Phyre2

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Description	P76446
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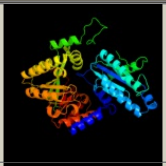
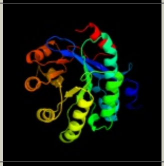
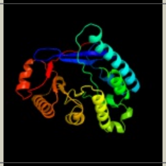
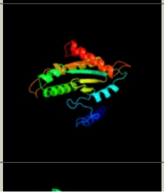
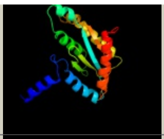
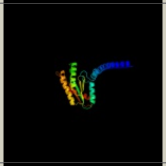
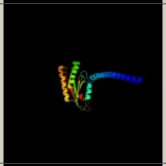
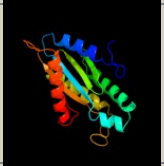
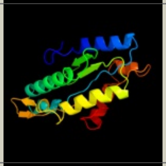
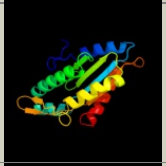
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	Alignment		100.0	18	**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	18	**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	21	**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	c3s83A_	Alignment		100.0	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef family protein; **PDBTitle:** crystal structure of eal domain from caulobacter crescentus cb15
5	c3hv9A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
6	c3pfmA_	Alignment		100.0	24	**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	20	**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	19	**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		99.4	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		99.3	11	**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	c3i5cA_	Alignment		98.9	9	**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
14	c3breA_	Alignment		98.8	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
15	c3i5aA_	Alignment		98.8	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wspr from pseudomonas syringae
16	c3i5bA_	Alignment		98.7	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wspr from2 pseudomonas aeruginosa
17	c3ignA_	Alignment		98.6	11	**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
18	c3qyyB_	Alignment		98.6	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	c3hvaA_	Alignment		98.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
20	c3iclA_	Alignment		98.5	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
21	c3mtkA_	Alignment	not modelled	98.5	5	**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
22	d1w25a3	Alignment	not modelled	98.5	7	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
23	c3hvwA_	Alignment	not modelled	98.2	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	d1p6qa_	Alignment	not modelled	95.4	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
25	c3khtA_	Alignment	not modelled	95.4	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis
26	c3hebB_	Alignment	not modelled	95.3	18	**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
27	d1mvoa_	Alignment	not modelled	95.0	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
28	c2zayA_	Alignment	not modelled	94.6	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from

						desulfuromonas2 acetoxidans
29	c2ayxA_	Alignment	not modelled	94.3	19	**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
30	c3rqiA_	Alignment	not modelled	94.3	11	**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
31	c3crnA_	Alignment	not modelled	94.1	16	**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
32	d1w25a1	Alignment	not modelled	93.9	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
33	d1qkka_	Alignment	not modelled	93.6	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
34	d1a53a_	Alignment	not modelled	93.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
35	c3eulB_	Alignment	not modelled	93.6	12	**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
36	c2yxbA_	Alignment	not modelled	93.6	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
37	c2jk1A_	Alignment	not modelled	93.4	8	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
38	c3nhzA_	Alignment	not modelled	93.4	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
39	d1h5ya_	Alignment	not modelled	93.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
40	c3gt7A_	Alignment	not modelled	93.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
41	c3qvqB_	Alignment	not modelled	93.0	11	**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
42	d1krwa_	Alignment	not modelled	92.8	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
43	d1u0sy_	Alignment	not modelled	92.6	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
44	c2j48A_	Alignment	not modelled	92.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
45	d1zesa1	Alignment	not modelled	92.3	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
46	d1heya_	Alignment	not modelled	92.2	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	c2pz0B_	Alignment	not modelled	92.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
48	d1jbea_	Alignment	not modelled	92.0	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
49	d1xhfa1	Alignment	not modelled	91.8	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
50	d1k68a_	Alignment	not modelled	91.7	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
51	d1dbwa_	Alignment	not modelled	91.5	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
52	c3q58A_	Alignment	not modelled	91.5	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
53	c3hv2B_	Alignment	not modelled	91.4	12	**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
54	d1k66a_	Alignment	not modelled	91.4	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
55	c3gl9B_	Alignment	not modelled	91.3	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
56	d1i3ca_	Alignment	not modelled	91.2	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
57	c2zwmA_	Alignment	not modelled	91.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
58	c2p0oA_	Alignment	not modelled	91.2	21	**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
59	c2qr3A_	Alignment	not modelled	91.2	11	**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
60	c3c3mA_	Alignment	not modelled	91.1	11	**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
61	d1kgsa2	Alignment	not modelled	91.1	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
62	c3cg0A_	Alignment	not modelled	90.9	14	**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
63	d1ny5a1	Alignment	not modelled	90.8	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
64	c2c3zA_	Alignment	not modelled	90.8	23	**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
65	c3i42A_	Alignment	not modelled	90.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey- **PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
66	d2r25b1	Alignment	not modelled	90.5	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
67	d1y0ea_	Alignment	not modelled	90.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
68	c3b2nA_	Alignment	not modelled	90.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
69	c3hdgE_	Alignment	not modelled	90.3	13	**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
70	d1dz3a_	Alignment	not modelled	90.1	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	d2ayxa1	Alignment	not modelled	90.1	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	c2rjnA_	Alignment	not modelled	90.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
73	d1mb3a_	Alignment	not modelled	89.7	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
74	d1ys7a2	Alignment	not modelled	89.7	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
75	c3grcD_	Alignment	not modelled	89.7	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
76	d2pl1a1	Alignment	not modelled	89.4	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
77	d1yioa2	Alignment	not modelled	89.4	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:signaling protein, transferase **Chain:** A: **PDB Molecule:**signal transduction histidine kinase;

78	c3c97A_	Alignment	not modelled	89.4	11	**PDBTitle:** crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
79	c2h6rG_	Alignment	not modelled	89.3	16	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
80	c3cnbC_	Alignment	not modelled	89.2	14	**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
81	c3cu5B_	Alignment	not modelled	89.1	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
82	d1a04a2	Alignment	not modelled	88.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
83	c3lteH_	Alignment	not modelled	88.1	13	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
84	d2a9pa1	Alignment	not modelled	87.9	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
85	d1ua7a2	Alignment	not modelled	87.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
86	d1peya_	Alignment	not modelled	87.5	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c1jibA_	Alignment	not modelled	87.4	28	**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.
88	c3ffsC_	Alignment	not modelled	87.4	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
89	c3cg4A_	Alignment	not modelled	87.3	13	**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
90	c3igsB_	Alignment	not modelled	87.2	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
91	c3gr7A_	Alignment	not modelled	87.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
92	c2rdmB_	Alignment	not modelled	86.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
93	c3f6cB_	Alignment	not modelled	86.4	16	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
94	d2d3na2	Alignment	not modelled	86.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	c2nt3A_	Alignment	not modelled	85.7	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
96	c2qxyB_	Alignment	not modelled	85.7	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
97	d1dcfa_	Alignment	not modelled	85.5	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
98	c3cfyA_	Alignment	not modelled	85.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
99	d1hvxa2	Alignment	not modelled	84.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
100	d1s8na_	Alignment	not modelled	84.7	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
101	c2jrlA_	Alignment	not modelled	84.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
102	c2vw3E_	Alignment	not modelled	84.6	17	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-

102	c2yw3[illegible]_	Alignment	not modelled	84.6	17	**PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
103	c2y85D_	Alignment	not modelled	84.4	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**phosphoribosyl isomerase a; **PDBTitle:** crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
104	d1zgza1	Alignment	not modelled	84.2	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
105	c1qhoA_	Alignment	not modelled	84.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
106	d2guya2	Alignment	not modelled	84.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
107	d1uoka2	Alignment	not modelled	84.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
108	d2gjpa2	Alignment	not modelled	83.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
109	d1ob0a2	Alignment	not modelled	83.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
110	c3nhmA_	Alignment	not modelled	83.7	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from myxococcus xanthus
111	c2qzjC_	Alignment	not modelled	83.3	11	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
112	c2gjlA_	Alignment	not modelled	83.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein pa1024; **PDBTitle:** crystal structure of 2-nitropropane dioxygenase
113	d1mxga2	Alignment	not modelled	83.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
114	c1cygA_	Alignment	not modelled	83.0	18	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
115	d1g5aa2	Alignment	not modelled	82.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	d1h3ga3	Alignment	not modelled	82.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
117	c3hdvB_	Alignment	not modelled	82.4	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
118	c3luaA_	Alignment	not modelled	82.4	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
119	d1ud2a2	Alignment	not modelled	82.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
120	d1zh2a1	Alignment	not modelled	82.2	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related