Phyre^2

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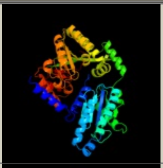
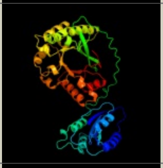
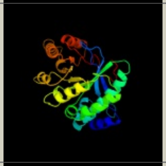
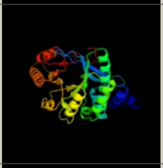
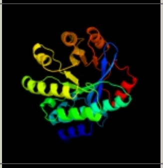
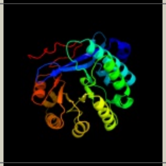
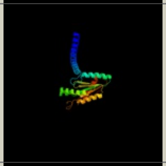
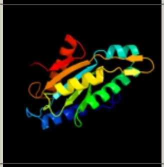
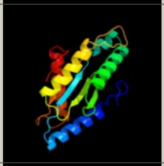
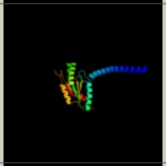
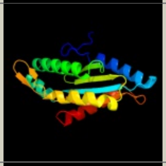
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	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
2	c3gfzB_	Alignment		100.0	21	**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	25	**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	25	**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	26	**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	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
10	c3kzpA_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative diguanylate cyclase/phosphodiesterase; **PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes
11	c1w25B_	Alignment		99.5	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		99.4	10	**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		99.3	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
14	c3iclA_	Alignment		99.2	9	**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
15	c3i5cA_	Alignment		99.1	8	**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
16	c3ignA_	Alignment		99.1	9	**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
17	c3i5aA_	Alignment		99.1	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
18	c3i5bA_	Alignment		99.1	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
19	c3hvaA_	Alignment		99.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
20	c3mtkA_	Alignment		99.0	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
21	d1w25a3	Alignment	not modelled	99.0	9	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
22	c3qyyB_	Alignment	not modelled	99.0	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	98.5	8	**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	c3khtA_	Alignment	not modelled	95.1	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
25	d1mvoa_	Alignment	not modelled	94.7	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
26	c3hebB_	Alignment	not modelled	94.7	19	**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	94.5	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
28	c2p0oA_	Alignment	not modelled	94.3	18	**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
						PDB header:signaling protein

29	c2zayA_	Alignment	not modelled	93.9	14	**Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
30	c2pz0B_	Alignment	not modelled	93.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
31	d1zesa1	Alignment	not modelled	92.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
32	d1w25a1	Alignment	not modelled	92.9	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
33	c2ayxA_	Alignment	not modelled	92.8	15	**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
34	c2yxbA_	Alignment	not modelled	92.1	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
35	d1heya_	Alignment	not modelled	91.6	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
36	c3q58A_	Alignment	not modelled	91.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
37	c2jk1A_	Alignment	not modelled	91.2	11	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
38	d1xhfa1	Alignment	not modelled	91.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
39	c2c3zA_	Alignment	not modelled	90.6	21	**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
40	d2ayxa1	Alignment	not modelled	90.4	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	d1jbea_	Alignment	not modelled	90.4	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
42	d1krwa_	Alignment	not modelled	90.4	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
43	d1a53a_	Alignment	not modelled	90.4	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
44	d1yioa2	Alignment	not modelled	90.3	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
45	d1qkka_	Alignment	not modelled	90.1	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
46	d1ua7a2	Alignment	not modelled	90.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
47	c3hv2B_	Alignment	not modelled	89.9	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
48	d1y0ea_	Alignment	not modelled	89.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
49	c3gt7A_	Alignment	not modelled	89.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
50	c2rjnA_	Alignment	not modelled	89.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
51	d1dz3a_	Alignment	not modelled	89.5	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
52	c3eulB_	Alignment	not modelled	88.7	12	**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
53	c3i42A_	Alignment	not modelled	88.5	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
54	c3nbzA	Alignment	not modelled	88.4	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional

54	c3hhzA_		Alignment	not modelled	88.4	16	regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
55	c3cg0A_		Alignment	not modelled	88.4	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
56	d1ny5a1		Alignment	not modelled	88.3	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c2j48A_		Alignment	not modelled	88.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
58	d1k68a_		Alignment	not modelled	88.3	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
59	d1u0sy_		Alignment	not modelled	88.2	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
60	d1ys7a2		Alignment	not modelled	88.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	d2pl1a1		Alignment	not modelled	88.0	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	c1cygA_		Alignment	not modelled	87.7	16	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
63	c3a23A_		Alignment	not modelled	87.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase; **PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
64	c2qr3A_		Alignment	not modelled	87.4	13	**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
65	c3gl9B_		Alignment	not modelled	87.4	16	**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
66	d1h5ya_		Alignment	not modelled	87.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
67	d1i3ca_		Alignment	not modelled	87.1	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
68	c2zwmA_		Alignment	not modelled	87.0	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
69	c3l12A_		Alignment	not modelled	87.0	13	**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
70	d1kgsa2		Alignment	not modelled	87.0	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	c3igsB_		Alignment	not modelled	86.9	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
72	d2r25b1		Alignment	not modelled	86.6	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
73	c2h6rG_		Alignment	not modelled	86.6	19	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
74	c3crnA_		Alignment	not modelled	86.6	16	**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
75	d1k66a_		Alignment	not modelled	86.3	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
76	c3b2nA_		Alignment	not modelled	86.2	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
77	d1dbwa_		Alignment	not modelled	86.2	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
78	c3cnbC_		Alignment	not modelled	86.1	15	**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
79	d2a9pa1	Alignment	not modelled	86.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
80	c3c97A_	Alignment	not modelled	86.0	9	**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
81	d1fmfa_	Alignment	not modelled	86.0	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
82	c3qvqB_	Alignment	not modelled	85.4	14	**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
83	c3c3mA_	Alignment	not modelled	85.1	10	**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
84	c3grcD_	Alignment	not modelled	85.0	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
85	c3cg4A_	Alignment	not modelled	85.0	10	**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
86	c3edeB_	Alignment	not modelled	84.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
87	c1bagA_	Alignment	not modelled	84.7	16	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
88	c3qjaA_	Alignment	not modelled	84.6	13	**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
89	c2rdmB_	Alignment	not modelled	84.2	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
90	c3t6kB_	Alignment	not modelled	83.8	18	**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
91	d1zh2a1	Alignment	not modelled	83.7	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
92	c2nt3A_	Alignment	not modelled	83.5	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
93	c3ffsC_	Alignment	not modelled	83.3	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
94	c1jibA_	Alignment	not modelled	83.3	21	**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.
95	c3a47A_	Alignment	not modelled	83.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
96	d2d3na2	Alignment	not modelled	83.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
97	c3cu5B_	Alignment	not modelled	82.8	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
98	c3rqiA_	Alignment	not modelled	82.6	10	**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
99	d1a04a2	Alignment	not modelled	82.6	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
100	c1uasA_	Alignment	not modelled	82.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
101	c2qzjC_	Alignment	not modelled	82.5	10	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
102	c3lteH_	Alignment	not modelled	82.4	11	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver

						domain) from2 bermanella marisrubri
103	d1hvxa2	Alignment	not modelled	82.3	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
104	c3ch0A_	Alignment	not modelled	82.0	32	**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
105	c3hdgE_	Alignment	not modelled	81.8	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
106	d1w0ma_	Alignment	not modelled	81.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
107	c1m53A_	Alignment	not modelled	80.9	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
108	d1s8na_	Alignment	not modelled	80.5	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
109	c2jrlA_	Alignment	not modelled	80.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
110	d1eh9a3	Alignment	not modelled	80.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
111	d2gjpa2	Alignment	not modelled	80.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
112	c2v82A_	Alignment	not modelled	80.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
113	d1mb3a_	Alignment	not modelled	79.9	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
114	d1ud2a2	Alignment	not modelled	79.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
115	d1lwha2	Alignment	not modelled	79.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	c3cfyA_	Alignment	not modelled	79.4	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
117	d2guya2	Alignment	not modelled	79.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
118	c2ze0A_	Alignment	not modelled	79.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
119	d1uoka2	Alignment	not modelled	79.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
120	c3bw2A_	Alignment	not modelled	79.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase; **PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes