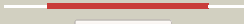



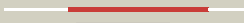



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1354c_(-)_1520011_1521882
Date	Wed Jul 31 22:05:45 BST 2019
Unique Job ID	e6405ca02b00832b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xgdA_	 Alignment		100.0	29	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
2	c5m3cB_	 Alignment		100.0	38	PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575 from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
3	c4rnhA_	 Alignment		100.0	36	PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
4	c3pjwA_	 Alignment		100.0	26	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
5	c3gfbB_	 Alignment		100.0	22	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
6	c3sy8C_	 Alignment		100.0	25	PDB header: transcription regulator Chain: C: PDB Molecule: rocr; PDBTitle: crystal structure of the response regulator rocr
7	c4hjfA_	 Alignment		100.0	36	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea in complex with c-di-gmp and ca++
8	c4fokA_	 Alignment		100.0	22	PDB header: protein binding Chain: A: PDB Molecule: fimx; PDBTitle: 1.8 a crystal structure of the fimx eal domain in complex with c-digmp
9	c4rniA_	 Alignment		100.0	38	PDB header: hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora phosphodiesterase domain, apo form
10	c3hvbB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of fimx from2 pseudomonas aeruginosa
11	c4lykB_	 Alignment		100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: cyclic di-gmp phosphodiesterase yaha; PDBTitle: crystal structure of the eal domain of c-di-gmp specific2 phosphodiesterase yaha in complex with activating cofactor mg++

12	c3hv9A_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx eal domain from pseudomonas aeruginosa
13	c3s83A_	Alignment		100.0	35	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea
14	c4f48A_	Alignment		100.0	23	PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the x-ray structural of fimxeal-c-di-gmp-pilz complexes from2 xanthomonas campestris
15	c4y8eA_	Alignment		100.0	32	PDB header: metal binding protein Chain: A: PDB Molecule: pa3825 eal; PDBTitle: pa3825-eal ca-apo structure
16	c4q6jB_	Alignment		100.0	31	PDB header: unknown function Chain: B: PDB Molecule: lmo0131 protein; PDBTitle: crystal structure of eal domain protein from listeria monocytogenes2 egd-e
17	c3pfmA_	Alignment		100.0	25	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
18	c4hu4B_	Alignment		100.0	35	PDB header: signaling protein,hydrolase Chain: B: PDB Molecule: oxygen sensor protein dosp; PDBTitle: crystal structure of eal domain of the e. coli dosp - dimeric form
19	c2w27A_	Alignment		100.0	23	PDB header: signaling protein Chain: A: PDB Molecule: ykui protein; PDBTitle: crystal structure of the bacillus subtilis ykui protein, with an eal2 domain, in complex with substrate c-di-gmp and calcium
20	c5m1tB_	Alignment		100.0	41	PDB header: signaling protein Chain: B: PDB Molecule: mucr phosphodiesterase; PDBTitle: pamucr phosphodiesterase, c-di-gmp complex
21	c5yrpB_	Alignment	not modelled	100.0	60	PDB header: biosynthetic protein Chain: B: PDB Molecule: sensory box/response regulator; PDBTitle: crystal structure of the eal domain of mycobacterium smegmatis dcpa
22	c2r6oB_	Alignment	not modelled	100.0	37	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative diguanylate cyclase/phosphodiesterase (ggdef & eal PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
23	d2basa1	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain
24	c3tlqB_	Alignment	not modelled	100.0	16	PDB header: transcription Chain: B: PDB Molecule: regulatory protein ydiv; PDBTitle: crystal structure of eal-like domain protein ydiv
25	c3kzpA_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative diguanylate cyclase/phosphodiesterase; PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes
26	c5hxgA_	Alignment	not modelled	100.0	18	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein stm1697; PDBTitle: stm1697-flhd complex
27	c1w25B_	Alignment	not modelled	100.0	32	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
28	c4zmuD_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas

					aeruginosa
29	c6d9mA_	Alignment	not modelled	100.0	26 PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin,response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
30	c5llxB_	Alignment	not modelled	100.0	23 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
31	c3ezuA_	Alignment	not modelled	100.0	25 PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
32	c4h54B_	Alignment	not modelled	100.0	22 PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase ydeh; PDBTitle: crystal structure of the diguanylate cyclase dgcz
33	c3tvkA_	Alignment	not modelled	100.0	25 PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase dgcz; PDBTitle: diguanylate cyclase domain of dgcz
34	c3icIA_	Alignment	not modelled	100.0	35 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium target mcr174c
35	c3mtkA_	Alignment	not modelled	100.0	28 PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase; PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
36	c3ignA_	Alignment	not modelled	100.0	27 PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of the ggdef domain from marinobacter aquaeolei2 diguanylate cyclase complexed with c-di-gmp - northeast structural3 genomics consortium target mqr89a
37	c3breA_	Alignment	not modelled	100.0	30 PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
38	c3i5cA_	Alignment	not modelled	100.0	27 PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wspr response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
39	c3i5bA_	Alignment	not modelled	100.0	28 PDB header: signaling protein Chain: A: PDB Molecule: wspr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wspr from2 pseudomonas aeruginosa
40	c3hvaA_	Alignment	not modelled	100.0	22 PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas aeruginosa
41	c4zmmB_	Alignment	not modelled	100.0	30 PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: ggdef domain of dcsbis complexed with c-di-gmp
42	c4ymeA_	Alignment	not modelled	100.0	36 PDB header: lyase Chain: A: PDB Molecule: sensory box/ggdef family protein; PDBTitle: crystal structure of a sensory box/ggdef family protein (cc_0091) from2 caulobacter crescentus cb15 at 1.40 a resolution (psi community3 target, shapiro)
43	c4wxoA_	Alignment	not modelled	100.0	32 PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
44	c5euhA_	Alignment	not modelled	100.0	35 PDB header: membrane protein Chain: A: PDB Molecule: putative ggdef domain membrane protein; PDBTitle: crystal structure of the c-di-gmp-bound ggdef domain of p. fluorescens2 gcbc
45	c4zvHb_	Alignment	not modelled	100.0	28 PDB header: signaling protein Chain: B: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of ggdef domain of the e. coli dosc - form iv
46	c3qyyB_	Alignment	not modelled	100.0	29 PDB header: signaling protein/inhibitor Chain: B: PDB Molecule: response regulator; PDBTitle: a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
47	c3i5aA_	Alignment	not modelled	99.9	27 PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wspr from pseudomonas syringae
48	d1w25a3	Alignment	not modelled	99.9	37 Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
49	c6eibC_	Alignment	not modelled	99.9	26 PDB header: transferase Chain: C: PDB Molecule: sensory box/ggdef family protein; PDBTitle: structure of the active ggeef domain of a diguanylate cyclase from2 vibrio cholerae.
50	c4iobA_	Alignment	not modelled	99.9	35 PDB header: lyase Chain: A: PDB Molecule: diguanylate cyclase tpbb; PDBTitle: crystal structure of the ggdef domain of pa1120 (yfin or tpbb) from2 pseudomonas aeruginosa at 2.7 ang.
51	c4urgB_	Alignment	not modelled	99.9	33 PDB header: lyase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from t.maritima (active-like dimer)
52	c4dmzB_	Alignment	not modelled	99.9	16 PDB header: nucleotide-binding protein Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo

						form
53	c4euvA	Alignment	not modelled	99.9	16	PDB header: signaling protein Chain: A: PDB Molecule: peld; PDBTitle: crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
54	c3hvwA	Alignment	not modelled	99.9	22	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567 protein from2 pseudomonas aeruginosa, northeast structural genomics consortium3 target par365c
55	c4bwiA	Alignment	not modelled	98.6	14	PDB header: transferase Chain: A: PDB Molecule: phytochrome-like protein cph2; PDBTitle: structure of the phytochrome cph2 from synechocystis sp. pcc6803
56	d2o9ca1	Alignment	not modelled	98.6	16	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
57	d2oola1	Alignment	not modelled	98.6	12	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
58	d3c2wa1	Alignment	not modelled	98.6	13	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
59	c4fofA	Alignment	not modelled	98.4	15	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the blue-light absorbing form of the2 thermosynechococcus elongatus pixj gaf-domain
60	c2lb5A	Alignment	not modelled	98.3	18	PDB header: transferase Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
61	d2veaa1	Alignment	not modelled	98.3	9	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
62	c6oeiA	Alignment	not modelled	98.3	16	PDB header: structural protein Chain: A: PDB Molecule: spindle pole body component spc42,sigma-54-dependent PDBTitle: yeast spc42 n-terminal coiled-coil fused to pdb: 3k2n
63	c3w2zA	Alignment	not modelled	98.3	13	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cyanobacterial protein
64	c6g20A	Alignment	not modelled	98.3	16	PDB header: fluorescent protein Chain: A: PDB Molecule: bacteriophytochrome protein; PDBTitle: crystal structure of a fluorescence optimized bathy phytochrome2 pairfp2 derived from wild-type app2 in its functional meta-f3 intermediate state.
65	c4wkkA	Alignment	not modelled	98.2	15	PDB header: signaling protein Chain: A: PDB Molecule: bacteriophytochrome protein; PDBTitle: the photosensory module (pas-gaf-phy) of the bacterial phytochrome2 agp1 (atbphp1) in the pr form, chromophore modelled with an exocyclic3 double bond at pyrrole ring a.
66	c3c2wB	Alignment	not modelled	98.2	12	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
67	c5dfxA	Alignment	not modelled	98.1	14	PDB header: transferase Chain: A: PDB Molecule: histidine kinase; PDBTitle: structure of the parental state of gaf3 from slr1393 of synechocystis2 sp. pcc6803 (in vivo assembled protein/chromophore)
68	c3trcA	Alignment	not modelled	98.1	15	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
69	c3hcyB	Alignment	not modelled	98.1	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative two-component sensor histidine kinase protein; PDBTitle: the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
70	c4s21B	Alignment	not modelled	98.0	14	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: crystal structure of the photosensory core module of2 bacteriophytochrome rpa3015 from r. palustris
71	d2k2na1	Alignment	not modelled	98.0	18	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
72	c2zmfA	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: A: PDB Molecule: camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase PDBTitle: crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a
73	c6mghB	Alignment	not modelled	98.0	14	PDB header: fluorescent protein Chain: B: PDB Molecule: mirfp670nano; PDBTitle: x-ray structure of monomeric near-infrared fluorescent protein2 mirfp670nano
74	c3p01C	Alignment	not modelled	98.0	11	PDB header: signaling protein Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
75	c3ci6B	Alignment	not modelled	98.0	14	PDB header: transferase Chain: B: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
						PDB header: transcription regulator Chain: B: PDB Molecule: sigma-54-dependent transcriptional

76	c3k2nB	Alignment	not modelled	98.0	15	regulator; PDBTitle: the crystal structure of sigma-54-dependent transcriptional regulator2 domain from chlorobium tepidum t1s
77	c4e04B	Alignment	not modelled	97.9	14	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: rpbph2 chromophore-binding domain crystallized by homologue-directed2 mutagenesis.
78	c3mmhA	Alignment	not modelled	97.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
79	c3p7nB	Alignment	not modelled	97.9	17	PDB header: dna binding protein Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
80	c3o5yA	Alignment	not modelled	97.9	10	PDB header: transcription regulator Chain: A: PDB Molecule: sensor protein; PDBTitle: the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
81	c3p01A	Alignment	not modelled	97.8	11	PDB header: signaling protein Chain: A: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
82	c2oolA	Alignment	not modelled	97.8	13	PDB header: signaling protein Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbph3 from r. palustris
83	c4rq9A	Alignment	not modelled	97.8	15	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
84	c4ehoD	Alignment	not modelled	97.7	14	PDB header: signaling protein Chain: D: PDB Molecule: bacteriophytochrome, pas/pac sensor; PDBTitle: crystal structure of the bacteriophytochrome rpbphp1
85	c3oovA	Alignment	not modelled	97.7	13	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein, putative; PDBTitle: crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
86	c5w10A	Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-specific phosphodiesterase; PDBTitle: lcd1 gaf domain in complex with camp ligand
87	c3dbaB	Alignment	not modelled	97.7	9	PDB header: hydrolase Chain: B: PDB Molecule: cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit PDBTitle: crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
88	c3eeaB	Alignment	not modelled	97.7	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: gaf domain/hd domain protein; PDBTitle: the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
89	c6mzbA	Alignment	not modelled	97.6	12	PDB header: signaling protein Chain: A: PDB Molecule: rod cgmp-specific 3',5'-cyclic phosphodiesterase subunit PDBTitle: cryo-em structure of phosphodiesterase 6
90	c6fhtB	Alignment	not modelled	97.6	16	PDB header: lyase Chain: B: PDB Molecule: bacteriophytochrome,adenylate cyclase; PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
91	c4g3vB	Alignment	not modelled	97.6	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator nh2; PDBTitle: crystal structure of a. aeolicus nh2 gaf domain in an inactive state
92	c1mc0A	Alignment	not modelled	97.5	8	PDB header: hydrolase Chain: A: PDB Molecule: 3',5'-cyclic nucleotide phosphodiesterase 2a; PDBTitle: regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
93	c6ifnA	Alignment	not modelled	97.5	20	PDB header: rna binding protein Chain: A: PDB Molecule: type iii-a crispr-associated protein csm1; PDBTitle: crystal structure of type iii-a crispr csm complex
94	c1vhmB	Alignment	not modelled	97.4	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein yebr; PDBTitle: crystal structure of an hypothetical protein
95	c2veaA	Alignment	not modelled	97.3	10	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.
96	c4mcwA	Alignment	not modelled	97.3	12	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent phosphohydrolase; PDBTitle: metallo-enzyme from p. marina
97	c6iqwA	Alignment	not modelled	97.3	19	PDB header: rna binding protein/rna Chain: A: PDB Molecule: csm1; PDBTitle: cryo-em structure of csm effector complex
98	d1vhma	Alignment	not modelled	97.2	13	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
99	c3ungC	Alignment	not modelled	97.2	22	PDB header: unknown function Chain: C: PDB Molecule: cmr2dhd; PDBTitle: structure of the cmr2 subunit of the crispr rna silencing complex
100	c4iukB	Alignment	not modelled	97.2	13	PDB header: nitrate-binding protein Chain: B: PDB Molecule: nrea protein; PDBTitle: crystal structure of nrea of staphylococcus carnosus with bound2 nitrate

101	c2o9bA	Alignment	not modelled	97.2	14	PDB header: transferase Chain: A: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of bacteriophytochrome chromophore binding domain
102	c2vjwA	Alignment	not modelled	97.2	15	PDB header: hydrolase Chain: A: PDB Molecule: gaf family protein; PDBTitle: crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
103	c3rfbB	Alignment	not modelled	97.1	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of frmsr
104	c4uw2A	Alignment	not modelled	97.1	15	PDB header: immune system Chain: A: PDB Molecule: csm1; PDBTitle: crystal structure of csm1 in t.onnurineus
105	c3ibjB	Alignment	not modelled	97.0	15	PDB header: hydrolase Chain: B: PDB Molecule: cgmp-dependent 3',5'-cyclic phosphodiesterase; PDBTitle: x-ray structure of pde2a
106	c3e0yA	Alignment	not modelled	97.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca
107	c4w8yA	Alignment	not modelled	96.9	20	PDB header: rna binding protein Chain: A: PDB Molecule: crispr system cmr subunit cmr2; PDBTitle: structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
108	d1mc0a2	Alignment	not modelled	96.9	7	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
109	d1mc0a1	Alignment	not modelled	96.8	11	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
110	c4pauA	Alignment	not modelled	96.8	14	PDB header: unknown function Chain: A: PDB Molecule: nitrogen regulatory protein a; PDBTitle: hypothetical protein sa1058 from s. aureus.
111	c2qybA	Alignment	not modelled	96.8	13	PDB header: membrane protein Chain: A: PDB Molecule: membrane protein, putative; PDBTitle: crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
112	c2w3gA	Alignment	not modelled	96.7	10	PDB header: transferase Chain: A: PDB Molecule: two component sensor histidine kinase devs (gaf) PDBTitle: air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
113	c3ksiA	Alignment	not modelled	96.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of frmsr of staphylococcus aureus (complex with 2-propanol)
114	c4o01D	Alignment	not modelled	96.5	14	PDB header: transferase Chain: D: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of d. radiodurans bacteriophytochrome photosensory2 core module in its illuminated form
115	c4g3kB	Alignment	not modelled	96.3	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator nh1; PDBTitle: crystal structure of a. aeolicus nh1 gaf domain in an inactive state
116	c3mf0A	Alignment	not modelled	96.3	9	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-specific 3',5'-cyclic phosphodiesterase; PDBTitle: crystal structure of pde5a gaf domain (89-518)
117	c2k31A	Alignment	not modelled	96.1	10	PDB header: hydrolase Chain: A: PDB Molecule: phosphodiesterase 5a, cgmp-specific; PDBTitle: solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
118	c3khtA	Alignment	not modelled	96.0	9	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
119	c4mmnD	Alignment	not modelled	96.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: putative uncharacterized protein ta0848; PDBTitle: structural and biochemical analysis of type ii free methionine-r-2 sulfoxide reductase from thermoplasma acidophilum
120	c2pz0B	Alignment	not modelled	95.9	9	PDB header: hydrolase Chain: B: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis