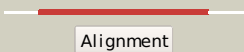

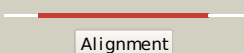

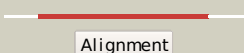

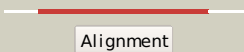

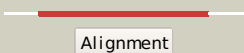

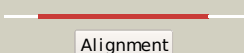

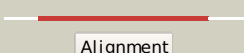

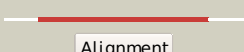
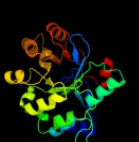
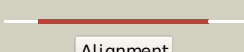

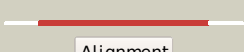




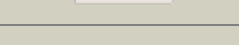


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hvbB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa
2	c3hv9A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx eal domain from pseudomonas aeruginosa
3	c3s83A_	 Alignment		100.0	19	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: crystal structure of eal domain from caulobacter crescentus cb15
4	c3pjwA_	 Alignment		100.0	18	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	19	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
6	c3pfmA_	 Alignment		100.0	18	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
7	c2w27A_	 Alignment		100.0	15	PDB header: signaling protein Chain: A: PDB Molecule: ykui protein; PDBTitle: crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium
8	c2r6oB_	 Alignment		100.0	21	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
9	d2basa1	 Alignment		100.0	14	Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain
10	c3kzpA_	 Alignment		100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative diguanylate cyclase/phosphodiesterase; PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listeria monocytigenes
11	d1p6qa_	 Alignment		94.0	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

12	dlheya_	Alignment		93.5	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
13	c3eulB_	Alignment		93.0	14	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narI from mycobacterium tuberculosis
14	c3khtA_	Alignment		93.0	10	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
15	dl dz3a_	Alignment		92.9	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
16	dlmvoa_	Alignment		92.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
17	c3hebB_	Alignment		91.5	13	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator receiver domain protein (chey); PDBTitle: crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
18	c2zayA_	Alignment		91.4	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
19	dljbea_	Alignment		89.7	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
20	c3b2nA_	Alignment		89.5	14	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
21	d2ayxa1	Alignment	not modelled	88.8	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
22	dlw25a1	Alignment	not modelled	88.6	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
23	c3gt7A_	Alignment	not modelled	87.4	21	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
24	dlqkka_	Alignment	not modelled	86.4	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
25	c2pz0B_	Alignment	not modelled	85.8	8	PDB header: hydrolase Chain: B: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
26	c2ayxA_	Alignment	not modelled	85.2	14	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
27	d2r25b1	Alignment	not modelled	84.9	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
28	c3i42A_	Alignment	not modelled	84.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-

					like)2 from methylobacillus flagellatus
29	c3luaA	Alignment	not modelled	84.1	14 PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
30	d1a04a2	Alignment	not modelled	82.7	12 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
31	d1zesal	Alignment	not modelled	82.6	14 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
32	c2yxba	Alignment	not modelled	82.2	9 PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
33	c3cnbc	Alignment	not modelled	81.1	13 PDB header: dna binding protein Chain: C: PDB Molecule: dna-binding response regulator, merr family; PDBTitle: crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
34	c3t8ya	Alignment	not modelled	80.9	13 PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
35	d1yioa2	Alignment	not modelled	79.3	13 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
36	d1ys7a2	Alignment	not modelled	78.3	15 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
37	d1y0ea	Alignment	not modelled	77.0	14 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
38	c2jk1A	Alignment	not modelled	76.8	13 PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
39	c1w25B	Alignment	not modelled	76.7	17 PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
40	c3cz5B	Alignment	not modelled	76.4	11 PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
41	c3t6kB	Alignment	not modelled	76.4	12 PDB header: signaling protein Chain: B: PDB Molecule: response regulator receiver; PDBTitle: crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
42	d1k66a	Alignment	not modelled	75.4	15 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
43	c2qvga	Alignment	not modelled	75.2	10 PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
44	d1kgsa2	Alignment	not modelled	75.1	11 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
45	c3f6cB	Alignment	not modelled	74.2	13 PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
46	d1rd5a	Alignment	not modelled	74.0	11 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
47	c3nhza	Alignment	not modelled	73.9	16 PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
48	d2a9pa1	Alignment	not modelled	73.4	12 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
49	c2qr3A	Alignment	not modelled	73.3	8 PDB header: transcription Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
50	d1h5ya	Alignment	not modelled	73.1	16 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
51	c3c3mA	Alignment	not modelled	72.8	12 PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
52	c3ktsA	Alignment	not modelled	72.5	25 PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365

53	c3cu5B_	 Alignment	not modelled	72.3	13	PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
54	d1i3ca_	 Alignment	not modelled	72.1	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
55	c3gl9B_	 Alignment	not modelled	70.7	15	PDB header: signaling protein Chain: B: PDB Molecule: response regulator; PDBTitle: the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
56	c3h1gA_	 Alignment	not modelled	69.5	9	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
57	c2zwmA_	 Alignment	not modelled	68.0	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
58	c3lteH_	 Alignment	not modelled	67.3	11	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
59	d1krwa_	 Alignment	not modelled	67.1	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
60	c3edeB_	 Alignment	not modelled	66.9	17	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltoextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
61	c3ffsC_	 Alignment	not modelled	66.2	11	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
62	c1zfiA_	 Alignment	not modelled	65.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
63	d1vd6a1	 Alignment	not modelled	65.4	13	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
64	c3breA_	 Alignment	not modelled	65.4	12	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
65	d1ny5a1	 Alignment	not modelled	65.3	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
66	d1zh2a1	 Alignment	not modelled	64.0	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
67	c3rlhA_	 Alignment	not modelled	63.3	10	PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d lisictox-alpha1a1a; PDBTitle: crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
68	d1a53a_	 Alignment	not modelled	62.6	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
69	c2p76H_	 Alignment	not modelled	62.2	11	PDB header: hydrolase Chain: H: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus
70	c3o63B_	 Alignment	not modelled	62.0	14	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
71	c2qr6A_	 Alignment	not modelled	61.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase; PDBTitle: crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
72	c3ch0A_	 Alignment	not modelled	61.7	15	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphodiester phosphodiesterase; PDBTitle: crystal structure of glycerophosphoryl diester phosphodiesterase2 (yp_677622.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
73	c2y85D_	 Alignment	not modelled	61.6	20	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdp
74	c3c97A_	 Alignment	not modelled	59.4	15	PDB header: signaling protein, transferase Chain: A: PDB Molecule: signal transduction histidine kinase; PDBTitle: crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
75	d1ua7a2	 Alignment	not modelled	59.1	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
76	d1s8na_	 Alignment	not modelled	58.9	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

77	c3l12A_	 Alignment	not modelled	58.3	16	PDB header: hydrolase Chain: A: PDB Molecule: putative glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silici bacter pomeroyi dss-3 at3 1.60 a resolution
78	d1xi3a_	 Alignment	not modelled	57.8	9	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
79	c3r0jA_	 Alignment	not modelled	57.7	11	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
80	c2rjnA_	 Alignment	not modelled	57.5	16	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
81	c3es8D_	 Alignment	not modelled	57.2	6	PDB header: isomerase, lyase Chain: D: PDB Molecule: muconate cycloisomerase; PDBTitle: crystal structure of divergent enolase from oceanobacillus2 iheyensis complexed with mg and l-malate.
82	d1qwga_	 Alignment	not modelled	56.9	15	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
83	d1u0sy_	 Alignment	not modelled	56.6	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
84	d1zgza1	 Alignment	not modelled	56.6	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
85	c3r2gA_	 Alignment	not modelled	55.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
86	d1gjwa2	 Alignment	not modelled	55.3	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
87	c2h6rG_	 Alignment	not modelled	54.9	10	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
88	d1vc4a_	 Alignment	not modelled	54.4	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
89	c3cg0A_	 Alignment	not modelled	54.0	17	PDB header: lyase Chain: A: PDB Molecule: response regulator receiver modulated diguanylate cyclase PDBTitle: crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
90	c2qv0A_	 Alignment	not modelled	53.6	13	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
91	c3hdgE_	 Alignment	not modelled	53.5	9	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
92	d1xhfa1	 Alignment	not modelled	53.1	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
93	c2j48A_	 Alignment	not modelled	52.7	16	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
94	d2tpsa_	 Alignment	not modelled	52.3	12	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
95	c3bw2A_	 Alignment	not modelled	52.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
96	c1qhoA_	 Alignment	not modelled	52.0	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
97	d1dbwa_	 Alignment	not modelled	52.0	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
98	c1u83A_	 Alignment	not modelled	50.8	14	PDB header: lyase Chain: A: PDB Molecule: phosphosulfolactate synthase; PDBTitle: psl synthase from bacillus subtilis
99	d1u83a_	 Alignment	not modelled	50.8	14	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
100	c3ilhA_	Alignment	not modelled	50.8	11	PDB header: transcription regulator Chain: A: PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii
101	c3hzhA_	Alignment	not modelled	50.7	9	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis response regulator (cheY-3); PDBTitle: crystal structure of the cheX-cheY-bef3-mg+2 complex from2 borrelia burgdorferi

102	d1zfja1	Alignment	not modelled	50.6	11	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
103	c2nt3A_	Alignment	not modelled	50.2	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator homolog; PDBTitle: receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
104	d1mb3a_	Alignment	not modelled	49.4	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
105	c3snkA_	Alignment	not modelled	49.2	13	PDB header: signaling protein Chain: A: PDB Molecule: response regulator chey-like protein; PDBTitle: crystal structure of a response regulator chey-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution
106	d1pdza1	Alignment	not modelled	49.1	11	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
107	c2qzjC_	Alignment	not modelled	48.7	17	PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
108	c3a0rB_	Alignment	not modelled	48.0	13	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
109	c3crnA_	Alignment	not modelled	47.6	14	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
110	c2chrA_	Alignment	not modelled	47.6	10	PDB header: isomerase Chain: A: PDB Molecule: chloromuconate cycloisomerase; PDBTitle: a re-evaluation of the crystal structure of chloromuconate2 cycloisomerase
111	c3qjaA_	Alignment	not modelled	47.6	11	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
112	c2otdC_	Alignment	not modelled	47.0	8	PDB header: hydrolase Chain: C: PDB Molecule: glycerophosphodiester phosphodiesterase; PDBTitle: the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a
113	c2jrlA_	Alignment	not modelled	46.6	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
114	c3m6mF_	Alignment	not modelled	46.4	24	PDB header: lyase/transferase Chain: F: PDB Molecule: sensory/regulatory protein rpfc; PDBTitle: crystal structure of rpff complexed with rec domain of rpfc
115	c2a7rD_	Alignment	not modelled	46.3	11	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
116	c3kruC_	Alignment	not modelled	45.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
117	c3hv2B_	Alignment	not modelled	45.8	14	PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
118	d1piia2	Alignment	not modelled	44.8	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
119	c3ktoA_	Alignment	not modelled	44.3	12	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein2 from pseudomonas atlantica
120	c3ozbF_	Alignment	not modelled	44.2	18	PDB header: transferase Chain: F: PDB Molecule: methylthioadenosine phosphorylase; PDBTitle: crystal structure of 5'-methylthioinosine phosphorylase from2 pseudomonas aeruginosa in complex with hypoxanthine