Phyre^2

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Description	P37649
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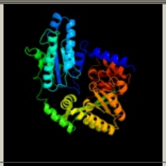
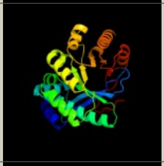
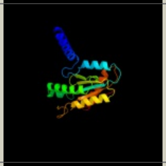
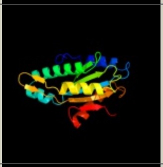
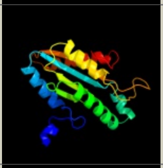
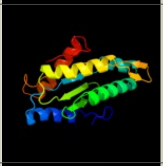
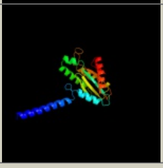
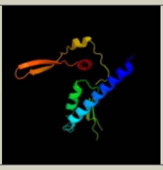
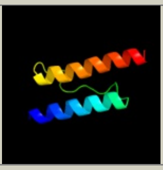
Detailed template information

#	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	22	**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	24	**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	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
5	c3s83A_	Alignment		100.0	35	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
6	c2w27A_	Alignment		100.0	21	**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	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
8	d2basa1	Alignment		100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
9	c2r6oB_	Alignment		100.0	31	**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
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		100.0	18	**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	18	**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	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
14	c3iclA_	Alignment		99.9	25	**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	c3i5aA_	Alignment		99.9	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
16	c3ignA_	Alignment		99.9	13	**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	c3mtkA_	Alignment		99.9	19	**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
18	c3hvaA_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
19	c3i5bA_	Alignment		99.9	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
20	c3i5cA_	Alignment		99.9	17	**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
21	c3qyyB_	Alignment	not modelled	99.9	20	**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
22	d1w25a3	Alignment	not modelled	99.9	18	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
23	c3hvwA_	Alignment	not modelled	99.9	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	c3pjvD_	Alignment		98.6	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd periplasmic domain
25	c3p7nB_	Alignment	not modelled	97.4	9	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
26	c3khtA_	Alignment	not modelled	96.0	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
27	c2p0oA_	Alignment	not modelled	95.6	13	**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
						Fold: Flavodoxin-like

28	d1mvoa_	Alignment	not modelled	95.3	13	**Superfamily:**CheY-like **Family:**CheY-related
29	c3hebB_	Alignment	not modelled	95.2	15	**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
30	d1p6qa_	Alignment	not modelled	95.2	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
31	c2pz0B_	Alignment	not modelled	95.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
32	c3q58A_	Alignment	not modelled	94.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
33	c2zayA_	Alignment	not modelled	94.8	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
34	d1w25a1	Alignment	not modelled	94.7	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
35	c2c3zA_	Alignment	not modelled	94.7	18	**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
36	d1a53a_	Alignment	not modelled	94.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
37	c3qvqB_	Alignment	not modelled	93.9	16	**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
38	c3igsB_	Alignment	not modelled	93.8	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
39	d1i3ca_	Alignment	not modelled	93.7	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
40	d1zesa1	Alignment	not modelled	93.6	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	d1jbea_	Alignment	not modelled	93.5	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
42	c3gt7A_	Alignment	not modelled	93.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
43	c3qjaA_	Alignment	not modelled	93.4	20	**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
44	d1ny5a1	Alignment	not modelled	93.3	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
45	d1zh2a1	Alignment	not modelled	93.0	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
46	d1heya_	Alignment	not modelled	92.7	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	d2asxa1	Alignment		92.7	25	**Fold:**HAMP domain-like **Superfamily:**HAMP domain-like **Family:**HAMP domain
48	d1krwa_	Alignment	not modelled	92.7	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	d2guya2	Alignment	not modelled	92.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	d1h3ga3	Alignment	not modelled	92.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
51	d1xm3a_	Alignment	not modelled	92.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
52	c3i42A_	Alignment	not modelled	92.2	18	**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
53	d1k66a_	Alignment	not modelled	92.2	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
54	c3b2nA_	Alignment	not modelled	92.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
55	c3dhuC_	Alignment	not modelled	92.1	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
56	d1qkka_	Alignment	not modelled	92.1	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c3cg0A_	Alignment	not modelled	91.8	21	**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
58	c3nhzA_	Alignment	not modelled	91.6	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
59	c3lnrA_	Alignment	not modelled	91.5	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**aerotaxis transducer aer2; **PDBTitle:** crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
60	d2pl1a1	Alignment	not modelled	91.3	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c3czkA_	Alignment	not modelled	91.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
62	c2rjnA_	Alignment	not modelled	91.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
63	d1g5aa2	Alignment	not modelled	91.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
64	d1ua7a2	Alignment	not modelled	91.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
65	c2yxbA_	Alignment	not modelled	90.9	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
66	c3hv2B_	Alignment	not modelled	90.9	8	**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	d1eh9a3	Alignment	not modelled	90.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	d1a04a2	Alignment	not modelled	90.9	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
69	c3ffsC_	Alignment	not modelled	90.8	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
70	d1ys7a2	Alignment	not modelled	90.6	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	d1dz3a_	Alignment	not modelled	90.6	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	c1cjkA_	Alignment	not modelled	90.5	9	**PDB header:**lyase/lyase/signaling protein **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
73	d2ayxa1	Alignment	not modelled	90.5	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
74	c3c3mA_	Alignment	not modelled	90.1	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
75	c1jgiA_	Alignment	not modelled	90.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of the active site mutant glu328gln of2 amylosucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
76	d1dbwa_	Alignment	not modelled	90.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
77	d2bhua3	Alignment	not modelled	90.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

78	c3eulB_	Alignment	not modelled	89.9	17	**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
79	c1cygA_	Alignment	not modelled	89.8	14	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
80	d1yioa2	Alignment	not modelled	89.6	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
81	c3a47A_	Alignment	not modelled	89.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
82	c3edeB_	Alignment	not modelled	89.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
83	c2jk1A_	Alignment	not modelled	89.5	12	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
84	c1zjaB_	Alignment	not modelled	89.3	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
85	c3rqiA_	Alignment	not modelled	89.3	19	**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
86	d1azsa_	Alignment	not modelled	89.2	9	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
87	d1vd6a1	Alignment	not modelled	89.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
88	c2wcsA_	Alignment	not modelled	89.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
89	c2ayxA_	Alignment	not modelled	89.0	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
90	d2aaaa2	Alignment	not modelled	88.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	d1u0sy_	Alignment	not modelled	88.9	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
92	c3cnbC_	Alignment	not modelled	88.7	20	**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
93	c1qhoA_	Alignment	not modelled	88.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
94	d2a9pa1	Alignment	not modelled	88.6	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
95	d1cgta4	Alignment	not modelled	88.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
96	c3cg4A_	Alignment	not modelled	88.4	17	**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
97	d1cyga4	Alignment	not modelled	88.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
98	d1gjwa2	Alignment	not modelled	88.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
99	c3ch0A_	Alignment	not modelled	88.4	24	**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
100	c2zwmA_	Alignment	not modelled	88.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
101	c1gcyA_	Alignment	not modelled	88.1	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
102	d1xi3a_	Alignment	not modelled	88.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase

						Family: Thiamin phosphate synthase
103	d1lwha2	Alignment	not modelled	88.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
104	d1pama4	Alignment	not modelled	87.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
105	c1tcmB_	Alignment	not modelled	87.7	14	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
106	d1kgsa2	Alignment	not modelled	87.6	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
107	c2h6rG_	Alignment	not modelled	87.5	17	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
108	c3cfyA_	Alignment	not modelled	87.5	13	**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
109	d1m7xa3	Alignment	not modelled	87.4	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
110	c3crnA_	Alignment	not modelled	87.4	12	**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
111	d1xhfa1	Alignment	not modelled	87.3	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
112	c3f6cB_	Alignment	not modelled	87.3	19	**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
113	c2qv6D_	Alignment	not modelled	87.1	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
114	d1e43a2	Alignment	not modelled	87.1	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
115	d1qhoa4	Alignment	not modelled	87.1	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	d1m53a2	Alignment	not modelled	87.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
117	d1ea9c3	Alignment	not modelled	87.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
118	d2gjpa2	Alignment	not modelled	86.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
119	c1jibA_	Alignment	not modelled	86.9	25	**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.
120	c3rlhA_	Alignment	not modelled	86.8	16	**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