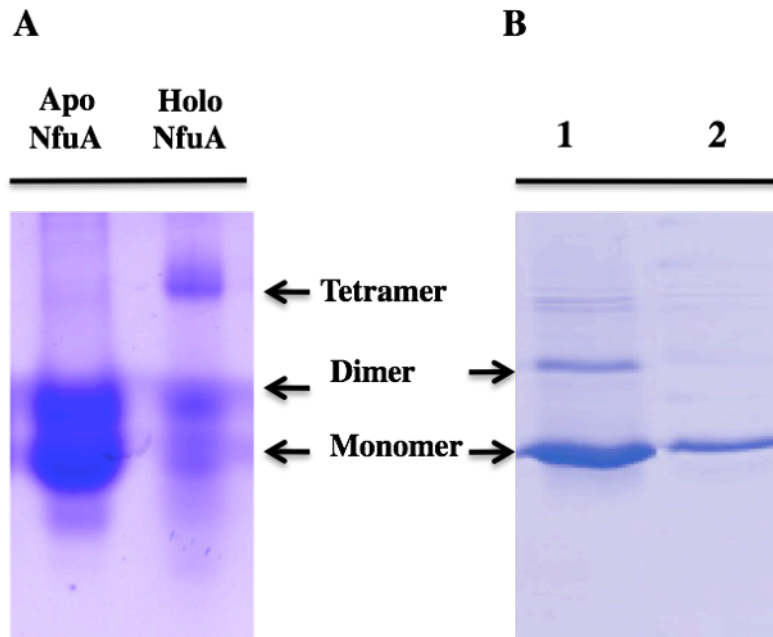


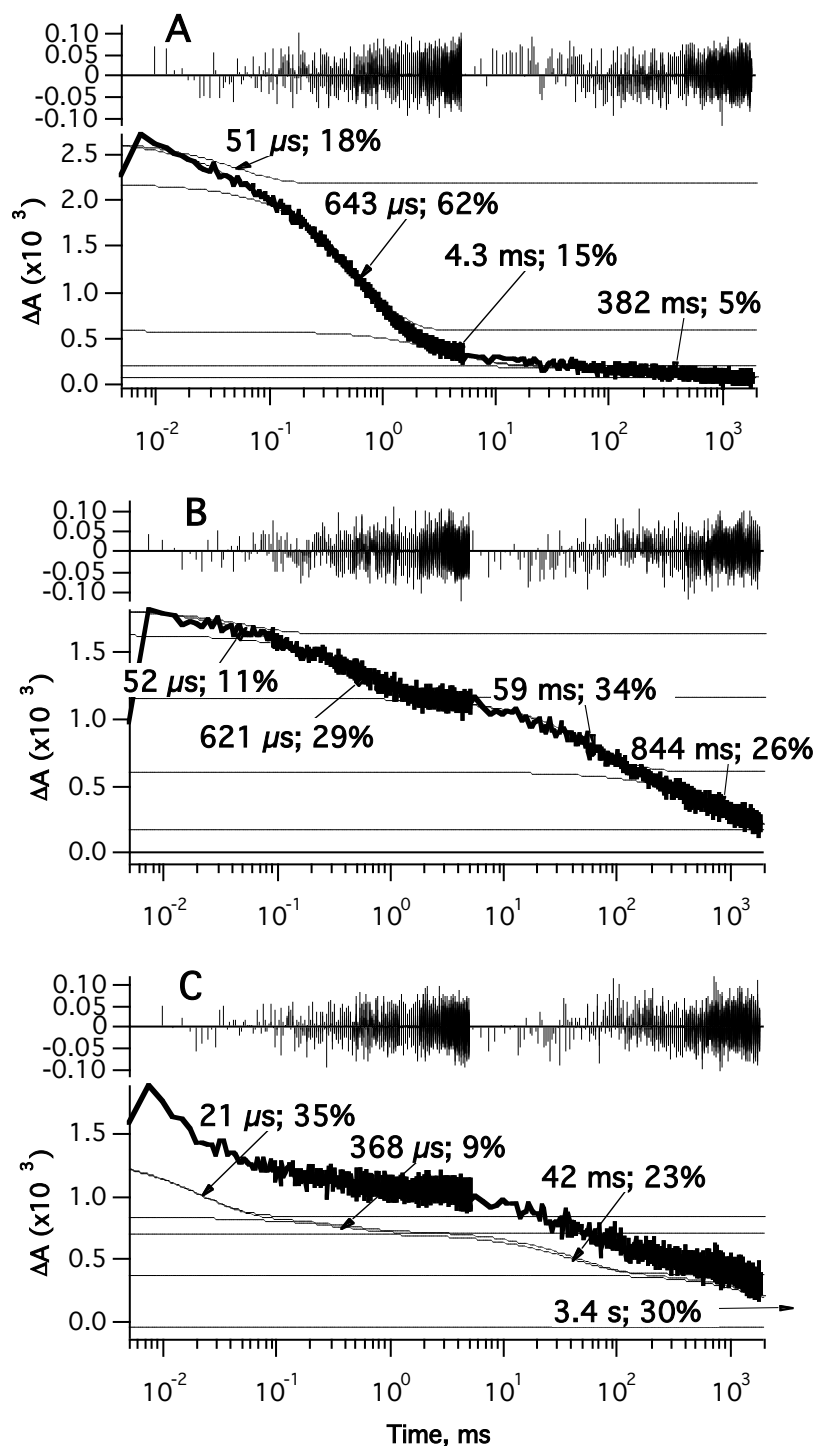
Supplemental Figure 1: **Sequence alignment of the selected cyanobacterial NfuA, NifU and NfuB proteins.** Amino acid sequences of NfuA, NfuB and NifU proteins from *Synechococcus* sp. PCC 7002 (7002), *Nostoc punctiforme* PCC 73102 (73102) and *Nodularia spumigena* CYY9414 (9414) were compared.

9414	NifU	1	MWDYTDKVLLELFYNPQNQGAIEETGEAGVKVAMGEIGSIACGDALRLHLKVE	55
73102	NifU	1	MWDYTDKVLLELFYDPKNQGEIEETGEAGVKVATGEIGSIACGDALRLHLKVE	55
9414	NifU	55	VESDKILDARFQTFGCTSAIASSSALTEMVKGLTLDEALKVSNKQIADYLGGLPEAKMHCSVMGQ	119
73102	NifU	55	VESDKILDARFQTFGCTSAIASSSALTEMVKGLTLDEALKVSNKDIADYLGGLPEAKMHCSVMGQ	119
9414	NifU	120	EALEAAIYNRGIPLATHDDDDGALICSCFGISEAKIRRVILENHLTDAEQVTNYVKAGGGCGS	184
73102	NifU	120	EALEAAIYNRGIPLATHDDDDGALICSCFGISESKIRRVILENHLTDAEQVTNYVKAGGGCGS	184
9414	NfuB	1	MTKLEELIQEINRFEAIISQWEESQRCVAVGLKRAIEDLHK	41
73102	NfuB	1	MTNLEELIQEINRFEAIISEWDESQRCVAVGLKRAIEALHK	41
7002	NfuA	1	MALALTENVEATLD-ELRPYLKADG	25
9414	NfuA	1	MELTTENVETVLD-EMRPYLMSDG	23
73102	NfuA	1	ELTIDNVETVLD-EMRPYLMSDG	22
9414	NifU	185	CLANIDDIIRDVKEKAAPALNTHSVAVAN---SQQSKPLTNVQRIALIQKVLDEEVRPVLADG	249
73102	NifU	185	CLANIDDIIRSVQQEYASPALNNGVQVATEIVTSKERSLTVQKIALIQKVLDEEVRPVLADG	249
9414	NfuB	42	AALTHLIKSLKQESMSALRQAVDDDDIVYVLLYHELKPPQA--PLIERINTALEEVRPGLKSHD	104
73102	NfuB	42	AALTNLIKNLKQESMPALRHAVADELVYAVLLYHELKPPK--PLAQRIETALEEVRPGLKSHD	104
7002	NfuA	26	GNVELVEIDGPVVK-LRLQGACGSCPSSTMTLRMGIERRLRENIPEIAEVEQVF	78
9414	NfuA	24	GNVELVELDGPVVK-LRLQGACGSCPSSTMTLRMGIERRLKEMIEPIAEIEQVI	76
73102	NfuA	23	GNVELVELDGPVVK-LRLQGACGSCPSSTMTLRMGIERRLKEMIEPIAEIEQVV	75
9414	NifU	250	GDVELYDVEGDKVK-VVLQGACGSCSSSTATLTKIAIEARLQDRVSKNLVVEAVAP	311
73102	NifU	240	GDVELYDVEGDRVK-VVLQGACGSCSSSTATLTKIAIEARLQDRVSKSLVVEAV	299
9414	NfuB	105	GDVEFVAIKPPDTVEVKLIGSCSSCPTSTLTLTQSVQAIKNHCPEITKVVAVNHTSTVN-----	165
73102	NfuB	105	GDVELVAIKSPDTVEVRLIGTCSSCPASTLTLTSLQVQAIKNHCPEITKVVAVNNSPAVNNANS	170
9414	NfuB	166	--SPFTPEDTATWVKLTIDQIPESGILTKGVGKNSLILYRQGENITCYLNACPHLATPLDMGKL	226
73102	NfuB	171	LISPFSSKITCTWMKVATLDEVPEFSVVVQLAGTSLILHRQGVTVKCYRNACTHLGSPLEKGV	235
9414	NfuB	227	DNGILTCKSHGFQYNLETGECLETVADVPLQSYYPVQIKGEKVFVKLPKYSI	277
73102	NfuB	236	ENGIITCPAHGFQYKLETGKCLTVPDVSLQSYYPVKVDDKVFVKLQK	281

Supplementary Figure 2: **Gel electrophoretic characterization of NfuA stained with Coomassie blue.** (A) Native gel electrophoresis of apo-NfuA and reconstituted Holo-NfuA under anoxic conditions. (B) SDS-PAGE analysis of apo-NfuA: *lane 1*, crosslinked with EDC and *lane 2*, without EDC crosslinking treatment.



Supplemental Figure 3: **Decay kinetics of the P700⁺ flash-induced absorption change at 820 nm.** (A) Sample with 1 μM P700-F_X core, 20 μM apo-PsaC, 20 μM PsaD, 4 μM DCPIP, 4 μM ascorbate, 0.04% (w/v) DM and 4 mM DTT (negative control). (B) Sample with 1 μM P700-F_X core, 20 μM holo-PsaC, 20 μM PsaD, 4 μM DCPIP, 4 μM ascorbate, 0.04% (w/v) DM and 4 mM DTT (positive control). (C) Sample with 1 μM P700-F_X core, 42 μM holo-NfuA, 20 μM apo-PsaC, 20 μM PsaD, 4 μM DCPIP, 4 μM ascorbate, 0.04% (w/v) DM and 4 mM DTT.



Supplemental Figure 4: **Phylogenetic analysis of NfuA, NifU and NfuB proteins from cyanobacteria.** Amino acid sequences of proteins with similarity to NifU (*i.e.*, NfuA, NifU, and NfuB) were compared from *Synechococcus* sp. PCC 7002 (7002), *Synechococcus elongatus* PCC 7942 (7942), *Synechococcus* sp. PCC 6301 (6301), *Trichodesmium erthraeum* IMS101 (IMS101), *Crocospaera watsonii* WH8501 (8501), *Cyanothece* sp. CCY 0110 (0110), *Synechococcus* sp. BL107 (BL107), *Synechocystis* sp. PCC 6803 (6803), *Anabaena* sp. PCC 7120 (7120), *Nostoc punctiforme* PCC 73102 (73102), *Anabaena variabilis* ATCC 29413 (29413), *Thermosynechococcus elongatus* BP-1 (BP 1), *Gloeobacter violaceus* PCC 7421 (7421), *Synechococcus* sp. WH7803 (7803), *Synechococcus* sp. WH7805 (7805), *Lyngbya* sp. PCC 8106 (8106), *Synechococcus* sp. JA-3-3Ab (JA33Ab), *Synechococcus* sp. JA-2-3Ba (JA23Ba), *Synechococcus* sp. RCC307 (RCC307), *Synechococcus* sp. WH5701 (5701), *Synechococcus* sp. CC9902 (9902), *Synechococcus* sp. WH8102 (8102), *Synechococcus* sp. CC9605 (9605), *Synechococcus* sp. CC9311 (9311), *Nodularia spumigena* CCY9414 (9414), *Synechococcus* sp. RS9916 (9916), *Synechococcus* sp. RS9917 (9917), *Prochlorococcus marinus* CCMP1375 (1375), *Prochlorococcus marinus* CCMP1986 (1986), *Prochlorococcus marinus* MIT9211 (9211), *Prochlorococcus marinus* MIT9301 (9301), *Prochlorococcus marinus* MIT9303 (9303), *Prochlorococcus marinus* MIT9312 (9312), *Prochlorococcus marinus* MIT9313 (9313), *Prochlorococcus marinus* MIT9515 (9515), *Prochlorococcus marinus* AS9601 (9601), *Prochlorococcus* sp. CC9605 (9605), *Prochlorococcus* sp. CC9902 (9902), *Prochlorococcus marinus* NATL2A (NATL2A), and *Azotobacter vinelandii* (Azot). The sequence alignment was generated using the ClustalW module within the MacVector version 10.0.1 (MacVector, Inc., Cary, NC). The neighbor-joining phylogenetic tree was generated using the phylogenetic analysis program PAUP (Sinauer Associates, Sunderland, MA).

