Supplemental Data for "Natural diversity provides a broad spectrum of cyanobacteriochrome-based diguanylyl cyclases"

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Five figures, one table and one citation.

Supplemental Figure S1. Spectral analysis of selected fusion CBCR-DGC proteins. Absorbance spectra of: (A) NpR6012g4-GGDEF(1), (B) NpR6012g4-GGDEF(2), (C) NpR6012g4-GGDEF(3), (D) NpR6012g4-GGDEF(4), (E) NpR6012g4-GGDEF(5), (F) RcaE-GGDEF(1), (G) RcaE-GGDEF(2), (H) RcaE-GGDEF(3), (I) RcaE-GGDEF(4) (J) DGC enzyme assay data; values (\pm SD, n = 3) are shown. For all panels, 15Z = blue trace/bar, 15E = orange trace/bar).



Supplemental Figure S2. CBCR GAF domain alignment. Amino acid sequence alignment of CBCR (GAF) domain of CBCR-DGC proteins. Bold lettering indicates proteins examined in this work. Blue highlighting denotes canonical '1st cysteine' residue. Yellow highlighting denotes DXCF motif. Red highlighting denotes 2^{nd} cysteine residue of Lyn8106_0097 Δ and Lyn.aest_0230 Δ .

WD 044070540	
WP_0113/0310	
KGG/1800	
WP_015113918	Q E I LFNLVA E IR ESLNLDT LFKTTVREVRKALRADRVG I FRFDTKSSGEFVSENVLPDYDSVIAI KVK <mark>DHCF</mark> GKRYTVAYHQGR I QVLSNI YQAGLKD <mark>C</mark> HLLVLEQFQI KAQI VVPLMKG
Nodo_0172	Q EV LFNLIA E IR ES LD LKT LFKTTAR EV RKALHT DR V G I FQ FD PD S S G E FV S EN LL PEY D SA IA I KV S <mark>DHCF</mark> GD KYVEQYQKGH IQ V LSD V SQA G LTQ <mark>C</mark> H LE LL EN FQ I KAQ I I V PLMKG
WP_015210266	A I L L R D I T Q R I NQ S L D L S N I F E I A S Q K I R E L I HA D R V G I F K F Y S D A D G E F V A E S V L Q G F N S H L A R K I H <mark>D H C F</mark> G K Q Y A S Y Y Q Q G R I Q A L D D I D N A G L A D <mark>C</mark> H R R I L A K L Q I R A N L V V P L L N G
WP_010873764	EKLVLKIANKIRASLNINDILYSTVTEVRQFLNTDRVVLFKFNSQWSGQVVTESHNDFCRSIINDEID <mark>DPCF</mark> KGHYLRLYREGRVRAVSDIEKADLAD <mark>C</mark> HKELLRHYQVKANLVVPVVFN
AIE73515	EKLVLKIANKIRASLNINDILHSTVTEVRQFLNTDRVVLFKFNSQWSGRVQTESHNDFCQSIINQEID <mark>D</mark> PCFKGHYLRLYREGRVRAISDIEMADLAECHRELLRHYQVKANLVVPVVFN
WP_015955649	ER I IMDVAQK I RASLNLDDI LNTTVSE I RHLLNTDRVFI Y RFDENWYGK VVVESVAC PEFSI LGEWI D <mark>EPCF</mark> RDQYVK Y Y RQGRI KAIEDI AQIELTP <mark>C</mark> HRELLNRYQVKANLVL PI VYQ
WP_013321179	ERIFREVAPKICSSHRLDDILNTIVTEVRHLLHSDRVFLYRFNEHWVGTVVESVAAPEFSILGESID <mark>EPCF</mark> RDQVKYYHQGRVKAIEDIEQAEIAL <mark>C</mark> HRELLKRYQVKANLVLPVVAF
WP_006529598	ER LYMEVAQK I RQSLNLEE I METT VT EV RHLLQADRVFLYQF NADWSGT VV ESVSESELSILGDLID <mark>D</mark> PCF REQYIKHYRQGRIKAIADVTKEELASCHLELLTRYQVKSNLVLPIVHQ
WP_009783799	EKLYME I VHKI ROSLNLNDI LKTAADEVRR LLDT DRVI LFRFD SOWNGT VVVESVLT DYPVSLDDE I DDPCFRENYVKYY ROGRVRAIEN I ROANLNECHIELLERY AVKANLVVPI I YO
WP_039728489	EHLVLEIANKI BOSI DI GYLLETI VTEVBOVI GCDBI ELEOFDEHWAGEVTVESVSDPVYSI LGEWIDEPCEBNEVVKI Y BOGRVBAI DDI TOVGI HACHI HMI ODVOVKSNI VI PILIYO
WP_015111021	FRIVAAVTORI BOSI FI DE LI OTTA DEVROI FAVDRVVI VOFEPDWSGI VAVESIAPGCI SI I GENYM <mark>DT CE</mark> OSTRADYVOGOT BAI EN I ETA GI SPCHI FI I OBIO I BANI VVPI I OO
NoR1060	FRI VAANTORI BOSI FI DE LI OTTAAFVROI FENDRULI VOFESDWSGI VANES LAFECMSTI GEHMADT EKSTRALV FOOGNTRALEDVETAGI SPCHI DI LRSI O I BANI VVPLI OK
WD 0177/5705	
KCC72205	
MD 046076404	ENTYARY (QLINING) LEEDING I CANTALEVADI FENDRUVI (V FEDWSOFYAVES) LIGENMULTER QSI NATY (QQUINALEDI ELGENALLA) LEVIALLA) LEVIANLI (QLINING) LEOLA CANTALENSE (CANTALENSE (VAN EVAFEZVALE) LIGENMULTER QSI NATY (QQUINALEDI ELGENALLA) LEVIANLI (QLINING) LEOLA CANTALENSE (VAN EVAFEZVALE) LIGENMULTER QSI NATY (QQUINALEDI ELGENALLA) LEVIANLI (VAN EVAFEZVALE) LIGENMULTER (VAN EVAFEZVALE) LIGENMULTER (QUINALEDI ELGENALLA) LIGENMULTER (VAN EVAFEZVALE) LIGENMULTER (VAN E
WP_0100/0404	
WP_011317683	ENTYAAVIQ HAQSILLEELLQII ADEVRQLFEEDKVLITKEEP DWSGLVA VESLEEGSMSILGEFTILDILEEQSINAATIQQGNI KAMEDI ENAGLSPLHLQLLQSIQ HANLIVPILQK
VVP_029632327	EN VAAVIQKI ROSLEENEI LOTI AAEVKOL FEVDKVVI TOFKVDWSOLVAVESLAEGOMSI LOFNYMDI EFOSI HASTYDDON TISTEDI ENAOLSYCHVKLLKSLOTKANU VVPI LOO
WP_035988295	EN VAAVIQEIRQSLDLNEILQIIADEVEQLEV DRVVIYEFESDWSGLVAVESLAAGSPSILGFHYMDICFEIHAAYYQQGNIRAIENIEIAGLSPCHVDLLESLNIKANLVVPILHQ
WP_017320093	ERIVATVTQR I RQSLDLEE I LQTTAFEVRQLFDVDRVVI YR FEPDWSGLVAVESLAPGCMSI LGFHVM <mark>DTCF</mark> QSNRAAYYQQGNAKA I ADI ESAGLSACHVELLRSLQI RANLI VPI LQQ
WP_036012702	DRIVAAVTQRIHQSLNLTEILQTTATEIRQLFDVDRVVLYRFEPDWSGKVAVESVAEGWMPILGLHVM <mark>DTCF</mark> QMTYAYEYQQGQIKAIEDIYSAELTQ <mark>C</mark> HVELLQQFQIRANLVVPILQQ
Os6304_3201	ERVMSAMRDRIRSSLNLKEILNTTVAEVRQFLNTDRVIIYRFHPDWSGKVVVESCGTRAREILNLTIL <mark>DPCF</mark> GETHAQLYKKGRLKATPDIYTEPISP <mark>C</mark> HRNLLAQFQVKANLVVPILLN
WP_015174564	ER LIAQIQ SRIR SSLDIQDILNTTVA EVR EFLAT DRVLVFR FRPDWNGDVVV ESVGEGWMPLKGMGID <mark>D</mark> C C <mark>F</mark> ANTY I GQYLKGRIRA I EDIHA SNLT E <mark>C</mark> HMNFLAGCQVKANLVVPI VQQ
WP_006633119	ER LIAQIQ SRIR SSLDLQDILNTT VAEVREFLAT DRVLIFRFRPDWNGDV VVESVAEGWIPLKGMGID <mark>D</mark> CC <mark>F</mark> ATT YIGQYLKGRIRAIEDVHT SNLSE <mark>C</mark> HLNFLEACQVKANLVVPIVQQ
YP_007122690	ELLIAGMCDRIRQSLNLGEILNTTVEEVRQFLRTDRVIIYRFEPDWSGTVVVESVAPEYLATLDIVIH <mark>D</mark> PCFGADQIVPYQQGRIQAFADICAAGLTPCYADFLRQLQVRANLVVPILYG
WP_038082070	ERLIGIIAQNIRQFLHLDSILTTTVEEVRQFLQVDRVVIYQFDAEWHGTVIAESISDPSFSILGQNVQ <mark>DPCF</mark> QKTISHSYFQGRIHAVNDILKANLDPCYVNLLTTLQARAVLVLPVVIH
WP_033335474	ERLIGVIAQNIRQFLHLDSILTTTVEEVRQFLQIDRVVIYQFDSDWYGTVIAESISDPSFSILGQSIQ <mark>DPCF</mark> QKTISHSYFQGRIHAVNDILKANLDPCYVNLLKMLQVRAILVVPIIIH
WP_038332578	EKLIGSMQARIRRSLDIDTIINTTVEEVRNFLQCDRVLVYRMNPDWSGTIVAESIHFDWPSVMGITIQDPCFTPDLARRYREGHIHYFDDIESCELSPCHTQLLSPLEVKANLVVPILQQ
S.hof 0333	ORLLAEITOOIHKSLDFHEILTAT VTO SROILOVDRVLIFOLNSDGSGVVIOESVDPAFPTTLGLKFL <mark>DRCF</mark> PSECYDFYWRGOSOIIFDT NODDLSNCLKSFMOOIGVKSKVVTPIIOH
KGG76686	OR LLAE IT KOIHKSLDFNEILTTT VTOVROILOVDRVLI FOLKSDGSGIVIOESVDPAFIST LGLOFL DRCFPSHCYDLYCRGOSOVI FDT NOEDLSGCLKNFMOOIGVKSKVVTPIIOH
Tir0924	EMINSTI JODI ROSI RI FETI ORAVNSJOOTI I SDRVI I YR FI GDGSG I VAV FATTI POYSI JOVI HDPCFTK FTARRFI EGRTI SI SDVNDAOLOD, YR FI I TRIOVOANI VYPI I OG
WP 024125851	EMINSTILIODIROSIRI EFILORAVTSIOOILISDRVILYRFIADGSGIVAVEATALPOYSILGRVIHDPCFTKETAORFIEGRTITISDVNOAOLODC VRFILTSIOVOANIVVPILOG
WP_015123238	EFITISTISON IR STATISTISTISTISTISTISTISTISTISTISTISTISTIST
WP_01520260	En la cita da la cita da la cita da cita
WP_010202402	
WP_006623407	
VDD66702	
MD 016170600	
WP_015179000	
WP_000032122	
WP_012594761	ENLINSTATIKTINGSTELLATISTAEMARQFLIHTURLITAKTAKTUWSGEVITEDSVOSPWIKSLIGATILUDEEFTAATLEPARTALGKIHLIPULEMSELSPLIHUWLTELQVKANLUTPIVUG
WP_0333/4512	QI LVNATAQKI RKSLETEATLETTVQEVQNLLLDRAFLYRDDFDWSGTVVEALKSPDTSLLGRRTTDTEFTANYVELYQRGRTHVVDDVQQSNLSELYTNWLTDLQVRANLVVPVLHD
AGZ05265	ERM I SA I AQH I R DS L D L D E I L N T V A E V RQ F L K T D R V I I Y R F N P DWS G V V I E SVAR G CQA I L NME I T E I Y F V E T Q AQ F Y Q N T V K A I S D I Y I A G L T P. H L E L L K K L Q V R A K L V P I L Q G
WP_036834157	ERT I YT I TOR I ROS LDLDE I LOTT VAE V ROF LOT DR VM I YR FNSDWSGLVYKESY SPGTKAI LKME I TD SY FVENHGO Y YOONT I KATP DI Y TAGLT PEHFELLEK LOV RAK LV VPI LOT
WP_012599180	ERMMHD I TRHIRQSLDLDE I LNTT VT DVRQFLQT DRV I I YR LNPDWSG I VYT ESVAPKWI A I LNME I TD SY FV ET EGGDY HRGY I NNVPD I YHAGFT Q <mark>C</mark> HLELL ER LQVRAKL VVP I LQQ
Cyan7822_5462	ERMIHE1AHKIRQSLDLTEILNTTVAQVREFLQTDRVIIYRLNPDCSGIVVTESVAPGWLAIVNREITDSYFVETEAGNYHGGKINNVPDIYTAGFSP <mark>C</mark> HLELLERLQVRAKLVVPIVQK
WP_015079858	EQLIAK I TQK I RT S LN LE LI L S TT A I EV R K L L K T D R V I V Y R F H P D G S G Y V I V E S V A E WD S M L G R V F Q D T Y F S D Q C G Y D Y R Q S N I Y V I E D I D N A G L S Q C H I D L L S Q L Q A K A N L V V P I Q E
WP_015148692	ER LV SRT LAR I RQ SLN LEE I LNT AV SEVRQ FLDC DR V V V R I WP DQ SG SV VT ESV I P PWP SMMEQ SFGEE I FP FSC Y ER Y C NGT V KA I DD LKAAN SP DC LI EF LQ SFG V NG KM I AP LL HE
WP_035989320	EQT LWQ IT QK I RQT LD LP S I LAT A T A EVQ SY LQ V DRT L I FQ FT SDH SGA I I QTT AQ A SC PT PT AQ EWQ A DG LR QR C Y HY Y SQ GQ A K A I A G LT A D L N E LC S PW I E LT E A K SA I V A P I LQ P
WP_039730111	EHA LRM ITQH I R ES LD LA PILA A V V E E V Q L L Q A D RT L I FQ L T S A H S G I V V Q E Q S R T E F PT I L A MQ WE D E H F S P N C Y A F Y Q Q A Q G R I V Q D I T Q D D W G D C L I E F MQ S I G V Q S K M V A P I T Q T
WP_008308234	E AV LTT VT NT I Q ET F D I Q S I L D A AV LT I L H F F Q A D R V L V Q I T D Q Q R G I V V S E AV E G D W P S M Q D V T I D E P C L G E Q R T Q A Y R R G K V Q A I A D I D A V P L A S C Y R E L L Q R Y Q V R A N L V P I V Q E
Lyn. aest_0230	EKLLA EINDRIRQ SLELDQIL VTAVTEVQEILQADRVLIYR FNPDWSGTIITES VVPGFDSILDKS <mark>T</mark> TD SYLLQTR GEA FRQGNIQ VVNDIYTANLTP <mark>C</mark> HQELLTQLQIRA SLLLPIVNS
Lyn8106_0097	EKLLGEINDRIRQSLELDQILATAVTEVQQILQVDRVLIYRFNPDWSGTIITESVVAGFNSILNKS <mark>I</mark> QDSYLVQTQGEAFSQGNIQVMNDIYTANLTP <mark>C</mark> HQELLIQLQIRASLLLPIVVQ
WP 039729794	ER LIDEIAQQIRQSLQLDAILNTAVTEVREFLDVDRVLVYRFRPDWSGIITFESIAPEATPTRYSAFEEPCFRORYVEQYQAGRVRAIADIYTADIOECYROLLETYOVRANLVVPILOG
WP 039725076	ER LIDT I SQR I Y ECT ELDE I LDTT V AQVR LFLRT DR VV LYR FKP DWSGT VAV E SV SP GVMP I LYTH I EESC FR DGY I SLY EQGR VRA I AD I YTA FI DACHLELLRG FGV RAN LVV PV LOE
-	

Supplemental Figure S3. DGC GGDEF domain alignment. Amino acid sequence alignment of GGDEF domain of CBCR-DGC proteins. Bold lettering indicates proteins examined in this work. Blue highlighting denotes RxxD inhibition site motif. Yellow highlighting denotes 'GGDEF' DGC active site motif.

l vn aost 0230	DOLTO LANRRY EDEVE FO FWHRIKR FO API SI LLOV DY FKYYNDTYGHLAGDROLVOVA FALSRGY		VII PNTNTEGAVEVVRCIONEIOAINIPHSTSNOITIS
Lyn8106_0097	DO I TO I ANDRY EDEVE EDEWSRIPREOVALSTITCOVOVEKHVNDTYCHLACOOCLYOVAEATSRO	DADIVARYGGEEEV	VII DNT NMEGALEVVHCIONELLAINI DHST STOITI S
Lyno 00000000			
WP_030062070	DGLTQTANKKSFDECLEKEWQKSNKEQSPLSLLLCDTDHFKLTNDTFGHQAGDNCLQQFAQTLDKVV	PIULVARTGGEEFA	ILLPNIDIMGATQIVEQTQQAVAQLQIPHLRSVCVTVS
WP_033335474	DGLIQIANKKSFDEFLDKEWQKSKKEQSPISLLLCDIDHFKLTNDTTGHQAGDKCLQQFAQILDIVV	PIULVARYGGEEFA	ILLP SI DI VGAVQIA EQIQQAVAQLQIPHVR SVCIIVS
WP_015210266	DG LTQ I ANR R C FNDR L LQ EWLR L C R EQQ P L S L L L FD V DY FK R Y ND FY GHQ L G DD C L T K L AQ A AQQ V V	P A D L V A R Y G G E E F V	I I L P N T D A E G A G A V A E R V H A A MQ A L N I P HQ A S V T V T I S
WP_015179608	D G L T Q I A N R R C F N D R L E H EWQ R L Y R EQ K P I S L L L F D V D Y F K R Y N D C Y G H Q M G D N C L F K L A Q T V Q E V V	P A <mark>D</mark> L V A R Y <mark>G G E E F</mark> G	I I L P N T D I E G A S A V A K R I H A A I Q A L H I P H K T S V V V T I S
WP_006632122	D G L T Q I A N R R C F N G R L E H EWQ R L Y R EQ K P I S L L L F D V D Y F K R Y N D C Y G H Q M G D D C L F K L A Q T V Q E V V	P A <mark>D</mark> L V A R Y <mark>G G E E F</mark> A	I I L P NT D L E G A S S V A Q R I HA A I K A L H I P H K T S V V V T I S
AGZ05265	DQ LTQ I P N R R C F D T R L D C V W K N L L R EQ G F L S L L L C D I D Y F K A Y N D T Y G H T G G D D C L R L V AQ A F K Q S V	S R <mark>D</mark> L A A R Y <mark>G G E E F</mark> V I	V I L P N T S I H K A FQ V AQ E I HQ A I KQ L N I P H L A S V H V T L S
WP_012599180	DQ LTQ I P N R R C F D H D L E R H WQ N L A R Q K R P L S L L L C D I D Y F K Q Y N D T Y G H S G G D V C L T Q V A Q A L K A S A	A S <mark>D</mark> L V A R Y <mark>G G E E F</mark> V	I I L P D T D N F G A I A V A Q N I Q K T L K E L R L P H R A S V Y V T V S
Cyan7822_5462	D E L T Q I A N R R C F E R D F N H EWY R L T R E K R F L S L L L C D I D Y F K Q Y N D T Y G H P A G D I C L K Q V A Q A L K Q A A	M T <mark>D</mark> L V A R Y <mark>G G E E F</mark> V	I L L P NT D S Y G A T Q V A V A V Q Q A I D H L H I P H L A S V S V T I S
WP_036834157	DK LTQ I A N R R C F D E I L HQ EWHR L V R EK R P L S L L L C D I D Y F KQ Y N D T Y G H S Q G D I C L Q Q V AQ A L Q Q G V	S I <mark>D</mark> L V A R Y <mark>G G E E F</mark> V V	VILPHT DQ E G A LQ V A K K I Q D V L E Q F N L P H R R S V R V T M S
YP_007122690	DG LT Q V A N R R F D E Y L H E EWR R L A R EQ S P L S L I L C D I D Y F K L Y ND N Y G H L A G D F C L Q Q V A A V L R Q C V	P P <mark>D</mark> L V A R Y <mark>G G E E F</mark> A	L I L P N T D A R G A A F V A E T V R Q R V R G L R I P H V K S V Y V T L S
WP_015955649	D G L T Q V A N R H R F D M Y L D Q E W R R L M R S Q Q F L S L I L C D V D H F K G Y N D T Y G H L A G D Q C L Q Q V A Q V I K N A V	P A <mark>D</mark> L V A R Y <mark>G G E E F</mark> A	I I L P D T P L R G A L Y V A EQ I R Q Q V Q Y L T I P H P Q S T W V T L S
WP 013321179	DG LT Q V A N R H R F D V Y L E Q E W R R L M R S R H S L S L I L S D V D H F K W Y N D T Y G H L A G D H C L Q Q I A R V I K T S V	P A <mark>D</mark> L V A R Y <mark>G G E E F</mark> A	I V L P E T S L K G A L F V A EQ I R Q K V K N L T I P H T K S A C V T L S
WP 009783799	DG LT Q I A N R H C F D R V L E K EWQR LMR S P DQ L S L I L C D I DN F K L Y NDT Y G HQ A G D Y C LQQ V AQ A I Q A G V	P A <mark>D</mark> L V A R Y <mark>G G E E F</mark> A ^V	VILPNT SLEGALR VAEEIR VR VR GLGV SHT G SAC VT L S
WP 012594761	D S L T E V A N R R F D E Y LOO E WR R L T R A KO P L S L I V C D V D F F K F Y N D T Y G H P A G D N C LOO V A O V LOO S V	P A <mark>D</mark> L V A R H <mark>G G E E F</mark> A	I V L P N T D I S G A V H I A G E I R S R L R G L K L E H R A S V Y V T L S
WP_038332578	DGITKVANRRCEDAYLOA FWRRMAR SROPI SILICDIDY FK SYNDTYGHOAGDVCIOOVAAALKETV	PADIVARYGGEEEV	A LI PHTNI EGAVHIAOT I RDRTTALO I PHOA SVYVTI S
WP_006529598	DG LTO VAN RYR FDNYLO FOWNRILLR S FDVL SLILCDVDYFKOYNDTYGHOO GD FCLIAIAKA I A SVL	P D D L V A R Y G G F F F A Y	VVLPNTSLTGTLTIARRIOAAIKALEIPHVNS-IVTLS
WP_039728489	DG I TO I PNRRK EDEHLAHEWRRALR SHOSI SI LI CDI DHEKOYNDSYGHOAGDYCI OOVAOTI SOLV	PSOLVTRYGGEEEA	IVI P DTTA E GALHI AO KIO A HVRALSI PHO HSI VVTI S
WP_015111021	DG I TO VAN R R C EDDT I KT EWORLAR FOAC I SI LI COVDC FKI YNDTYGHI SGDDVI ROVAOA I SMTA	PADIVARYGGEEEAV	VII PNTDTEGALAVATEIONNIRALOIIHSNSIIITIS
KCC72205	DG I TOVANDOCEDDI I NA EWORIADEOA SI SI I I COVOCEVI YNDTYGUI AGDDVI DUVAVA I SOTV	DADIVADVGGEEEAN	VII DNTGIEEAITVADEIOTNVSAIOIDUDNSIEITIS
MD 016976404	DG LT LVANDR CEDDT LVA EWERTAR EQA DE SET LECOVOCE VELVNDT VCHLAGDDALD SVAVAL ETV		VIERNIGIEERIIVATEIOSNUSALVIDUDNOVVITUS
WP_0100/0404			VILENT NVACALAVANT LOVNICALOLDUDNEVENTIC
WP_017320093	DGLTUVANRPCFDERLQVEWQRLAREQAPLSLTLCDVDCFRLTNDTHGHLAGDEALTHVANATSQAV	SAULVARTOGEEFA	VILPNINVAGATAVAKI TUKNI SALULPHPNSV FVILS
WP_015148092	DGLIHVANKKAFDECLQKEWKKIIKEHSMMSLILCDIDFFKLTNDIYGHQAGDSCLKQVAQAIASAA	PAULVARYGGEEFA	VILPHINGEGAMQVAQIIKNHVKALKIDHAKSVYVSIS
WP_015202462	DGLIQLANKKTFNETLNSEWNKLAKEEAVLSLILCDIDFFKITNDITGHLAGDKCLIEVANAIKSAT	PAULVARYGGEEFA	VILPNIDASGAMHLAELIKKIVKILKISHLNSEGVILS
WP_006623497	DGLIQVPNRRQFDIYLIIEWRRCIREFIPISLILCDVDFFRHYNDIYGHQEGDRCLQEVAQALIRSI	PGOLVARYGGEEFA	IIILPNIDAEGMCNVAGIIREQILQLQRIHEISIYISVS
KDR55793	DG LTQ V P N R R Q F D T Y L M T EWR R C I R E C T P I S L I L C D V D F F K H Y N D T Y G H Q E G D R C L Q E V A Q A L A R S I	P G D L V A R Y G G E E F A	I I L P NT D A E G M C N V A DT I R E Q I L Q L Q R I H E T S I Y I S V S
WP_015079858	D G L T Q I P N R R S F D E V L E R E WK R L E R E K V P L S L I L C D I D F F K N Y N D T Y G H Q S G D E C L K E V A Q I L Y Q V A	P G <mark>D</mark> L A A R Y <mark>G G E E F</mark> A	LVLPHTDIAGAICIAEIILSSIRSKGLIHKSSIYLTLS
WP_008308234	DA LT R I P N R R Y FMKHLGQ EWK R AHR DQ T V LT L V L C D V DH F K R Y N DT Y GH V M G D K C L AQ V A A A LQ G AM	P A <mark>D</mark> L V A R F <mark>G G E E F</mark> V I	M V L P N T T V T G A I A V V E S I Q Q A L H D R Y L P H R T S V R V T L S
KGG71856	DA LT K I A N R R C F D E F L E Q E W N R L T G T E N Y L S L I L F D I D Y F K D Y N D C Y G H L V G D E C L I Q V A R A A K S V L	P T <mark>D</mark> L L A R Y <mark>G G E E F</mark> I V	V V L P N T N K S G A I K V T Q L I Q R S I Q K L N I P H T R N C I V T V S
WP_015113918	DG LT K I ANR R C F D E L L E R EWHR L Q R T G N Y L S L V L F D I D N F K D Y N D Y Y G H L A G D E C L I K V A R A A Q A V L	P T <mark>D</mark> L L A R Y <mark>G G E E F</mark> I V	V L L P N T N E S G A I K V T N L I H K S I E E L K I S H P K N S F V T I S
Nodo_0172	DA LTQ V SNR R F F DN S L E A EWER S L R A GT Y L S L I L F D I D Y F K F Y ND H Y G H P A G D Q C L I E I T Q A A Q G V L	P	V I L P E T GQ A G A A K I A E Y I R N A V R G L K I P NQ G I L Y V T I S
WP_033374512	D S L T Q V G N R R S F D E A L P R EWEKMA L SQ A S L S L V L V D V D F F K A Y ND T Y G H P A G D E C L R A V A Q T L R T A V	ST <mark>D</mark> L V T R Y <mark>G G E E F</mark> A	I L L P HT D A NG A V Q V A G E I L S R V R Q L K I P H S Q S V H I S V S
WP_039730111	DG LT R I A N R R Q F D N T L T V E W Q R A Q R E H R E L T L V L C D I D Y F K Q Y N D T Y G H P A G D D C L I A V A Q A L K N C V	S T <mark>D</mark> C V A R Y <mark>G G E E F</mark> A	I I L P N T N L T G A I V V L K Q M Q A A I A E L N L A H D T H T R V T L S
WP_035989320	DQ LTQ I A N R Y F D T V LQ R EWK R L S R S H S P L A L I M F D V D H F KQ F N D C H G H P S G D D C L I T V A K T S Q A V V	P S <mark>D</mark> I V A R Y <mark>G G E E F</mark> A ¹	V V L P H T T L T G A A T L A E A I R A R I R A L N I V N F Q S T Y V T V S
Tir0924	D S L T D I G N R R C F D E L F L K EWR R C Q R E Q K P L S L I M L D I D C F K A Y N D H Y G H L Q G D E I L K Q V A R I L E S H L	A G <mark>D</mark> L A T R F <mark>G G E E F</mark> A	L I L P D T D Q R G A I H I V E K I Q G A L A E A N I T H A K S V K L T A S
WP_024125851	D S L T D I G N R R C F D E L F P K EWR R C Q R A Q K P L S L I M V D I D C F K A Y N D H Y G H L Q G D E I L K Q V A Q I L E S H L	A G <mark>D</mark> L A T R F <mark>G G E E F</mark> A	L I L P D T D H R G A I H I A E N I Q A A L A A A N I T H A K S V K L T A S
WP_015123238	D G L T Q I G N R R Q F T D I S L A EWR R A A R E Q T P I S L V L V D I D Y F K L Y N D H Y G H Q Q G D V I L Y R I A Q Q L A A G L	P G <mark>D</mark> L A T R Y <mark>G G E E F</mark> A	LILP DTP EAGAIQ VV EQIQEAIAT LAIPHAASIHLT LS
WP 010873764	DA LTQ V GNR Y L F D ST L E R E WQ R L Q R I R E P L A L L L C D V D F F K G F N D N Y G H P A G D R C L K K I A D A M A K V A	P T <mark>D</mark> L V A R Y <mark>G G E E F</mark> A	I I L S ET S L E G A I N V T E A L Q V E V A N L A I P H T V S T H V T L S
AIE73515	DA LT Q V G N R Y L F D S T L E R E W Q R L Q R G S E P L A L L L C D V D F F K G F N D N Y G H P A G D R C L K E I A NAMA K V A	P T <mark>D</mark> L V A R Y <mark>G G E E F</mark> A ^V	VIL SQT DLEGAIHVTKALQAGVANLAVPH SE ST YVT LS
WP 039729794	DA LT Q LANR R R F D Q Y L A E G W Q H Q R R Q A A I A I L L L D I D F F K R Y N D H Y G H P Q G D E C L R Q V S Q A L S Q A A	T V <mark>D</mark> L V A R Y <mark>G G E E F</mark> A	I V L P D T D L A G A H E V A T A MQ A A I A D L Q L E H P E S F Q I T L S
WP 039725076	DG LT GV ANR R F DHY LEEC WOEOOT R G ST LT LI LADID F F KOYNDCYGH PAGDT CLK R V A ST IOS V F	SO DLVARY GGEEFV	ILLPDT EEDAAVELLGLLRRRLOALAIQHQESYYLTLS
WP 011378510	DG LTO I P NR R F D E Y F N D V W L W G C R D H T P V A L L L I D V D Y F K T Y N D F Y G H L A G D E V L R K I G L L L N S V V	AT DLVARY GGEEFV	AV LP STT LEGADAVARR LOADLOR LO I PHNH SVWVT V S
WP 017745795	DG LTOVAN R C FDD I L NA EWOR LAR EOA S L S L I L C DV DC FK L Y NDT Y GH L A GDDA L R H I A KA I FOT V	IP A D L V A R Y G G E E F A V	VILPNT DIE EA LAVARKIOT NV SALOLSYPNSV FITLS
WP 029632327	DG LTOVAN R C FDDT L K V EWOR LA SEOA SL SL I L C DV DY FK L Y NDT Y GH LA GDDA L R H V A KA I SO SV	IP A D L V A R Y G G E E F A V	VILPNTDVEEALILAREIOTNISALOLPHRNSVEITLS
NoR1060	DG I TO V GNRR C EDDT ENTOWOR LAR FOGSLSTILL CDV DV FKLYNDTHGHLAGDDAL ROVAKVI SOTV	PADIVARY	VII PNT DIEGALAVAK DIOT NISALKMPHPHSVEITIS
WP 011317683	DG I TO VANRR C FDNT I A I VWFHI AR FOGSI SI LI COVOC FKI YNDT I GHI A GDDVI RHVAGA I SR SV.		VII PNT DA EGA LAVAK E LO SNV SILO I PHP S SVI I SI S
WP_036012702	DGI TOVANRRCEDEVEFA EWORI ARKO SPI SI LICOVOVEKI VNOTVGHLAGODA LPOVAKA LAPTI	IPADI VARY GGEEEA	VII SSTDAKAA ITVAFKIOANI SFIOI PHARSVVVTI S
WP 035088205			VVIDETTAFFALAVANA IOASIAAI GMDHEOAADVTI C
S hof 0333		PADIVARVGGEEEA	
0.1101_0333	UNLINTAMANA FUEILUUUWERLINEUN FUSILUUUN FNSTNUM I UNFVOULUUE FAKALIKAV	PADLVARTOOEEFA	VILENTATEAEQUAVELOEQUAVELOEQUAVELOEULOSTUS
NGG/0000	UNITED AND DEDEVIEVENUESENCOS IST TO DEEKI VNDTVODAODOGU VVATALISEN	COEAABY CCEEFA	VILENINGIGAEQVAVRIQEQIAQEQISTESSVIVIAS
WP_00/300010	DULIGLANKKUTDETLETEWLKSLKNGGSISLILUDVDFFKLTNDITGHQAGDECLKKVAEAINEAKI	IT OUT AAKT OUE LTAT	VILPURENURALEVAEDIKKKIAVLUIPHAISVEVS
WP_0151/4564	USLIQLANKKKEDEVINKEWERS-SSSEPLSLIMCDIDCFKLTNUNTGHQAGDACLQQVARAIGDAC.	IPAELAARY GGEEFG	VILPNIDIVAAQAVAESIKSKVKALAIPHIKSVSVILS
WP_006633119	USLIQLANKKKFUEVINKEWEQS-SSLEPLSLIMCDIDCFKLYNDNYGHQAGDACLQQVARAIGDAC.	IPPELAARY GGEEFA	VILPNIDIVAAQAVAEGIRSRVKALAIPHIKSVCVTLS
Os6304_3201	D G L I Q V A N K K C F D G F L D H EWR R L T R E P A D L S L I L C D I D Y F K P Y N D T Y G H Q A G D E C L Q R V A A A L R Q C I I	' K L E L I A R Y <mark>G G E E F</mark> A /	A V L P N I D L K S A L E L A E R I R Ť E V A G L Q I P H A Q S V Y I T M S

Supplemental Figure S4. CBCR-DGC linker alignment. Amino acid sequence alignment of linker region between CBCR and GGDEF domains. Bold lettering indicates proteins further discussed in this work. Blue highlighting denotes conserved leucine residue discussed in previous work (Blain-Hartung et al., 2017). Red highlighting denotes conserved polar, hydrophilic residue discussed in text. Yellow highlighting denotes residues that are conserved in \geq 90% of observed proteins.

AGZ05265.1	QLA	I A I		SE	. Y Q A NQQ L E	муму	DQ L	TQ
AIE73515.1	QVA	I A	I HO	GE	Y E	ISSL	DAL	TQ
Cyan7822 5462	QVA	I A	IG	SE	YQQLQAQ	- I L V	DEL	TQ
KDR55793.1	OLG	I A	100	AE	YOO	LATL		то
KGG72295.1	0 A A	I A	100	SE	YHOLOOANOELOF	LASS		то
KGG75138.1	OLA	I A	100	SE	YOOLEEANRELOR	LAKL		то
KGG76686.1	NIA	I A	100	SF	Y0 K100 AK001 FR	LAKI	DAI	ТН
Lvn. aest 0230	A LO	IT!	voo	SA	Y F	LAHY		TO
Lyn8106_0097	KIA	i A	100	SA	Y F	ману		TO
Nodo 0172	OFS	v A				ISNI		TO
S hof 0333	NIA			C E				T LL
W/D 006520508 1	OTA		1 11			LCCM		10
WP_006623407.1		12	100					
WP_000023497.1								
WP_000032122.1	QLA							LQ LO
WP_000033119.1	Q V A							I Q
VVP_000300234.1	K L S	1 A	IKU	AH		LANH		I K
WP_009/83/99.1	QIA	1 A	н	QGQ	YHQLEIANQELEH	LAAK	DGL	Q
WP_0108/3/64.1	QVA	IA	I HO	GE	Y E	1 S S L		Q
11/0924	PLI	V A	LQC	AF	Y E A NINLQ	MVYI		D
WP_011317683.1	QAA	I A	IQC	2 S E	Y L		DGL	TQ
WP_011378510.1	QLS	I A		SQ	. L K	QVRI	DGL	TQ
NpR1060	QAA	I A	IQC	S E	. Y H	LACS	DGL	TQ
WP_012594761.1	YIG	I A	LEC	Q E Q	. Y R E L R L A N E E <mark>L</mark> E <mark>C</mark>	LAFV	D S L	ΤE
WP_012599180.1	QLA	I A	IQ	2 S E	. HQ	LALI	DQ L	TQ
WP_013321179.1	TAA	I A	I H (GE	. HQ	LSAI	DGL	TQ
WP_015111021.1	QAA	I A	I H C	SE	. Y H	LAAS	DGL	TQ
WP_015113918.1	QFN	VA	LE	I S E	. L D Q S R S Q A N Q L A Q A N H A L A L A N S K <mark>L</mark> E <mark>K</mark>	LSKL	DGL	ΤK
WP_015123238.1	ALA	I A I	V N C	AE	. Y Q	LVYV	DGL	TQ
WP_015148692.1	QLA	I A	IQ	ST	. F K Q L E A A N E E <mark>L</mark> Q R	IASL	DGL	ТН
Os6304_3021	QVA	I A	IQ	2 S T	. F E Q L Q A A N Q E <mark>L</mark> H R	IASL	DGL	TQ
WP 015174564.1	QVA	I A	I E C	SL	YQQLAAANQR <mark>L</mark> DG	LANL	D S L	TQ
WP 015179608.1	QLA	I A	IK	AD	F Q K L Q K E L A E R Q Q A Q A R M R E I N Q Q L A L S N E E L A R A T H L <mark>L</mark> E Q	VVNI		TQ
WP 015202462.1	QLA	I A	100	DAO	YQQLESANIK LQS	LANL		TO
WP 015955649.1	GAA	I A	I HO	GE	YQQLESANLELK	LSCL		то
WP 016876404.1	0 A A	I A	IK	SE	Y H A NO F LO F	LASS	DGL	TI
WP 017320093 1	0 A A	I A	100	50	Y0 0L0K ANO FLOR	LASL		TO
WP_017745795.1	0 A A	I A	100	SF	Y H 0100 ANO FLOR	LASS	DGI	TO
WP_024125851_1	PIT	V A	100	AF	Y F AL FO ALANIO	MVYI		TD
WP 020632327 1	0 4 4	IΔ	100	SE		VASS		TO
WP_03335474.1	014		100	SE		LATI		TO
WP_033374512.1	OVA		100					
WD 02509205 1	0.4.4							
WP_035080230.1			vo					
WP_033909320.1	QLA							
WP_030012702.1	QAG					LACS		
WP_030034157.1	QLA							LQ LO
WP_030062070.1	QLA					LAKL		
WP_030332576.1	QVG	I A		250	Y N			T C
WP_039/250/6.1	QFG		VYU	AE		LAIM		G
WP_039728489.1	QAA	IA	н	GE	1 Q E L Q A A NA S L E Q	LAHL		Q
VVP_039/29/94.1	QLG	V A	IKC	2 5 É	Y A Q LQC	QAIT		Q
VVP_039/30111.1	QLA	I A	LQC	2 SQ	HQANHELE	LSII		I R
WP_0150/9858.1	PLV	MA	Q	AÉ	Y Q	LASI	JGL	1.
YP_007122690.1	QVA	IA	Q	255	FEQLEAANQE <mark>L</mark> QF	LASI	DGL	<u> </u>
WP_007356015.1	QGA	IA	IQC	2 S Q	YQRLEAANGE <mark>L</mark> QF	LASL	DGL	1.
WP_015210266.1	QLT	I A	I Q (SD	. F Q K S Q K E L A E R É Q A E A R L R E S N Q Q L A F S N E E L A C A T R L L E K	LVNI	DGL	T
		d,		- 1				
Conservation								
Consci /dtion					le e se le			
	457	9 + !	956	583	5 2 2 1 0 0 + 3 2	6622	+ 6 +	+ 1

Consensus QLA I A I QQ S E L Y Q + + Q K E + A E R QQ A Q A R M R E I N QQ L A + + N + Q L QQ F S N E E L A A N Q E L Q R L A S L D G L T Q

Supplemental Figure S5. Spectroscopic characterization of 2^{nd} cysteine mutant constructs of novel R/B CBCR proteins and the GAF1-only construct, Nod_0172(GAF1). (A) Lyn.aest_0230 Δ (C₇₃A), (B) Lyn8106_0097 Δ (C₅₃A), (C) Nod_0172(GAF1). 15*Z*, blue traces; 15*E*, orange traces.



Supplemental Ta	able S1: Accession	information for	r proteins in	this study ¹
1 1			1	•

Protein	Genbank	DOE-IMG locus tag	Organism
	accession		
Os6304_3021	AFY82617	Oscil6304_3021	Oscillatoria acuminata
			PCC 6304
S.hof_0333	KYC42878	WA1DRAFT_10042	Scytonema hofmannii
			PCC 7110
NpR1060	ACC79786	Npun_R1060	Nostoc punctiforme PCC
			73102
Lyn8106_0097	EAW38947	L8106_01492	Lyngbya sp. PCC 8106
Lyn.aest_0230	ERT07933	M595_2050	Lyngbya aestuarii BL J
Cyan7822_5462	ADN17337	Cyan7822_5462	Gloeothece verrucosa
			PCC 7822 ²
Nod_0172	WP_155523487	Lepto7104DRAFT_1266	Nodosilinea nodulosa
			PCC 7104

1. Current Genbank accessions, DOE-IMG locus tags, and current organism/strain designations are provided for each newly characterized protein in this study (Fig. 3).

2. Gloeothece verrucosa PCC 7822 is also known as Cyanothece sp. PCC 7822.

Supplemental Citation

Blain-Hartung MD, Rockwell NC, Lagarias JC (2017) Light-regulated synthesis of cyclic-di-GMP by a bidomain construct of the cyanobacteriochrome Tlr0924 (SesA) without stable dimerization. Biochemistry 56: 6145-6154.