Phyre2

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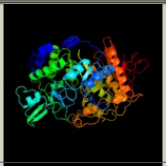
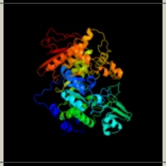
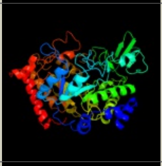
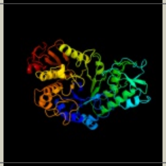
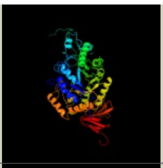
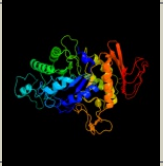
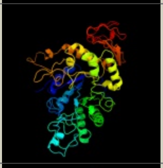
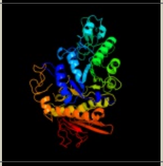
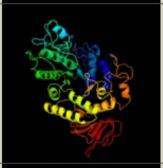
Description	P76041
Date	Thu Jan 5 12:17:40 GMT 2012
Unique Job ID	01efecf8db48614c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1jgiA_	Alignment		100.0	27	**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
2	c3ucqA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis
3	c3czkA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
4	d1g5aa2	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
5	c1uokA_	Alignment		100.0	21	**PDB header:**glucosidase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of b. cereus oligo-1,6-glucosidase
6	c2gdvA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sucrose phosphorylase; **PDBTitle:** sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
7	c3edeB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
8	c3a47A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
9	c1m53A_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
10	c1zjaB_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
11	c1gviA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd

12	c3k8kB_	Alignment		100.0	20	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
13	c1jibA_	Alignment		100.0	20	**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.
14	c2zidA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dextran glucosidase; **PDBTitle:** crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
15	c1ea9D_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
16	c2ze0A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
17	c2d0gA_	Alignment		100.0	18	**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
18	c1wzaA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase a; **PDBTitle:** crystal structure of alpha-amylase from h.orenii
19	d1m53a2	Alignment		100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
20	c2wcsA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
21	c2ya1A_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
22	d1uoka2	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
23	c2ya0A_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
24	c3faxA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
25	d1r7aa2	Alignment	not modelled	100.0	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
26	c1lwhA_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
27	c2e8yA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
28	c3bmwA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor

29	c2vncB_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
30	c1qhoA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
31	c1tcmB_	Alignment	not modelled	100.0	17	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
32	c1bf2A_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
33	c2z1kA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
34	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
35	c1cygA_	Alignment	not modelled	100.0	21	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
36	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
37	c2wanA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
38	c3m07A_	Alignment	not modelled	100.0	17	**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.
39	c2wskA_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycogen debranching enzyme; **PDBTitle:** crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
40	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
41	c1ehaA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
42	c3amkA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
43	c2aaaA_	Alignment	not modelled	100.0	14	**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
44	d1lwha2	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
45	c3amlA_	Alignment	not modelled	100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
46	c2taaA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase (o-glycosyl) **Chain:** A: **PDB Molecule:**taka-amylase a; **PDBTitle:** structure and possible catalytic residues of taka-amylase a
47	d2fhfa5	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
48	d1wzla3	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
49	d1wzaa2	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	c2fhfA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
51	d1gvia3	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
52	c2dh3A_	Alignment	not modelled	100.0	12	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
53	c2x4bA_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin
54	d1cgta4	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
						Fold:TIM beta/alpha-barrel

55	d1ea9c3	Alignment	not modelled	100.0	21	**Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
56	d3bmva4	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
57	d1qhoa4	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
58	d1bf2a3	Alignment	not modelled	100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
59	d1j0ha3	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
60	c1gjuA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
61	d1pama4	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
62	c3dhuC_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
63	d1h3ga3	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
64	d1cxla4	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
65	d1ji1a3	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
66	c2by0A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
67	d1cyga4	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	d2guya2	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
69	d2aaaa2	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
70	d1m7xa3	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
71	c2qpuB_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme; **PDBTitle:** sugar tongs mutant s378p in complex with acarbose
72	c1wpcA_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltohexaosidase; **PDBTitle:** crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
73	c1e40A_	Alignment	not modelled	100.0	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
74	c1hvxA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** bacillus stearothermophilus alpha-amylase
75	c1ud8A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
76	d2bhua3	Alignment	not modelled	100.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
77	c1bagA_	Alignment	not modelled	100.0	15	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
78	d1eh9a3	Alignment	not modelled	100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
79	c1jaeA_	Alignment	not modelled	100.0	15	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
80	c3blpX_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
81	d1gjwa2	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
82	c1jdaA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase;

						PDBTitle: maltotetraose-forming exo-amylase
83	c1jd7A_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
84	c1gcyA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
85	d1ob0a2	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
86	c1mwoA_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase; **PDBTitle:** crystal structure analysis of the hyperthermostable2 pyrococus woesei alpha-amylase
87	c3bc9A_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** alpha-amylase b in complex with acarbose
88	c1iv8A_	Alignment	not modelled	100.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**maltooligosyl trehalose synthase; **PDBTitle:** crystal structure of maltooligosyl trehalose synthase
89	d1e43a2	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
90	d1ht6a2	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
91	d1avaa2	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
92	d1ud2a2	Alignment	not modelled	100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
93	d1hvxa2	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
94	d2gjpa2	Alignment	not modelled	100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	d1mxga2	Alignment	not modelled	100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
96	d2d3na2	Alignment	not modelled	100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
97	d1gcya2	Alignment	not modelled	100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
98	d1ua7a2	Alignment	not modelled	100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
99	d1jaea2	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
100	d1g94a2	Alignment	not modelled	100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
101	d1hx0a2	Alignment	not modelled	100.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
102	d3dhpa2	Alignment	not modelled	100.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
103	c3hjeA_	Alignment	not modelled	100.0	16	**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	15	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
105	d1iv8a2	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
106	c1bplA_	Alignment	not modelled	99.9	15	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
107	c3aicC_	Alignment	not modelled	99.8	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucosyltransferase-si; **PDBTitle:** crystal structure of glucansucrase from streptococcus mutans
108	c3hz3A_	Alignment	not modelled	99.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucansucrase; **PDBTitle:** lactobacillus reuteri n-terminally truncated glucansucrase2 gtf180(d1025n)-sucrose complex
109	d1g5aa1	Alignment	not modelled	99.1	34	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain

						Family:alpha-Amylases, C-terminal beta-sheet domain
110	d1uoka1	Alignment	not modelled	99.0	21	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
111	d1m53a1	Alignment	not modelled	99.0	13	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
112	c2xn1B_	Alignment	not modelled	98.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
113	d1j0ha2	Alignment	not modelled	98.5	9	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
114	d1wzla2	Alignment	not modelled	98.4	19	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
115	c3mi6A_	Alignment	not modelled	98.3	17	**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.
116	c3cc1B_	Alignment	not modelled	98.3	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
117	c2yfnA_	Alignment	not modelled	98.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
118	d1zy9a2	Alignment	not modelled	98.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
119	d2f2ha4	Alignment	not modelled	98.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
120	c1zy9A_	Alignment	not modelled	98.3	14	**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