

Additional file 2: Figure S2

	Opsin domain	
<i>Cr2c-Cyc1op1</i> : MKLRQRTVGAQLRSQPVSSAGGPANSGPPATPSGGGIAPVSIFGAAEALADPEARWMLTWSWTFITGFFVYITASWLSGLWYTTDPLAYAALRAQVPTLVYQMSSTAFFTALVLNLSLLFEDNAPKRQLALLSCAIKGAA : 140		
<i>Vc2c-Cyc1op1</i> : —MRKRT—GLPLPRQ—RENAPAQN—————SVNSTLG—EDNGDPEAFRGWYKWTWITWLTGFCFYMTASWVVDACL PANPVASVELFKVPLLVYQMSSTAFFTALVLNLSLLFEDNAPKRQLALLSCAIKGAA : 123		
<i>Cr2c-Cyc1op1</i> : CHTDLLLVTTGGATVLYDAYGSICIPQRVYQWLVTTPTMVYILSKISDFTPRQTATATIGLDVLMVLSGLVANFLRSPYL—WVAFLTSTAATIGVLYMMGLMVYSAVKEHTSANSRRSLFFIYMCTLFIWNLFPALWILHVY : 279		
<i>Vc2c-Cyc1op1</i> : CHTDMLLVTRARVVFDAFGAIVIPQRVYQWLVTTPTMVYILSKISDFTPQQTATATICMDVVMVLSGLMANFAPGPLYNLWLMFVSMLSFVGLYMMGRMVFSVAVKEHSSPSSRRSLFFIYMCTLLIWSMFPVAVWLHLL : 263		
<i>Cr2c-Cyc1op1</i> : HRGSPAEEYLVNFANFMAKVLFSSSIMYGNMTIAQRRLLAQQDAENANRVQMIQDLRDSVTRKQDFMSLMSHELRTPLNGIIQLSDALVRGAGGEMNPQGQHFVRTIKNSSNHLNIINDILDVAALKHGLTIKHEVC : 419	dimerization and histidine phosphotransferase (DHP) domain	
<i>Vc2c-Cyc1op1</i> : NSSSPYGEYLNI FANFMAKVLFSSSIMYGNMTIAQRRLLAQQAENAHVRVMTIQELRDAVTRKQDFMSLMSHELRTPLNGIIQLSDALVRGAGGEMNPQGQHFVRTIKNSSNHLNIINDILDVAALKHGLTIKHEL C : 403		
<i>Cr2c-Cyc1op1</i> : SLAKAVDHVVDIVAPLAKKEVTMERWDPATPLIIDFSRVIQILYNLTGNALKFTNKGVRVGRVPSADGTHVLLQVSDTIGIIPKDRLHSIWGAPEQVDMSVTRKYGGTGLGLNIVKQVEAHEGTIEVASVEGRGTT : 559	catalytic and ATPase (CA) domain	
<i>Vc2c-Cyc1op1</i> : SLAKAVEHVVDIVAPLAKKDAVIERSDPHPLIIDFSRVIQILYNLAGNALKFTHRGVRCVRVSPSADGSSVTLQVADTIGIPPERISG IWGAPEQVDMSVTRKYGGTGLGLNIVKQVEAHEGTIEVASVEGRGTT : 543		
<i>Cr2c-Cyc1op1</i> : FTVLPVLQSSSTRRSLEGVQLDSLTRCGHAAARDTMVQRRTSRP———SLGLEDITITQFARGVQRRASGLLVAKAAQEAGSNAGTGPAGSTGAGAGGGGGAGGGGQDLSLDREEQEQLLRKRTHELEHESRLDLAR : 694		
<i>Vc2c-Cyc1op1</i> : FVTLPVLQPCTRQSLQLQVMESSLCKGHASARAARVSRRRSNRLASTSGRKPSEETASKLARGTTRHASGLTSPSRDDAAD—————GNVSGNSQKEEDVLYRRRTQLEARENLMGELQR : 659		
<i>Cr2c-Cyc1op1</i> : RTVHKQSMEEADLASRQLLLSDYERRAERDTRSLERIDSGQPGLTNGGEGAGGAAGGAGSGGGGSGAPGSAGKAVGAGGSCRGDVRGGGTDGRGGGGGGAGGAGG———GGGGGGGGGASGGGGRSGAPTSGRAS : 829		
<i>Vc2c-Cyc1op1</i> : RAEHKRSMEEAHRYSRQLQLSEPERQAERDSRSLERLDLQIAARPPPS—————LPAPAAAAAGGSLRNSSETGVKSSPGSITAAAGSLGSFQAWRGSEASEVAHRAVTHGSSRTS———GEAR : 771		
<i>Cr2c-Cyc1op1</i> : LIGELPSGGSGGGGGGGGGGGDGTPESPRSATARRGLLAMRQSSLSNLRGATSARAGGAAGGAAASGGVSVGRWASTTDTGFANQAAAAAWRGDSHRTLPGVGGGCVSVSSANGNSIADVYEALQLARASNESGGGGGG : 969		
<i>Vc2c-Cyc1op1</i> : E—ALATRGSVGGGGGGGG—CSG—————STAVSTGNSLADV EYHLLLARGSDSHSHGL : 824		
<i>Cr2c-Cyc1op1</i> : GGGGGGGGNGSSLKASGSLARMSAYRTGYGGAGGGGGGA—NGLNYGGGGGALGGSGASGLLSALESDLRYNRPSPRDPYDCDASSVGADSEYEWVGDDGGAGGGGAGGGRSRGPTSTGSLALGDMACPGGRR : 1108		
<i>Vc2c-Cyc1op1</i> : VRKLSATSVGGGSKSNTVREALRMSITYGRTPGGGGCGGGGGGGGGGMIHSIS——GP——VPGGTSHILLKALDSILYRGARESHD———DGSSVGADSESDGLRA—————AGRRS : 924		
<i>Cr2c-Cyc1op1</i> : HQPPKPSLRSGKLTPLMSNA———AAAAAITAVPPGLTLDKLAYSMDYGTIQVLSVDDEDIQIVLEEILTDSGYAFARCMGDAEAEWL CASDTPMDLILLDDCMPVMSGHEFCATLRKVIPGNVLPVIMVSAKSDEE : 1244	Response regulator	
<i>Vc2c-Cyc1op1</i> : QKGPVPVSRGKIMPASASLNSTNALVTASSLSPPPGLTLDKLPYSMDYGTIQVLSVDEEVNQIVLEEILTSTGYHFARCMGDEALDWLCASETMPDLILLDDCMPVMSGHEFCATLRKVIPGNVLPVIMVSAKSDEE : 1064		
<i>Cr2c-Cyc1op1</i> : NIVEGLRSGSNDFVRKPYQREELLARIETQLRLKSDSWWLAELVNNVDGRETESMKLLKNILPESI IARMQQQKQFVADSHIHVILFSDIVGFTLSLSSKLPTAEVFLMLSNMFTAFLDKLDRFSVYKVTETIGDAYMVA A : 1384	Guanylyl cyclase	
<i>Vc2c-Cyc1op1</i> : NIVEGLRSGSNDFVRKPYRREELLARIETQLRLKSDSWWLAELVNNVDGRETESMKLLKNILPESI IARMQQQKQFVADSHIHVILFSDIVGFTLSLSSKLPTAEVFLMLSNMFTAFLDKLDRFSVYKVTETIGDAYMVA A : 1204		
<i>Cr2c-Cyc1op1</i> : GHDEDEKAEKGSPLMRVLGFARAML DVVRNITAPNGERLIRIGVHC GPAFAGVIGMKPCRYCFLGDTVNTASRMESTGFPMC IHVSENVFKHHPAEAELEQVGERDIKGGKHMRTYVVRGTGAWEQALRDFAA RQQA A : 1524		
<i>Vc2c-Cyc1op1</i> : GHDEDEDKARKGSP LTRVLGFAKAML DVVRNITAPNGERMRI RIGVHC GPAFAGVIGMKPCRYCFLGDTVNTASRMESTGFPMC IHVSEVDYQHHPNMEGEFVEVGEREVKGGKRMRTYLVVRGTGAWEQALRDYAPRQQT A : 1344		
<i>Cr2c-Cyc1op1</i> : AAAAQAAQQLTALA———RQQAALLQQQHEQLQLQLQ———ANGGGGGGA——TAN———AAKAAADAL AQLPASLSPDSASAGSTS SMLPLSGGSVAGAAARTANS LAPAGGGGAAAAGADGGGGN : 1639		
<i>Vc2c-Cyc1op1</i> : AASTSASASAAGQQQQQHQHQPAAQTMMQQQQQLQQQQQLSCQQPEREGLHGGAAGAKSTGVSSGLGGGLHPQQLSQLSHRASFGAVSPGGSRS———AGQ———VMLCPSSSSAAAAAAA———AAA : 1466		
<i>Cr2c-Cyc1op1</i> : GCGGGGGAVRMGHILLSTVAEEGSLPGSPSSFAAAAAAALSPSAAAQQQQQAAPGYHPSHL—RTASAGAGRSP LSRGELPAAAS SPLQPGGGAAGAAGSSPLLPPLLRGANHYTDPRLAGGLRPSFSTGGVYLEDSD D : 1778		
<i>Vc2c-Cyc1op1</i> : ANDGNHNNGRFVHILLSTVAEEVSVPPSPLLLPDATAAVTD———GNGVGFGLVRPQLTSGAMGVRSP LSRPELSA———PRLP———PRTTFGSEAYYCDETSDD : 1559		
<i>Cr2c-Cyc1op1</i> : GGTSTNTGVGGGTGHGMSSLGEGRAGSISTLTGIGAR—SFTGASCGGAGGGGGGGGLRMLNSPTQYDTG DAGENGSSGPGSGGGGGGEGVGGSGGTGSLRVHVPRLSGLSGGSGVSGGSTGIGMSRAGLGSATAAA A : 1917		
<i>Vc2c-Cyc1op1</i> : GANSTLNGMIMASGGALRSC———SGSLTGLLPASPFLLQT——APATGAGAGARRAVSDASGYGNTGD———GGDSGRQPGHASVL DVAA——— : 1639		
<i>Cr2c-Cyc1op1</i> : AASGACFLTSDAADASFSGGVLAAATTSHAALSGGAADQHAPSAGAVMGSSPAALQVSPASPGGAAAGGLGSLSPQSSLYGGAQLLSPNSAGLHSGHANTHTLAYLEQRIASLGTQLATEALSRQRLQDELDAER R : 2057		
<i>Vc2c-Cyc1op1</i> : —————EFLGVGGAATA—PAVA———HLREDGLAFAPATA——AGGAG——R———VGSVTGGAVIPATGYLEQQITRLGTQLAAETSKRQLQADLDEERR : 1722		
<i>Cr2c-Cyc1op1</i> : RAAGAMQASLLMQQLRNATQAAGGSGGAPSSVAAAAAAGQEQHLARLQLGSGGGGADAASGGGGGALPSPAAYL SRLPPPP———RGAGGAVASLRAAGANELL———PTSN—EANSNADADVITGG : 2181		
<i>Vc2c-Cyc1op1</i> : RSASALQHVTLLQQQAALATAAATSSAT———SSTAGRQDSTD R———NGAVATSYGS———CSASTKHPCNNLPSGGPSAKNGTKHGGNSVYRQQQLLEQLRDQEQQQQQQQPISQCDSSYAPDAEIVILG : 1844		
<i>Cr2c-Cyc1op1</i> : GGMSTVVPAAQPSSSAFSGAGAATSGGSGNDQQ———EITLASPFVSDLPAYALEAGDVVPNSLDFASQGFDPGSSGAGGRGGGGGSRHAGRAAAQQRPSSKVKQRMNVDAAALLMQPPKAQ———QLQPGSQ : 2309		
<i>Vc2c-Cyc1op1</i> : PADDADIG———DGSGGSGGSGGAAGTAGPDSDEGPAL EQQRVPSRFPLHLPAASS—GSVEG——GASPRAGLDPRVTTMQG———TGNSSNLMRDSPLVLTDIEWHSNGLRRPDD : 1951		
<i>Cr2c-Cyc1op1</i> : STAFVEA———GGVGRSGASGGGIAEPLPGSAEAYSGSRQQLEDQLLPVMPMPTSI TAL—MPGGGTAAATAAVGTATAASTT———TTTTTYSHHRHVFHTSAAAGALSAHPAPGSPSLPAPSSSSPCTALQP : 2437		
<i>Vc2c-Cyc1op1</i> : ATAAAE TGSP EAAVAVGRRE—TGGGVHVHAT———DARGGT———GGALYSSPVSPPLHPLHSPAGL LAARPASDSTNTDITDQKLFYDSGARVNAVEPHTLSHLGKAAVIVRAG———TAGGTGGCHVQS : 2076		
<i>Cr2c-Cyc1op1</i> : LQLQPPPI PCYSLDALFVDLGLPEYLPFRFDRATRILDMILSMDAQQLERLGLKPLGYRTRVREAVYBLARGLLRSSDEAAVLVEMSQHQHQQQYRSQQAQQLQQHQHQLER——— : 2549		
<i>Vc2c-Cyc1op1</i> : ——GWLMPRYSLDVLFELGLIPLYLGAQFEATRILDQLIGMDTQLERLGLRPLGYCLIR EAVLDLARRLLRACEEARLPLQPLALDAAPV LGAPHAAAAEAPSSINSGGGGGGGGGGGGGGGGGGGGAAMRSG : 2210		