Phyre^2

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Description	P15977
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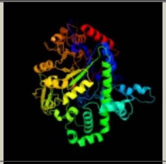
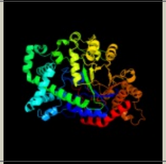
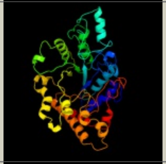
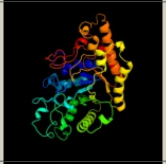
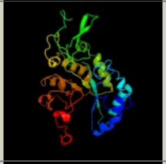
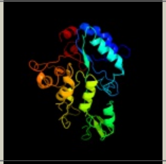
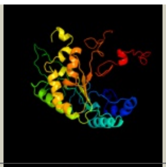
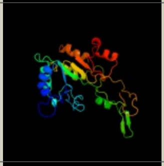
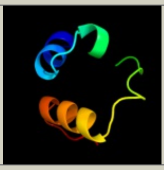
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1x1na1	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
2	d1eswa_	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
3	d1tz7a1	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
4	c3zt5D_	Alignment		98.6	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucanohydrolase pep1a; **PDBTitle:** glge isoform 1 from streptomyces coelicolor with maltose2 bound
5	c3amkA_	Alignment		98.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
6	c3amlA_	Alignment		98.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
7	c1m53A_	Alignment		98.2	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
8	d1uoka2	Alignment		98.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
9	d1j0ha3	Alignment		98.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
10	c1uokA_	Alignment		98.1	21	**PDB header:**glucosidase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of b. cereus oligo-1,6-glucosidase
11	d1bf2a3	Alignment		98.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

12	c1zjaB_	Alignment		98.1	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
13	d1m53a2	Alignment		98.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
14	d1ua7a2	Alignment		98.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
15	d1gvia3	Alignment		97.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
16	c1wpcA_	Alignment		97.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltohexaosidase; **PDBTitle:** crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
17	c3a47A_	Alignment		97.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
18	c1tcmB_	Alignment		97.9	21	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
19	d1m7xa3	Alignment		97.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
20	d1lwha2	Alignment		97.9	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
21	c3dhuC_	Alignment	not modelled	97.9	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
22	c1jibA_	Alignment	not modelled	97.8	16	**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.
23	d2d3na2	Alignment	not modelled	97.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
24	c2ya1A_	Alignment	not modelled	97.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
25	d2guya2	Alignment	not modelled	97.8	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
26	c2ze0A_	Alignment	not modelled	97.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
27	c2ya0A_	Alignment	not modelled	97.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
28	c2wcsA_	Alignment	not modelled	97.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)

29	c3bmwA_	Alignment	not modelled	97.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
30	c3k1dA_	Alignment	not modelled	97.6	19	**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
31	c2dh3A_	Alignment	not modelled	97.6	23	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
32	c1ehaA_	Alignment	not modelled	97.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
33	c1ea9D_	Alignment	not modelled	97.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
34	d1h3ga3	Alignment	not modelled	97.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
35	c2zidA_	Alignment	not modelled	97.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dextran glucosidase; **PDBTitle:** crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
36	d1eh9a3	Alignment	not modelled	97.3	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
37	c2by0A_	Alignment	not modelled	97.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
38	d3bmva4	Alignment	not modelled	97.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
39	d2bhua3	Alignment	not modelled	97.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
40	c2taaA_	Alignment	not modelled	97.2	28	**PDB header:**hydrolase (o-glycosyl) **Chain:** A: **PDB Molecule:**taka-amylase a; **PDBTitle:** structure and possible catalytic residues of taka-amylase a
41	c2wskA_	Alignment	not modelled	97.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycogen debranching enzyme; **PDBTitle:** crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
42	c2qpuB_	Alignment	not modelled	97.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme; **PDBTitle:** sugar tongs mutant s378p in complex with acarbose
43	d1gcya2	Alignment	not modelled	97.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
44	c1hvxA_	Alignment	not modelled	97.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** bacillus stearothermophilus alpha-amylase
45	c2z1kA_	Alignment	not modelled	97.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
46	c1gviA_	Alignment	not modelled	97.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
47	c1qhoA_	Alignment	not modelled	96.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
48	c2wanA_	Alignment	not modelled	96.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
49	d1cyga4	Alignment	not modelled	96.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	d1ob0a2	Alignment	not modelled	96.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
51	c1cygA_	Alignment	not modelled	96.4	15	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
52	d1e43a2	Alignment	not modelled	96.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
53	d1pama4	Alignment	not modelled	96.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
54	c1jaeA_	Alignment	not modelled	96.1	16	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
55	c2fhfA_	Alignment	not modelled	96.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase;

55	[illegible]	Alignment	not modelled	96.0	19	**PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
56	c3edeB_	Alignment	not modelled	95.8	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
57	c1lwhA_	Alignment	not modelled	95.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
58	d1ht6a2	Alignment	not modelled	95.7	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
59	d1avaa2	Alignment	not modelled	95.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
60	d1ea9c3	Alignment	not modelled	95.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
61	c2gdvA_	Alignment	not modelled	95.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sucrose phosphorylase; **PDBTitle:** sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
62	c1bplA_	Alignment	not modelled	95.3	13	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
63	d1gjwa2	Alignment	not modelled	95.2	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
64	d2gjpa2	Alignment	not modelled	95.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
65	d1cxla4	Alignment	not modelled	95.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
66	c1gcyA_	Alignment	not modelled	95.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
67	d2fhfa5	Alignment	not modelled	95.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	c2e8yA_	Alignment	not modelled	94.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
69	d1ud2a2	Alignment	not modelled	94.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
70	c3k8kB_	Alignment	not modelled	94.5	19	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
71	c1jdaA_	Alignment	not modelled	94.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
72	d1r7aa2	Alignment	not modelled	94.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	d2aaaa2	Alignment	not modelled	94.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
74	c1gjuA_	Alignment	not modelled	94.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
75	c1m7xC_	Alignment	not modelled	94.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
76	c3faxA_	Alignment	not modelled	93.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
77	c1jgiA_	Alignment	not modelled	93.4	22	**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
78	c3bc9A_	Alignment	not modelled	93.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** alpha-amylase b in complex with acarbose
79	c1e40A_	Alignment	not modelled	93.3	18	**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
80	c2x4bA_	Alignment	not modelled	93.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin
81	c1bf2A_	Alignment	not modelled	92.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
82	c3czkA_	Alignment	not modelled	92.6	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase;

82	c3czkA_	Alignment	not modelled	92.6	8	**PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
83	d1mxga2	Alignment	not modelled	92.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
84	c2aaaA_	Alignment	not modelled	92.5	17	**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
85	c1jd7A_	Alignment	not modelled	92.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
86	c3m07A_	Alignment	not modelled	92.3	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.
87	c3blpX_	Alignment	not modelled	91.9	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
88	d1hvxa2	Alignment	not modelled	91.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
89	d1g5aa2	Alignment	not modelled	91.5	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
90	c1bplB_	Alignment	not modelled	91.5	12	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
91	d1qhoa4	Alignment	not modelled	91.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
92	d1wzla3	Alignment	not modelled	90.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
93	d1hx0a2	Alignment	not modelled	90.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
94	c1bagA_	Alignment	not modelled	90.2	23	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
95	d1jaea2	Alignment	not modelled	89.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
96	c1wzaA_	Alignment	not modelled	88.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase a; **PDBTitle:** crystal structure of alpha-amylase from h.orenii
97	d1g94a2	Alignment	not modelled	88.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
98	d3dhpa2	Alignment	not modelled	87.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
99	c2yfnA_	Alignment	not modelled	87.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
100	c2vncB_	Alignment	not modelled	86.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
101	d1ji1a3	Alignment	not modelled	86.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
102	d1wzaa2	Alignment	not modelled	83.4	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
103	d1cgta4	Alignment	not modelled	82.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
104	c1mwoA_	Alignment	not modelled	80.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase; **PDBTitle:** crystal structure analysis of the hyperthermostable2 pyrococus woesei alpha-amylase
105	c1ud8A_	Alignment	not modelled	79.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
106	c2bnoA_	Alignment		75.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
107	c2d0gA_	Alignment	not modelled	73.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase i; **PDBTitle:** crystal structure of thermoactinomyces vulgaris r-47 alpha-2 amylase 1 (tvai) mutant d356n/e396q complexed with p5, a3 pullulan model oligosaccharide

108	c3hjeA_	Alignment	not modelled	73.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**704aa long hypothetical glycosyltransferase; **PDBTitle:** crystal structure of sulfolobus tokodaii hypothetical2 maltooligosyl trehalose synthase
109	c3cc1B_	Alignment	not modelled	65.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-n-acetylgalactosaminidase; **PDBTitle:** crystal structure of a putative alpha-n-acetylgalactosaminidase2 (bh1870) from bacillus halodurans c-125 at 2.00 a resolution
110	d1j0ha2	Alignment		63.2	21	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
111	d1h9aa1	Alignment	not modelled	62.8	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
112	c2bhlB_	Alignment	not modelled	61.4	20	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
113	d2a6ca1	Alignment	not modelled	60.9	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
114	c1qkiE_	Alignment	not modelled	59.7	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
115	c3pxpA_	Alignment	not modelled	58.7	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**helix-turn-helix domain protein; **PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
116	d1l1ya_	Alignment	not modelled	58.7	25	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
117	c1l2aD_	Alignment	not modelled	58.7	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
118	d2ofya1	Alignment	not modelled	56.9	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
119	d1g9ga_	Alignment	not modelled	55.9	21	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
120	c3gzaB_	Alignment	not modelled	55.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution