Phyre^2

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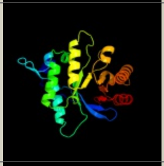
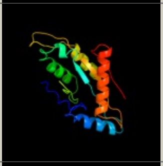
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gfzB_	Alignment		100.0	37	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
2	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
3	c3hvbB_	Alignment		100.0	15	**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	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
5	c2w27A_	Alignment		100.0	15	**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
6	c3s83A_	Alignment		100.0	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
7	c3pfmA_	Alignment		100.0	18	**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	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**EAL domain-like **Family:**EAL domain
9	c2r6oB_	Alignment		100.0	23	**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	18	**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	c3ezuA_	Alignment		99.8	15	**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

12	c1w25B_	Alignment		99.8	13	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
13	d1w25a3	Alignment		99.6	14	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
14	c3iclA_	Alignment		99.5	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
15	c3breA_	Alignment		99.5	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
16	c3i5bA_	Alignment		99.5	12	**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	c2kb2A_	Alignment		99.4	42	**PDB header:**signaling protein, hydrolase regulator **Chain:** A: **PDB Molecule:**blrp1; **PDBTitle:** blrp1 bluf
18	c3qyyB_	Alignment		99.4	7	**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
19	c3ignA_	Alignment		99.4	12	**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
20	c3hvaA_	Alignment		99.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
21	d2buna1	Alignment	not modelled	99.3	28	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**BLUF domain
22	c3i5aA_	Alignment	not modelled	99.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
23	c2hfnJ_	Alignment	not modelled	99.3	29	**PDB header:**electron transport **Chain:** J: **PDB Molecule:**synechocystis photoreceptor (slr1694); **PDBTitle:** crystal structures of the synechocystis photoreceptor slr1694 reveal2 distinct structural states related to signaling
24	c3i5cA_	Alignment	not modelled	99.3	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
25	d1x0pa1	Alignment	not modelled	99.3	28	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**BLUF domain
26	d2byca1	Alignment	not modelled	99.3	38	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**BLUF domain
27	c3mtkA_	Alignment	not modelled	99.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diguanylate cyclase/phosphodiesterase; **PDBTitle:** x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c

28	d1yrxa1	Alignment	not modelled	99.2	27	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**BLUF domain
29	c3hvwA_	Alignment	not modelled	98.7	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate-cyclase (dgc); **PDBTitle:** crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
30	d1ua7a2	Alignment	not modelled	94.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
31	d1gjwa2	Alignment	not modelled	93.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
32	c1qhoA_	Alignment	not modelled	93.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
33	c3edeB_	Alignment	not modelled	92.3	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
34	c3khtA_	Alignment	not modelled	92.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
35	c2p0oA_	Alignment	not modelled	91.6	15	**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
36	d1y0ea_	Alignment	not modelled	91.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
37	d1kkoa1	Alignment	not modelled	91.0	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
38	d1h3ga3	Alignment	not modelled	90.9	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
39	d2guya2	Alignment	not modelled	90.7	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
40	d1a53a_	Alignment	not modelled	90.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
41	c1cygA_	Alignment	not modelled	90.3	12	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
42	c2c3zA_	Alignment	not modelled	90.2	16	**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
43	c1jibA_	Alignment	not modelled	89.9	11	**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.
44	d1lwha2	Alignment	not modelled	89.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
45	c3q58A_	Alignment	not modelled	89.7	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
46	c1bagA_	Alignment	not modelled	89.7	12	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
47	d1qhoa4	Alignment	not modelled	89.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
48	d2aaaa2	Alignment	not modelled	89.6	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
49	c1tcmB_	Alignment	not modelled	89.1	18	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
50	c1lwhA_	Alignment	not modelled	88.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
51	c3igsB_	Alignment	not modelled	88.6	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2; **PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
52	c3czkA_	Alignment	not modelled	88.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
53	d1gcya2	Alignment	not modelled	88.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

54	c3bmwA_	Alignment	not modelled	88.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
55	c1gjuA_	Alignment	not modelled	88.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
56	c1jdaA_	Alignment	not modelled	88.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
57	d1z41a1	Alignment	not modelled	87.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
58	c2wcsA_	Alignment	not modelled	87.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
59	c2aaaA_	Alignment	not modelled	87.4	7	**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
60	c2h6rG_	Alignment	not modelled	87.2	11	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
61	d1ht6a2	Alignment	not modelled	86.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
62	c1jgiA_	Alignment	not modelled	86.2	8	**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
63	d1bf2a3	Alignment	not modelled	85.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
64	c3hebB_	Alignment	not modelled	85.3	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
65	d1g5aa2	Alignment	not modelled	85.2	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
66	c1gcyA_	Alignment	not modelled	85.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
67	d1p6qa_	Alignment	not modelled	85.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
68	c3k8kB_	Alignment	not modelled	84.8	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
69	d1mvoa_	Alignment	not modelled	84.7	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
70	d1cxla4	Alignment	not modelled	83.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
71	c1zjaB_	Alignment	not modelled	83.7	14	**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	d1wzla3	Alignment	not modelled	83.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	c2zayA_	Alignment	not modelled	83.5	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
74	c2jk1A_	Alignment	not modelled	83.4	11	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
75	d1pama4	Alignment	not modelled	83.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
76	d1eh9a3	Alignment	not modelled	82.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
77	c1gviA_	Alignment	not modelled	82.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
78	c3q94B_	Alignment	not modelled	82.7	15	**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'
79	c3kruC_	Alignment	not modelled	82.6	18	**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
80	c3ffsC_	Alignment	not modelled	82.5	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
81	d3bmva4	Alignment	not modelled	82.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
82	d1cgta4	Alignment	not modelled	82.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
83	c3dhuC_	Alignment	not modelled	81.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
84	c2z1kA_	Alignment	not modelled	81.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
85	d1krwa_	Alignment	not modelled	81.1	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
86	c2pz0B_	Alignment	not modelled	81.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
87	c3gr7A_	Alignment	not modelled	80.9	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
88	c2ya0A_	Alignment	not modelled	80.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
89	c1m53A_	Alignment	not modelled	80.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
90	d1m53a2	Alignment	not modelled	80.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	c2ze0A_	Alignment	not modelled	79.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
92	d1heya_	Alignment	not modelled	78.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	d1w25a1	Alignment	not modelled	78.6	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
94	d1avaa2	Alignment	not modelled	78.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	c2wskA_	Alignment	not modelled	77.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycogen debranching enzyme; **PDBTitle:** crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
96	d1ea9c3	Alignment	not modelled	77.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
97	c1ea9D_	Alignment	not modelled	77.2	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
98	d1vhna_	Alignment	not modelled	77.1	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
99	c2qpuB_	Alignment	not modelled	76.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme; **PDBTitle:** sugar tongs mutant s378p in complex with acarbose
100	d1xm3a_	Alignment	not modelled	76.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
101	d1j0ha3	Alignment	not modelled	76.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
102	c3a47A_	Alignment	not modelled	76.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
103	c1jd7A_	Alignment	not modelled	75.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
104	d1uoka2	Alignment	not modelled	75.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
105	d2bhua3	Alignment	not modelled	74.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
						PDB header:hydrolase

106	c3ch0A_	Alignment	not modelled	74.9	27	**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
107	d1w0ma_	Alignment	not modelled	74.5	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
108	c1bf2A_	Alignment	not modelled	74.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
109	c2otdC_	Alignment	not modelled	74.1	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a
110	d1cyga4	Alignment	not modelled	74.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
111	d1rd5a_	Alignment	not modelled	73.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
112	c2by0A_	Alignment	not modelled	73.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
113	c2iswB_	Alignment	not modelled	73.1	12	**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
114	c3ozbF_	Alignment	not modelled	72.8	25	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
115	d1m7xa3	Alignment	not modelled	72.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	c3qvqB_	Alignment	not modelled	72.5	10	**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
117	d1cb0a_	Alignment	not modelled	72.4	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
118	d1qyia_	Alignment	not modelled	72.2	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
119	c3m07A_	Alignment	not modelled	72.0	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative alpha amylase; **PDBTitle:** 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium.
120	d1ps9a1	Alignment	not modelled	70.6	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases