK and AtPRK) and SEC-SAXS (CrPRK) data collection parameters.

	<i>CrPRK</i>	<i>AtPRK</i>	<i>CrPRK</i> SEC-mode
Detector	Pilatus 2M	ADSC Quantum Q315r	Pilatus 1M
Beam geometry (mm ²)	0.1 × 0.1	0.1 × 0.1	0.7 × 0.7
Wavelength (Å)	1.240	0.940	0.990
Capillary diameter (mm)	/	/	1.8
Sample-to-detector Distance (mm)	239.85	393.43	2872
Δϕ (°)	0.5	0.7	/
q* range (nm ⁻¹)	/	/	0.033-4.9
Exposure time (s)	5	5	1
Flow (ml/min)	/	/	0.5
Temperature (K)	100.0	100.0	277.15

* $q = 4\pi \sin(\theta)/\lambda$, where 2θ is the scattering angle and λ is the X-ray wavelength.

Table S5. X-ray data collection and refinement statistics.

	CrPRK	AtPRK
<i>Data collection</i>		
Unit cell (Å)	77.68, 83.55, 133.15, 90.00, 90.00, 90.00	116.30, 116.30, 106.81, 90.00, 90.00, 90.00
Space group	P2 ₁ 2 ₁ 2 ₁	I4 ₁
Resolution range* (Å)	44.38 – 2.60 (2.72 – 2.60)	82.23 – 2.47 (2.58 – 2.47)
Unique reflections	27230 (3280)	24824 (3107)
Completeness* (%)	99.6 (100.0)	97.6 (99.6)
R _{merge} *	0.076 (0.770)	0.091 (0.435)
CC _{1/2}	0.997 (0.743)	0.997 (0.947)
I/σ(I) *	13.6 (1.7)	11.2 (2.3)
Multiplicity*	5.1 (5.3)	6.9 (6.5)
<i>Refinement</i>		
Resolution range* (Å)	39.86 – 2.60 (2.69 - 2.60)	46.77 – 2.47 (2.57 – 2.47)
Reflection used	27162 (2666)	24672 (2786)
R/R _{free} *	0.227/0.262	0.226/0.281
rmsd from ideality (Å, °)	0.004, 0.915	0.011, 1.128
<i>N° atoms</i>		
Non-hydrogen atoms	5360	5385
Protein atoms	5319	5355
Solvent molecules	31	30
Hetero atoms	10	/
<i>B value</i> (Å ²)		
Mean	62.4	78.4
Wilson	59.0	52.5
Protein atoms	62.3	78.4
Solvent molecules	56.2	70.3
Hetero atoms	85.5	/
<i>Ramachandran plot (%)[§]</i>		
Most favoured	91.1	91.4
Allowed	7.4	6.0
Disallowed	1.5	2.7

*Values in parentheses refer to the last resolution shell

[§]As defined by MolProbity (35)

Table S6. Proteins used for phylogeny.

Organism - full description	Uniprot used	other Ref.	Kingdom	Phylum	Photosynthetic	Reference and/or status of the uniprot entry
<i>A. profundus</i>	D3REPF9		Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5)
<i>M. concilii</i>	FABW53	AE65433 AE65434	Archae	Euryarchaeota	no	Kono et al., 2017 (5)
<i>Methanospirillum hungatei</i>	Q2V045	P0B-S85F	Archae	Euryarchaeota	no	Kono et al., 2017 (5)
<i>M. marburgii</i>	ABCNW0	ABK15221	Archae	Euryarchaeota	no	Kono et al., 2017 (5)
<i>Methanococcus thermophila</i>	ABG847		Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5) / protein predicted
<i>A. veneficus</i>	B5ICQ8		Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5) / protein predicted
<i>F. plancius</i>	F2KMR8		Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5) / protein predicted
<i>A. boonei</i>	D3RZ92	A7A4V6	Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5) / protein predicted
<i>Ferrovibrio placidus</i> (strain DSM 1195 / Snip 56)	G7WJ21	H3YH11	Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5) / protein predicted
<i>Methanoregula a boonei</i> (strain DSM 1154 / ICM 14090 / 648)	J0SA78	J0SA78	Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5) / protein predicted
<i>Methanococcus hungaricus</i> (strain 64c)	BEGG52		Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5) / protein predicted
<i>Methanococcus limicola</i> DSM 4140	EUR155	AGAQQVL5	Euryarchaeota	Euryarchaeota	no	Kono et al., 2017 (5) / protein predicted
<i>Methanospirillum limicola</i> DSM 1021 (Strain WSM19) Enriched medicea)	B71555		Bacteria	Acidithiobacillia	no	Kono et al., 2017 (5) / protein inferred from homology
<i>Methanospirillum palustris</i> (strain DSM 11571 / OCM 486 / SER 487) (<i>Methanoplatus petrolearius</i>)			Bacteria	α-Proteobacteria	yes (purple non-sulfur)	Hallbeck and Kaplan, 1987 (36)
<i>M. palustris</i>			Bacteria	α-Proteobacteria	no	Inferred by homology
<i>M. petroleica</i>			Bacteria	α-Proteobacteria	no	Inferred by homology
<i>Methanolinea</i> sp. SDB			Bacteria	α-Proteobacteria	yes (purple non-sulfur)	Inferred by homology
<i>A. ferrooxidans</i>			Bacteria	α-Proteobacteria	yes (purple non-sulfur)	Inferred by homology
(<i>Ferrobacillus ferrooxidans</i> (strain ATCC 23270) / DSM 14882 / CIP 104768 / NCIMB 8455)			Bacteria	α-Proteobacteria	no	Kono et al., 2017 (5) / protein inferred from homology
<i>R. ephemeroides</i>	A4A26113	P12033	PDB:1A71	Bacteria	α-Proteobacteria	Kono et al., 2017 (5) / protein inferred from homology
<i>N. vulgaris</i>	P27100		Bacteria	α-Proteobacteria	no	Meijer et al., 1991 (37)
<i>R. metalli</i>	P58347		Bacteria	α-Proteobacteria	no	Experimental evidence at transcript level
<i>S. mediterranea</i>	P56887		Bacteria	α-Proteobacteria	yes (purple non-sulfur)	Kobayashi et al., 2003 (38)
<i>R. palustris</i> DV	ADU61566		Bacteria	α-Proteobacteria	yes (purple non-sulfur)	Kono et al., 2017 (5)
<i>R. rubrum</i>	ABC23204		Bacteria	α-Proteobacteria	yes (purple non-sulfur)	Kono et al., 2017 (5) / protein predicted
<i>A. cryptum</i>	AF5FW9		Bacteria	α-Proteobacteria	no	Kono et al., 2017 (5) / protein inferred from homology
<i>N. hamburgensis</i>	Q3QGD6		Bacteria	α-Proteobacteria	no	Kono et al., 2017 (5) / protein inferred from homology
<i>R. palustris</i> Bi	Q37064		Bacteria	α-Proteobacteria	no	Kono et al., 2017 (5) / protein inferred from homology
X. flava	P23015		Bacteria	Cyanobacteria	yes	Meijer et al., 1991 (37)
<i>Synechocystis</i> sp.	P37101		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>S. elongatus</i>	Q31FL2		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>A. variabilis</i>	Q3MF31		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>G. violaceus</i>	Q7N187		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>T. elongatus</i>	Q8DHN2		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>Cyanobacter</i> sp.	B7XK62		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>G. kloetens</i>	USQDM9		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>M. aeruginosa</i>	I4IN9		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>N. spumigena</i>	AQZEL11		Bacteria	Cyanobacteria	yes	Inferred by homology
<i>E. amylovora</i>	E5BA03		Bacteria	γ-Proteobacteria	no	Inferred by homology
<i>S. flexneri</i>	P0A262		Bacteria	γ-Proteobacteria	no	Inferred by homology
<i>M. capsulatus</i>	Q6ZL2X		Bacteria	γ-Proteobacteria	yes (purple sulfur)	Inferred by homology
<i>A. vinosum</i>	D3R02		Bacteria	γ-Proteobacteria	yes (purple sulfur)	Kono et al., 2017 (5) / protein predicted
<i>P. luminescens</i>	AGAIBYKCS		Bacteria	γ-Proteobacteria	no	Kono et al., 2017 (5) / protein inferred from homology
<i>P. profundum</i>	QBL1E1		Bacteria	γ-Proteobacteria	no	Kono et al., 2017 (5) / protein inferred from homology
<i>C. M. xonera</i>	DSM144		Bacteria	γ-Proteobacteria	no	Kono et al., 2017 (5) / protein predicted
T. identificans	Q3SG56		Bacteria	γ-Proteobacteria	no	Kono et al., 2017 (5) / protein predicted
<i>C. nector</i>	P15923		Bacteria	β-Proteobacteria	no	Kossmann et al., 1993 (39)
<i>E. gracilis</i>	Q24110		Eukaryota	Ciliophora	yes	Experimental evidence at transcript level
<i>G. theta</i>	Q24114		Haccolia#	Ciliophora	yes	Experimental evidence at transcript level
<i>D. lutheri</i>	Q241LS		Haccolia#	Haplophyceae	yes	Experimental evidence at transcript level
<i>P. parvum</i>	E1ZF27		Virdiplantae	Chlorophyce	yes	Predicted protein
<i>C. variabilis</i>	C1FFW3		Virdiplantae	Chlorophyce	yes	Inferred by homology
<i>M. commoda</i>	AOA090N369		Virdiplantae	Chlorophyce	yes	Inferred by homology
<i>Ostreococcus tauri</i>	D5TRR7	A8TP4	Virdiplantae	Chlorophyce	yes	Inferred by homology
<i>V. carteri</i>	P15824		Virdiplantae	Chlorophyce	yes	Roelie and Ogen, 1990 (40)
<i>C. reinhardtii</i>	M2X242		Virdiplantae	Chlorophyce	yes	Kono et al., 2017 (5) / protein predicted
<i>G. subtiluria</i>	P93681	COP566	Virdiplantae	Streptophytina	yes	Experimental evidence at transcript level
<i>P. sativum</i>			Virdiplantae	Streptophytina	yes	Experimental evidence at transcript level
<i>P. sticticensis</i>			Virdiplantae	Streptophytina	yes	Experimental evidence at transcript level
<i>P. tremulae</i>			Virdiplantae	Dinoflagellata	yes	SAR-Alveolates*
<i>Populus tremuloides</i> (Western balsam poplar) (<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>)	B9GZT5	D8SL148	Virdiplantae	Dinoflagellata	yes	SAR-Rhizaria*
<i>S. moellendorffii</i>	P27774		Virdiplantae	Stramenopiles*	yes	SAR-Stramenopiles*
<i>M. crystallinum</i>	P09559		Virdiplantae	Stramenopiles*	yes	SAR-Stramenopiles*
<i>S. olacea</i>	P26302		Virdiplantae	Stramenopiles*	yes	SAR-Stramenopiles*
<i>T. aestivum</i>	P255897		Virdiplantae	Stramenopiles*	yes	This Study and Roessle and Ogen, 1990 (40)
<i>A. thaliana</i>			Virdiplantae	Stramenopiles*	yes	Experimental evidence at transcript level
<i>L. Linguidum</i>	Q24L13		Virdiplantae	Stramenopiles*	yes	Predicted protein
<i>Pyrocystis lunula</i>	Q24L12		Virovirus	Stramenopiles*	yes	Experimental evidence at transcript level
<i>B. natans</i>	Q25157		Virovirus	Stramenopiles*	yes	Inferred by homology
<i>O. sinensis</i>	Q50533		Virovirus	Stramenopiles*	yes	Inferred by homology
<i>P. tricornutum</i>	B5Y5F0		Virovirus	Stramenopiles*	yes	Inferred by homology
<i>T. pseudonana</i>	B5B240		Virovirus	Stramenopiles*	yes	Inferred by homology

*Member of the SAR group (42); #Member of the Hacrobia Kingdom (43)

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