Phyre^2

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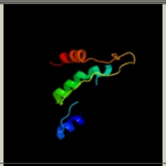
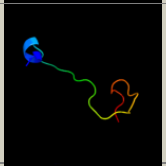
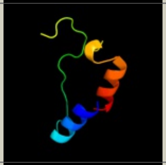
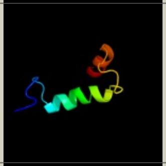
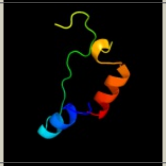
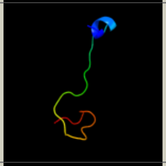
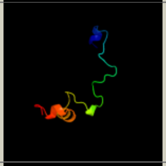
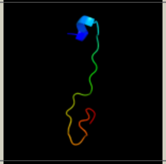
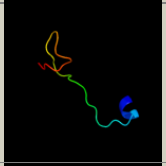
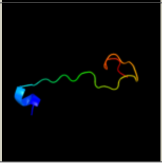
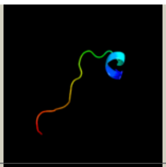
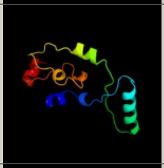
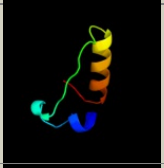
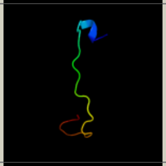
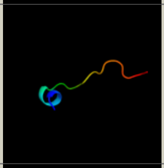
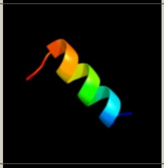
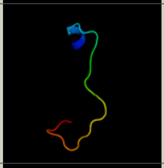
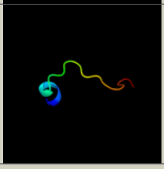
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tv8a_	Alignment		82.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**MoCo biosynthesis proteins
2	d1g5aa2	Alignment		57.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
3	c3k1dA_	Alignment		52.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme; **PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
4	c2kgrA_	Alignment		51.0	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a
5	c3amkA_	Alignment		49.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
6	c1jgiA_	Alignment		49.1	16	**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
7	c2fhfA_	Alignment		48.8	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
8	c3amlA_	Alignment		44.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
9	d1tz7a1	Alignment		42.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
10	c3czkA_	Alignment		40.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
11	c3ucqA_	Alignment		39.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis

12	c3faxA_	Alignment		36.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
13	c3l51B_	Alignment		35.6	13	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**structural maintenance of chromosomes protein 4; **PDBTitle:** crystal structure of the mouse condensin hinge domain
14	d2obba1	Alignment		35.3	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
15	d2aaaa2	Alignment		34.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
16	c2ya1A_	Alignment		34.4	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
17	c3eyiB_	Alignment		33.9	27	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
18	d1gjwa2	Alignment		33.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
19	d1iq3a_	Alignment		33.5	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
20	c2e8yA_	Alignment		33.3	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
21	c1bf2A_	Alignment	not modelled	32.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
22	c2wanA_	Alignment	not modelled	32.2	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
23	d1fi6a_	Alignment	not modelled	28.1	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
24	c2wd5A_	Alignment	not modelled	25.6	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**structural maintenance of chromosomes protein 1a; **PDBTitle:** smc hinge heterodimer (mouse)
25	c2ya0A_	Alignment	not modelled	24.1	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
26	c2vncB_	Alignment	not modelled	23.9	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
27	c3m07A_	Alignment	not modelled	23.0	19	**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.
28	c1bagA_	Alignment	not modelled	22.9	14	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
						Fold:EF Hand-like

29	d1eg3a1	Alignment	not modelled	22.6	17	**Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
30	c3rh3A_	Alignment	not modelled	22.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized duf3829-like protein; **PDBTitle:** crystal structure of an uncharacterized duf3829-like protein (bt_1908)2 from bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
31	d1bf2a3	Alignment	not modelled	21.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
32	d1br1b_	Alignment	not modelled	21.5	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
33	c2wskA_	Alignment	not modelled	21.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycogen debranching enzyme; **PDBTitle:** crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
34	c1gjuA_	Alignment	not modelled	21.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
35	d1ugla_	Alignment	not modelled	20.2	57	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Plant defensins
36	d1mxga2	Alignment	not modelled	19.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
37	d1ibia1	Alignment	not modelled	19.2	26	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
38	d1ua7a2	Alignment	not modelled	19.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
39	c2x4bA_	Alignment	not modelled	19.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin
40	d1m7xa3	Alignment	not modelled	18.9	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
41	d1vlia2	Alignment	not modelled	18.6	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
42	d1avaa2	Alignment	not modelled	18.4	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
43	c3fmfA_	Alignment	not modelled	18.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
44	d1cyga4	Alignment	not modelled	17.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
45	c2taaA_	Alignment	not modelled	17.3	13	**PDB header:**hydrolase (o-glycosyl) **Chain:** A: **PDB Molecule:**taka-amylase a; **PDBTitle:** structure and possible catalytic residues of taka-amylase a
46	d2bvca1	Alignment	not modelled	17.2	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Glutamine synthetase, N-terminal domain **Family:**Glutamine synthetase, N-terminal domain
47	c1m7xC_	Alignment	not modelled	17.2	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
48	c2k7bA_	Alignment	not modelled	17.1	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** nmr structure of mg2+-bound cabp1 n-domain
49	c2by0A_	Alignment	not modelled	16.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
50	c2amiA_	Alignment	not modelled	16.4	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**caltractin; **PDBTitle:** solution structure of the calcium-loaded n-terminal sensor2 domain of centrin
51	c1jaeA_	Alignment	not modelled	15.9	15	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
52	d2fhfa5	Alignment	not modelled	15.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
53	d2guya2	Alignment	not modelled	15.8	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
54	c3edeB_	Alignment	not modelled	15.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
55	d2r7ca1	Alignment	not modelled	15.3	22	**Fold:**HIT-like **Superfamily:**Rotavirus NSP2 fragment, C-terminal domain **Family:**Rotavirus NSP2 fragment, C-terminal domain
						PDB header:hydrolase

56	c1jd7A_	Alignment	not modelled	15.0	13	**Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
57	c3sibA_	Alignment	not modelled	14.9	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ure3-bp sequence specific dna binding protein; **PDBTitle:** crystal structure of ure3-binding protein, wild-type
58	d1h3ga3	Alignment	not modelled	14.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
59	c1gviA_	Alignment	not modelled	14.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
60	d1v95a_	Alignment	not modelled	14.5	13	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
61	c3nwcA_	Alignment	not modelled	14.2	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**smc protein; **PDBTitle:** crystal structure of the pyrococcus furiosus smc protein hinge domain
62	c2k7cA_	Alignment	not modelled	14.1	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** nmr structure of mg2+-bound cabp1 c-domain
63	d1u1ha2	Alignment	not modelled	13.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
64	d1c07a_	Alignment	not modelled	13.7	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
65	c3dhuC_	Alignment	not modelled	13.4	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
66	c2fcdA_	Alignment	not modelled	13.1	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**myosin light chain 1; **PDBTitle:** solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae
67	c1lwhA_	Alignment	not modelled	13.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
68	c2dh3A_	Alignment	not modelled	13.0	11	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
69	c1e40A_	Alignment	not modelled	12.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
70	c1ehaA_	Alignment	not modelled	12.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
71	c1mwoA_	Alignment	not modelled	12.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase; **PDBTitle:** crystal structure analysis of the hyperthermostable2 pyrocoocus woesei alpha-amylase
72	c1ea9D_	Alignment	not modelled	12.5	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
73	d1ea9c3	Alignment	not modelled	12.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
74	d1x1na1	Alignment	not modelled	12.3	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
75	d1w7jb1	Alignment	not modelled	12.2	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
76	d1gvia3	Alignment	not modelled	12.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
77	c2bl0B_	Alignment	not modelled	12.1	18	**PDB header:**muscle protein **Chain:** B: **PDB Molecule:**myosin regulatory light chain; **PDBTitle:** physarum polycephalum myosin ii regulatory domain
78	c3l7sA_	Alignment	not modelled	11.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate--homocysteine **PDBTitle:** crystal structure of mete coordinated with zinc from streptococcus2 mutans
79	c2wcsA_	Alignment	not modelled	11.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
80	d1uoka2	Alignment	not modelled	11.6	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
81	c1jibA_	Alignment	not modelled	11.3	10	**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.
82	d1lwha2	Alignment	not modelled	11.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases

						Family: Amylase, catalytic domain
83	c2aaaA_	Alignment	not modelled	11.0	10	**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
84	c3ghgD_	Alignment	not modelled	10.9	19	**PDB header:**blood clotting **Chain:** D: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of human fibrinogen
85	d2cuja1	Alignment	not modelled	10.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
86	d1j0ha3	Alignment	not modelled	10.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
87	d1wzla3	Alignment	not modelled	10.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
88	d1tn4a_	Alignment	not modelled	10.7	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
89	d1qhoa4	Alignment	not modelled	10.5	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
90	d1eswa_	Alignment	not modelled	10.5	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	c3ogzA_	Alignment	not modelled	10.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-sugar pyrophosphorylase; **PDBTitle:** protein structure of usp from l. major in apo-form
92	c3p09A_	Alignment	not modelled	10.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase; **PDBTitle:** crystal structure of beta-lactamase from francisella tularensis
93	c3blpX_	Alignment	not modelled	10.2	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
94	d2b4jc1	Alignment	not modelled	10.1	14	**Fold:**N-cbl like **Superfamily:**HIV integrase-binding domain **Family:**HIV integrase-binding domain
95	c2jmiA_	Alignment	not modelled	10.1	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein yng1; **PDBTitle:** nmr solution structure of phd finger fragment of yeast yng12 protein in free state
96	c3ey5A_	Alignment	not modelled	10.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase-like, gnat family; **PDBTitle:** putative acetyltransferase from gnat family from bacteroides2 thetaiotaomicron.
97	c2jmlA_	Alignment	not modelled	9.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
98	c2xtdB_	Alignment	not modelled	9.9	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tbl1 f-box-like/wd repeat-containing protein tbl1x; **PDBTitle:** structure of the tbl1 tetramerisation domain
99	c2yx0A_	Alignment	not modelled	9.8	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1