Phyre^2

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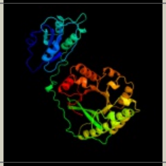
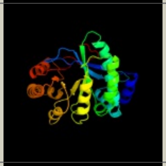
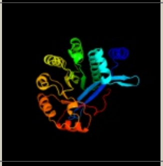
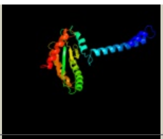
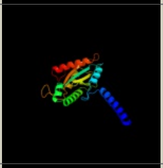
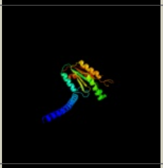
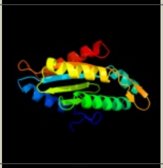
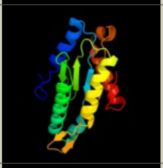
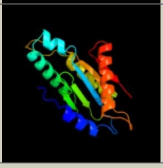
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	Alignment		100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
2	c3gfzB_	Alignment		100.0	17	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
3	c3hvbB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa
4	c3hv9A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
5	c3s83A_	Alignment		100.0	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
6	c3pfmA_	Alignment		100.0	21	**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	23	**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	32	**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	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
10	c3kzpA_	Alignment		100.0	21	**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	c1w25B_	Alignment		99.7	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp

12	c3ezuA_	Alignment		99.6	5	**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
13	c3iclA_	Alignment		99.5	4	**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 consortium3 target mcr174c
14	c3i5cA_	Alignment		99.4	9	**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
15	c3i5bA_	Alignment		99.4	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
16	c3breA_	Alignment		99.4	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
17	c3hvaA_	Alignment		99.3	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
18	c3ignA_	Alignment		99.3	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase; **PDBTitle:** crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
19	c3mtkA_	Alignment		99.3	8	**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
20	d1w25a3	Alignment		99.2	9	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
21	c3i5aA_	Alignment	not modelled	99.2	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
22	c3qyyB_	Alignment	not modelled	99.1	8	**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
23	c3hvwA_	Alignment	not modelled	98.8	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
24	d1mvoa_	Alignment	not modelled	95.4	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
25	c3khtA_	Alignment	not modelled	95.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
26	c3hebB_	Alignment	not modelled	95.1	18	**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
27	d1p6qa_	Alignment	not modelled	94.9	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
28	d1w25a1	Alignment	not modelled	94.6	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

29	c2zayA_	Alignment	not modelled	94.6	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
30	c2yxbA_	Alignment	not modelled	94.5	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
31	c3q58A_	Alignment	not modelled	94.5	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
32	c2p0oA_	Alignment	not modelled	94.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf871; **PDBTitle:** crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
33	c2pz0B_	Alignment	not modelled	94.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
34	c3qvqB_	Alignment	not modelled	94.1	13	**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
35	c3gt7A_	Alignment	not modelled	94.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
36	d2ayxa1	Alignment	not modelled	94.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
37	c2ayxA_	Alignment	not modelled	94.0	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
38	c3nhzA_	Alignment	not modelled	93.7	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
39	d1zesa1	Alignment	not modelled	93.7	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
40	d1xhfa1	Alignment	not modelled	93.5	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	c3crnA_	Alignment	not modelled	93.4	13	**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
42	c3cg0A_	Alignment	not modelled	93.3	15	**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
43	c3eulB_	Alignment	not modelled	93.1	9	**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
44	c3gl9B_	Alignment	not modelled	93.1	12	**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
45	d1k66a_	Alignment	not modelled	93.1	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
46	d1a53a_	Alignment	not modelled	93.1	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
47	d1qkka_	Alignment	not modelled	93.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	c3igsB_	Alignment	not modelled	92.9	11	**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
49	d1krwa_	Alignment	not modelled	92.6	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
50	d1heya_	Alignment	not modelled	92.5	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
51	c3rqiA_	Alignment	not modelled	92.5	7	**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
52	c2y85D	Alignment	not modelled	92.4	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a;

52	c2y85D_	Alignment	not modelled	92.4	14	**PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
53	d1mb3a_	Alignment	not modelled	92.3	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
54	c2rjnA_	Alignment	not modelled	92.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
55	c2jk1A_	Alignment	not modelled	92.2	12	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
56	d1dz3a_	Alignment	not modelled	92.2	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c3hv2B_	Alignment	not modelled	92.1	10	**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
58	d1h5ya_	Alignment	not modelled	92.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
59	d1jbea_	Alignment	not modelled	92.0	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
60	d2a9pa1	Alignment	not modelled	91.9	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c3c3mA_	Alignment	not modelled	91.8	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
62	c2nt3A_	Alignment	not modelled	91.5	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
63	c2c3zA_	Alignment	not modelled	91.4	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
64	d1dbwa_	Alignment	not modelled	91.4	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
65	c3cnbC_	Alignment	not modelled	91.4	12	**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
66	d2pl1a1	Alignment	not modelled	91.2	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	c3grcD_	Alignment	not modelled	91.1	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
68	d1ua7a2	Alignment	not modelled	90.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
69	d1kgsa2	Alignment	not modelled	90.9	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	d1yioa2	Alignment	not modelled	90.8	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	d1ny5a1	Alignment	not modelled	90.8	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	c3i42A_	Alignment	not modelled	90.6	10	**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
73	c3b2nA_	Alignment	not modelled	90.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
74	c2zwmA_	Alignment	not modelled	90.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
75	d1ys7a2	Alignment	not modelled	90.4	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	d1i3ca_	Alignment	not modelled	90.2	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
77	d1k68a_	Alignment	not modelled	90.2	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:transcription

78	c2qr3A_	Alignment	not modelled	90.1	9	**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
79	d1y0ea_	Alignment	not modelled	89.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
80	c3lteH_	Alignment	not modelled	89.6	13	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
81	c1cygA_	Alignment	not modelled	89.4	16	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
82	c2rdmB_	Alignment	not modelled	89.4	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
83	d1fmfa_	Alignment	not modelled	89.3	10	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
84	c2j48A_	Alignment	not modelled	89.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
85	d1zh2a1	Alignment	not modelled	89.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
86	d1u0sy_	Alignment	not modelled	88.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c1qhoA_	Alignment	not modelled	88.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
88	c2qxyB_	Alignment	not modelled	88.4	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
89	c1bagA_	Alignment	not modelled	88.3	12	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
90	c3cu5B_	Alignment	not modelled	88.2	9	**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
91	c3t6kB_	Alignment	not modelled	88.2	14	**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
92	c3cfyA_	Alignment	not modelled	87.9	10	**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
93	d2guya2	Alignment	not modelled	87.9	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
94	c1gcyA_	Alignment	not modelled	87.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
95	c3edeB_	Alignment	not modelled	87.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
96	c1yadD_	Alignment	not modelled	87.5	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
97	c1jibA_	Alignment	not modelled	87.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neopullulanase; **PDBTitle:** complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
98	d1zgza1	Alignment	not modelled	87.1	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
99	c3qjaA_	Alignment	not modelled	87.0	8	**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
100	c2h6rG_	Alignment	not modelled	86.9	16	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
101	c3hdgE_	Alignment	not modelled	86.8	14	**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
102	c3a47A_	Alignment	not modelled	86.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
						Fold:TIM beta/alpha-barrel

103	d1cgta4	Alignment	not modelled	86.3	26	**Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
104	c3ffsC_	Alignment	not modelled	86.3	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
105	c3hzhA_	Alignment	not modelled	86.2	12	**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
106	d1a04a2	Alignment	not modelled	86.1	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
107	d1hvxa2	Alignment	not modelled	85.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
108	c3cg4A_	Alignment	not modelled	85.6	13	**PDB header:**structural genomics, unknown function **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
109	c2qzjC_	Alignment	not modelled	85.5	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
110	c3hdvB_	Alignment	not modelled	85.4	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
111	c2v82A_	Alignment	not modelled	85.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
112	c3c97A_	Alignment	not modelled	85.2	11	**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
113	d1h3ga3	Alignment	not modelled	85.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
114	d1peya_	Alignment	not modelled	85.1	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
115	d1ud2a2	Alignment	not modelled	84.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	c3nhmA_	Alignment	not modelled	84.7	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from myxococcus xanthus
117	d1s8na_	Alignment	not modelled	84.6	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
118	d1pama4	Alignment	not modelled	84.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
119	c2qvgA_	Alignment	not modelled	84.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
120	d2d3na2	Alignment	not modelled	84.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain