Phyre2

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Description	P13518
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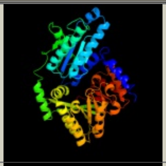
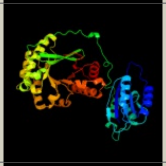
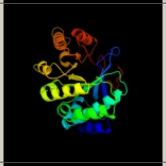
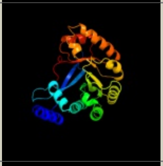
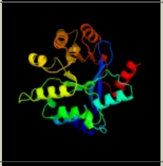
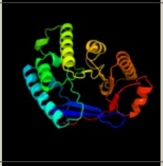
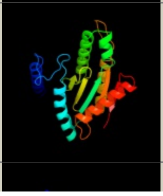
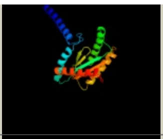
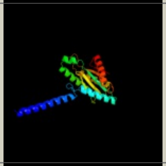
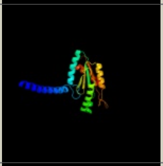
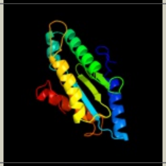
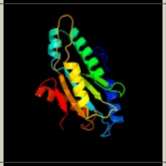
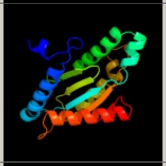
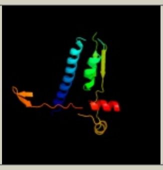
Unique Job ID	0fba59284080d6c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	Alignment		100.0	23	**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	19	**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	23	**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	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
5	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
6	c3pfmA_	Alignment		100.0	20	**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	14	**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	19	**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	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	c1w25B_	Alignment		100.0	22	**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		100.0	15	**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	c3breA_	Alignment		99.9	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
14	c3i5cA_	Alignment		99.9	22	**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		99.9	24	**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	c3i5aA_	Alignment		99.9	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
17	c3ignA_	Alignment		99.9	20	**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
18	c3iclA_	Alignment		99.9	21	**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
19	c3qyyB_	Alignment		99.9	14	**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
20	c3hvaA_	Alignment		99.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
21	c3mtkA_	Alignment	not modelled	99.9	15	**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
22	d1w25a3	Alignment	not modelled	99.9	24	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
23	c3hvwA_	Alignment	not modelled	99.8	18	**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	c3p7nB_	Alignment	not modelled	97.8	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
25	c3pjvD_	Alignment		96.9	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd periplasmic domain
26	c3khtA_	Alignment	not modelled	96.2	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
27	d1mvoa_	Alignment	not modelled	96.0	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

28	c3b2nA_	Alignment	not modelled	95.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
29	d1p6qa_	Alignment	not modelled	95.6	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
30	d1krwa_	Alignment	not modelled	95.5	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
31	c2zayA_	Alignment	not modelled	95.4	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
32	c3hebB_	Alignment	not modelled	95.2	11	**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
33	c2qv6D_	Alignment	not modelled	95.1	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
34	c2p0oA_	Alignment	not modelled	94.9	16	**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
35	d1w25a1	Alignment	not modelled	94.9	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
36	d1zesa1	Alignment	not modelled	94.8	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
37	c3gt7A_	Alignment	not modelled	94.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
38	c2ayxA_	Alignment	not modelled	94.7	11	**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
39	d1a53a_	Alignment	not modelled	94.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
40	d1jbea_	Alignment	not modelled	94.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	d1u0sy_	Alignment	not modelled	94.6	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
42	c3hv2B_	Alignment	not modelled	94.3	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
43	c2rjnA_	Alignment	not modelled	94.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
44	d1dbwa_	Alignment	not modelled	94.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
45	c3nhzA_	Alignment	not modelled	94.2	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
46	c3t6kB_	Alignment	not modelled	94.2	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
47	d2a9pa1	Alignment	not modelled	94.1	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	d2ayxa1	Alignment	not modelled	94.1	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	c3q58A_	Alignment	not modelled	94.0	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
50	d1dz3a_	Alignment	not modelled	94.0	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
51	d1heya_	Alignment	not modelled	94.0	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
52	c2yxbA_	Alignment	not modelled	94.0	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
						PDB header:lyase/lyase/signaling protein

53	c1cjkA_	Alignment	not modelled	94.0	7	**Chain:** A: **PDB Molecule:**adenylate cyclase, type v; **PDBTitle:** complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
54	c2qr3A_	Alignment	not modelled	93.9	15	**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
55	d1qkka_	Alignment	not modelled	93.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
56	d2pl1a1	Alignment	not modelled	93.8	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c2c3zA_	Alignment	not modelled	93.7	14	**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
58	d1ny5a1	Alignment	not modelled	93.7	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
59	c3c97A_	Alignment	not modelled	93.6	4	**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
60	d1xhfa1	Alignment	not modelled	93.6	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	d1kgsa2	Alignment	not modelled	93.3	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	c3eulB_	Alignment	not modelled	93.3	13	**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
63	d1y0ea_	Alignment	not modelled	93.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
64	c3i42A_	Alignment	not modelled	93.2	8	**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
65	c3mr7B_	Alignment	not modelled	93.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold **PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
66	d1a04a2	Alignment	not modelled	93.1	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	d1peya_	Alignment	not modelled	93.1	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
68	d1yioa2	Alignment	not modelled	93.0	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
69	c2zwmA_	Alignment	not modelled	93.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
70	c2jk1A_	Alignment	not modelled	92.9	10	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
71	c2jrlA_	Alignment	not modelled	92.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
72	c3lteH_	Alignment	not modelled	92.6	8	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
73	c2pz0B_	Alignment	not modelled	92.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
74	c3cg0A_	Alignment	not modelled	92.6	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
75	c3gl9B_	Alignment	not modelled	92.5	10	**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
76	c2qvgA_	Alignment	not modelled	92.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila

77	d1i3ca_	Alignment	not modelled	92.3	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
78	c3crnA_	Alignment	not modelled	92.3	15	**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
79	c3igsB_	Alignment	not modelled	92.3	12	**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
80	d1ys7a2	Alignment	not modelled	92.3	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
81	c3c3mA_	Alignment	not modelled	92.1	8	**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
82	c3cu5B_	Alignment	not modelled	92.1	10	**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
83	d2r25b1	Alignment	not modelled	91.7	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
84	d1k66a_	Alignment	not modelled	91.4	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
85	d1vhna_	Alignment	not modelled	91.2	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
86	c3f6cB_	Alignment	not modelled	91.1	10	**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
87	d1zgza1	Alignment	not modelled	91.0	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
88	c3grcD_	Alignment	not modelled	90.9	5	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
89	c3cnbC_	Alignment	not modelled	90.8	9	**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
90	d1tz9a_	Alignment	not modelled	90.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
91	c3qvqB_	Alignment	not modelled	90.5	11	**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	d1zh2a1	Alignment	not modelled	90.4	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	c3cfyA_	Alignment	not modelled	90.4	16	**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
94	c3cg4A_	Alignment	not modelled	90.2	8	**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
95	c3ffsC_	Alignment	not modelled	90.2	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
96	d1s8na_	Alignment	not modelled	90.2	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
97	c2h6rG_	Alignment	not modelled	90.0	7	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
98	d1w0ma_	Alignment	not modelled	90.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
99	c2w01C_	Alignment	not modelled	90.0	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the guanylyl cyclase cya2
100	d1xm3a_	Alignment	not modelled	89.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
101	c2qxyB_	Alignment	not modelled	89.8	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from

						thermotoga2 maritima
102	c2j48A_	Alignment	not modelled	89.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
103	d1k68a_	Alignment	not modelled	89.7	7	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
104	c2nt3A_	Alignment	not modelled	89.5	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
105	d1azsa_	Alignment	not modelled	89.5	8	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
106	c3hdgE_	Alignment	not modelled	89.4	7	**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
107	c3cz5B_	Alignment	not modelled	89.4	13	**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
108	d1mb3a_	Alignment	not modelled	89.3	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
109	c2qv0A_	Alignment	not modelled	89.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
110	c3gr7A_	Alignment	not modelled	88.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
111	d1gjwa2	Alignment	not modelled	88.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
112	d1ua7a2	Alignment	not modelled	88.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
113	c3dzdA_	Alignment	not modelled	88.6	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
114	c2gjlA_	Alignment	not modelled	88.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
115	c2qzjC_	Alignment	not modelled	88.5	15	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
116	c3uvjC_	Alignment	not modelled	88.4	8	**PDB header:**lyase **Chain:** C: **PDB Molecule:**guanylate cyclase soluble subunit alpha-3; **PDBTitle:** crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
117	c3hzhA_	Alignment	not modelled	88.3	6	**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
118	d1fx2a_	Alignment	not modelled	88.3	13	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
119	c3ucqA_	Alignment	not modelled	88.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis
120	c1ybuA_	Alignment	not modelled	87.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.