Phyre2

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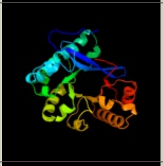
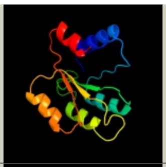
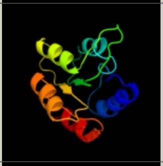
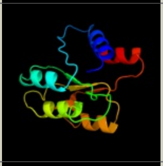
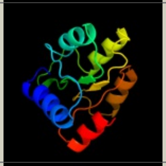
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hvbB_	Alignment		100.0	12	**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	c3s83A_	Alignment		100.0	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
3	c3hv9A_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
4	c3pjwA_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
5	c3gfzB_	Alignment		100.0	12	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
6	c2w27A_	Alignment		100.0	13	**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
7	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
8	c2r6oB_	Alignment		100.0	20	**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	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
10	c3kzpA_	Alignment		100.0	14	**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
11	c3b2nA_	Alignment		94.8	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus

12	c3khtA_	Alignment		94.0	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
13	d1zesa1	Alignment		93.5	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
14	d1dz3a_	Alignment		93.5	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
15	c2ayxA_	Alignment		92.9	12	**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
16	c3hebB_	Alignment		92.7	9	**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
17	d1heya_	Alignment		92.2	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
18	d1p6qa_	Alignment		92.2	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
19	d1w25a1	Alignment		91.8	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
20	d1mvoa_	Alignment		91.7	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
21	d1u0sy_	Alignment	not modelled	91.6	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
22	d1qkka_	Alignment	not modelled	91.5	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
23	d1jbea_	Alignment	not modelled	91.3	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
24	c2pz0B_	Alignment	not modelled	90.8	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
25	c3cz5B_	Alignment	not modelled	90.6	6	**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
26	c3gt7A_	Alignment	not modelled	90.3	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
27	c2zayA_	Alignment	not modelled	90.3	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
28	d1krwa_	Alignment	not modelled	90.1	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

29	d2a9pa1	Alignment	not modelled	90.0	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
30	c2qr3A_	Alignment	not modelled	89.5	9	**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
31	d2pl1a1	Alignment	not modelled	89.0	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
32	d2r25b1	Alignment	not modelled	88.5	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
33	c3nhzA_	Alignment	not modelled	88.3	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
34	d1a04a2	Alignment	not modelled	88.2	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
35	c3gl9B_	Alignment	not modelled	87.9	6	**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
36	c2yxbA_	Alignment	not modelled	87.7	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
37	c3f6cB_	Alignment	not modelled	87.6	14	**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
38	c2jk1A_	Alignment	not modelled	87.5	15	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
39	d1h5ya_	Alignment	not modelled	87.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
40	c2qvgA_	Alignment	not modelled	87.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
41	d2ayxa1	Alignment	not modelled	87.2	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
42	c2zwmA_	Alignment	not modelled	87.0	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
43	c3luaA_	Alignment	not modelled	86.7	12	**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
44	c3rqiA_	Alignment	not modelled	86.5	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein; **PDBTitle:** crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
45	d1peya_	Alignment	not modelled	86.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
46	d1ka9f_	Alignment	not modelled	85.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
47	c3cg0A_	Alignment	not modelled	84.7	13	**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
48	c3m6mF_	Alignment	not modelled	84.6	8	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
49	c3lteH_	Alignment	not modelled	84.5	8	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
50	c3cnbC_	Alignment	not modelled	84.5	10	**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
51	d1k68a_	Alignment	not modelled	84.3	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
52	d1k66a_	Alignment	not modelled	84.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:signaling protein

53	c3t6kB_	Alignment	not modelled	84.0	7	**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
54	d1yioa2	Alignment	not modelled	83.6	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
55	c3eulB_	Alignment	not modelled	83.6	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 narl from mycobacterium tuberculosis
56	d1s8na_	Alignment	not modelled	83.3	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c3i42A_	Alignment	not modelled	83.1	12	**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
58	d1i3ca_	Alignment	not modelled	82.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
59	c2nt3A_	Alignment	not modelled	82.2	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
60	c3cu5B_	Alignment	not modelled	82.1	11	**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
61	c1w25B_	Alignment	not modelled	82.1	11	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
62	c3eodA_	Alignment	not modelled	81.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
63	d1xhfa1	Alignment	not modelled	81.4	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
64	d1xi3a_	Alignment	not modelled	81.3	5	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
65	d1kgsa2	Alignment	not modelled	81.2	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
66	c3hv2B_	Alignment	not modelled	81.1	11	**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
67	d1ys7a2	Alignment	not modelled	80.4	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
68	c2qxyB_	Alignment	not modelled	80.4	6	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
69	c3c97A_	Alignment	not modelled	80.0	13	**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
70	d1y0ea_	Alignment	not modelled	80.0	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
71	d1ny5a1	Alignment	not modelled	80.0	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	d1dbwa_	Alignment	not modelled	79.5	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
73	c3ch0A_	Alignment	not modelled	79.1	8	**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
74	c2rjnA_	Alignment	not modelled	78.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
75	c3ktoA_	Alignment	not modelled	78.3	7	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
76	c3hdgE_	Alignment	not modelled	77.9	8	**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
77	c2y85D_	Alignment	not modelled	77.7	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis

						phosphoribosyl2 isomerase with bound rcdrp
78	d1vd6a1	Alignment	not modelled	77.6	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
79	d1mb3a_	Alignment	not modelled	77.5	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
80	d1thfd_	Alignment	not modelled	77.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
81	c2otdC_	Alignment	not modelled	76.8	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a
82	c3rlhA_	Alignment	not modelled	76.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sphingomyelin phosphodiesterase d lisictox-alphaia1a; **PDBTitle:** crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
83	c2p76H_	Alignment	not modelled	76.2	0	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase from2 staphylococcus aureus
84	c3crnA_	Alignment	not modelled	76.1	7	**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
85	c2qr6A_	Alignment	not modelled	75.9	15	**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
86	c1yadD_	Alignment	not modelled	75.9	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
87	d1znna1	Alignment	not modelled	75.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
88	c3q58A_	Alignment	not modelled	75.5	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
89	c3l12A_	Alignment	not modelled	75.3	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution
90	c2h6rG_	Alignment	not modelled	74.9	14	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
91	c3qvqB_	Alignment	not modelled	74.8	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase olei02445; **PDBTitle:** the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate
92	d1piia2	Alignment	not modelled	74.3	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
93	d1fmfa_	Alignment	not modelled	74.3	10	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
94	c1znnF_	Alignment	not modelled	72.9	15	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
95	c3cfyA_	Alignment	not modelled	72.7	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
96	c3ffsC_	Alignment	not modelled	72.4	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
97	d1zgza1	Alignment	not modelled	72.3	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
98	c2jrlA_	Alignment	not modelled	71.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
99	d1zh2a1	Alignment	not modelled	71.5	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
100	c3mmnA_	Alignment	not modelled	71.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase homolog; **PDBTitle:** crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
101	c2qzjC_	Alignment	not modelled	70.9	7	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator

						from2 clostridium difficile
102	c3igsB_	Alignment	not modelled	70.7	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2; **PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
103	c3uj2C_	Alignment	not modelled	70.2	7	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** crystal structure of an enolase from anaerostipes caccae (efi target2 efi-502054) with bound mg and sulfate
104	c3ilhA_	Alignment	not modelled	70.0	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
105	c3grcD_	Alignment	not modelled	69.7	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
106	c2v82A_	Alignment	not modelled	69.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
107	d1o1za_	Alignment	not modelled	69.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
108	d1dcfa_	Alignment	not modelled	69.3	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
109	d1a53a_	Alignment	not modelled	68.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
110	d2al1a1	Alignment	not modelled	66.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
111	c1piiA_	Alignment	not modelled	66.5	8	**PDB header:**bifunctional(isomerase and synthase) **Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase; **PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
112	c3t8yA_	Alignment	not modelled	66.1	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
113	c3hdvB_	Alignment	not modelled	66.1	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
114	d1xm3a_	Alignment	not modelled	66.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
115	c3gr7A_	Alignment	not modelled	66.0	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
116	c3h1gA_	Alignment	not modelled	65.3	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
117	c3ktsA_	Alignment	not modelled	65.2	22	**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
118	c2qv0A_	Alignment	not modelled	65.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
119	c3hzhA_	Alignment	not modelled	65.0	3	**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
120	c3kruC_	Alignment	not modelled	64.3	10	**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