

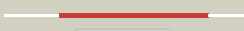


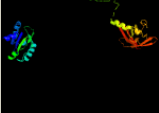


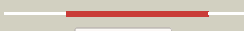














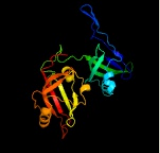


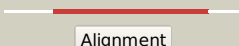

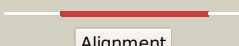
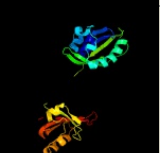
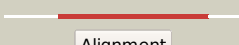

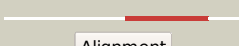
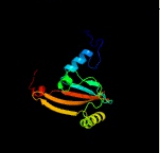







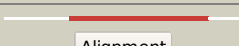








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3651_(-)_4092020_4093057
Date	Fri Aug 9 18:20:34 BST 2019
Unique Job ID	b393e9893eec8c44

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4q6uA_	 Alignment		100.0	98	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
2	c4f3IA_	 Alignment		100.0	9	PDB header: transcription/activator Chain: A: PDB Molecule: circadian locomoter output cycles protein kaput; PDBTitle: crystal structure of the heterodimeric clock:bmal1 transcriptional2 activator complex
3	c4hh2D_	 Alignment		100.0	16	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator, ppsr; PDBTitle: structure of ppsr without the hth motif from rb. sphaeroides
4	c4f3IB_	 Alignment		100.0	6	PDB header: transcription/activator Chain: B: PDB Molecule: bmal1b; PDBTitle: crystal structure of the heterodimeric clock:bmal1 transcriptional2 activator complex
5	c3rtyA_	 Alignment		99.9	11	PDB header: circadian clock protein Chain: A: PDB Molecule: period circadian protein; PDBTitle: structure of an enclosed dimer formed by the drosophila period protein
6	c4zp4D_	 Alignment		99.9	8	PDB header: protein transport/transcription Chain: D: PDB Molecule: endothelial pas domain-containing protein 1; PDBTitle: crystal structure of the heterodimeric hif-2a:arnt complex
7	c5sy5B_	 Alignment		99.9	13	PDB header: transcription Chain: B: PDB Molecule: neuronal pas domain-containing protein 1; PDBTitle: crystal structure of the heterodimeric npas1-arnt complex
8	c3gecA_	 Alignment		99.9	13	PDB header: circadian clock protein Chain: A: PDB Molecule: period circadian protein; PDBTitle: crystal structure of a tandem pas domain fragment of2 drosophila period
9	c4zprB_	 Alignment		99.9	8	PDB header: protein transport/transcription/dna Chain: B: PDB Molecule: hypoxia-inducible factor 1-alpha; PDBTitle: crystal structure of the heterodimeric hif-1a:arnt complex with hre2 dna
10	c4ehoD_	 Alignment		99.9	11	PDB header: signaling protein Chain: D: PDB Molecule: bacteriophytochrome, pas/pac sensor; PDBTitle: crystal structure of the bacteriophytochrome rbbphp1
11	c4dj2C_	 Alignment		99.9	10	PDB header: protein binding Chain: C: PDB Molecule: period circadian protein homolog 1; PDBTitle: unwinding the differences of the mammalian period clock proteins from2 crystal structure to cellular function

12	c3gdiB_	 Alignment		99.9	8	PDB header: transcription Chain: B; PDB Molecule: period circadian protein homolog 2; PDBTitle: mammalian clock protein mper2 - crystal structure of a pas domain2 fragment
13	c4dj3B_	 Alignment		99.9	7	PDB header: protein binding Chain: B; PDB Molecule: period circadian protein homolog 3; PDBTitle: unwinding the differences of the mammalian period clock proteins from2 crystal structure to cellular function
14	c4lrzG_	 Alignment		99.9	11	PDB header: transferase/transcription regulator Chain: G; PDB Molecule: pts-dependent dihydroxyacetone kinase operon regulatory PDBTitle: crystal structure of the e.coli dhar(n)-dhal complex
15	c4zp4A_	 Alignment		99.9	9	PDB header: protein transport/transcription Chain: A; PDB Molecule: aryl hydrocarbon receptor nuclear translocator; PDBTitle: crystal structure of the heterodimeric hif-2a:arnt complex
16	c5sy7B_	 Alignment		99.9	11	PDB header: transcription/dna Chain: B; PDB Molecule: neuronal pas domain-containing protein 3; PDBTitle: crystal structure of the heterodimeric npas3-arnt complex with hre dna
17	c3caxA_	 Alignment		99.9	9	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein pf0695; PDBTitle: crystal structure of uncharacterized protein pf0695
18	c3bw1A_	 Alignment		99.9	14	PDB header: transferase Chain: A; PDB Molecule: sensor protein; PDBTitle: crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
19	c1wa9A_	 Alignment		99.9	10	PDB header: circadian rhythm Chain: A; PDB Molecule: period circadian protein; PDBTitle: crystal structure of the pas repeat region of the2 drosophila clock protein period
20	d1ew0a_	 Alignment		99.9	12	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
21	c4hj6A_	 Alignment	not modelled	99.9	14	PDB header: signaling protein Chain: A; PDB Molecule: lov protein; PDBTitle: crystal structure of rhodobacter sphaeroides lov protein
22	c3ewkA_	 Alignment	not modelled	99.8	14	PDB header: flavoprotein Chain: A; PDB Molecule: sensor protein; PDBTitle: structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
23	c6i20A_	 Alignment	not modelled	99.8	13	PDB header: transcription Chain: A; PDB Molecule: aureochrome1-like protein; PDBTitle: flavin analogue sheds light on light-oxygen-voltage domain mechanism
24	c3mr0B_	 Alignment	not modelled	99.8	11	PDB header: transcription regulator Chain: B; PDB Molecule: sensory box histidine kinase/response regulator; PDBTitle: crystal structure of sensory box histidine kinase/response regulator2 from burkholderia thailandensis e264
25	c2r78D_	 Alignment	not modelled	99.8	12	PDB header: transferase Chain: D; PDB Molecule: sensor protein; PDBTitle: crystal structure of a domain of the sensory box sensor2 histidine kinase/response regulator from geobacter3 sulfurreducens
26	c3sw1B_	 Alignment	not modelled	99.8	11	PDB header: signaling protein Chain: B; PDB Molecule: sensory box protein; PDBTitle: structure of a full-length bacterial lov protein
27	c4gczB_	 Alignment	not modelled	99.8	12	PDB header: signaling protein, de novo protein Chain: B; PDB Molecule: blue-light photoreceptor, sensor protein fixl; PDBTitle: structure of a blue-light photoreceptor
28	c4wujB_	 Alignment	not modelled	99.8	11	PDB header: circadian clock protein Chain: B; PDB Molecule: glycoside hydrolase family 15, cellulose signaling PDBTitle: structural biochemistry of a fungal lov domain

						photoreceptor reveals2 an evolutionarily conserved pathway integrating blue-light and3 oxidative stress
29	c3mqoB_	Alignment	not modelled	99.8	15	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
30	c3k3dA_	Alignment	not modelled	99.8	6	PDB header: signaling protein Chain: A: PDB Molecule: protein rv1364c/mt1410; PDBTitle: the n-terminal pas domain crystal structure of rv1364c from2 mycobacterium tuberculosis at 2.3 angstrom
31	c3ue6C_	Alignment	not modelled	99.8	8	PDB header: signaling protein Chain: C: PDB Molecule: aureochrome1; PDBTitle: the dark structure of the blue-light photoreceptor aureochrome1 lov
32	c2pr6A_	Alignment	not modelled	99.8	11	PDB header: flavoprotein, signaling protein Chain: A: PDB Molecule: blue-light photoreceptor; PDBTitle: structural basis for light-dependent signaling in the dimeric lov2 photosensor ytva (light structure)
33	c2v1bA_	Alignment	not modelled	99.8	9	PDB header: transferase Chain: A: PDB Molecule: nph1-1; PDBTitle: n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
34	c3luqC_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: C: PDB Molecule: sensor protein; PDBTitle: the crystal structure of a pas domain from a sensory box histidine2 kinase regulator from geobacter sulfurreducens to 2.5a
35	c3eehA_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: putative light and redox sensing histidine kinase; PDBTitle: the crystal structure of the domain of the putative light and redox2 sensing histidine kinase from haloarcula marismortui
36	c2qj3A_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: nitrogen fixation regulatory protein; PDBTitle: crystal structure of the fad-containing pas domain of the protein nif2 from azotobacter vinelandii.
37	c5xgdA_	Alignment	not modelled	99.7	21	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
38	c3mfxA_	Alignment	not modelled	99.7	10	PDB header: transcription Chain: A: PDB Molecule: sensory box/ggdef family protein; PDBTitle: crystal structure of the sensory box domain of the sensory-box/ggdef2 protein so_1695 from shewanella oneidensis, northeast structural3 genomics consortium target sor288b
39	c3volA_	Alignment	not modelled	99.7	8	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: x-ray crystal structure of pas-hamp aer2 in the cn-bound form
40	c3h9wA_	Alignment	not modelled	99.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: diguanylate cyclase with pas/pac sensor; PDBTitle: crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr66c
41	c2vlqD_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: D: PDB Molecule: sporulation kinase a; PDBTitle: kina pas-a domain, homodimer
42	c2mwgB_	Alignment	not modelled	99.7	11	PDB header: protein binding Chain: B: PDB Molecule: blue-light photoreceptor; PDBTitle: full-length solution structure of ytva, a lov-photoreceptor protein2 and regulator of bacterial stress response
43	c5hvvA_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase tod5; PDBTitle: crystal structure of pas1 complexed with toluene
44	c2ykfA_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: A: PDB Molecule: probable sensor histidine kinase pdtas; PDBTitle: sensor region of a sensor histidine kinase
45	d1y28a_	Alignment	not modelled	99.7	13	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
46	c3lyxA_	Alignment	not modelled	99.7	16	PDB header: transcription Chain: A: PDB Molecule: sensory box/ggdef domain protein; PDBTitle: crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b
47	c3mxqC_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: C: PDB Molecule: sensor protein; PDBTitle: crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
48	c3oloB_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: two-component sensor histidine kinase; PDBTitle: crystal structure of a pas domain from two-component sensor histidine2 kinase
49	d1p97a_	Alignment	not modelled	99.7	11	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Hypoxia-inducible factor Hif2a, C-terminal domain
50	c3icyB_	Alignment	not modelled	99.7	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: sensor protein; PDBTitle: the crystal structure of sensory box histidine kinase/response2 regulator domain from chlorobium tepidum tls
51	c3mjgB_	Alignment	not modelled	99.7	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the pas domain of q24qt8_deshy protein from2 desulfitobacterium hafniense. northeast structural genomics3 consortium target dhr85c.
52	c3niaC_	Alignment	not modelled	99.7	7	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable ggdef family protein;

52	c3njac_	Alignment	not modelled	99.7	7	PDBTitle: the crystal structure of the pas domain of a ggdef family protein from2 chromobacterium violaceum atcc 12472.
53	c3kx0X_	Alignment	not modelled	99.7	7	PDB header: signaling protein Chain: X: PDB Molecule: uncharacterized protein rv1364c/mt1410; PDBTitle: crystal structure of the pas domain of rv1364c
54	c5svuD_	Alignment	not modelled	99.7	12	PDB header: circadian clock protein Chain: D: PDB Molecule: adagio protein 1; PDBTitle: structure and kinetics of the lov domain of zeitlupe determine its2 circadian function in arabidopsis
55	c2qkpD_	Alignment	not modelled	99.7	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
56	c2l4rA_	Alignment	not modelled	99.7	13	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: nmr solution structure of the n-terminal pas domain of herg
57	c3f1oB_	Alignment	not modelled	99.7	11	PDB header: transcription Chain: B: PDB Molecule: aryl hydrocarbon receptor nuclear translocator; PDBTitle: crystal structure of the high affinity heterodimer of hif2 alpha and2 arnt c-terminal pas domains, with an internally-bound artificial3 ligand
58	c5iu1A_	Alignment	not modelled	99.7	14	PDB header: plant protein Chain: A: PDB Molecule: ctr1-like protein; PDBTitle: n-terminal pas domain homodimer of ppanr map3k from physcomitrella2 patens.
59	c5akpA_	Alignment	not modelled	99.6	15	PDB header: signaling protein Chain: A: PDB Molecule: phytochrome-like protein; PDBTitle: crystal structure of the dark-adapted full-length2 bacteriophytochrome xccbphp from xanthomonas campestris3 bound to bv chromophore
60	c1v9yA_	Alignment	not modelled	99.6	11	PDB header: signaling protein Chain: A: PDB Molecule: heme pas sensor protein; PDBTitle: crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
61	d1v9ya_	Alignment	not modelled	99.6	11	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
62	c2pdtD_	Alignment	not modelled	99.6	11	PDB header: circadian clock protein Chain: D: PDB Molecule: vivid pas protein vvd; PDBTitle: 2.3 angstrom structure of phosphodiesterase treated vivid
63	c2wkqA_	Alignment	not modelled	99.6	9	PDB header: transferase, cell adhesion Chain: A: PDB Molecule: nph1-1, ras-related c3 botulinum toxin substrate 1; PDBTitle: structure of a photoactivatable rac1 containing the lov2 c450a mutant
64	c4hoiB_	Alignment	not modelled	99.6	14	PDB header: transport protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: crystal structure of pas domain from the mouse eag1 potassium channel
65	c4wn5A_	Alignment	not modelled	99.6	10	PDB header: transcription Chain: A: PDB Molecule: hypoxia-inducible factor 3-alpha; PDBTitle: crystal structure of the c-terminal per-arnt-sim (pasb) of human hif-2 3alpha9 bound to 18:1-1-monoacylglycerol
66	c2kdkA_	Alignment	not modelled	99.6	8	PDB header: transcription regulator Chain: A: PDB Molecule: aryl hydrocarbon receptor nuclear translocator-like protein PDBTitle: structure of human circadian clock protein bmal2 c-terminal pas domain
67	d1bywa_	Alignment	not modelled	99.6	9	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
68	c4i5sA_	Alignment	not modelled	99.6	10	PDB header: transferase Chain: A: PDB Molecule: putative histidine kinase covs; vick-like protein; PDBTitle: structure and function of sensor histidine kinase
69	c4hp4A_	Alignment	not modelled	99.6	9	PDB header: transport protein Chain: A: PDB Molecule: eag-like k[+] channel; PDBTitle: crystal structure of pas domain from the fruit-fly elk potassium2 channel
70	c5va1A_	Alignment	not modelled	99.6	10	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: cryo-em structure of the human ether-a-go-go related k+ channel
71	c3cloC_	Alignment	not modelled	99.6	14	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
72	c3b33A_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus
73	d1n9la_	Alignment	not modelled	99.5	13	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
74	c3t50B_	Alignment	not modelled	99.5	2	PDB header: transferase Chain: B: PDB Molecule: blue-light-activated histidine kinase; PDBTitle: x-ray structure of the lov domain from the lov-hk sensory protein from2 brucella abortus (dark state).
75	c6rhgB_	Alignment	not modelled	99.5	10	PDB header: fluorescent protein Chain: B: PDB Molecule: multi-sensor hybrid histidine kinase; PDBTitle: structure of chloroflexus aggregans cagg_3753 lov domain
						Fold: Profilin-like

76	d1xj3a1	Alignment	not modelled	99.5	13	Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
77	c2z6dB	Alignment	not modelled	99.5	12	PDB header: transferase Chain: B: PDB Molecule: phototropin-2; PDBTitle: crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana
78	d1jnua	Alignment	not modelled	99.5	8	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
79	c4kuoA	Alignment	not modelled	99.5	13	PDB header: signaling protein Chain: A: PDB Molecule: blue-light photoreceptor; PDBTitle: a superfast recovering full-length lov protein from the marine2 phototrophic bacterium dinoroseobacter shibae (photoexcited state)
80	d1l18a	Alignment	not modelled	99.4	19	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: N-terminal PAS domain of Pas kinase
81	c5f6aA	Alignment	not modelled	99.4	9	PDB header: circadian clock protein Chain: A: PDB Molecule: protein cycle; PDBTitle: drosophila melanogaster cycle w398a pas-b with empty pocket
82	c3fg8B	Alignment	not modelled	99.4	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rha05790; PDBTitle: crystal structure of pas domain of rha05790
83	c2jheB	Alignment	not modelled	99.4	12	PDB header: transcription Chain: B: PDB Molecule: transcription regulator tyrr; PDBTitle: n-terminal domain of tyrr transcription factor (residues 1-190)
84	c4mn5A	Alignment	not modelled	99.3	11	PDB header: transferase Chain: A: PDB Molecule: sensor protein kinase walk; PDBTitle: crystal structure of pas domain of s. aureus yycg
85	d1oj5a	Alignment	not modelled	99.3	9	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PAS domain of steroid receptor coactivator 1A, NCo-A1
86	c3p7nB	Alignment	not modelled	99.3	11	PDB header: dna binding protein Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
87	c4m4xA	Alignment	not modelled	99.3	11	PDB header: transcription Chain: A: PDB Molecule: aryl hydrocarbon receptor; PDBTitle: structure and dimerization properties of the aryl hydrocarbon receptor2 (ahr) pas-a domain
88	c2w0nA	Alignment	not modelled	99.3	9	PDB header: transferase Chain: A: PDB Molecule: sensor protein dcus; PDBTitle: plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
89	c3fc7B	Alignment	not modelled	99.3	7	PDB header: transferase Chain: B: PDB Molecule: htr-like protein; PDBTitle: the crystal structure of a domain of htr-like protein from haloarcula2 marismortui atcc 43049
90	c6dgiA	Alignment	not modelled	99.2	8	PDB header: unknown function Chain: A: PDB Molecule: rpfr; PDBTitle: cronobacter turicensis rpfr quorum-sensing receptor pas domain in2 complex with bdsf
91	c4r3aA	Alignment	not modelled	99.2	10	PDB header: signaling protein Chain: A: PDB Molecule: blue-light-activated histidine kinase 2; PDBTitle: erythrobacter litoralis el346 blue-light activated histidine kinase
92	c5nwmA	Alignment	not modelled	99.2	11	PDB header: signaling protein Chain: A: PDB Molecule: nuclear receptor coactivator 1; PDBTitle: insight into the molecular recognition mechanism of the coactivator2 ncoa1 by stat6
93	c6ceqC	Alignment	not modelled	99.2	10	PDB header: signaling protein Chain: C: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: the aer2 receptor from vibrio cholerae is a dual pas-heme oxygen2 sensor
94	d1nwza	Alignment	not modelled	99.2	8	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
95	c5k7lA	Alignment	not modelled	99.2	13	PDB header: metal transport/calcium binding protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin
96	c5fq1A	Alignment	not modelled	99.1	7	PDB header: transferase Chain: A: PDB Molecule: histidine kinase; PDBTitle: structure of the cytoplasmic pas domain of the geobacillus2 thermodenitrificans histidine kinase cita
97	c5hzbB	Alignment	not modelled	99.1	9	PDB header: signaling protein Chain: B: PDB Molecule: intersectin-1,nph1-1,intersectin-1; PDBTitle: crystal structure of photoinhibitable intersectin1 containing wildtype2 lov2 domain in complex with cdc42
98	c2o9bA	Alignment	not modelled	99.1	14	PDB header: transferase Chain: A: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of bacteriophytochrome chromophore binding domain
99	c4e04B	Alignment	not modelled	99.1	11	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: rpbphp2 chromophore-binding domain crystallized by homologue-directed2 mutagenesis.
100	c4rq9A	Alignment	not modelled	99.1	8	PDB header: signaling protein Chain: A: PDB Molecule: photoreceptor-histidine kinase bphp; PDBTitle: crystal structure of the chromophore-binding domain of stigmatella2 aurantiaca bacteriophytochrome (thr289his mutant) in the pr state
101	d1lotda	Alignment	not modelled	99.1	11	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain)

						Family: PYP-like
102	d1mzua_	Alignment	not modelled	99.0	8	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
103	c3a0rA_	Alignment	not modelled	99.0	7	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
104	c4o01D_	Alignment	not modelled	98.9	15	PDB header: transferase Chain: D: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of d. radiodurans bacteriophytochrome photosensory2 core module in its illuminated form
105	c3a0vA_	Alignment	not modelled	98.9	9	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
106	c5y7yA_	Alignment	not modelled	98.8	10	PDB header: transcription Chain: A: PDB Molecule: aryl hydrocarbon receptor repressor; PDBTitle: crystal structure of ahrr/arnt complex
107	c6ideA_	Alignment	not modelled	98.8	13	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
108	d1xfna1	Alignment	not modelled	98.8	10	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
109	c2oolA_	Alignment	not modelled	98.7	6	PDB header: signaling protein Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
110	c2veaA_	Alignment	not modelled	98.7	7	PDB header: transferase Chain: A: PDB Molecule: phytochrome-like protein cph1; PDBTitle: the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
111	c6bapC_	Alignment	not modelled	98.6	7	PDB header: signaling protein Chain: C: PDB Molecule: photoreceptor-histidine kinase bphp; PDBTitle: stigmatella aurantiaca bacterial phytochrome pas-gaf-phy, t289h mutant
112	c4r70B_	Alignment	not modelled	98.3	5	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: crystal structure of bacteriophytochrome rpbphp3 from photosynthetic2 bacterium r. palustris
113	c5v0lB_	Alignment	not modelled	98.3	12	PDB header: transcription/dna Chain: B: PDB Molecule: aryl hydrocarbon receptor; PDBTitle: crystal structure of the ahr-arnt heterodimer in complex with the dre
114	c3c2wB_	Alignment	not modelled	94.4	7	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of the photosensory core domain of p. aeruginosa2 bacteriophytochrome pabphp in the pfr state
115	c5llxB_	Alignment	not modelled	91.8	10	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase (ggdef) domain-containing protein; PDBTitle: bacteriophytochrome activated diguanylyl cyclase from idiomarina2 species a28l with gtp bound
116	c6d9mA_	Alignment	not modelled	86.1	9	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
117	c3gwrA_	Alignment	not modelled	78.4	7	PDB header: protein binding Chain: A: PDB Molecule: putative calcium/calmodulin-dependent protein kinase type PDBTitle: crystal structure of putative calcium/calmodulin-dependent protein2 kinase type ii association domain (yp_315894.1) from thiobacillus3 denitrificans atcc 25259 at 2.00 a resolution
118	d2o9ca2	Alignment	not modelled	73.0	12	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: BphP N-terminal domain-like
119	c3u2aA_	Alignment	not modelled	71.7	11	PDB header: hydrolase Chain: A: PDB Molecule: ggdef family protein; PDBTitle: adaptor dependent degradation of a cell-cycle regulator reveals2 diversity in substrate architectures
120	c4ovmE_	Alignment	not modelled	48.9	14	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus