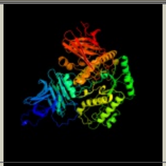
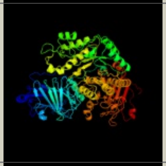
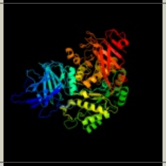
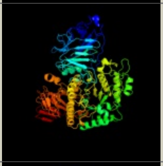
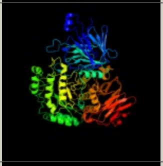
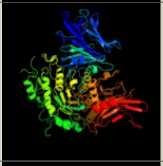
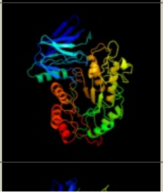
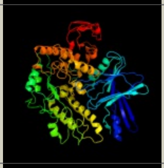
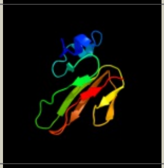
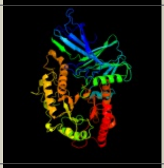
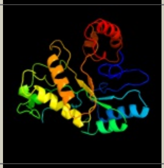
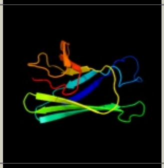
Email	l.a.kelley@imperial.ac.uk
Description	P31434
Date	Thu Jan 5 11:47:24 GMT 2012
Unique Job ID	9d24d38e7c8bffef

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xsiF_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative family 31 glucosidase yici; **PDBTitle:** structure of a family 31 alpha glycosidase
2	c3topA_	Alignment		100.0	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**maltase-glucoamylase, intestinal; **PDBTitle:** crystral structure of the c-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
3	c3lppA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrase-isomaltase; **PDBTitle:** crystal complex of n-terminal sucrase-isomaltase with kotalanol
4	c2qmjA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltase-glucoamylase, intestinal; **PDBTitle:** crystral structure of the n-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
5	c2xvgA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha xylosidase; **PDBTitle:** crystal structure of alpha-xylosidase (gh31) from2 cellvibrio japonicus
6	c2g3nA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of the sulfolobus solfataricus alpha-2 glucosidase mala in complex with beta-octyl-glucopyranoside
7	c2x2iB_	Alignment		100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-1,4-glucan lyase isozyme 1; **PDBTitle:** crystal structure of the gracilariopsis lemaneiformis alpha-2 1,4-glucan lyase with acarbose
8	c3ffjA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase (family 31); **PDBTitle:** the crystal structure of the glycosyl hydrolase (family 31) from2 ruminococcus obeum atcc 29174
9	d2f2ha4	Alignment		100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
10	d2f2ha2	Alignment		100.0	100	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**YicI N-terminal domain-like
11	c1zy9A_	Alignment		100.0	18	**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

12	c2yfnA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
13	c2xn1B_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
14	d2f2ha3	Alignment		99.9	100	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**Putative glucosidase YicI, domain 3
15	d1zy9a2	Alignment		99.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
16	c3mi6A_	Alignment		99.8	12	**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.
17	c3cc1B_	Alignment		99.7	13	**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
18	d2f2ha1	Alignment		99.6	100	**Fold:**Putative glucosidase YicI, C-terminal domain **Superfamily:**Putative glucosidase YicI, C-terminal domain **Family:**Putative glucosidase YicI, C-terminal domain
19	d1uasa2	Alignment		99.6	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
20	c1uasA_	Alignment		99.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
21	d1szna2	Alignment	not modelled	99.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
22	d1r46a2	Alignment	not modelled	99.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
23	c3a5vA_	Alignment	not modelled	99.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase i from mortierella vinacea
24	c3lrmB_	Alignment	not modelled	99.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase 1; **PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
25	c3a23A_	Alignment	not modelled	99.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase; **PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
26	c1r46B_	Alignment	not modelled	99.2	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase a; **PDBTitle:** structure of human alpha-galactosidase
27	c1t0oA_	Alignment	not modelled	99.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
28	c1ktbA_	Alignment	not modelled	99.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** the structure of alpha-n-acetylgalactosaminidase
29	d1ktba2	Alignment	not modelled	99.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

30	c3dhuC_	Alignment	not modelled	98.9	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
31	c2wskA_	Alignment	not modelled	98.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycogen debranching enzyme; **PDBTitle:** crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
32	c1jibA_	Alignment	not modelled	98.4	17	**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.
33	c1jd7A_	Alignment	not modelled	98.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
34	c1gviA_	Alignment	not modelled	98.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
35	c1bagA_	Alignment	not modelled	98.1	12	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
36	c3czkA_	Alignment	not modelled	98.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
37	c1lwhA_	Alignment	not modelled	97.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
38	d1g5aa2	Alignment	not modelled	97.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
39	d1ua7a2	Alignment	not modelled	97.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
40	d1m53a2	Alignment	not modelled	97.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
41	c3ucqA_	Alignment	not modelled	97.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis
42	d1gvia3	Alignment	not modelled	97.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
43	c1jgiA_	Alignment	not modelled	97.8	18	**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
44	c1jdaA_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
45	d1ea9c3	Alignment	not modelled	97.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
46	c2wcsA_	Alignment	not modelled	97.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
47	c1wzaA_	Alignment	not modelled	97.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase a; **PDBTitle:** crystal structure of alpha-amylase from h.orenii
48	d1gcya2	Alignment	not modelled	97.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
49	c2z1kA_	Alignment	not modelled	97.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
50	c1zjaB_	Alignment	not modelled	97.8	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
51	d1uoka2	Alignment	not modelled	97.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
52	c1m53A_	Alignment	not modelled	97.7	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
53	d1lwha2	Alignment	not modelled	97.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
54	c1gcyA_	Alignment	not modelled	97.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
55	d1j0ha3	Alignment	not modelled	97.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

56	c1cygA_	Alignment	not modelled	97.7	18	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
57	c2zidA_	Alignment	not modelled	97.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dextran glucosidase; **PDBTitle:** crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
58	c2ze0A_	Alignment	not modelled	97.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
59	c1uokA_	Alignment	not modelled	97.6	13	**PDB header:**glucosidase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of b. cereus oligo-1,6-glucosidase
60	c1tcmB_	Alignment	not modelled	97.6	16	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
61	d1h3ga3	Alignment	not modelled	97.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
62	c1jaeA_	Alignment	not modelled	97.6	11	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
63	c2wanA_	Alignment	not modelled	97.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
64	c1ehaA_	Alignment	not modelled	97.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
65	c1qhoA_	Alignment	not modelled	97.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
66	c3zt5D_	Alignment	not modelled	97.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucanohydrolase pep1a; **PDBTitle:** glge isoform 1 from streptomyces coelicolor with maltose2 bound
67	c3a47A_	Alignment	not modelled	97.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
68	d1avaa2	Alignment	not modelled	97.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
69	d1ht6a2	Alignment	not modelled	97.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
70	c3edeB_	Alignment	not modelled	97.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
71	d1wzaa2	Alignment	not modelled	97.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
72	d1wzla3	Alignment	not modelled	97.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	c2vncB_	Alignment	not modelled	97.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
74	c1ea9D_	Alignment	not modelled	97.3	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
75	c3faxA_	Alignment	not modelled	97.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
76	c2e8yA_	Alignment	not modelled	97.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
77	d1jaea2	Alignment	not modelled	97.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
78	c2qpuB_	Alignment	not modelled	97.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme; **PDBTitle:** sugar tongs mutant s378p in complex with acarbose
79	d2bhua3	Alignment	not modelled	97.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
80	c2aaaA_	Alignment	not modelled	97.2	15	**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
81	d1qhoa4	Alignment	not modelled	97.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
82	c3bmwA_	Alignment	not modelled	97.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p

						complexed with a maltoheptaose3 inhibitor
83	d1eh9a3	Alignment	not modelled	97.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
84	d1cyga4	Alignment	not modelled	97.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
85	c2taaA_	Alignment	not modelled	97.2	16	**PDB header:**hydrolase (o-glycosyl) **Chain:** A: **PDB Molecule:**taka-amylase a; **PDBTitle:** structure and possible catalytic residues of taka-amylase a
86	c3m07A_	Alignment	not modelled	97.1	12	**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	d1m7xa3	Alignment	not modelled	97.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
88	d2aaaa2	Alignment	not modelled	97.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
89	c2ya0A_	Alignment	not modelled	97.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
90	d1pama4	Alignment	not modelled	97.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	c1bf2A_	Alignment	not modelled	97.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
92	c1e40A_	Alignment	not modelled	97.1	13	**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
93	d2guya2	Alignment	not modelled	97.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
94	c1hvxA_	Alignment	not modelled	97.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** bacillus stearothermophilus alpha-amylase
95	c3blpX_	Alignment	not modelled	97.0	16	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
96	d3bmva4	Alignment	not modelled	97.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
97	c2ya1A_	Alignment	not modelled	97.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
98	d1bf2a3	Alignment	not modelled	97.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
99	d1cxla4	Alignment	not modelled	96.9	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
100	c2dh3A_	Alignment	not modelled	96.9	15	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
101	c1wpcA_	Alignment	not modelled	96.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltohexaosidase; **PDBTitle:** crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
102	c2by0A_	Alignment	not modelled	96.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
103	c3k1dA_	Alignment	not modelled	96.9	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
104	d1cgta4	Alignment	not modelled	96.8	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
105	c2x4bA_	Alignment	not modelled	96.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin
106	d3dhpa2	Alignment	not modelled	96.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
107	d1g94a2	Alignment	not modelled	96.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
108	d1hx0a2	Alignment	not modelled	96.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
109	c2aamA	Alignment	not modelled	96.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein tm1410;

109	c2aamA_	Alignment	not modelled	96.6	9	**PDBTitle:** crystal structure of a putative glycosidase (tm1410) from thermotoga2 maritima at 2.20 a resolution
110	d2aama1	Alignment	not modelled	96.6	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**TM1410-like
111	c1m7xC_	Alignment	not modelled	96.5	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
112	c3amkA_	Alignment	not modelled	96.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
113	c1ud8A_	Alignment	not modelled	96.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
114	c3amlA_	Alignment	not modelled	96.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
115	d2fhfa5	Alignment	not modelled	96.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	d1hvxa2	Alignment	not modelled	96.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
117	c2fhfA_	Alignment	not modelled	96.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
118	d2gjpa2	Alignment	not modelled	96.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
119	d1ud2a2	Alignment	not modelled	95.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
120	c3k8kB_	Alignment	not modelled	95.3	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg