# Supplementary Material

# An alternative plant-like cyanobacterial ferredoxin with unprecedented structural and functional properties

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Supplementary Figure 1: ESI-MS data of purified Fd1 and Fd2 from *T. elongatus*.A) ESI-MS spectrum of Fd1 in the denaturing mode





## B) ESI-MS spectrum of Fd2 in the denaturating mode

## C) ESI-MS spectrum of Fd1 in the native mode



The main peak (m/z = 10889.12 Da) corresponds to the experimental mass for native Fd1. Indeed, the theoretical mass of the protein with the [2Fe-2S] cluster (calculated mass of 176 Da) and without four Cys thiol protons is 10887.8 Da. A *circa* +23 Da Na-adduct was observed at 10910.92 and a +38 Da K-adduct was observed at 10927.18 Da. The peak at 10822.81 Da probably corresponds to the protein with two Fe attached to it, but without the bridging sulfurs. The detection of such a peak suggests that a fraction of the proteins has lost the two bridging sulfurs of the [2Fe-2S] cluster in the conditions used to record the ESI-MS spectra.



The main peak at 10921,28 Da corresponds to the mass of native Fd1 with the [2Fe-2S] cluster bound (*i.e.* m/z = 10889.12 Da) and with a mass adduct of circa + 32 Da. We also observe the peak at m/z = 10888,21 Da which corresponds to a fraction of native Fd1.

E) ESI-MS spectrum obtained with Fd1' in denaturating mode, after exchange in acetate buffer



The larger peak at m/z = 10714,48 Da corresponds to the theoretical mass of Fd1. Another large peak is observed at m/z = 10745,62 Da, which corresponds to an adduct of *circa* 32 Da. Another adduct is observed at m/z = 10776,49 Da (*circa* + 62 Da).

## Supplementary Figure 2: Redox midpoint potentials of Fd1, Fd2, Fd1' and FdN

The determination of the midpoint potentials of Fd1, Fd1', Fd2 and FdN was done by spectroelectrochemical titrations in the UV-Vis range.

A- Superposition of the titrations in the oxidative mode for Fd1 (orange), Fd1' (black), Fd2 (green) and FdN (blue) at pH 7.5. The experimental data were fitted by a Nernst equation with n=1.  $E_m$  values given in Table 2 are an average of data obtained in oxidation and reduction mode.



B – Superposition of the titrations in the reductive mode for Fd1 (orange), Fd1' (black), Fd2 (green) and FdN (blue) at pH 7.5.



C - Superposition of titrations in the reductive (red) and in the oxidative (blue) mode for FdN, Fd1, Fd1' and Fd2 at pH 7.5.



D - Effect of pH on the midpoint potential of Fd1: Electrochemical titration of Fd1, pH 7,5 (blue) and pH 10 (green).



E) - Summary of the midpoint potentials and  $R^2$  values resulting from the fit of experimental data using a Nernst curve with n fixed to 1.

		Fd2	Fd1	FdN	Fd1'
Oxidation	Em	-427	-375	-375	-343
	<b>R</b> <sup>2</sup>	0.9976	0.9996	0.9958	0.9997
Reduction	Em	-453	-369	-392	-344
	<b>R</b> <sup>2</sup>	0.9996	0.9993	0.9986	0.9983

# Supplementary Figure 3: Crystals of Fd2 from *T. elongatus*.

A plate-shaped crystal with a brown color was grown from urchin-like crystal by the sitting drop vapor diffusion method. The bar represents  $50 \,\mu$ m.



**Supplementary Figure 4**: FoFc map near residues Val65, Asp66, Ser68, Asp69 and His70, Val83, Cys94 and Ser97.

Green: positive, red: negative.



#### **Supplementary Figure 5:** Comparison of RMSDs between the C $\alpha$ of Fd1, Fd2 and FdN.

The distance differences between the C $\alpha$  atoms of three Fds were calculated based on secondary structure matching, using lsqkab [1]. Distance differences between (A) Fd1 (PDB ID: 5AUI, [2]) and Fd2 (present study), (B) Fd1 and FdN (PDB ID: 1fxa, [3], A monomer), (C) Fd2 and FdN. The overall RMSDs are given at the bottom of each figure and are represented as a horizontal orange line in each figure panel.

A) Fd1 vs Fd2 3.5 α<u>2-h</u>el Loop 1 **원** 3.0 C-ter 0.0 GLY 12 THR 15 ASP 18 GLU 21 TYR 24 ASP 27 GLU 30 GLU 54 SER 60 GLN 62 LEU 65 ASP 68 GLU 71 PHE 74 THR 77 ALA 80 ARG 83 CSO 86 CSO 86 CLU 89 GLU 95 ALA 1 LYS 4 LEU 7 GLY 33 SER 39 ALA 42 CYS 45 CYS 48 LYS 51 VAL 57 36 Leu ence -RMSD (=0.9975 Å ) Ed1 s





C)

B)

## Supplementary Figure 6: Comparison of the Loop 1 structure in Fd1 and Fd2.

The structures of loop 1 of Fd2 (**A**) and Fd1 (PDBID: 5aui [2]) (**B**) are shown. The dashed lines indicate hydrogen bonds between the residues. The bond lengths are as follows: (**A**) A16-R19, 2.91 Å; N16-G20, 2.94 Å; N16-L21, 2.97 Å; N16-T98, 2.98 Å; (**B**) R10-S14, 2.84 Å; R10-T91, 2.76 Å; R10-N92, 2.90 Å; P11-G13, 2.84 Å; D12-S14, 3.06 Å. **C**) Superimposition of the loop 1 structures of Fd1 and Fd2.



С



Supplementary Figure 7: Comparison of the Loop 2 structure in Fd1 and Fd2.

The structures of loop 2 in Fd2 (**A**) and Fd1 (PDBID: 5aui [2]) (**B**) are shown. The dashed lines indicate hydrogen bonds between the residues. The bond lengths are as follows: (**A**) T64-C94, 3.04 Å; D66-R4, 2.77Å; Q67-L84, 2.81 Å; S68-H70, 2.70 Å and 2.84 Å; S68-S71, 3.02 Å; S68-A87, 2.83 Å; F72-G51, 2.74 Å; K74-K77, 2.76 Å (peptide N-side chain O) and 2.86 Å (side chain N- side chain O), K76-A108, 2.68 Å; (**B**) E57-CSO87, 2.79 Å (peptide N-side chain O) and 2.94 Å (peptide O-side chain O); Q60-Q63, 2.87 Å; Q60-L77, 2.95Å; D62-Y25, 3.05 Å; Q63-F65, 2.96 Å; Q63-L66, 2.75 Å; S64-G44, 2.79 Å; D67-Q70, 2.88 Å (side chain O-peptide N) and 2.98 Å (peptide N-side chain O). (**C**) Superimposition of loop 2.



**Supplementary Figure 8:** Effect of  ${}^{1}\text{H}_{2}\text{O}/{}^{2}\text{H}_{2}\text{O}$  exchange on the reduced-*minus*-oxidized FTIR difference spectra recorded with Fd1 and Fd2.

## A) Effect of <sup>1</sup>H<sub>2</sub>O/<sup>2</sup>H<sub>2</sub>O exchange in the mid infrared for Fd1 (top) and Fd2 (bottom)

Spectra in H<sub>2</sub>O are in orange for Fd1 and in green for Fd2. The corresponding spectra recorded in  ${}^{2}\text{H}_{2}\text{O}$  are in dark grey. The inset presents the absorption region of v(S- ${}^{2}\text{H}$ ) modes in the reduced-minus-oxidized FTIR difference spectrum recorded with Fd1 in  ${}^{2}\text{H}_{2}\text{O}$ .



Down shifts by less than 10 cm<sup>-1</sup> are expected upon  ${}^{1}\text{H}_{2}\text{O}/{}^{2}\text{H}_{2}\text{O}$  exchange for amide v(C=O) modes, *i.e.* up to 10 cm<sup>-1</sup> for  $\alpha$ -helix and less than 5 cm<sup>-1</sup> for  $\beta$ -sheet secondary structures [4, 5]. The band frequencies at 1694 and 1639 cm<sup>-1</sup> are not sensitive to H<sub>2</sub>O/{}^{2}\text{H}\_{2}\text{O} exchange while the bands at 1668 and 1652 cm<sup>-1</sup> are downshifted by -4 and -3 cm<sup>-1</sup>, respectively. This supports the assignment to peptide carbonyl groups from random coil and/or  $\alpha$  helix at 1668 and 1653

cm<sup>-1</sup>, to carbonyl groups involved in β-sheet structures at 1640 cm<sup>-1</sup>, or to carbonyl groups free of hydrogen bonding interactions above 1680 cm<sup>-1</sup>. For Fd1, an additional band observed at 1680 cm<sup>-1</sup> in  ${}^{2}$ H<sub>2</sub>O for oxidized Fd1 shows that at least two different groups contribute to the broad band at *circa* 1700-1694 cm<sup>-1</sup> in H<sub>2</sub>O. The behavior upon  ${}^{1}$ H<sub>2</sub>O/ ${}^{2}$ H<sub>2</sub>O exchange in the 1800-1620 cm<sup>-1</sup> region is similar for Fd2. This suggests a dominating contribution of Amide I bands. They appear almost at the same frequencies for Fd2 and Fd1, with a slightly higher frequency of the v(C=O) mode at 1642 cm<sup>-1</sup> (1641 cm<sup>-1</sup> in  ${}^{2}$ H<sub>2</sub>O), and at 1672 cm<sup>-1</sup> (*vs* 1668 cm<sup>-1</sup> in Fd1) and with different relative band intensities.

Amide II modes are expected to largely downshift in  ${}^{2}\text{H}_{2}\text{O}$ . They are identified in  ${}^{1}\text{H}_{2}\text{O}$  at 1503 cm<sup>-1</sup> and at 1551 and 1522 cm<sup>-1</sup> for Fd1<sub>ox</sub> and Fd1<sub>red</sub>, respectively, by their large downshift to 1413 cm<sup>-1</sup> (-88) and 1476 (-75) and 1452 cm<sup>-1</sup> (-70) in  ${}^{2}\text{H}_{2}\text{O}$ . For Fd2<sub>ox</sub>, in contrast to Fd1, two bands are identified at 1433 and 1406 cm<sup>-1</sup> in  ${}^{2}\text{H}_{2}\text{O}$ , which should result from the downshift of the Amide II mode at 1503 cm<sup>-1</sup>. They suggest different properties of the Amide II modes sensitive to the [2Fe-2S] cluster reduction as compared to Fd1.

In the spectrum recorded in  ${}^{2}$ H<sub>2</sub>O, bands at 1561 and 1511 cm<sup>-1</sup> for Fd1<sub>ox</sub> and at 1576, 1516 and 1504 cm<sup>-1</sup> for Fd2<sub>ox</sub> cannot result from Amide II modes with deuterated N<sup>2</sup>H. These bands result either from Amide II modes where the NH has not been exchanged in N<sup>2</sup>H or from contributions of amino acid side chains. Bands at 1516-1504 cm<sup>-1</sup> are typical for a tyrosine  $v_{19}(CC)$  side chain mode [6, 7]. This mode is expected to shift by a maximum of -3 cm<sup>-1</sup> upon <sup>1</sup>H/<sup>2</sup>H exchange. These modes could be superimposed to contributions from Amide II modes in H<sub>2</sub>O. The FTIR data thus suggest that a tyrosine side-chain contributes to the redox-induced structural changes in both Fd1 and Fd2. The bands at 1561 and 1576 cm<sup>-1</sup> are in the range where carboxylate  $v_{as}(COO^{-})$  modes of aspartate or glutamate contribute [6]. These modes are expected either at the same frequency or upshifted by a few wavenumbers in <sup>2</sup>H<sub>2</sub>O. For Fd1<sub>red</sub> and Fd2<sub>red</sub>, bands at 1544 and 1539 cm<sup>-1</sup> could correspond to these modes, and the low frequency would indicate a strong interaction with a positively charged group. The positive band at 1396 cm<sup>-1</sup> in the spectra recorded with all Fds is tentatively assigned to the corresponding  $v_s(COO^{-})$  mode of a glutamate or aspartate residue. The latter mode is less sensitive to changes in hydrogen bonding interactions. Finally, the band at  $1622 \text{ cm}^{-1}$  for Fd1<sub>ox</sub>, which disappears or is largely downshifted in <sup>2</sup>H<sub>2</sub>O could correspond to a lysine or arginine side-chain mode. This band seems downshifted to  $1608 \text{ cm}^{-1}$  in Fd2<sub>ox</sub>.

Finally the bands at 1866/1853 cm<sup>-1</sup> in the figure inset recorded with Fd1 and not with Fd2 or FdN are typical for a cysteine  $v(S^{-2}H)$  mode [8]. It corresponds to the v(S-H) mode observed

at 2567/2548 cm<sup>-1</sup> of Fd1 in H<sub>2</sub>O, assigned to a cysteine side chain, which is sensitive to the change in redox state of the [2Fe-2S] cluster.

## B) Effect of <sup>1</sup>H<sub>2</sub>O/<sup>2</sup>H<sub>2</sub>O exchange on the 1400-1000 cm<sup>-1</sup> region.

Reduced-*minus*-oxidized FTIR difference spectra recorded with FdN (blue line), Fd1 (orange line), Fd1' (black line) and Fd2 (green line) in the region between 1400 and 1000 cm<sup>-1</sup> in H<sub>2</sub>O. For Fd1 and Fd2, spectra recorded in  $^{2}$ H<sub>2</sub>O are shown with grey lines.



Two IR modes from threonine and serine side chains are expected in the 1300-900 cm<sup>-1</sup> region: the  $\delta$ (COH) bending mode, which is largely downshifted upon deuteration, and the v(CO) mode, only slightly shifted in <sup>2</sup>H<sub>2</sub>O ([9] and references therein). In the region where  $\delta$ (COH) modes are expected to contribute, bands observed at 1295(+) cm<sup>-1</sup>, 1279(-) cm<sup>-1</sup>, and 1247(-)

cm<sup>-1</sup> in the spectra recorded with Fd1, FdN and Fd1' seem absent or largely shifted in  ${}^{2}\text{H}_{2}\text{O}$ . The bands at 1295/1279 cm<sup>-1</sup> are also absent in the spectrum recorded with Fd2, while the band at 1247 cm<sup>-1</sup> is conserved in Fd2. Bands at 1072(-) cm<sup>-1</sup>, 1063(+) cm<sup>-1</sup> and 1049(+) cm<sup>-1</sup> observed in the spectra recorded with Fd1, FdN and Fd1' are still present and only slightly modified in the spectrum recorded in  ${}^{2}\text{H}_{2}\text{O}$ . The bands at 1073/1063 cm<sup>-1</sup> are absent in the spectrum recorded with Fd2.

We thus assign the bands at 1295(+)/1279(-) cm<sup>-1</sup> to the  $\delta$ (COH) bending mode of either threonine or serine and propose that they are shifted to 999(+)/977(-) cm<sup>-1</sup> in <sup>2</sup>H<sub>2</sub>O, in the spectrum recorded with Fd1, in agreement with literature data. The bands at 1072(-)/1063(+)cm<sup>-1</sup> are tentatively assigned to corresponding v(CO) mode. Since the difference bands at 1295(+)/1279(-) cm<sup>-1</sup> and 1072(-)/1063(+) cm<sup>-1</sup> are absent in the reduced-minus-oxidised spectrum of Fd2, (as well as the difference band at 999(+)/977(-) cm<sup>-1</sup> in the spectrum recorded in <sup>2</sup>H<sub>2</sub>O), they are tentatively assigned to the CysSerThrCys motif, present in Fd1 and FdN and replaced by the CysValAsnCys motif in Fd2. The structural change at the level of the Ser47 described for FdN reduction could explain the changes in the IR mode frequencies of Ser 47 or Thr48 side chains upon Fd reduction. Supplementary Figure 9: Hydrogen bonding interactions of the fifth  $CysS\gamma$  in Fd1 and Fd2 structures.

The environment around the fifth Cys is compared for Fd2 (green), Fd1 (in orange transparent for PDB ID: 5aui [2], and in pink for the new Fd1 structure), and FdN (in blue PDB ID: 1fxa [3]). The hydrogen bonds are shown in dashed lines in black for Fd2 and red for Fd1 (new structure). Both Cys-S $\gamma$  can form hydrogen bonding interactions: Cys87S $\gamma$  in Fd1 (new Fd1 structure) with the peptide carbonyl oxygen of Glu57 at 3.14 Å, and for Cys94S $\gamma$  in Fd2 with the peptide carbonyl oxygen of Thr64 at 3.05 Å.



**Supplementary Figure 10:** Orientation of the arginine and serine residues. Consequences on Cys46 environment

The environment around Arg42 (**A**) and Cys46, Ser40 and Thr48 (Fd1 numbering) (**B**) is compared for Fd2 (transparent green) and Fd1 (orange for PDB ID: 5aui [2] and pink for the new Fd1 structure) as well as for FdN (in blue, PDB ID: 1fxa, [3]). The hydrogen bonds are shown with dashed lines in black for Fd2, magenta for Fd1 PDB ID: 5aui, red for the new Fd1 structure and in blue for FdN.

#### Α





**Supplementary Figure 11:** Crystal structure of a major ferredoxin, Fd1 coded by *tlr1009* in *T. elongatus*.

(A) Ribbon model of the whole structure. The crystal structure contains residues 2-98 (the full length of the protein is 98 residues), a [2Fe-2S] type iron-sulfur cluster (shown in ball), and a tentatively assigned sulfate ion and two benzamidines (shown in sticks). The color of the Fd1 structure is in cyan, iron atoms are in brown, sulfur and oxygen atoms of the sulfate iron are shown in yellow and red, and the benzamidines are shown in gray.

(B) Superposition of the Fd1 structure determined in the present study with that reported previously (PDB ID: 5aui [2], protein body, orange ; benzamidine, blue). The structures of the two Fd1 were superposed by the SSM protocol in Coot [10]. Residues having remarkable difference structures are shown in sticks. In the new structure (PDB ID :6jo2), Ser40 has two conformations, one with its side chain facing the iron cluster with 0.33 occupancy, and the other one facing Asp36 from the adjacent molecule with 0.67 occupancy. The main-chains of Leu35 and Asp36 were flipped, which may be caused by crystal packing because Ser40 was close to the Leu35 and the Asp36 residues, as well as Glu31 of the adjacent molecule in the crystal. Arg42 has also two conformations in the new structure, and no remarkable environmental differences were found near Arg42. The 87<sup>th</sup> residue in the new structure is cysteine, in agreement with the amino acid sequence but not S-hydroxycysteine that was reported in the previous structure (PDB ID : 5aui).

A

В







Flash-induced absorption measurements were performed at 580 nm with increasing Fd2 concentrations (0, 1.00, 2.02, 4.01, 7.93  $\mu$ M from a to e) and with [PSI] decreasing from 0.218 to 0.206  $\mu$ M along with Fd2 addition (or buffer in the reference cuvette). Best-fits were performed with real PSI concentrations but data in the figure were normalized to 0.218  $\mu$ M PSI for easier comparison. **Part A** displays raw kinetics. Both P700 oxidation and (F<sub>A</sub> F<sub>B</sub>) reduction give rise to an initial fast bleaching (negative absorption signal) whereas Fd reduction by (F<sub>A</sub> F<sub>B</sub>)<sub>1red</sub> gives rise to a further bleaching with kinetics depending upon the Fd concentration (traces b to e). In trace a (no Fd), the slow signal decay is due to a recombination reaction between P700<sup>+</sup> and (F<sub>A</sub> F<sub>B</sub>)<sub>1red</sub>. In the presence of Fd, the fastest component of the decay kinetics (up to *c*. 0.5 ms after the flash) is first-order with its rate being constant (not [Fd]-dependent) and its amplitude increasing with [Fd]. It is attributed to intracomplex ET from (F<sub>A</sub> F<sub>B</sub>)<sub>1red</sub> to Fd within PSI:Fd complexes which are preformed before flash excitation. It is followed by a second-order component with its rate being [Fd]-dependent and its amplitude is much smaller

in traces d and e. It is attributed to Fd reduction by the part of PSI which does not bind Fd before flash excitation and where diffusion-limited binding of Fd to PSI-(FA FB)1red precedes Fd reduction itself and limits the rate of this reduction. After completion of Fd reduction (i.e. after  $\approx$  30 ms for b, 15 ms for c and less than 10 ms for d and e), the slow decay is attributed to P700<sup>+</sup> reduction by the exogenous electron donor DCPIPH<sub>2</sub> (DCPIP reduced by ascorbate). Traces b and c were fitted between 1 and 60 ms with a biexponential function to take into account both the second-order process of Fd reduction and the slow P700<sup>+</sup> decay (black traces with fits extrapolated to time 0). The best-fit rates of the fastest component (due to Fd reduction) are kobs = 75 and 151 s<sup>-1</sup> for b and c, respectively. Assuming pseudo-first order conditions with  $k_{obs}$  =  $k_{on} \times [Fd]_{free}$  (k<sub>on</sub> = second-order rate of Fd reduction; [Fd]<sub>free</sub> = [Fd not bound to PSI] = 0.93 and 1.91  $\mu$ M from the K<sub>d</sub> fit (see Supp. Figure 13), one obtains k<sub>on</sub> = 8.0 and 7.9 × 10<sup>7</sup> M<sup>-1</sup>s<sup>-1</sup> from the independent fits of b and c. On short time scales ( $t < 20 \ \mu s$ , see orange ellipse), fastdecaying signals due to  $\beta$ -carotene triplet states are present which obscure the signals due to ET. These triplet signals are Fd-independent and are eliminated by subtracting the signal without Fd from those with Fd, as shown in **Part B**. Moreover, the subtraction procedure allows the signals due to PSI charge separation (P700<sup>+</sup> (F<sub>A</sub> F<sub>B</sub>)<sub>1red</sub>) to be eliminated so that only Fd reduction by (FA FB)1red is observed. The difference kinetics are essentially first-order with only a minor contribution due to second-order Fd reduction (see black traces at short times in Part A). The signal increase with [Fd] reflects the binding equilibrium between PSI and Fd with the first-order signal amplitude being proportional to the amount of PSI:Fd complex formed before flash excitation.

### Supplementary Figure 13: Titration of Fd binding to PSI.



The amplitude of the first-order components of Fd reduction (see Supp. Figure 12 for Fd2, see also single difference kinetics in Figure 7) were plotted as a function of [Fd]. Amplitudes were quantified as the average signal sizes between 0 and 100  $\mu$ s for Fd1 (orange squares and triangles for 2 different titrations) and Fd1' (black crosses) and between 0 and 400  $\mu$ s for Fd2 (green circles). The continuous curves were obtained by fitting the data with a simple-binding equilibrium model where the amount of PSI:Fd is solution of a quadratic equation involving the dissociation constant K<sub>d</sub> and the concentrations of PSI and Fd. For each Fd, K<sub>d</sub> and the asymptotic signal amplitude (100% of PSI binding Fd) were adjustable parameters and the data are plotted as a fraction of the 100% amplitude. K<sub>d</sub> values of 0.50, 1.32 and 1.84  $\mu$ M were determined for Fd1, Fd1' and Fd2, respectively.



Flash-induced absorption measurements were performed at 580 nm with decreasing [PSI] from 0.209 to 0.197  $\mu$ M along with Fd1 and FNR additions (or buffer in the reference cuvette). Best-

fits were performed with real PSI concentrations but data in the figure were normalized to 0.2  $\mu$ M PSI for easier comparison. Concentrations of Fd1 and FNR are indicated for each trace. **Part A** displays raw kinetics. After measurement without addition (black), Fd1 was added first at a concentration of  $\approx 4 \,\mu$ M (red), then FNR was added at concentrations increasing from  $\approx 2$  to 15  $\mu$ M (green, blue, cyan and magenta) and another Fd1 addition was eventually made (giving  $\approx 7.5 \,\mu$ M, orange). Fd reduction leads to a signal decrease which is followed from 0.2 to 3 ms by a small signal increase (red trace). This signal has been investigated in detail [11] and was shown to be due to a non-redox absorption change attributed to an increase in the Fd<sub>ox</sub> absorption upon binding to PSI. Fd<sub>ox</sub> binding to PSI occurs after Fd<sub>red</sub> dissociation, as a diffusion-limited process. Moreover, it occurs similarly whether FNR is present or not and is eliminated when the signal from the reference cuvette (Fd alone) is subtracted from the sample cuvette (Fd + FNR). Addition of FNR induces the appearance of a large positive signal increase following the initial Fd-reduction signal and concomitant with the Fd-binding induced signal. This signal is attributed to the formation of singly-reduced FNR<sub>sq</sub> in its protonated form (FADH<sup>•</sup>).

**Part B** displays the differences between the sample and reference cuvettes. The final signal level increases with [FNR] and decreases with the final addition of Fd1. This shows that FNR reduction by Fd<sub>red</sub> is only partial and the redox equilibrium: Fd<sub>red</sub> + FNR<sub>ox</sub>  $\leftrightarrow$  Fd<sub>ox</sub> + FNR<sub>sq</sub> must be considered. The amplitudes of the final signal levels (between 10 and 15 ms) were fitted using this equilibrium reaction and neglecting the presence Fd:FNR complexes in different redox states. Two adjustable parameters were used, the equilibrium constant K<sub>eq</sub> = [Fd<sub>ox</sub>]×[FNR<sub>sq</sub>]/([Fd<sub>red</sub>]×[FNR<sub>ox</sub>]), and the signal amplitude corresponding to full FNR reduction. With [Fd<sub>red</sub>] + [FNR<sub>sq</sub>] = [PSI], the equation giving the ET extent, that is [FNR<sub>sq</sub>]/[PSI], is a simple quadratic equation. The best-fit parameters are K<sub>eq</sub> = 1.26,  $\Delta A$  for 100% ET = 6.72 × 10<sup>-4</sup> and the resulting best-fit signal levels are shown as horizontal lines. Data can also be read as ET extent using the right vertical scale.

**Part C** displays kinetics of part A with emphasis on the short time scale. The kinetics between 0 and 0.5 ms were globally fitted using the following kinetic model:  $Fd_{red} + FNR_{ox} \rightarrow Fd_{ox}$ :  $FNR_{sq} \rightarrow Fd_{ox} + FNR_{sq}$ . The rates  $k_{on}$  and  $k_{limit}$  of the two consecutive reactions were taken as adjustable parameters whereas the 100% ET signal was used as a fixed value. From the best fit values ( $k_{on} = 4.1 \times 10^8 \text{ M}^{-1}\text{s}^{-1}$  and  $k_{limit} = 640 \text{ s}^{-1}$ ), the kinetics were calculated up to completion of the reactions (black traces). The cyan trace ([FNR] = 7.82 µM) and the corresponding calculated kinetics are also shown in Figure 8.





Flash-induced absorption measurements were performed at 520 nm with decreasing [PSI] from 0.243 to 0.231  $\mu$ M along with Fd1/2 and NiR additions (or buffer in the reference cuvette). All data in the figure were normalized to 0.243  $\mu$ M  $\mu$ M PSI for easier comparison. **Part A** displays

raw kinetics. In the absence of Fd (trace no Fd), charge separation leads to a positive signal resulting from a major positive contribution due to P700 oxidation and a minor negative contribution due to (F<sub>A</sub> F<sub>B</sub>) reduction. Addition of either Fd1 (4.79 µM) or Fd2 (4.77 µM) leads to a signal decrease (traces Fd1 and F2). In the case of Fd1, this initial decrease is followed by a smaller increase at t < 2 ms, which results from Fd<sub>ox</sub> binding to PSI (see Supp. Figure 14A) for a similar signal at 580 nm). No such signal is observable with Fd2, although preliminary experiments (not shown) suggest that it may be present at higher [Fd2]. NiR at increasing concentrations was added with both Fds: 3.11 µM for a and b, 6.32 µM for c and d and 12.74 µM for e and f. Traces a, c, e and b, d, f were recorded with Fd1 and Fd2, respectively. Parts **B** and **C** display the signal differences between the sample cuvettes (Fd + NiR) and the reference cuvettes (Fd) for Fd1 and Fd2, respectively. With each Fd, the final levels are identical for every [NiR], which indicates complete single reduction of NiR, in contrast to what is observed with FNR. These levels are different for Fd1 and Fd2, which also suggests that their respective contributions are different. For each Fd, the kinetics were globally fitted using the following simple kinetic model:  $Fd_{red} \rightarrow free Fd_{red} + NiR_{ox} \rightarrow Fd_{ox} + NiR_{1red}$  with rate constants  $k_{off}$  and  $k_{on}$  for the 2 consecutive reactions. Starting from  $[Fd_{red}] = [PSI]$  at t = 0 and within the first-order approximation ([NiR<sub>ox</sub>] >> [Fd<sub>red</sub>]), one gets: [NiR<sub>1red</sub>](t) = [PSI]×[-k<sub>2</sub> e<sup>-koff t</sup> + k<sub>off</sub> e<sup>-</sup>  $k^{2}t + k_{2} - k_{off}/(k_{2}-k_{off})$  with  $k_{2} = k_{on} \times [NiR_{ox}]$ . For each Fd, the adjustable parameters were the following: kon, koff, the final signal amplitude, and an offset to take into account the fact that all signals do no start from 0 (very small in all cases except for trace e). The following best-fit parameters were obtained: for Fd1,  $k_{on} = 1.43 \times 10^8 \text{ M}^{-1}\text{s}^{-1}$  and  $k_{off} = 5231 \text{ s}^{-1}$ ; for Fd2,  $k_{on} =$  $0.47 \times 10^8$  M<sup>-1</sup>s<sup>-1</sup> and k<sub>off</sub> = 1410 s<sup>-1</sup>. These values are similar to those obtained by single fits of the kinetics in Figure 9. However these global fits are rather poor, especially for the highest [NiR] (traces e and f). In the case of Fd1, this may arise, at least partially, from the fact that some Fd1:NiR complex is formed in darkness, as indicated by the significant initial offset in trace e. Fd1:NiR complex formation should result in a lower amount of PSI:Fd1 through binding competition. In turn, subtraction of the reference cuvette is not perfect as there is more PSI:Fd complex in this cuvette and then, a larger amount of fast Fd reduction than in the sample cuvette, and this is expected to result in the observed offset. In the case of Fd2, there is no significant offset in f, which indicates that the dark amount of Fd2:NiR can be neglected. One (partial) explanation for the bad fit of trace f could be that Fd2 reduction should be explicitly taken into account in the kinetic model, as it is not that fast compared to the following processes of Fd<sub>red</sub> dissociation and NiR reduction. It was not checked further by numerical simulations of the kinetics that the above explanations for the poor global fits are correct, as the main conclusion of this study, which is that NiR reduction by Fd1 is about 3-times faster than by Fd2, is approximately valid for the 3 tested [NiR].

**Supplementary Figure 16:** Phylogenetic analysis of photosynthetic-type Fds from cyanobacteria.

**Part A:** Phylogenetic unrooted tree of all photosynthetic-type [2Fe-2S] Fds from 83 different cyanobacterial strains and from maize, *Arabidopsis thaliana* and *Chlamydomonas reinhardtii*. Sequence alignment was performed with MUSCLE and tree construction was done with the neighbor-joining method, both methods being provided in the SeaView integrated software. Bootstrap values (from 0 to 100) were obtained from 1000 repetitions. The branches and leaves are colored according to the value of the X:Y doublet: blue for Val:Phe, Phe:Phe, Ile:Phe, Ile:Ile and Thr:Phe; red for Ser:Phe; green and dashed light green for Thr:Gly. Values of X:Y are indicated at the end of the labels. Labels of eucaryotic Fds are colored green. The dashed light green branch correspond to Fds with a large C-terminal extension. It includes Fed2 from *Synechocystis* 6803, Fd3 from *T. elongatus*, FdC2 from *Arabidopsis thaliana* and Fdx6 from *Chlamydomonas reinhardtii*.



**Part B:** Sequence alignment which was used for building the phylogenetic tree of Figure 10. The sequences are grouped by cyanobacterial strain. All strains have at least one "red" Fd, have one "light green" Fd (with a C-terminal extension) and all except one (*Synechococcus* sp. PCC 7002) have one "green" Fd. The cluster-liganding Cys are shown on a yellow background whereas the residues X and Y are on a cyan background.

637313626_Thermosynechococcus_elongatus_BP_1_XY=SF	MATY-KVTLVRPDGSETTIDVPEDEYILDVA-EEQGLD-LPFSCRAGACSTCAGKLLE-GEVDQSDQSFLDDDQIEKGFVLTCVAYPRSDCKILTNQEEELY	
637313857_Thermosynechococcus_elongatus_BP_1_XY=VF	MTKRDHNKVY-NVTLVN	
637313101_Thermosynechococcus_elongatus_BP_1_XY=TG	MTQTF-RVEILHQQTYTFEASADKPLLRSA-TAAGID-LPSS <mark>C</mark> NAGV <mark>CTTC</mark> AAQIQE-GTVDHGDAM <mark>G</mark> LSPELREKGYVLL <mark>C</mark> VARPCSDLKLISEKEEEVYNFQFQQFQKA	
637314283_Thermosynechococcus_elongatus_BP_1_XY=TG	MSTPQTY-TVTIHVRPLKSEDPPPRTYTITVPSDRYILQHA-ESQGLE-LPFSCRNGACTTCAVRILS-GHVYQPEAMSLSPALQAQGYALLCVSYARSDLEVETQDEDEVYELQFGRYFGKGRVQLGLPL	DED
2598118050_Thermosynechococcus_sp_NK55a_XY=SF	MATY-KVTLVRPDGSETTIDVPEDEYILDVA-EEQGLD-LPFS <mark>C</mark> RAGA <mark>C</mark> STCAGKLLE-GEVDQSDQS <mark>F</mark> LDDDQIEKGFVLTCVAYPRSDCKILTNQEEELY	
2598118883_Thermosynechococcus_sp_NK55a_XY=VF	MTKRDHNKVY-NVTLVNBBBBBB-	
2598119820_Thermosynechococcus_sp_NK55a_XY=TG	MTQAF-RVEILHQQQQTYTFEASADKPILQSA-TAAGID-LPSS CNAGVCTTCAAQIQE-GTVDHGDAMGLSPELREKGYVLLCVARDSDLKLISEKEEEVYHFQFGQFQKA	
2598119066_Thermosynechococcus_sp_NK55a_XY=TG	MSTPQTY-TVTIHVRPLKSGDPPTRTYTITVPGDRYILQHA-ESQGLE-LPFS <mark>G</mark> RNGA <mark>CTTC</mark> AVRILS-GHVYQPEAM <mark>G</mark> LSPALQARGYALL <mark>C</mark> VSYARSDLEVETQDEDEVYELQFGRYFGKGRVQLGLPL	LDED
2515004633_Synechocystis_sp_PCC_6803_XY=SF	MASY-TVKLITPPDGESSIECSDDTYILDAA-EEAGLD-LPYS <mark>C</mark> RAGA <mark>CSTC</mark> AGKITA-GSVDQSDQS <mark>FL</mark> DDDQIEAGYVLT <mark>C</mark> VAYPTSDCTIET-HKEEDLY	
2515004363_Synechocystis_sp_PCC_6803_XY=VF	MGAIY-SVNLVNPATGSDVTIEVAEDELILEAA-ENQGLD-LPYS <mark>C</mark> RAAS <mark>CVAC</mark> AGRLLE-GTVEHTDKGSD <mark>F</mark> LKPEELAAGCVLL <mark>C</mark> AAYATSDCKILTHQEEALFG	
2515003158_Synechocystis_sp_PCC_6803_XY=TG	MVNTY-TAEIQHQQQTYTISVPEDKTVLQAA-DDEGIQ-LPTS <mark>Q</mark> GAGVC <mark>TTC</mark> AALITE-GTAEQADGM <mark>G</mark> VSAELQAEGYALL <mark>C</mark> VAYPRSDLKIITEKEDEVYQRQFGGQG	
2515004036_Synechocystis_sp_PCC_6803_XY=TG	MSRSH-RVLIHDRENEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVE	DED
2810310233_Synechocystis_sp_PCC_6714_XY=SF		
2810311673_Synechocystis_sp_PCC_6714_XY=VF		
2810311846_Synechocystis_sp_PCC_6714_XI=IG		
2810310322_Synechocystis_sp_PCC_6/14_A1=1G	wroth	טטענ
6412E4E12 Manwooklavia mavina MPTC11017 XV-CE		
oficitors_marine_mercerologic_set		
641253039 Agerwochlorig marine MBIC11017 XV-SE		
641254216 Agerwochlorig marine MBIC11017 XV-SF		
641256388 Agerwochlorig marine MBIC11017 XV-II		
641250751 Agerwochlorig marine MBIC11017 XV-II		
641251779 Agerwochlorig marine MBIC11017 XV-TG		
641253070 Agarwoghloris marina MBIC11017 XV-TG		OFF
VI2550/0_Acaryochioris_marina_mbicrior/_Arero		101515
2503365403 Cvanobacterium stanieri PCC 7202 XV=SF		
2503365836 Cyanobacterium stanieri PCC 7202 XX=VE		
2503367054 Cyanobacterium stanieri PCC 7202 XY=TG		
2503367346 Cvanobacterium stanieri PCC 7202 XY=TG		IEDD
2503746716_Cyanobacterium_sp_PCC_10605_XY=SF	MATY-NVTLITPDGEQTIEVPDDEYILDVA-EEQGID-LPYSCRAGACSTCAGKLVE-GTVDQSDQSFLDDDQIEAGYVLTCVAYPTSDCKIETHKEEDLY	
2503744606_Cyanobacterium_sp_PCC_10605_XY=VF	MANSY-KIKLINEEEKGIDNVIEVNADEYILDAA-ERQGFN-LPYSCRAGVCVSCTAKIVE-GTVNHDYDFLKDKEIEAGFFLTCKAYATSDGVIKTHQEDALLDL	
2503745149_Cyanobacterium_sp_PCC_10605_XY=TG	MSNTY-TVKIHNA	
2503744961_Cyanobacterium_sp_PCC_10605_XY=TG	MTKTY-KVTIHHRQENRIQTIEVPEDQYILATA-EKQAVE-PFFSCRNGACTTCAVRVLE-GKLYQPEA-MCLSPELQRKGYALLCVSYPRSDLVVETQD-EDEVYELQFGRYFGRGKVRFGIPI	IEDD
2503792835_Gloeocapsa_sp_PCC_7428_XY=SF	MATY-KVTLINDBEGLNQTIEVDDDTYILDAA-EEAGLD-LPYS <mark>C</mark> RAGAC <mark>STC</mark> AGKLVS-GSIDQSDQS <mark>F</mark> LDDDQIEAGYVLTCVAYPTSDCTIETHKEEDLY	
2503794358_Gloeocapsa_sp_PCC_7428_XY=SF	MTTY-QVHLINKKKSLDVTIPVDEKTTILDAA-ENEGLD-LPFS <mark>C</mark> HSGS <mark>CS</mark> SCVGKVVE-GEIDQSDQV <mark>E</mark> LDEDQVAKGFVLLCVAYPRSDCTIRTHQEAYLV	
2503795939_Gloeocapsa_sp_PCC_7428_XY=SF	MYY-QVRLVNPDMALDRTILVPEEQYILDIA-EEAGIR-LPAG <mark>C</mark> HQGNC <mark>SAC</mark> VAKIIS-GEVDQSEQR <mark>F</mark> LQPAEIAAGYTLTCVAYPLSDCTLQTHQEKVLYHSSLYYSTEQSG	
2503793157_Gloeocapsa_sp_PCC_7428_XY=VF	MLNRNSDKIY-KVTLVSBBHKLNSTIEVCGDEYILDAA-EVQNIE-LPYA <mark>C</mark> RAGA <mark>CVVC</mark> IGKVLE-GSVDQSDHS <mark>F</mark> LNEKELKAGFVLT <mark>C</mark> RAYPQSDCIIKTHQEEELFELY	
2503796502_Gloeocapsa_sp_PCC_7428_XY=IA	$MKTY-RIELVNRNHFVVEVAENQYILDAV-EAAGLR-LPVG_{C}RYGA_{C}I_{C}AAHLVA-GKVNQSQG-+V_{A}LKASHEGMGYVLL_{C}VAYPQSDCKLEVGLES-QEQLYVNPFKGC$	
2503792624_Gloeocapsa_sp_PCC_7428_XY=TG	mpqTy-TVQIQHQQQTHTIEVPEDKIILRAA-SAAGLD-LPSS <mark>Q</mark> NAGVC <mark>TTC</mark> AALLLE-GTVEQSDGM <mark>G</mark> LSPELQQKGYALL <mark>C</mark> VSYPRSNLKIETEKEDEVYDLQFGQFQRS	
2503794822_Gloeocapsa_sp_PCC_7428_XY=TG	MTRYY-KIQIRDRCRCQNYTLEVPEDGYILQNA-EKQGVE-LPFS <mark>G</mark> RNGA <mark>GTTG</mark> AVRVLS-GEIYQPEAM <mark>G</mark> LSPELRAKGYALL <mark>G</mark> VSYPLSDLEVETQDEDEVYELQFGRYFGKGKVRAGLPL	LDED
C10105000 @		
648185082_Cyanothece_sp_PCC_7822_XY=SF	WITY-KVTLKL	
646166603_Cyanothece_sp_PCC_/622_X1=SF		
648185081_Cyanothece_sp_PCC_7822_XY=SF	MATY-KVTLKT	
648185320_Cyanothece_sp_PCC_7822_XY=FF		
646166096_Cyanothece_sp_PCC_/622_XI=VF		
646166237_Cyanothece_sp_PCC_7622_XI=IG		
overesting_cyanochece_sp_rcc_/ezz_x1=10		JEED
643583891 Cvanothece sp PCC 7425 XY=SF		
643587771 Cyanothece sp PCC 7425 XY=SF		
643584071 Cvanothece sp PCC 7425 XY=TF		
643587430 Cvanothece sp PCC 7425 XY=TG		
643586875 Cvanothece sp PCC 7425 XY=TG		LDED
2509428395 Synechococcus sp PCC 6312 XY=SF	MATY-KVTLIN	
2509429422 Synechococcus sp PCC 6312 XY=VF	MKRDHSRVY-SVTLVNE	
2509429821 Synechococcus sp PCC 6312 XY=TG		
2509429932_Synechococcus_sp_PCC_6312_XY=TG	MTTTY-SVTIHDRQRQQTYQVRVPADRYILHSA-EATGTE-LPFACRNGACTTOAVQVKS-GSLRQPEAMCLSPKLQAQGYALLCVSYAESDLVVETQDEDEVYELOFGQYF6KGKVQIGLPL	LDED
641676090_Cyanothece_sp_ATCC_51142_XY=SF	MATY-KVTLKSEGINTTIEVPDDEYILDVA-EEQGLE-LPYS <mark>C</mark> RAGA <mark>CSTC</mark> AGKLVS-GSVDQSDQS <b>F</b> LDDDQIEAGFVLTCVAYPTSDCTIETHQEEALY	
641676089_Cyanothece_sp_ATCC_51142_XY=SF	MASY-KVTLKTPP-EGENTIEVPEDEYILDVA-EEEGLD-LPYSCRAGACSTCAGKLVS-GTIDQSDQSELDDDQIEAGFVLTCVAYPTSDCTIETHQEENLY	
641675038_Cyanothece_sp_ATCC_51142_XY=SF	$\text{MTATY}-\text{QVRLMKTFK}\text{QKNKETGKKEE}\text{IAEIDVTLEVPEDVYIFDAA}-\text{EEEGLD}-\text{LPSS}_{C}^{C}\text{CSGAC}_{S}^{C}\text{VGRIVE}-\text{GEVD}\text{QED}_{Q}-\text{S}_{L}^{F}\text{DDE}\text{QVEK}\text{GWVLL}_{C}^{C}\text{VAYPRSNCTIKT}-\text{H}_{Q}-\text{EAYL}_{A}$	

MNCDOFFF-SUTI TN		WOACKUTE-CTUFOTAOAUOPLCYALUDACUU.T	A SPTSNOUTLT DOFFFTF
	PKIGAGKIIQVADDQVIIDIA-KQQGID-DFACCCAAAC	FDOLCKVIS-CKVEOTEKAESELKEDELDOCVUL	
MSNTV_TVFINU		TTCACKULE_CEVEOCDCMCLSPELOAECVALL	
MSRYH-TIRIYH		TTCAVELLS-GEVDOPEAVCLSPELRKKGVALL	USYAKSDIEVETODEDEVYELOFGRYFGKGKVKLGEPLDDD
Mokin-Tikiin		TOAVITID-GEVDQTERVOIDTEDRIGGTADE	
MATY-NVTLKT	PDGEHTIEVPDDEYILDVA-EEOGLD-LPYSCRAGAC	STCAGKIES-GSVDOSDOSFLDDDOIEAGYVLT	CVAYPTSDCTILTHOEEELY
MNTTTKTY-NUTLTN	E	FDCI CKULO-COVECTAKAL FELSEDELKACYTLT	
		TTCAAKI SE-GEVEOTDCMCI SPELOAECVALI	
MESU KITUUV		TSCARCIDE-GEVEQIDG-MOIDFEIQAEGIAIL	OVSTPRODIGING - MO - M
		TOCAVEISS-GEIEGPERMOLSPELERQGIRLE	
		CTCACKLES_CSUDOSDOSELDDDOTEACUUT	
CR	WEEKS DEFUDUTIDUA FDTVIFDAA - FENGID - DE SCROAC	SCUCRIFE-GEVNODDOVELDDDOLAKKEVLI	
		POCICKWE-CKVEOTCOASSELKSDETKACEVIJ	
MSKTU-TVFTDU		TTCAAOTLO-GEVDPCDA-MCTSPELOSECVULL	
		TTOAVEVIS-GETVOREA-MOISPELSOEGIVIL	OVERATED SKILL SKALL SK
MIRIT QIRIN		CAVICUD-GETTQTEA AGUDTEDRQRGTADE	
MATY FUTTI TH		CENTRAL VIE - CENTROS DO CENTRO DO DO VIA A CENTR	
MAII-KVILIN	WENGDEMONTS EVERYTI SUN - EDECID-LESSCRAGAC		CVAIFESDCTIEI-HQ-EBALI
		BOOLOWINE CTUEOTAKALEEL DDDELLERGWALL	
MTOTY TUETUU	ECTTUTTEVAEDOKILEVA-DKACLE-LDCC	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
MTOYY OTRINU		TICARQUEE-GIVDQSDG-MGISFELQIKGIALL	OVERAREDITET-EK-EBEVIIQUE PUT
MIQII-QIRIMA	QEGRATILEVFDDATTEASX-EDQGTE-EFF3CRAGAC	ACAVELVS-GEVIQPERVELSPELKERGIALE	<mark>o</mark> vsiaksbieveiQDEDEviEuQrokirokokkeloirMDDI
		CCUCRTUE-CENNICEDOCEIDDELTERCUNIT	CUANDERDOTTET - HO - FAVI D
GR	KRIQFFEIDVILEVFEDEIILSVA-EDEGLD-LFSSCASGAC		
	EQEGINITIDVFEDETIDDAA-EEQGID-DFSSCRAGAC		CVAIFRODUITEI - HQ - BEALI
MINDINRAF-SVILVN	EKGLEKTIEVNSDQIILDIA-ESQGVN-HPSSCRAGC	PDCLGRVLE-GIVEQIARALEPLRPNELKAGIVLL	CAASPISNCKIIIHQAEEILD
MIQII-IVEIHH	QGITHTIEVAEDQKILEVA-DKAGLE-LPSSCNAGV	TICAAQLLE-GIVDQSDGMGISPELQIKGIALL	CVSIPRSNLIIEIEKEEEVIIQQFPQP
MTQYY-QIRINH	RQEGKHYTLEVPDDHYILHSA-EDQGYE-LPFS <mark>C</mark> RNGA <mark>C</mark>	TACAVRIVS-GEVYQPEAVCLSPELKERGYALL	<mark>G</mark> VSYARSDLEVETQDEDEVYELQFGRYFGRGKKRLGIFMDDI
MATY-KVTLIN	EEQGINTTLEVPDDEYILDVA-EEQGLE-LPYSCRAGAC	STCAGKIQS-GTVDQSDQSFLDDDQIGAGYVLT	CVAYPTSDCTILT-HQEEELY
GS	/SKKKPPEMDVTITVPEDTYIFDAA-EDEGID-LPSSCRSGAC	SCVGRIES-GEIDQSDQSFLDDEQIAKGYVLL	CVAYPRSDCTIRTHQEAYLV
MSRTPRIDETF-SVTLIN	EKRDLDKTILVSEREIILDIA-EQEQLK-LPYSCRAGAC	IDOLGKVVK-GQVDQSEKALEFLKPDELKAGYVLL	CACSPRSDCVIETHQAEELFGED
MPKTY-SVEIIH	QGTTHTIEVSEDQTILKAA-LDAGIE-LPNSCNAGV	TTCAAQLLE-GTVEQSDGMGLSPELQKEGYALL	CVAFPRSNLKLESEKEDMVYHRQFGQS
MSQFH-TIRVNN	RQTGEHLTVSVPDDQYILHSI-EAQGYN-LPFS <mark>C</mark> RNGA <mark>C</mark>	TTOAVRIRS-GELYQPEAVGLSPELKQKGYALL	<mark>G</mark> VSYARSDLEVETQDEDEVYELQFGRFFARGRVRFGLPLDEI
MATY-KVTLVN	AAEGLNTTIDVADDTYILDAA-EEQGID-LPYSCRAGAC	STCAGKVVS-GTVDQSDQSFLDDDQIAAGFVLT	CVAYPTSDVTIETHKEEDLY
MATY-QVEVIY	QGQSQTFTADSDQSVLDSA-QAAGVD-LPAS <mark>C</mark> LTGV <mark>C</mark>	TTCAARILS-GEVDQPDAM <mark>G</mark> VGPEPAKQGYTLL	CVAYPRSDLKIETHKEDELYALQFGQPG
MSDTY-TVRIRD	RRTDEEFTVQVPPDRYILQTA-EEQGYE-LPFSCRNGAC	TACAVRVLG-GAIEQTEAMCLSAPLRQRGYALL	<mark>C</mark> VSYPRSDVIVETQDEDEVYMLQFGRYFGQGKVSFGLPLDEE
MATY-KVTLIS	·EAEGINETIDCDDDTYILDAA-EEAGLD-LPYS <mark>C</mark> RAGA <mark>C</mark>	STCAGKITS-GSIDQSDQSFLDDDQIEAGYVLI	CVAYPTSDCTIQTHQEEGLY
MSNTY-RVEIHH	·EGQIHQIDVPSDKYILQVA-EEAGFS-LPNS <mark>C</mark> NAGV <mark>C</mark>	TTCAAKILE-GEVDQSEGM <mark>G</mark> LSPDLQAQGYVLL	CIAHPRSDLKVETGKEEEVYQRQFGASS
MSAYHTIRIND	RQRDKSYCVQVPEDRYILPCA-ENQGSD-LPYS <mark>C</mark> RNGA <mark>C</mark>	TTCAVRVIS-GELYQPEAMCLSPELQEEGYALL	<mark>C</mark> VSYPRSDLEVETQDEDEVYELQFGRYFGKGKVRSGLPLDEI
MATF-KVTLIN	·EAEGTKHEIEVPDDEYILDAA-EEQGYD-LPFS <mark>C</mark> RAGA <mark>C</mark>	STCAGKLVS-GTVDQSDQSFLDDDQIEAGYVLI	CVAYPTSDVVIQTHKEEDLY
MASY-QVRLIN	·KKQDIDTTIEIDEETTILDGA-EENGIE-LPFS <mark>C</mark> HSGS <mark>C</mark>	SSCVGKVVE-GEVDQSDQIFLDDEQMGKGFALL	CVTYPRSNCTIKTHQEPYLA
MSKTY-TVEILH	·QGKTHTLQVPEDKTILSVA-DEQGLD-LPSS <mark>C</mark> HAGV <mark>C</mark>	TTCAGQIIT-GTVDQSDGM <mark>G</mark> VSPELQQQGYALL	CVAYPRSDLKIETEKEDTVYQMQFGK
MSETH-TVKVRD	P ATCKOVTI KUPEDPVTI UTA-FOOCUF-I PECOPNCA	TTCAVRVVS-GDIYQPEAVCLSLELRRQGYALL	CVSYARSDLEVETQDEDEVYELQFGRYFAKGRVKAGLPLDE
MATY-KVTLID	LEGASTTIDVPDDEYILDAA-EEQGLD-LPFSCRAGAC	STCAGKLVS-GTVDQSDQSFLDDDQIQAGYVLT	CVAYPTSDVTIETHKEEELY
MATY-KVTLID	LEGASTTIDVPDDEYILDAA-EEQGLD-LPFSCRAGAC	STCAGKLVS-GTVDQSDQSFLDDDQIQAGYVLI SSCVGKVVE-GEINQDDQIFLDDEQMGKGFALL	CVAYPTSDVTIETHKEEELY CVTYPRSNCTIKTHQEPYLV
MATY-KVTLID MATY-QVRLIN	LEGASTIDVPDEVILDAA-EEQGLD-LPFSCHSGS KKUNLDTIEIDEDTILDAA-EENGIE-LPFSCHSGS Q	STCAGKLVS-GTVDQSDQSFLDDDQIQAGYVLI SSCVGKVVE-GEINQDDQIFLDDEQMGKGFALL TTCAGQIIS-GTVDQTDGMGVSPELQKEGYVLI	CVAYPTSDVTIETHKEEELY
MATY-KVTLID MATY-QVRLIN	LEGASTIDVPDCYILDAA-EEQGLD-LPFSGRAGAA KKNLDTTIEDEDTITLDGA-EENGIE-LPFSGRAGGA 	STCAGKLVS-GTVDQSDQSFLDDDQIQAGYVLT SSCVGKVVE-GEINQDDQIFLDDEQMGKGFALL TTCAQQIIS-GTVDQTDGMGVSPELQKEGYVLL TTCAVRVVS-GEIYQPEAVGLSLELRRQGYALL	VAYPTSDYTIETHKERELY- CVTYPRSNCTIKTHQEPYLV- CVAYPRSDVKVETEKEEVYYQQPGK- CVSYRSDEVETQDEDVYELQFGRYFAKGRVKAGLPLDEI
		STÖAGKLVS-GTVDQSDQSELDDDQIQAGYVLT SSGVGKVVE-GEINQDDQ-IFLDDBQMGKGFALL TTQAQQIIS-GTVDQTDGMGVSPELQKEGVVLI TTQAVQVS-GEIYQPEAVGLSLELRRQGYALL	CVAYPTSDVTIETHKEEELY CVTYPRSNCTIKTHQEPYLV- CVAYPRSDVKVETEKEEVVYQKQFGK CVAYPRSDVKVETEKEEVVYQKQFGK VSYARSDLEVETQDEDEVYELQFGRYFAKGRVKAGLPLDEI
		STÇAGKLVS-GTVDQSDQƏFLDDDQIQAGYVLT SSÇVGKVVE-GEINQDDQIFLDDBOMGKGFALL TIQAGQIIS-GTVDQTDGMGVSPELQKEGYVLI TIQARVVS-GEIYQPEAVULSLELRRQGYALI STÇAGKITA-GTVDQSDQSFLDDEQIENNYVLT	CVAYPTSDVTIETHKEEELY- CVAYPRSNCTIKTHQEPYLV- CVAYPRSDVKVETEKEEVYYQKQFGK- UYSYARSDLEVETQDEBYYELQFGRYFAKGKVKAGLPLDEI CVAYPTSDCTIQTHKEEELY-
	LEGASTIDVPDDEYILDAA-EEQGLD-LPFSGRAGA 	STËAGKLVS-GTVDQSDQSFLDDDDQIQAGVVI SSËVGKVVE-GEINQDDQIFLDDDQMGKGFALL TTCAQQIIS-GTVDQTDGMGVSPELQKEGVVLI TTCAVRVVS-GEIYQPEAVULSLELRRQGVALL STËAGKITA-GTVDQSDQSFLDDEQIENNYVLT SSËVGKITVE-GEVDQSDQIFLDDDQMKGFALL	CVAYPTSDVTIETHKEEELY CVTYPRSNCTIKTHQEPYLV- CVAYPRSDVKVETEKEEVVYQKQPGK CVSYARSDLEVETQDEDEVYELQFGRYFAKGRVKAGLPLDEI CVAYPTSDCTIQTHKEEELY CVTYPRSNCTIKTHQEPYLV
		STQAGKLVS-GTVDQSDQSFLDDDQIQAGYVI SSCVGKVVE-GEINQDDQ-IFLDDEDMGKGFALI TIAGQIIS-GTVDQTDG-MGVBCKGFALI TIAVRVVS-GEIYQPEAVGLSLELRRQGYALI STQAGKITA-GTVDQSDQSFLDDEQIENNYVLI SSCVGKIVE-GEVDQSDQ-IFLDDDQMGKGFALI TICAAKITNGGTVDQSEG-MGVSDLQKDGYVLI	CVAYPTSDVTIETHKEERLY- CVAYPTSDVTIETHKEERLY- CVAYPTSDVKVETEKEEVYLV VSYAREDLEVETEKEEVYLYGKQFGK
		STEAGKLVS-GTVDQSDQSFLDDDQIQAGVVLI SSCVGKVVE-GEINQDDQIFLDDEQMGKGFALL TTCAQQIIS-GTVQTDGMGVSPELQKEGVVLI TTCAVRVVS-GEIYQPEAVGLSLELRRQGVALL STEAGKITA-GTVDQSDQSFLDDEQIENNYVLI SSCVGKIVE-GEVDQSDQIFLDDQQMGKGFALL TTCAVRVIS-GEINQPEA-MGVSPDLQKDGVVLI TTCAVRVIS-GEINQPEA-MGVSPDLQKDGVVLI	VAYPTSDVTIET HKEEELY CVTYPRSNCTIKTHQEPYLV- CVAYPRSDVKVET EKEEVYPLQFGR- CVSYRSDLEVET QDEDEVYELQFGRYFAKGRVKAGLPLDET CVAYPTSDCTIQT HKEEELY CVTYPRSDLKIIT HQEEVIV- CIAYPRSDLKIIT HQEEVYLV- CIAYPRSDLKIIT DQEEVYLV- CVSYRSDLEVET QDEDVYELQFGRFFAKGRVRAGPPLDET
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-MATY-KVTLID 		STAAGKLVS-GTVDQSDQSFLDDDQIQAGVVLT SSCVGKVVE-GEINQDDQILDDEQMGKGFALL TTDAQIIS-GTVDQTDGMGVSPLQKEGVVLI TTDAVRUVS-GEIYQPEA-VGLSLERKQGVALL STCAGKITA-GTVDQSDQSFLDDDQIGNGVVLI TTDAXKITNGGTVDQSEQILDDDDMGKGFALL TTDAXKITNGGTVDQSEG-MGVSPDLQKDGVVLI TTDAXKITS-GEIHQPEA-JLSPELRKQGVALL STCAGKVTS-GSVDQSDQSFLDDDQLEAGFVLI	VAYPTSDVTIETHKEEELY- CVTYPRSNCTIKTHQEPYLV- CVTYPRSDVKVETEK-EEEVYEQQFGK- (VSYRABLEVETQDEDEVYEQQFGRYFAKGRVKAGLPLDET CVAYPTSDCTIQTHKEEELY- CVTYPRSNCTIKTHQEPYLV- LTAYPRSDLKIITDQEEVYEQQFGK- USYARSDLEVETQDEEVYEQQFGK- USYARSDLEVETQDEEVYEQQFGKFFAKGKVRAGFPLDET CVAYPTSDVTITTHAEEELY-
		STQAGKLVS-GTVDQSDQFLDDDQQQAGVVI SSCWGKVVE-GEINQDDQFLDDDGMGKGFALI TTQAQIIS-GTVDQTDQWGVSPELQKEGVVLI TTQAQIIS-GTVDQSDQSFLDDEQIENNYVI SSCWGKIVE-GEVQGDQFLDDDQMGKGFALI TTQAKINGGTVDQSGDFLDDDQMGKGFALI TTQAKINGGTVDQSGDSFLDDQLEAGFVI STGAGKVIS-GSVDQSDQSFLDDQLEAGFVI SGASRILE-GIVEQDAWGNDDQLEAGFVI	CVAYPTSDVTIET HKEEELY CVTYPRSNCTIKTHQEPYLV- CVAYPRSDVKVET KKEEVVYQKQPGK CVSYARSDLEVET QDEDEVYELQFGRYFAKGRVKAGLPLDEI CVAYPTSDCTIQT HKEEELY CTYPRSDLKIIT DQEEVVYQKQPGK CVSYARSDLEVET QDEDEVYELQFGRFFAKGRVRAGFPLDEI CVAYPTSDVTITT HAEEELY CVAYPTSDVTITT HAEEELY CVAYPTSDVVI GQCVEDLVNDQFGKYQE
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		STCAGKLVS-GTVDQSDQFLDDDQQQAGVVI SSCWGKVVE-GEINQDDQ-IFLDDEGMGKGFALI TTCAQIIS-GTVDQTDQ-MWSPELQKKGFVLI TTCAQINS-GTVDQDQ-STLDDEQIENNYVI SSCWGKIVE-GEVQGDQSFLDDEQIENNYVI TTCAAKINGGTVDQSBQSFLDDDQLGKGFALI TTCAAKINGGTVDQSBQ-SLBSPLRKQGYALI STCAGKVIS-GENQGDQ-SFLDDQLEAGFVI TSCASRILE-GIVEQDA-SFLDDQLEAGFVI TSCASRILE-GIVEQDA-MQVSQALKKGYALI	VAYPTSDVTIET HKEEELY CVTYPRSDVTVET EKEEELY CVTYPRSDVKVET EKEEVYELQFGRYPAGRVKAGLPLDEI CVSYARSDLEVET QDEDEVYELQFGRYPAGRVKAGLPLDEI CVYPRSDLKIIT HQEEVYLV CTYPRSDLKIIT DQEBVYUQFGK- CVSYARSDLEVET QDEDEVYELQFGRPFAGRVRAGPPLDEI CVSYARSDLEVET QDEDEVYELQFGRYFAKGRVRAGPPLDEI CVAYPKSDLHVVI GDQVEDLINDQFGKY
		STQAGKLVS-GTVDQSDQSFLDDDQIQAGYVLT SSCVGKVVE-GEINQDDQTFLDDDGMGKGFALL TTQAGQIIS-GTVDQTDGMGVSPELQKEGYVLI TTQARVVS-GEIYQPEAVULSLELRRQGYALI SSCVGKIVE-GEVDQSDQSFLDDDQIGNGYVLT TCAAKTINGGTVDQSEQSFLDDDQMKGFALL TTQAXFINGGTVDQSEQSFLDDDQLEAGFVLT TSGASKILE-GIVQSDAMGLMDDLRKGFALL SSCVKIXS-GELQGDAMGLMDDLRKGFALL SSCTGKITA-GELDQSDANFLDDDQIKAGFVLT	CVAYPTSDVTIET HKEEELY- CVAYPTSDVTIET HKEEELY- CVAYPTSDCTIKT HQEPYLV- CVAYPTSDCTIQT HKEEELY- CVAYPTSDCTIQT HKEEELY- CVAYPTSDCTIKT HQEPYLV- CVAYPTSDCTIKT HQEPYLV- CVAYPTSDVTITT HAEEELY- CVAYPTSDVTITT HAEEAUL-
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		STAGKLVS-GTVDQSDQSFLDDDQIQAGYVLT SSCVGKVVE-GEINQDDQFLDDDQMKGFALI TTDAQUIS-GTVDQTDGMGVSPELQKEGYVLI TTDAVEVVS-GEYLQDEA-VULSLEHKQGYALI STCAGKITA-GTVDQSDQSFLDDDQIENGYVLI TTCAAKUYS-GEYLQDEA-MGVSDDQKKGFALI TTCAAKUTNGGTVDQSBQSFLDDDQLEAGFVLT TSCAGKVTS-GSVDQSDQSFLDDDQLEAGFVLT TSCAGKVIS-GEIHQPEAMGVSDQLKKGFALI SSCTAGKTA-GTVQSDQSFLDDDQIKAGFVLT SGAVKIS-GEIQSDQSFLDDDQIKAGFVLT SSCTAGKTA-GEIQSDQSFLDDDQIKAGFVLT SSCTAGKTA-GEIQSDQSFLDDBQIKAGFVLT SSCTAGKTA-GEIQSDQSFLDDBQIKAGFVLT SSCTAGKTA-GEIQSDQSFLDDBQIKAGFVLT TSCAAKLTD-GTVDQSDQSFLDDBQIKAGFVLT SSCTAGKAG-GEVQSGDQ-SFLDDBQIKAGFVLT TTCAAQLLE-GTVEQSDQWLSPELAGXTVT TTCAAQLE-GTVEQSDQ-WLSPELAGXTVT	VAYPTSDVTIETHKEEELY- CVYPYRSNCTIKTHQEEYLY- CVYPYRSNCTIKTHQEEYLY- CVAYPTSDCTIQTHKEEELY- CVYPRSNCTIKTHQEEYLV- CUAYPTSDCTIQTHKEEELY- CVAYPTSDLKIITDQEEVYVQKQFGK- UIAYPRSDLKVITQDEEVYVQKQFGK- VYSYRSDLEVETQDEEVYVELQFGRFFAKGRVRAGPPLDEI CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHQEEAIL- CVAYPTSDCTIITHQEEAIL- CVAYPTSDCTIITHQEEAIL- CVAYPTSDCTIITHQEEAIL- CVAYPTSDCTIITHQEEAIL- CVAYPTSDCTIITHQEEAIL- CVAYPTSDCTIITHQEEAIL- CVAYPTSDCTIITHQEEAIL- CVAYPTSDCTIETHQEEAIL- CVAYPTSDCTIETHQEEAIL- CVAYPTSDCTIETHQEEAIL- CVAYPTSDCTIETHQEEAIL- CVAYPTSDCTIETHQEEAIL- CVAYPTSDCTIETHQEEAIL- CVAYPTSDCTIETHQEEAIL- CVAYPTSDCTUETHQHQHQHQHQHQHQHQHQH
	<ul> <li>LEGASTIDVPDEYILDAA-EEQGLD-LPFSGRAGA</li> <li>LEGASTIDVPDEYILDAA-EEQGLD-LPFSGRAGA</li> <li>CONLDTIEIDEDTILOGA-EENGIE-LPFSGRAGA</li> <li>CONLDTVEDETILSVA-DEQGLD-LPFSGRAGA</li> <li>CONTENTIOTEEDTILLOA-EENGIE-LPFSGRAGA</li> <li>EAEGLNTIDCEEDTYILDAA-EENGIE-LPFSGRAGA</li> <li>CONTENTIVEVPERTILSVA-EENGIE-LPFSGRAGA</li> <li>CONTENTIVEVPERTILSVA-EENGIE-LPFSGRAGA</li> <li>CONTENTIVEVPERTILSVA-EENGIE-LPFSGRAGA</li> <li>CONTENTIVEVPERTILSVA-EENGIE-LPFSGRAGA</li> <li>CONTENTIVEVPERTILSVA-EENGIE-LPFSGRAGA</li> <li>CONTENTIVEVPENTILISA-ENGGED-LPFSGRAGA</li> <li>CONTENTIVEVPENTILISA-ENGGED-LPFSGRAGA</li> <li>CONTENTIVEVPENTILSA-EENGID-LPFSGRAGA</li> <li>CONTENTIVEVPENTILSA-EENGID-LPFSGRAGA</li> <li>CONTENTIVEVPDEYILDAA-EENGID-LPFSGRAGA</li> <li>EAEGIDTIEVPDEYILDAA-EENGID-LPFSGRAGA</li> <li>EAEGIDTIEVPDEYILDAA-EENGID-LFFSGRAGA</li> <li>CKCRITTIEVPDEYILDAA-EENGID-LFFSGRAGA</li> <li>CKCRITTIEVPDENGILLAA-EENGID-LFFSGRAGA</li> <li>CKCRITTIEVPDENGILLAA-EENGID-LFFSGRAGA</li> <li>CKCRITTIEVPDENGILLAA-EENGID-LFFSGRAGA</li> <li>CKCRITTIEVPDENGILLAA-EENGID-LFFSGRAGA</li> <li>CKCRITTIEVPDENGILLAA-EENGID-LFFSGRAGA</li> </ul>	STQAGKLVS-GTVDQSDQSFLDDDQIQAGYVI SSCVGKVVE-GEINQDDQFLDDDGMGKGFALI TIAGQIIS-GTVDQTDQWIVSPELQKEGYVLI STQAGKITA-GTVDQSDQSFLDDEQIENNYVLI SSCVGKIVE-GEVQDSDQSFLDDDQMGKGFALI TTQAKITNGGTVDQSEQ-MQVSPDLQKGFVLI STQAGKVIS-GEINQSDQ-SFLDDDQLEAGFVLI SCASKILE-GTVEQDEAWIVSQALKDKGYALI SSCVGKVVE-GEIDQSDQWILDDDQLKAGFVLI STGAGKLTD-GTUQQFEAWIVSQALKDKGYALI SSCVGKVVE-GEIDQSDQWILDDDQLKAGFVLI STGAKLID-GTUQQFEAWIVSQALKDKGYALI SSCVGKVVE-GEIDQSDQWILDDDQLKAGFVLI SSCVGKVVE-GEIDQSDQWILDDQQLKAGFVLI SSCVGKVE-GEIDQSDQWILDDQLGKGFVLI SSCVGKVE-GEIDQSDQWILDDQLGKGFVLI SSCVGKVE-GEIDQSDQWILDDQLGKGFVLI SSCVGKVE-GEIDQSDQWILDDQLGKGFVLI SSCVGKVE-GEIDQSDQWILDDQLGKGFVLI SSCVGKVE-GEIDQSDQWILDDQLGKGFVLI SSCVGKVE-GEIDQSDQWILDDQLGKGFVLI SSCVGKVE-GEIDQSDQWILDDQLGKGFVLI SSCVGKVE-GEIDQSDQWILDQQLGAGYVLI A_AVRVIR-GEVYQPEAWILSPELAGYVLI	CVAYPTSDVTIET HK EERLY- CVAYPTSDVTIET HK EERLY- CVAYPTSDVTVET EK EEVYUQKQFGK- UYSTARSDLEVET QL EDEVYELQFGRYFAKGRVRAGLPLDET CVAYPTSDCTIQT HK EEELY- CVTYPRSNCTIKT HQ EEVVQKQFGK- CVSYARSDLEVET QD EDEVYELQFGRYFAKGRVRAGPPLDET CVAYPTSDVTITT HA EERLY- CVAYPTSDVTITT HA EERLY- CVAYPTSDVTITT HA EERLY- CVAYPTSDVTITT HQ EERVYDLQFGRYFAKGRVRAGPPLDET CVAYPTSDVTITT HQ EERLY- CVAYPTSDTTITT HQ EERLY- CVAYPTSDTUET HQ EERLY- CVAYPTSDTUET HQ EERLY- CVAYPTSDTUET HQ EERLY- CVAYPTSDLEVET QD EDEVYDLQFGQPQ- CVAYPTSDLEVET QD EDEVYDLQFGRYFAKGKVQFGLPLDET
-MATY-KVTLID -MATY-QVRLIN -MSKTY-TVFILH -MSTY-TIKVRD -MATY-KVTLIH -MATY-QVRLIN -MATY-VTLIH -MSY-VTLIN -MSY-NTLIS -MSY-NTLIS -MSY-KVTLIS -MSY-KVTLIS -MATY-KVRLIN -MATY-KVRLIN -MATY-KVRLIN -MATY-KVRLIN -MATY-KVRLIN -MATY-KVRLIN		STÜAGKLVS-GTVDQSDQSLDDDQIQAGYVLT SSCVGKVVE-GEINQDDQTLDDDSQMGKGFALL TTDAQQIIS-GTVDQTDGWGVSPELQKEGYVLI TTDAVRVVS-GEIYQPEAVGLSLELRRQGYALI STĞAGKITA-GTVDQSDQSLDDDQMGKGFALI TTQAXRVVS-GEIYQPEAVGLSDEKRQGYALI TTQAXRINGGTVDQSBQSLDDDQLEAGFVLT TSGASKILE-GIYQGEDAWGLNDDLRKGFALI SSCTGKITA-GEINQSDQSLDDDQLEAGFVLT SSCAKKIS-GIYQGEDAWGLNDDLRKGFALI SSCTGKITA-GEINQSDQSLDDDQIKAGFVLT SSCAKKIS-GEINQSDQSLDDEQIEAGFVLT TTQAQELE-GTVEQSDQSLDDEQIEAGFVLT TTQAQELE-GTVEQSDQNCLDDQUKAGFVLT TTCAQELE-GTVEQSDQSLDDEQIEAGFVLT TTCAQELE-GTVEQSDQNCLDSPELAGFVLT TTCAQUESCTVDQSDQSLDDEQIEAGFVLT TTCAQUESCTVDQSDQNCLSPSLQAGFVLT TTCAQUESCTVDQSDQNCLSPSLQAGFVLT TTCAQUESCTVDQSDQNCLSPSLQAGFVLT TTCAQUESCTVDQSDQNCLSPSLQAGFVLT TTCAQUESCTVDQSDQSLDDEQIEAGFVLT TTCAQUESCTVDQSDQSLDDEQUEAGFVLT	VAYPTSDVTIETHKEEELY- CVAYPTSDVTIETHQEEYIV VAYPRSDVKVETEKEEVYYQQQGGK- CVAYPTSDCTIQTHKEEELY- CVAYPTSDCTIQTHKEEELY- CVAYPTSDCTIQTHKEEELY- VSYARSDLEVETQDEEEVYQQQGGK- VSYARSDLEVETQDEEEVYELQFGRFFAKGRVRAGFPLDEI CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDTTITHAEEELY- CVAYPTSDTTITHAEEELY- CVAYPTSDTTITHAEEELY- CVAYPTSDTTITHQEEALY- CVAYPTSDTTITHQEEALY- CVAYPTSDTTITHQEEALY- CVAYPTSDTTITTHQEEALY- CVAYPTSDTTITTHQEEALY- CVAYPTSDTTITTHQEEALY- CVAYPTSDTTITTHQEEALY- CVAYPTSDTTITTHQEEALY- CVAYPTSDTTITTHQEEALY- CVAYPTSDTTITTHQEEALY- CVAYPTSDTTITTHQEEALY- CVAYPTSDLFVETQDEDEVYELQFGRYFAKGKVQFGLPLDEI EIAYPOSDLEVETQDEDEVYELQFGRYFAKGKVQFGLPLDEI EIAYPOSDLEVETQNEEENY-
	<ul> <li>LEGASTIDVPDEYILDAA-EEQGLD-LPFSGRAGA</li> <li>LEGASTIDVPDEYILDAA-EEQGLD-LPFSGRAGA</li> <li>CONDITIEIDEDTILOGA-EENGIE-LPFSGRAGA</li> <li>GATTILQVFERTILSVA-DEQGLD-LPFSGRAGA</li> <li>EAEGLNTIDCEEDTYILDAA-EEAGIE-LPFSGRAGA</li> <li>EQGNTIQVPERTILSVA-EEAGIE-LPFSGRAGA</li> <li>E</li></ul>	STQAGKLVS-GTVDQSDQFLDDDQIQAGYVI SGCWGKVE-GEINQDDQFLDDDGMGKGFALI TTAGQIIS-GTVDQDDQWISPERLQKGGYVLI TTAGQIIS-GTVDQSDQSFLDDEQIENYVIJ SGCWGKIVE-GEVQGDQSFLDDDQMGKGFALI TTAAKINGGTVDQSEQMCVSPDQLKGFVLI TTAAKINGGTVDQSEQMCVSDQLKGFVLI SGCAKIS-GTUQQFEAMUSQALKDKGYALI SGCAKIS-GTUQQFEAMUSQALKDKGYALI SGCAKIS-GTVQQSDQNFLDDDQIKAGFVLI STGAKLTD-GTUQQFEAMUSQALKDKGYALI SGCAKIS-GTVQQSDQNFLDDDQIKAGFVLI STGAKLTD-GTVQGDQNFLDDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI SGCAKIS-GTVQQSDQNFLDDQIKAGFVLI	CVAYPTSDVTIET HK EEELY- CVAYPTSDVTIET HK EEELY- CVAYPTSDVTVET CB EEVYUQKQFQK- CVAYPTSDCTIQT HK EEELY- CVAYPTSDCTIQT HK EEELY- CVAYPTSDCTIQT HK EEELY- CVAYPTSDVTITT HQ EEELY- CVAYPTSDVTITT HQ EEELY- CVAYPTSDVTITT HA EEELY- CVAYPTSDVTITT HA EEELY- CVAYPTSDVTITT HQ EEELY- CVAYPTSDVTITT HQ EEELY- CVAYPTSDVTITT HQ EEALY- CVAYPTSDTTITT HQ EEALY- CVAYPTSDCTIET HQ EEALY- CVAYPTSDCTUET HQ EEXYTDCQFQCY- CVAYPTSDLEVET QD EDEVYELQFGRYFAKGKVQFGLP LDEF CVAYPTSDLEVET QD EDEVYELQFGRYFAKGKVQFGLP LDEF CTAPPTSQUTTET HK EEELY
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	<ul> <li>LEGASTIDVPDDEYILDAA-EEQGLD-LPFSGRAGAK</li> <li>LEGASTIDVPDDEYILDAA-EEQGLD-LPFSGRAGAK</li> <li>CHNLDTIENDEDTIILOGA-EENGIE-LPFSGRAGAK</li> <li>GRUTTLQVPDDRYILHSA-EQQGVE-LPFSGRAGAK</li> <li>AGGENTLQVPDDRYILHSA-EQQGVE-LPFSGRAGAK</li> <li>GRUTTIDVEDETIILOGA-EERAGIE-LPFSGRAGAK</li> <li>GRUTTIEVPDRYILHSA-EQGID-LPFSGRAGAK</li> <li>GRUTTIEVPDRYILHSA-EQGID-LPFSGRAGAK</li> <li>GRUTTIEVPDRYILHSA-EQGID-LPFSGRAGAK</li> <li>GRUTTIEVPDRYILHSA-ERQGID-LPFSGRAGAK</li> <li>GRUTTIEVPDRYILHSA-ERQGID-LPFSGRAGAK</li> <li>GRUTTIEVPDDEYILDAA-EEQGID-LPFSGRAGAK</li> <li>GRUTTIEVPDDEYILDAA-EEQGID-LPFSGRAGAK</li> <li>GRUTTIEVPDDEYILDAA-EEQGLD-LPFSGRAGAK</li> <li>GRUTTEVPDDEYILDAA-EEQGUT-LPFSGRAGAK</li> <li>GRUTTEVPDDEYILDAA-EEQGUT-LPFSGRAGAK</li> <li>GRUTTEVPDDEYILDAA-EEQGUT-LPFSGRAGAK</li> <li>GRUTTEVPDDEYILDAA-EEQGUT-LPFSGRAGAK</li> </ul>	ST CAGKLVS-GTVDQSDQFLDDDQIQAGVVI SG CVGKVVE-GEINQDDQFLDDDGMGKGFALI TT CAGIIS-GTVDQDDQSLDDEGMGKGFALI TT CAGIIS-GTVDQSDQSLDDEQIENNYVLT SS CVGKIVE-GEVQGDQTLDDDQMGKGFALI TT CAKITNGGTVDQSEQ-SLDDDQLENGVVI TT CAKITNGGTVDQSEQ-SLDDDQLENGVVI SG CAGKLS-GTUQQFEAMUSQDQLKAGFVLT SG CASKLE-GTUQQFEAMUSQDLAGFVLT ST CAGKILS-GTUQQFEAMUSQDLAGFVLT ST CAGKILS-GTUQQFEAMUSQALKDKGYALI SG CAKILS-GEUQSDQNFLDDDQLENGFVLT ST CAGKILS-GTUQQFEAMUSQALKDKGYALI SG CAKILS-GEUQSDQNFLDDDQLAGFVLT TT CAUSTIG-GTUQQFEAMUSQALKDKGYALI SG CAKILS-GTUQQFEAMUSQFUAGSVLI TAAUKUS-GTUQQFEAMUSPELAGGYALI SG CAKILS-GTUQQFEAMUSPELAGGYALI TAAUKUS-GTUQGSQSLDDQUFAGSVLI TAAUKUS-GTUQGSQNLDSPQVAGSVLI TAAUKUS-GTUQGSQNLSFQVAAGSVLI TAAUKUS-GTUQGSQNLSFQVAAGSVLI TAAUKUS-GTUQGSQNLSFQVAAGSVLI TAAVKUS-GTUQGSQNLSFQVAAGSVLI TAAVKUS-GTUQGSQNLSFQVAAGSVLI	CVAYPTSDVTIETHKEEELY- CVAYPTSDVTIETHQEEYLV- CVAYPTSDVTVETEQEEYVIQKQPGK- VAYPTSDCTIQTHKEEELY- CVAYPTSDCTIQTHKEEELY- CVAYPTSDCTIQTHKEEELY- CVAYPTSDVTITTHQEEYVV- GVSTARBDLEVETQDEDEVYELQPGRPFAKGRVRAGPPLDE CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHQEEALY- CVAYATSDCTIQTHQEEALY- CVAYPTSDCTIITHQEEALY- CVAYPTSDCTIITHQEEALY- CVAYPTSDCTIITHQEEALY- CVAYPTSDCTIITHQEEALY- CVAYPTSDCTIITHQEEALY- CVAYPTSDCTIITHQEEALY- CVAYPTSDCTIITHQEEALY- CVAYPTSDCTIITHQEEALY- CVAYPTSDCTIETHQEEALY- CVAYPTSDCTIETHQEEALY- CVAYPTSDCTIETHQEEALY- CVAYPTSDCTIETHQEEXVICLQPGRYTAKGKVQFGLPLDE CTAYPTGQCVTIETHQEELY- CVAYPTSDCTUETHQEELY- CVAYPTSDCTUETHQEELY- CVAYPTSDCTUETHQEELY CVAYPTSDCTUETHQEELY CVAYPTSDCTUETHQEELY CVAYPTSDCTUETHQEELY CVAYPTSDCTUETHQEELY
		ST AGKLVS-GTVDQSDQSFLDDDQIQAGYVI SS CVGKVVS-GEINQDDQTFLDDEOMGKGFALL TT AGQIIS-GTVDQTDGMCVSPELQKEGYVLI TT AVRVVS-GEIYQPEAVLSLEILRRQGYALI ST AGKITA-GTVDQSDQSFLDDDQIENRYVVI SS CVGKIVE-GEVQSDQMCVSPDQUKGFALI TT AAKTVGGTVDQSEQSFLDDDQLEAGFVLT TS ASKILE-GIVGQEDAMCVSDLKKGFALI SS TGKITA-GELDQSDQNFLDDDQIKAGFVLT ST AGKLTD-GTVDQSDQNFLDDDQIKAGFVLT ST AGKLTD-GTVDQSDQNFLDDDQIKAGFVLT ST AGKLTD-GTVQSDQNFLDDDQIKAGFVLT ST AGKLTD-GTVQSDQNFLDDDQIKAGFVLT ST AGKLTD-GTVQSDQNFLDDDQIKAGFVLT ST AGKLTD-GTVQSDQNFLDDDQIKAGFVLT ST CAGKLTD-GTVQSDQNFLDDQIKAGFVLT ST CAGKLTD-GTVQSDQNFLDDQIKAGFVLT ST CAGKLTD-GTVQSDQNFLDDQIKAGFVLT ST CAGKLTD-GTVQSDQNFLDDQIKAGFVLT ST CAGKLTD-GTVQSDQNFLDDQIAGVVLT ST CAGKLS-GTVQDSDQSFLDDDQIEAGYVLT ST CAGKLS-GTVDQSDQNFLSPSQVAGYVLT ST CAGKLS-GTVDQSDQNFLSPSQVAGYVLT TT AVRUS-GDLEQKYANLSPNLRDQGYALW	CVAYPTSDVTIET HKEEELY- CVAYPTSDVTIET HKEEELY- CVAYPTSDVTIET HQEEYIV- VSYARSDLEVET QDEEEVYELQFGRYFAKGRVRAGLPLDEI CVAYPTSDCTIQT HKEEELY- CVAYPTSDCTIQT HKEEELY- CVAYPTSDVTITT HAEEELY- CVAYPTSDVTITT HQEEAXL CVAYPTSDVTITT HQEEAXL CVAYPTSDCTLET HQEEAXL CVAYPTSDCTLET HQEEXIL- CVAYPTSDVTLET HQEEXIL- CVAYPTSDVTLET HQEEXIL- CVAYPTSDVTLET HQEEXIY- CVAYPTSDVTLET HQEEXIY- CVAYPTSDVTLE HQEXIY- CVAYPTSDVTLE HQEXIY- CVAYPTSDVTLE HQEXIY- CVAYPTSDVTLE HQEXIY- CVAYPTSDVTLE HQEXIY- CVAYPT
	<ul> <li>LEGASTIDVPDDEYILDAA-EEQGLD-LPFSGRAGAA</li> <li>LEGASTIDVPDDEYILDAA-EEQGLD-LPFSGRAGAA</li> <li>K</li></ul>	ST CAGKLVS-GTVDQSDQFLDDDQIQAGVVI SS CVGKVVE-GEINQDDQFLDDDEQMGKGFALI TTCAQIIS-GTVDQDDQFLDDEQMGKGFALI TTCAQIIS-GTVDQDQDSLDDEQIENNYVLT SS CVGKIVE-GEVQGDQFLDDDQMGKGFALI TTCAAKINGGTVDQSEQ-SLDDDQLEAGFVLT STCAGKILG-GIVQQSDQSLDDDQLEAGFVLT SCARKLE-GIVEQDDA-MUNDDQIKAGFALI SGCAKLS-GIVQQSDQSLDDDQLEAGFVLT SGCAKLS-GIVQQSDQSLDDDQLEAGFVLT SGCAKLS-GIVQQSDQNUSDDQLKAGFVLT SS CAKLS-GIVQQSDQTLDDDQLKAGFVLT SS CAKLS-GIVQQSDQTLDDDQLKAGFVLT SS CAKLS-GIVQQSDQTLDDDQLKAGFVLT SS CAKLS-GIVQQSDQTLDDDQLKAGFVLT SS CAKLS-GIVQQSDQTLDDDQLKAGFVLT SS CAKLS-GIVQQSDQTLDDDQLKAGFVLT SS CAKLS-GIVQQSDQSLDDDQLEAGFVLT SS CAKLS-GIVQQSDQSLDDDQLEAGFVLT TTCAAQLEGISGIGSGISGISGUSAGA SS CAKLS-GIVQQSDQSLDDQLEAGFVLT TTCAAQLS-GIVQQSDQSLDDQLEAGFVLT TTCAAQLS-GIVQQSDQSLDDQLEAGFVLT TTCAAVLS-GIVQQSDQSLDDQLEAGFVLT TTCAAVLS-GIVQQSDQSLDDQLEAGFVLT SCAGKLS-GIVQSDQNLSPSQVAAGVVLT TTCAVRUS-GIVQQSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDDDQLEAGFVLT TTCAVRUS-GIVQSSDQSLDDDDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDDDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDDQLAGFVLT TTCAVRUS-GIVQSSDQSLDDDQLAGFVLT	CVAYPTSDVTIET HK EERLY- CVAYPTSDVTIET KK EERYUV (VAYPTSDVTIET KK EERYUVQKQFGK VAYPTSDCTIQT HK EERYVQKQFGK CVAYPTSDCTIQT HK EERYVQKQFGK CVAYPTSDCTIQT HK EERLY- CVAYPTSDVTITT HA EERLY- CVAYPTSDVTITT HA EERLY- CVAYPTSDVTITT HA EERLY- CVAYPTSDVTITT HA EERLY- CVAYPTSDVTITT HA EERLY- CVAYFTSDVTITT HA EERLY- CVAYFTSDVTITT HA EERLY- CVAYFTSDVTITT HG EERLY- CVAYFTSDVTITT HG EERLY- CVAYFTSDVTITT HG EERLY- CVAYFTSDVTITT HG EERLY- CVAYFTSDVTITT HG EERLY- CVAYFTSDVTITT HG EERLY- CVAYFTSDVTIET HK EERLY- CVAYFTSDVTIET HK EERLY- CVAYFTSDVTIET HK EERLY- CVAYFTSDVTIET HK EERLY- CVAYFTSDVTIET HK EERLY- CVAYFTSDVTIET HK EERLY- CVAYFTSDVTIET HG EERLY- CVAYFASDCTUET HG EERLY- CVAYFASDCTUET HG EERLY- CVAYFASDCTUET HG EERLY- CVAYFASDCTUET HG EERLY- CVAYFASDCTUET HG EERLY- CVAYFASDCTUET HG EERLY-
	<ul> <li>LEGASTIDVPDRYILMA ELGOID INTERNO</li> <li>LEGASTIDVPDRYILMA ELGOID IPPS RAGA</li> <li>K</li></ul>	ST AAGKLVS-GTVDQSDQSLDDDQQQAGVVI SS CVGKVVE-GEINQDDQTLDDDGMGKGFALL TT AAGQIIS-GTVDQTDGWVSPELQKBGVVLI TT AVRVVS-GEIYQPEAVULSLELRRQGVALI ST AAGKITA-GTVDQSDQSLDDDQMGKGFALI TT AAKTVGGTVDQSBQWUSPELQKBGVVLI TT AAKTVGGTVDQSBQWUSPELQKBGVVLI ST AAGKVTS-GSTUQGEDAWUSPELQKBGVVLI ST AAGKVTS-GSTUQGEDAWUSPELQKBGVVLI ST AAGKVTS-GSTUQGEDAWUSPELQKBGVVLI ST AAGKVTS-GSTUQGEDAWUSPELQKBGVVLI ST AAGKVTS-GSTUQGEDAWUSPELQKBGVVLI ST AAGKVTS-GSTUQGEDAWUSPELQKBGVVLI ST AAGKLTD-GTVDQSDQWUSPELQKBGVVLI ST CAAGKLTD-GTVDQSDQWUSPELQKBGVVLI ST CAAGKLTD-GTVDQSDQSLDDDQLAGBVVLI ST CAAGKLTD-GTVDQSDQWLSPELQABGVVLI SG CAKKLS-GTVDQSEQSLDDDQLBAGVVLI SG CAKKLS-GTVDQSEQSLDDDQLBAGVVLI SG CAKKLS-GTVDQSDQSLDDDQUFAGGVVLI SG CAKKLS-GTVDQSDQSLDDDQUFAGGVVLI SG CAKKLS-GTVDQSDQSLDDDQUFAGGVVLI SG CAKKLS-GTVDQSDQSLDDDQUFAGGVVLI SG CAKKLS-GTVDQSDQSLDDDQUFAGGVVLI SG CAKKLS-GTVDQSDQSLDDDQUFAGGVVLI SG CAKKLS-GTVDQSDQSLDDDQUFAGGVVLI SG CAKKLS-GTVDQSDQSLDDDQUFAGGVVLI ST CAGKKLDS-GUFQDQDQSLDSPQQGVALW ST CAKKLS-GUFQDQDQ-SLDDQUFAGGVVLI ST CAKKLS-GUFQCYQSLDDDQUFAGGVVLI ST CAKKLS-GUFQCYQSLDDDQUFAGGVVLI ST CAKKLS-GUFQCYQSLDDDQUFAGGVVLI ST CAKKLS-GUFQCYQSLDDDQUFAGGVVLI ST CAKKLS-GUFQCYQSLDDDQUFAGGVVLI ST CAKKLS-GUFQCYQSLDDDQUFAGGVVLI ST CAKKLS-GUFQCYQSLDDQUFAGGVVLI ST CAKKLS-GUFQCYQCASLDDQUFAGGVVLI ST CAKKLS-GUFQCYQCASLDDQUFAGGVVLI ST CAKKLS-GUFQCYQCASLDDQUFAGGVVLI ST CAKKLS-GUFQCYQCASLDDQUFAGGVVLI ST CAKKLS-GUFQCYQCASLDDQUFAGGVVLI ST CAKKLS-GUFQCASLDDQUFAGGVVLI ST CAKKLS-GUFQCASLDDQUFAGGVVLI ST CAKKLS-GUFQCASLDQUFAGGVVLI ST CAKKLS-GUFQCASLDQUFAGGVVLI ST CAKK	CVAYPTSDVTIETHKEEELY- CVAYPTSDVTIETHKEEELY- CVAYPTSDVTIETHQEPYIV- VSYARSDLEVETQDEDYYELQGGKYFAKGRVRAGLPLDEF CVAYPTSDCTIQTHKEEELY- CVAYPTSDCTIQTHKEEELY- CVAYPTSDVTITTQDEDEVYELQFGRFFAKGRVRAGFPLDEF CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDTTITTHAEEELY- CVAYPTSDTTTTHAEEELY- CVAYPTSDTTTTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTITTHAEEELY- CVAYPTSDVTIETHQEEAIL- CVAYPTSDLEVETQDEDEVYELQFGRYFAKGKVQFGLPLDED CVAYPTSDUFVETQDEDEVYELQFGRYFAKGKVQFGLPLDED CIAYPQSDVTIETNKEEELY- CIAYPCSDCTIETNKEEELY- CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKEEELY CVAYPASDCTIETNKCOV CVAYPASDCTIETNK

>641677669\_Cyanothece\_sp\_ATCC\_51142\_XY=TF >641676595\_Cyanothece\_sp\_ATCC\_51142\_XY=FF >641675121\_Cyanothece\_sp\_ATCC\_51142\_XY=TG >641676148\_Cyanothece\_sp\_ATCC\_51142\_XY=TG

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>2509576475 Pleurocapsa\_sp\_PCC\_7327\_XY=SF >2509575425\_Pleurocapsa\_sp\_PCC\_7327\_XY=SF >2509577373\_Pleurocapsa\_sp\_PCC\_7327\_XY=FF >2509574243\_Pleurocapsa\_sp\_PCC\_7327\_XY=TG >2509576177\_Pleurocapsa\_sp\_PCC\_7327\_XY=TG

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>644979811\_Cyanothece\_sp\_PCC\_8002\_XY=SF >644979243\_Cyanothece\_sp\_PCC\_8002\_XY=SF >644979103\_Cyanothece\_sp\_PCC\_8002\_XY=FF >644981264\_Cyanothece\_sp\_PCC\_8002\_XY=TG >644978511\_Cyanothece\_sp\_PCC\_8002\_XY=TG

>643480033\_Cyanothece\_gp\_PCC\_7424\_XY=SF >643480365\_Cyanothece\_gp\_PCC\_7424\_XY=SF >643479357\_Cyanothece\_gp\_PCC\_7424\_XY=TF >643482024\_Cyanothece\_gp\_PCC\_7424\_XY=TG >643478783\_Cyanothece\_gp\_PCC\_7424\_XY=TG

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>637234546\_Nostoc\_sp\_PCC\_7120\_XY=SF >637231797\_Nostoc\_sp\_PCC\_7120\_XY=SF >637231146\_Nostoc\_sp\_PCC\_7120\_XY=TG >637233304\_Nostoc\_sp\_PCC\_7120\_XY=TG

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>2509438340\_Microcoleus\_sp\_PCC\_7113\_XY=SF >2509434797\_Microcoleus\_sp\_PCC\_7113\_XY=SF >2509433114\_Microcoleus\_sp\_PCC\_7113\_XY=SF >2509433371\_Microcoleus\_sp\_PCC\_7113\_XY=SF >2509435084\_Microcoleus\_sp\_PCC\_7113\_XY=TG >2509434121\_Microcoleus\_sp\_PCC\_7113\_XY=TG

>641612336\_Synechococcus\_sp\_PCC\_7002\_XY=SF >641612335\_Synechococcus\_sp\_PCC\_7002\_XY=SF >641610634\_Synechococcus\_sp\_PCC\_7002\_XY=TG

>2504682534\_Crinalium\_epipsammum\_PCC\_9333\_XY=SF >2504683757\_Crinalium\_epipsammum\_PCC\_9333\_XY=SF >2504684382\_Crinalium\_epipsammum\_PCC\_9333\_XY=TG >2504686495\_Crinalium\_epipsammum\_PCC\_9333\_XY=TG **Part C:** Cyanobacteria having one (or two) Fds from the blue group are marked in blue in the phylogenetic tree of cyanobacteria published by Shih et al. [12].



**Supplementary Figure 17A:** Superimposition of Fd2 to the structure of the PSI:Fd1 complex Fd2 was aligned to Fd1 in the PSI:Fd co-crystal structure (PDB: 5ZF0) by using the  $\alpha$ -carbons. The PSI subunits in proximity to Fd2 are shown in cartoon mode: PsaA, C, D, E are colored grey, light pink, cyan (transparent) and yellow, respectively. Fd2 is shown in green. The Fd2 cluster, F<sub>B</sub> and F<sub>A</sub> are visible from left to right.

After alignment, PSI atoms within a distance of 2 Å from Fd are identified as belonging to Arg36 and Arg40 from PsaA and Lys34 from PsaC. These residues, colored by element, are displayed as sticks together with the Fd2 residues involved in steric hindrance (as well as Phe72). The pairs of residues involved in steric hindrance are labeled **a** (Arg40<sub>PsaA</sub>, Asp69<sub>Fd2</sub>), **b** (Arg36<sub>PsaA</sub>, Asp79<sub>Fd2</sub>) and **c** (Lys34<sub>PsaC</sub>, Tyr46<sub>Fd2</sub>). Whereas a very strong steric clash is involved in **a**, only a limited steric hindrance is involved in **b** and **c**.



Supp. Figure 17B: Discussion related to intracomplex reduction of Fds by PSI

It was initially proposed that the presence of several phases in the kinetics of intracomplex Fd reduction was due to different conformations of the PSI:Fd complex [13], leading to different ET electronic couplings (conformational model). More recently, an alternative explanation was proposed where only the fastest sub- $\mu$ s phase corresponds to real ET [11], in the sense of a non-adiabatic tunneling reaction [14, 15]. In this interpretation, intracomplex Fd reduction is incomplete during the initial sub- $\mu$ s phase due to a small equilibrium constant K<sub>ET</sub> of the reaction: PSI<sub>red</sub>:Fd<sub>ox</sub>  $\rightarrow$  PSI<sub>ox</sub>:Fd<sub>red</sub>. Then, further Fd reduction proceeds due to energetic relaxation of the PSI<sub>ox</sub>:Fd<sub>red</sub> and/or fast dissociation of Fd<sub>red</sub> from PSI (relaxation model). In this context, it must be recalled that there is some uncertainty about the midpoint potential of (F<sub>A</sub> F<sub>B</sub>) with published values which span between -440 and -550 mV [16-18]. Moreover, it has been recently found that the driving force for Fd reduction within the complex is lower than what can be calculated from the midpoint potentials of the separated partners [11], a situation which may favor a fast turnover of Fd reduction and release.

Within this model, the difference in the intracomplex kinetics of Fd reduction should mostly depend upon the driving force of Fd reduction (assuming similar distances and ET couplings with the different Fds). Indeed the higher midpoint potential of Fd1' (*vs* Fd1) would correspond to a higher value of  $K_{ET}$  and consequently a larger contribution of the sub-µs phase. The slow Fd2 kinetics would also be attributed to the fact that the Fd2 intracomplex reduction is endergonic with a very low value of  $K_{ET}$  and consequently no significant sub-µs phase.

Data collection	Fd2 (Native)	Fd1(Native)
Beamline	BL38XU (SPring-8)	BL41XU (SPring-8)
Wavelength (Å)	1.000	1.000
Average dose (MGy)	0.22	0.67
Space group	$P2_1$	<i>C</i> 2
Unit cell	a = 27.95 Å b = 51.12 Å c = 31.57 Å $\alpha = \gamma = 90.00^{\circ}, \beta = 116.15^{\circ}$	a = 56.17 Å b = 53.22 Å c = 32.29 Å $\alpha = \gamma = 90.00^{\circ}, \beta = 92.67^{\circ}$
Resolution (Å)	28.34-1.38 (1.47-1.38) <sup>b</sup>	38.61-1.55 (1.64-1.55) <sup>b</sup>
Unique reflections	16,325 (2,593)	13,408 (1,983)
Redundancy	3.68 (3.62)	3.30 (2.95)
Completeness	99.3 (98.9)	96.5 (90.1)
$R_{ m merge}$ <sup>c</sup>	5.6 (58.5)	6.4 (38.3)
$I/\sigma(I)$	12.82 (2.00)	12.04 (2.90)
<i>R</i> -means $d$ (%)	6.6 (68.8)	7.6 (46.8)
$CC(1/2)^{e}$	99.9 (71.8)	99.7 (86.6)
Structural refinement		
$R_{ m factor}$	0.1124	0.1327
$R_{ m free}$	0.1570	0.1759
Number of atoms		
Proteins	887	842
Ligands	9	27
Water	109	96
Number of residues	107	97
R.m.s.d. (bond)	0.0213	0.0111
R.m.s.d. (angle)	2.0860	1.4082
Mean B-factor	18.168	14.938
Ramachandran plot <sup>f</sup>		
Favored (%)	96.19	96.84
Allowed (%)	3.81	3.16
Outliers (%)	0.00	0.00

Supp. Table 1. Data collection and structural refinement statistics of Fd crystals.

<sup>*a*</sup> Average diffraction weighted dose calculated by RADDOSE-3D [19].

<sup>b</sup> Statistics for the highest resolution shell are shown in parentheses.

 ${}^{c}R_{merge} = \sum_{hkl} \sum_{i} |I_{i}(hkl) - \langle I(hkl) \rangle| / \sum_{hkl} \sum_{i} I_{i}(hkl)$ 

where  $I_i(hkl)$  is the intensity of the reflection and  $\langle I(hkl) \rangle$  is the mean intensity of a group of equivalent reflection.

 $^{d}$ *R*-factor independent of the redundancy.

<sup>e</sup> Percentage of correlation between intensities from two random half-datasets.

<sup>*f*</sup> Calculated with the MolProbity [20].

**Supp. Table 2.** Dipole moments characteristics of Fd2, Fd1 and orthologues of Fd1 in six other cyanobacteria, including FdN, and of the heterocyst Fd from *Nostoc* PCC7120.

Cyanobacterial strain	$\mu_{Fdox}$	μ <sub>Fdred</sub>	Angle	Total charge
	(Debyes)	(Debyes)	$(\mu_{Fdox}, \mu_{Fdred})$	(Fd <sub>ox</sub> )
			(degrees)	
<i>T. elongatus</i> Fd2 (tlr1236)	378	422	4.4	-6
<i>T. elongatus</i> Fd1 (ts11009)	186	234	6.5	-17
<i>Nostoc</i> . 7119 FdN (all4148)	285	334	3.3	-18
<i>Syn.</i> 6803 (ssl0020)	247	291	5.9	-18
Leptolyngbya boryana	239	292	0.6	-18
Mastigocladus laminosus	370	408	5.1	-15
Aphanothece sacrum	328	379	1.1	-15
Arthrospira platensis	234	279	5.4	-19
All strains Fd1	$270 \pm 62$	$316 \pm 61$	$4 \pm 2.4$	$-17.1 \pm 1.6$
Nostoc. 7120 heterocyst Fd (all1430)	453	481	5.6	-13

The following structures were used for the calculations: PDB 5AUI for *T. elongatus* Fd1 [2], PDB 1OFF for *Syn.* 6803 [21], PDB 1QT9 for *Nostoc* 7119 FdN [22], PDB 3B2G for *Leptolyngbya boryana* [23], PDB 4FXC for *Arthrospira platensis* [24], PDB 3AV8 for *Aphanothece sacrum* [25], PDB 1RFK for *Mastigocladus laminosus* [26], PDB 1FRD for *Nostoc* 7120 heterocyst Fd [27].

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