Phyre^2

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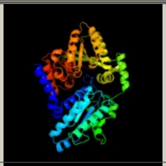
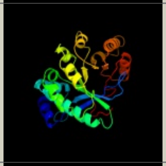
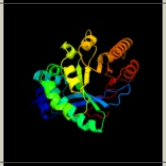
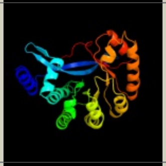
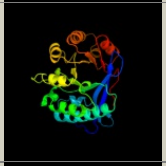
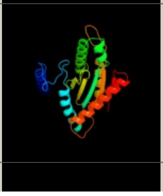
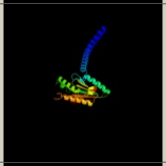
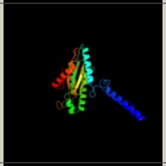
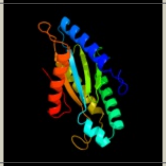
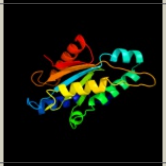
Detailed template information

#	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	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
3	c3hv9A_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
4	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
5	c3s83A_	Alignment		100.0	30	**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	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
7	c2w27A_	Alignment		100.0	19	**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	28	**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	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
10	c3kzpA_	Alignment		100.0	22	**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		98.3	6	**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		97.8	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		97.3	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
14	c3i5cA_	Alignment		97.3	10	**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	c3i5aA_	Alignment		97.0	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
16	c3i5bA_	Alignment		96.8	7	**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	c3iclA_	Alignment		96.7	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
18	c3mtkA_	Alignment		96.2	9	**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
19	d1w25a3	Alignment		96.0	4	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
20	c3ignA_	Alignment		95.9	8	**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
21	c3hvaA_	Alignment	not modelled	95.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
22	c3qyyB_	Alignment	not modelled	95.3	9	**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	94.5	11	**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	c2p0oA_	Alignment	not modelled	94.2	17	**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
25	d1p6qa_	Alignment	not modelled	93.9	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
26	c3khtA_	Alignment	not modelled	93.4	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
27	c2zayA_	Alignment	not modelled	93.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
28	d1mvoa_	Alignment	not modelled	93.0	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:transcription regulator

29	c3hebB_	Alignment	not modelled	93.0	16	**Chain:** B: **PDB Molecule:**response regulator receiver domain protein (chey); **PDBTitle:** crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
30	c2ayxA_	Alignment	not modelled	92.4	16	**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
31	d1heya_	Alignment	not modelled	90.9	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
32	d1gjwa2	Alignment	not modelled	90.9	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
33	d1w25a1	Alignment	not modelled	90.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
34	d1ua7a2	Alignment	not modelled	89.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
35	d1h5ya_	Alignment	not modelled	89.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
36	c2jk1A_	Alignment	not modelled	89.5	7	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
37	c3rqiA_	Alignment	not modelled	89.1	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
38	c2yxbA_	Alignment	not modelled	89.1	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
39	c2c3zA_	Alignment	not modelled	88.7	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
40	d2ayxa1	Alignment	not modelled	88.1	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	d1krwa_	Alignment	not modelled	88.0	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
42	d1qkka_	Alignment	not modelled	87.8	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
43	c3gt7A_	Alignment	not modelled	87.7	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
44	d1y0ea_	Alignment	not modelled	87.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
45	c2h6rG_	Alignment	not modelled	87.4	11	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
46	d1jbea_	Alignment	not modelled	87.4	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	d1k68a_	Alignment	not modelled	87.2	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
48	c3i42A_	Alignment	not modelled	87.1	14	**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
49	c2y85D_	Alignment	not modelled	86.0	21	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
50	c3eulB_	Alignment	not modelled	85.9	11	**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
51	c3gl9B_	Alignment	not modelled	85.7	14	**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
52	d2pl1a1	Alignment	not modelled	85.6	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
53	d1zesa1	Alignment	not modelled	85.6	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						Fold: Flavodoxin-like

54	d1yioa2	Alignment	not modelled	85.5	8	**Superfamily:**CheY-like **Family:**CheY-related
55	c3crnA_	Alignment	not modelled	85.1	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver domain protein, chey-like; **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
56	d1kgsa2	Alignment	not modelled	85.0	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c2v82A_	Alignment	not modelled	85.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
58	c3q58A_	Alignment	not modelled	85.0	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
59	d2r25b1	Alignment	not modelled	84.7	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
60	d1i3ca_	Alignment	not modelled	84.7	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c2pz0B_	Alignment	not modelled	84.3	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
62	d1u0sy_	Alignment	not modelled	84.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
63	c2j48A_	Alignment	not modelled	84.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
64	c3hv2B_	Alignment	not modelled	83.7	14	**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
65	c3nhzA_	Alignment	not modelled	83.3	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
66	d1ys7a2	Alignment	not modelled	83.2	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	d2d3na2	Alignment	not modelled	82.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	c1jibA_	Alignment	not modelled	82.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neopullulanase; **PDBTitle:** complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
69	d1ny5a1	Alignment	not modelled	82.5	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	c3gr7A_	Alignment	not modelled	82.5	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
71	d1dz3a_	Alignment	not modelled	82.3	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	d1hvxa2	Alignment	not modelled	82.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	c3b2nA_	Alignment	not modelled	81.4	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
74	c3cg0A_	Alignment	not modelled	81.3	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	c3c3mA_	Alignment	not modelled	80.8	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
76	d1uoka2	Alignment	not modelled	80.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
77	c3a23A_	Alignment	not modelled	80.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase; **PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
78	c3c97A_	Alignment	not modelled	80.4	10	**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

79	d2guya2	Alignment	not modelled	80.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
80	c1qhoA_	Alignment	not modelled	80.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
81	d1dbwa_	Alignment	not modelled	80.2	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	d2gjpa2	Alignment	not modelled	80.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
83	c3cnbC_	Alignment	not modelled	79.7	16	**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
84	d1k66a_	Alignment	not modelled	79.5	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
85	c1gjuA_	Alignment	not modelled	79.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
86	d1ob0a2	Alignment	not modelled	79.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
87	d1mxga2	Alignment	not modelled	79.1	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
88	d1xhfa1	Alignment	not modelled	79.0	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
89	d2p10a1	Alignment	not modelled	79.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
90	d1ud2a2	Alignment	not modelled	78.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	d1h3ga3	Alignment	not modelled	78.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
92	d1ea9c3	Alignment	not modelled	78.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
93	c1yadD_	Alignment	not modelled	78.2	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
94	c1cygA_	Alignment	not modelled	78.1	17	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
95	d1lwha2	Alignment	not modelled	78.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
96	c1ea9D_	Alignment	not modelled	77.8	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
97	d1g5aa2	Alignment	not modelled	77.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
98	d1rd5a_	Alignment	not modelled	77.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
99	d1cgta4	Alignment	not modelled	77.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
100	c2zwmA_	Alignment	not modelled	77.4	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
101	c3grcD_	Alignment	not modelled	77.4	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
102	c2rjnA_	Alignment	not modelled	77.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
103	c3lteH_	Alignment	not modelled	77.2	13	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
104	c3hdgE_	Alignment	not modelled	76.8	16	**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
105	c1ud8A_	Alignment	not modelled	76.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase;

						PDBTitle: crystal structure of amyk38 with lithium ion
106	d1e43a2	Alignment	not modelled	76.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
107	d2aaaa2	Alignment	not modelled	76.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
108	c3kruC_	Alignment	not modelled	76.2	16	**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
109	c1uasA_	Alignment	not modelled	76.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
110	c2aaaA_	Alignment	not modelled	75.8	12	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** calcium binding in alpha-amylases: an x-ray diffraction2 study at 2.1 angstroms resolution of two enzymes from3 aspergillus
111	d1pama4	Alignment	not modelled	75.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
112	c3bmwA_	Alignment	not modelled	75.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
113	c2jrlA_	Alignment	not modelled	75.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
114	c1jgiA_	Alignment	not modelled	75.0	15	**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
115	c3cg4A_	Alignment	not modelled	75.0	11	**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
116	c3cu5B_	Alignment	not modelled	74.9	14	**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
117	d1gvia3	Alignment	not modelled	74.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
118	c3igsB_	Alignment	not modelled	74.5	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2; **PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
119	d1a04a2	Alignment	not modelled	74.3	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
120	c3ffsC_	Alignment	not modelled	74.1	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase