Phyre^2

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Description	P75800
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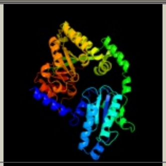
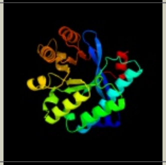
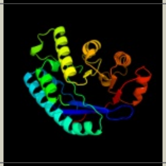
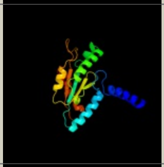
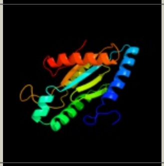
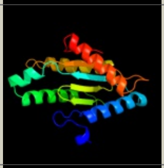
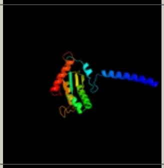
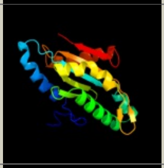
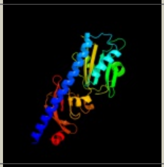
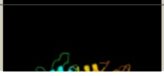
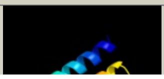
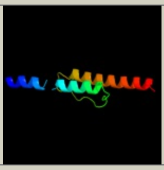
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	Alignment		100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
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	19	**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	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
5	c3s83A_	Alignment		100.0	29	**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	22	**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	22	**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	21	**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	20	**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	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		100.0	8	**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	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
14	c3i5aA_	Alignment		99.9	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
15	c3iclA_	Alignment		99.9	12	**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
16	c3i5bA_	Alignment		99.9	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
17	c3qyyB_	Alignment		99.9	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
18	c3i5cA_	Alignment		99.9	12	**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
19	c3mtkA_	Alignment		99.9	12	**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		99.9	11	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
21	c3ignA_	Alignment	not modelled	99.9	10	**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
22	c3hvaA_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
23	c3hvwA_	Alignment	not modelled	99.8	9	**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	c3c8cB_	Alignment		99.6	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of mcp_n and cache domains of methyl-2 accepting chemotaxis protein from vibrio cholerae
25	c3licA_	Alignment		99.5	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase sohk1s-z6
						**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical sensory transduction

26	c3libA_	Alignment		99.4	10	histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase mmhk1s-z3
27	c2p7jA_	Alignment	not modelled	99.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative sensory box/ggdef family protein; **PDBTitle:** crystal structure of the domain of putative sensory box/ggdef family2 protein from vibrio parahaemolyticus
28	c3liaA_	Alignment		99.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical sensory transduction histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase mmhk1s-z2
29	c3lifA_	Alignment	not modelled	99.2	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative diguanylate cyclase (ggdef) with pas/pac domain; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase rphk1s-z16
30	c3fosA_	Alignment	not modelled	99.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
31	c3e4pB_	Alignment	not modelled	99.1	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**c4-dicarboxylate transport sensor protein dctb; **PDBTitle:** crystal structure of malonate occupied dctb
32	c3by9A_	Alignment	not modelled	98.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the v. cholerae histidine kinase dctb2 sensor domain
33	d2p7ja2	Alignment	not modelled	98.3	12	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**YkuI C-terminal domain-like
34	c3p7nB_	Alignment	not modelled	98.2	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
35	c2qv6D_	Alignment	not modelled	97.0	9	**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
36	c3khtA_	Alignment	not modelled	95.6	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
37	d2basa2	Alignment	not modelled	95.4	16	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**YkuI C-terminal domain-like
38	c3q58A_	Alignment	not modelled	94.3	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
39	c2p0oA_	Alignment	not modelled	94.1	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
40	c1cjkA_	Alignment	not modelled	94.0	10	**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
41	d1a53a_	Alignment	not modelled	93.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
42	d1p6qa_	Alignment	not modelled	93.2	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
43	c3hebB_	Alignment	not modelled	93.2	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
44	c2c3zA_	Alignment	not modelled	93.2	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
45	c2zayA_	Alignment	not modelled	93.2	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
46	c1ybuA_	Alignment	not modelled	92.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
47	d1mvoa_	Alignment	not modelled	92.1	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	d1azsa_	Alignment	not modelled	91.5	9	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
						**Fold:**HAMP domain-like

49	d2asxa1	Alignment		91.5	19	**Superfamily:**HAMP domain-like **Family:**HAMP domain
50	c3b2nA_	Alignment	not modelled	91.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
51	d1ua7a2	Alignment	not modelled	91.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
52	d1h3ga3	Alignment	not modelled	90.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
53	c2w01C_	Alignment	not modelled	90.3	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the guanylyl cyclase cya2
54	c3lnrA_	Alignment		90.3	13	**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
55	c3edeB_	Alignment	not modelled	89.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
56	d1wc1a_	Alignment	not modelled	89.7	6	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
57	c1qhoA_	Alignment	not modelled	89.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
58	d1yioa2	Alignment	not modelled	89.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
59	c3hv2B_	Alignment	not modelled	89.3	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
60	d1gjwa2	Alignment	not modelled	89.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
61	c2jk1A_	Alignment	not modelled	89.1	10	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
62	d2guya2	Alignment	not modelled	89.0	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
63	c3lrmB_	Alignment	not modelled	89.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase 1; **PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
64	c1wc6B_	Alignment	not modelled	88.8	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
65	c3c97A_	Alignment	not modelled	88.7	17	**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
66	c2pz0B_	Alignment	not modelled	88.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
67	c3i42A_	Alignment	not modelled	88.6	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
68	d1bf2a3	Alignment	not modelled	88.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
69	d1w25a1	Alignment	not modelled	88.4	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	c1y10C_	Alignment	not modelled	88.2	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
71	d1heya_	Alignment	not modelled	88.1	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	d1qhoa4	Alignment	not modelled	87.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	c2h6rG_	Alignment	not modelled	87.4	8	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim)

						from2 methanocaldococcus jannaschii
74	c1cygA_	Alignment	not modelled	87.0	21	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
75	c3t8yA_	Alignment	not modelled	86.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
76	d1k68a_	Alignment	not modelled	86.9	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
77	c2rjnA_	Alignment	not modelled	86.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
78	d1krwa_	Alignment	not modelled	86.5	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
79	d1ps9a1	Alignment	not modelled	86.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
80	d1nvma2	Alignment	not modelled	86.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
81	c3kruC_	Alignment	not modelled	85.9	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
82	c2iswB_	Alignment	not modelled	85.8	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
83	d1lwha2	Alignment	not modelled	85.6	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
84	c1bagA_	Alignment	not modelled	85.6	15	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
85	c2wcsA_	Alignment	not modelled	85.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
86	d2bhua3	Alignment	not modelled	85.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
87	c3igsB_	Alignment	not modelled	85.0	13	**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
88	d1jbea_	Alignment	not modelled	84.9	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
89	d1u0sy_	Alignment	not modelled	84.9	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
90	d1k66a_	Alignment	not modelled	84.8	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
91	c3hf3A_	Alignment	not modelled	84.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
92	d1o1za_	Alignment	not modelled	84.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
93	d1ys7a2	Alignment	not modelled	84.3	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
94	c3qvqB_	Alignment	not modelled	84.2	12	**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
95	c3a23A_	Alignment	not modelled	84.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase; **PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
96	c3cg0A_	Alignment	not modelled	84.1	19	**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
97	c1tcmB_	Alignment	not modelled	84.0	18	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
						Fold: Flavodoxin-like

98	d1dz3a_	Alignment	not modelled	84.0	19	**Superfamily:**CheY-like **Family:**CheY-related
99	c3nhzA_	Alignment	not modelled	83.9	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
100	c1gjuA_	Alignment	not modelled	83.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
101	d1eh9a3	Alignment	not modelled	83.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
102	c3gt7A_	Alignment	not modelled	83.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
103	d1qkka_	Alignment	not modelled	83.3	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
104	c1jibA_	Alignment	not modelled	83.1	22	**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.
105	c2dh3A_	Alignment	not modelled	83.0	21	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
106	c1gviA_	Alignment	not modelled	83.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
107	c1gcyA_	Alignment	not modelled	82.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
108	d1uoka2	Alignment	not modelled	82.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
109	d1zesa1	Alignment	not modelled	82.5	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
110	d1dbwa_	Alignment	not modelled	82.4	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
111	c1zjaB_	Alignment	not modelled	82.4	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
112	d1piia2	Alignment	not modelled	82.3	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
113	d1y0ea_	Alignment	not modelled	82.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
114	d1pama4	Alignment	not modelled	82.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
115	c3rqiA_	Alignment	not modelled	81.9	15	**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
116	c3gr7A_	Alignment	not modelled	81.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
117	c2zwmA_	Alignment	not modelled	81.6	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
118	c3a47A_	Alignment	not modelled	81.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
119	c1m53A_	Alignment	not modelled	81.4	6	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
120	d1cgta4	Alignment	not modelled	81.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain