Phyre^2

Email	l.a.kelley@imperial.ac.uk
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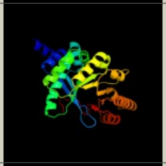
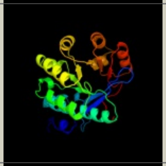
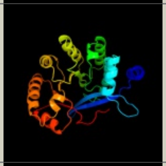
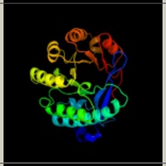
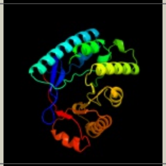
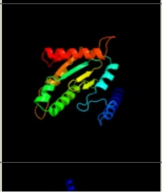
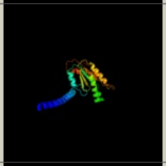
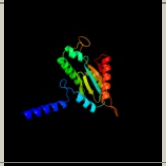
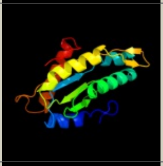
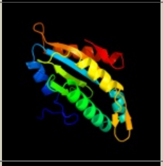
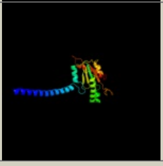
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	Alignment		100.0	21	**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	20	**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	23	**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	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	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
8	d2basa1	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
9	c2r6oB_	Alignment		100.0	30	**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	25	**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	14	**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	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		99.9	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
14	c3i5cA_	Alignment		99.9	16	**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	c3mtkA_	Alignment		99.9	14	**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
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	c3i5bA_	Alignment		99.9	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
18	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
19	c3hvaA_	Alignment		99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
20	c3i5aA_	Alignment		99.9	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
21	c3qyyB_	Alignment	not modelled	99.9	16	**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	16	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
23	c3hvwA_	Alignment	not modelled	99.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
24	c3p7nB_	Alignment	not modelled	97.6	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
25	c3khtA_	Alignment	not modelled	94.1	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
26	d1mvoa_	Alignment	not modelled	92.4	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
27	d1p6qa_	Alignment	not modelled	92.3	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
28	d1gjwa2	Alignment	not modelled	92.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
29	c2qv6D_	Alignment	not modelled	91.9	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii;

29	c2qv6D_	Alignment	not modelled	91.9	12	**PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
30	c2zayA_	Alignment	not modelled	91.7	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
31	c2pz0B_	Alignment	not modelled	91.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
32	c3gt7A_	Alignment	not modelled	90.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
33	c2c3zA_	Alignment	not modelled	90.2	19	**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
34	d1ua7a2	Alignment	not modelled	89.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
35	d1a53a_	Alignment	not modelled	89.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
36	c2p0oA_	Alignment	not modelled	88.6	12	**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
37	c3q58A_	Alignment	not modelled	88.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
38	d1jbea_	Alignment	not modelled	88.3	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
39	c2h6rG_	Alignment	not modelled	88.1	15	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
40	c3qvqB_	Alignment	not modelled	88.1	17	**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
41	c3t8yA_	Alignment	not modelled	88.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
42	c3nhzA_	Alignment	not modelled	87.9	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
43	c1cygA_	Alignment	not modelled	87.5	22	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
44	d1bf2a3	Alignment	not modelled	87.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
45	c3hebB_	Alignment	not modelled	87.5	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
46	d1vhna_	Alignment	not modelled	87.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
47	c1qhoA_	Alignment	not modelled	87.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
48	d1y0ea_	Alignment	not modelled	86.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
49	c3kruC_	Alignment	not modelled	86.8	17	**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
50	d1u0sy_	Alignment	not modelled	86.7	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
51	c1m53A_	Alignment	not modelled	86.7	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
52	c3a47A_	Alignment	not modelled	86.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
53	d2pl1a1	Alignment	not modelled	86.5	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-

54	c2rjnA_	Alignment	not modelled	86.5	11	dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
55	c3edeB_	Alignment	not modelled	86.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
56	c3b2nA_	Alignment	not modelled	86.0	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
57	d1krwa_	Alignment	not modelled	86.0	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
58	d1m7xa3	Alignment	not modelled	85.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
59	c3i42A_	Alignment	not modelled	85.5	17	**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
60	c2jk1A_	Alignment	not modelled	85.5	9	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
61	d1dz3a_	Alignment	not modelled	85.1	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	c3gr7A_	Alignment	not modelled	85.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
63	c1gjuA_	Alignment	not modelled	84.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
64	c3q94B_	Alignment	not modelled	84.6	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
65	d1m53a2	Alignment	not modelled	84.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
66	c1bagA_	Alignment	not modelled	84.4	11	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
67	c2ayxA_	Alignment	not modelled	84.3	14	**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
68	d1h3ga3	Alignment	not modelled	84.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
69	d1w25a1	Alignment	not modelled	83.8	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	d2guya2	Alignment	not modelled	83.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
71	c1zjaB_	Alignment	not modelled	83.5	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
72	d1yioa2	Alignment	not modelled	83.3	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
73	c1gcyA_	Alignment	not modelled	83.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
74	c2ze0A_	Alignment	not modelled	83.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
75	c3gl9B_	Alignment	not modelled	83.0	18	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
76	d1w0ma_	Alignment	not modelled	82.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
77	c2ya0A_	Alignment	not modelled	82.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
78	c3czkA_	Alignment	not modelled	82.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
79	d2bhua3	Alignment	not modelled	82.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
						Fold:TIM beta/alpha-barrel

80	d1g5aa2	Alignment	not modelled	82.2	13	**Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
81	d1a04a2	Alignment	not modelled	82.1	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	c1cjkA_	Alignment	not modelled	82.0	15	**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
83	d1eh9a3	Alignment	not modelled	81.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
84	c3faxA_	Alignment	not modelled	81.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
85	c2qr3A_	Alignment	not modelled	81.6	8	**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
86	d1heya_	Alignment	not modelled	81.5	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c2wcsA_	Alignment	not modelled	81.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
88	d1dbwa_	Alignment	not modelled	81.1	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
89	d2aaaa2	Alignment	not modelled	80.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
90	d1lwha2	Alignment	not modelled	80.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	c3ch0A_	Alignment	not modelled	80.3	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
92	c3igsB_	Alignment	not modelled	80.2	15	**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
93	d2r25b1	Alignment	not modelled	80.2	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
94	d1uoka2	Alignment	not modelled	80.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	d1ny5a1	Alignment	not modelled	80.1	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	c3dhuC_	Alignment	not modelled	80.1	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
97	d1qhoa4	Alignment	not modelled	80.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
98	c1tcmB_	Alignment	not modelled	80.0	16	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
99	c3crnA_	Alignment	not modelled	79.6	10	**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
100	c1jibA_	Alignment	not modelled	79.3	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.
101	c3eulB_	Alignment	not modelled	79.2	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
102	d1gcya2	Alignment	not modelled	79.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
103	c3ozbF_	Alignment	not modelled	79.0	20	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
104	c3rlhA_	Alignment	not modelled	78.8	13	**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
105	d1ys7a2	Alignment	not modelled	78.8	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
106	c1bf2A_	Alignment	not modelled	78.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
107	c2e8yA_	Alignment	not modelled	78.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
108	d2ayxa1	Alignment	not modelled	78.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
109	c3cg0A_	Alignment	not modelled	78.3	11	**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
110	d1nvma2	Alignment	not modelled	78.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
111	c3c97A_	Alignment	not modelled	77.9	15	**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
112	d1ea9c3	Alignment	not modelled	77.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
113	c2ya1A_	Alignment	not modelled	77.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
114	c2zidA_	Alignment	not modelled	77.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dextran glucosidase; **PDBTitle:** crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
115	c2dh3A_	Alignment	not modelled	77.4	25	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
116	c1jd7A_	Alignment	not modelled	77.3	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
117	d1tz9a_	Alignment	not modelled	77.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
118	d1cb0a_	Alignment	not modelled	77.0	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
119	d1k66a_	Alignment	not modelled	77.0	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
120	c3hf3A_	Alignment	not modelled	77.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01