Phyre2

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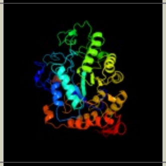
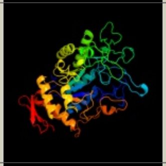
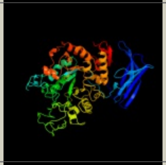
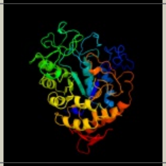
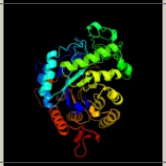
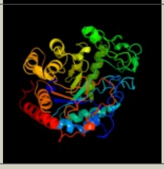
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3edeB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
2	c1tcmB_	Alignment		100.0	25	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
3	c3bmwA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
4	c1cygA_	Alignment		100.0	26	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
5	c1qhoA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
6	c1gviA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
7	c1jibA_	Alignment		100.0	25	**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.
8	c1ea9D_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
9	c2d0gA_	Alignment		100.0	23	**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
10	c3k8kB_	Alignment		100.0	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
11	d3bmva4	Alignment		100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

12	c2wcsA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
13	d1cgta4	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
14	c2taaA_	Alignment		100.0	25	**PDB header:**hydrolase (o-glycosyl) **Chain:** A: **PDB Molecule:**taka-amylase a; **PDBTitle:** structure and possible catalytic residues of taka-amylase a
15	d1pama4	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
16	d1h3ga3	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
17	d1cxla4	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
18	c2aaaA_	Alignment		100.0	23	**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
19	d1qhoa4	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
20	d2guya2	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
21	c3k1dA_	Alignment	not modelled	100.0	18	**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
22	d1cyga4	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
23	d2aaaa2	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
24	d1gvia3	Alignment	not modelled	100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
25	d1wzla3	Alignment	not modelled	100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
26	d1ji1a3	Alignment	not modelled	100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
27	c2z1kA_	Alignment	not modelled	100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
28	c2e8yA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
						PDB header:transferase

29	c1jgiA_	Alignment	not modelled	100.0	20	**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
30	d1j0ha3	Alignment	not modelled	100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
31	c3faxA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
32	c1bf2A_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
33	c2ya1A_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
34	c2wanA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
35	c2ya0A_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
36	d1ea9c3	Alignment	not modelled	100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
37	c3ucqA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis
38	c3a47A_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
39	c2vncB_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
40	d2fhfa5	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
41	c1uokA_	Alignment	not modelled	100.0	24	**PDB header:**glucosidase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of b. cereus oligo-1,6-glucosidase
42	c3zt5D_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucanohydrolase pep1a; **PDBTitle:** glge isoform 1 from streptomyces coelicolor with maltose2 bound
43	c1m53A_	Alignment	not modelled	100.0	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
44	c1zjaB_	Alignment	not modelled	100.0	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
45	d1m53a2	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
46	c3m07A_	Alignment	not modelled	100.0	21	**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.
47	c1m7xC_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
48	c2wskA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycogen debranching enzyme; **PDBTitle:** crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
49	d1g5aa2	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	d1uoka2	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
51	c3czkA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
52	c2zidA_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dextran glucosidase; **PDBTitle:** crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
53	c1ehaA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
54	c1wzaA_	Alignment	not modelled	100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase a; **PDBTitle:** crystal structure of alpha-amylase from h.orenii
55	d1bf2a3	Alignment	not modelled	100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases

						Family: Amylase, catalytic domain
56	c2gdvA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sucrose phosphorylase; **PDBTitle:** sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
57	c2ze0A_	Alignment	not modelled	100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
58	c2fhfA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
59	c1gjuA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
60	c3amkA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
61	c3amlA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
62	c2qpuB_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme; **PDBTitle:** sugar tongs mutant s378p in complex with acarbose
63	c2by0A_	Alignment	not modelled	100.0	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
64	d1wzaa2	Alignment	not modelled	100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
65	c1lwhA_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
66	c2x4bA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin
67	d1lwha2	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	c3dhuC_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
69	c1e40A_	Alignment	not modelled	100.0	20	**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	c1wpcA_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltohexaosidase; **PDBTitle:** crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
71	c1ud8A_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
72	d1gjwa2	Alignment	not modelled	100.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	c1hvxA_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** bacillus stearothermophilus alpha-amylase
74	c2dh3A_	Alignment	not modelled	100.0	22	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
75	d1m7xa3	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
76	c1jdaA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
77	c1gcyA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
78	c1jaeA_	Alignment	not modelled	100.0	18	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
79	c3bc9A_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** alpha-amylase b in complex with acarbose
80	d2bhua3	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
81	d1ob0a2	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
82	c3blpX	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1;

82	c3blpx_	Alignment	not modelled	100.0	18	**PDBTitle:** role of aromatic residues in human salivary alpha-amylase
83	c1bagA_	Alignment	not modelled	100.0	19	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
84	c1jd7A_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
85	d1mxga2	Alignment	not modelled	100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
86	d1eh9a3	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
87	c1mwoA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase; **PDBTitle:** crystal structure analysis of the hyperthermostable2 pyrocoocus woesei alpha-amylase
88	d1r7aa2	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
89	d1ud2a2	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
90	d1e43a2	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	d2gjpa2	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
92	d1hvxa2	Alignment	not modelled	100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
93	d1gcya2	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
94	d1avaa2	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	d2d3na2	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
96	d1ua7a2	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
97	d1ht6a2	Alignment	not modelled	100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
98	d1jaea2	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
99	d1g94a2	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
100	d1hx0a2	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
101	c1iv8A_	Alignment	not modelled	100.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**maltooligosyl trehalose synthase; **PDBTitle:** crystal structure of maltooligosyl trehalose synthase
102	d3dhpa2	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
103	c3hjeA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**704aa long hypothetical glycosyltransferase; **PDBTitle:** crystal structure of sulfolobus tokodaii hypothetical2 maltooligosyl trehalose synthase
104	c1bplB_	Alignment	not modelled	100.0	18	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
105	d1iv8a2	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
106	c1bplA_	Alignment	not modelled	99.9	38	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
107	c3aicC_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucosyltransferase-si; **PDBTitle:** crystal structure of glucansucrase from streptococcus mutans
108	c3hz3A_	Alignment	not modelled	99.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucansucrase; **PDBTitle:** lactobacillus reuteri n-terminally truncated glucansucrase2 gtf180(d1025n)-sucrose complex
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase

109	c2yfnA_	Alignment	not modelled	98.7	14	agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
110	c2xn1B_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
111	c3mi6A_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
112	d2f2ha4	Alignment	not modelled	98.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
113	d1uuqa_	Alignment	not modelled	97.8	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
114	c1uz4A_	Alignment	not modelled	97.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**man5a; **PDBTitle:** common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 intineraries for glucoside and mannoside hydrolysis
115	d1edga_	Alignment	not modelled	97.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
116	c3civA_	Alignment	not modelled	97.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase; **PDBTitle:** crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
117	c1zy9A_	Alignment	not modelled	97.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase (ec 3.2.1.22) (melibiase)2 (tm1192) from thermotoga maritima at 2.34 a resolution
118	c3pzqA_	Alignment	not modelled	97.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family **PDBTitle:** structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol
119	d1zy9a2	Alignment	not modelled	97.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
120	d2pb1a1	Alignment	not modelled	97.5	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases