







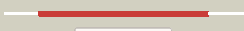















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1326c_glgB_1490123_1492318
Date	Wed Jul 31 22:05:42 BST 2019
Unique Job ID	938e9b25fa5b4e11

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k1dA	 Alignment		100.0	100	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
2	c5gquA	 Alignment		100.0	47	PDB header: transferase Chain: A: PDB Molecule: 1,4-alpha-glucan branching enzyme glgb; PDBTitle: crystal structure of branching enzyme from cyanothecce sp. atcc 51142
3	c3amlA	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
4	c1m7xC	 Alignment		100.0	52	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
5	c3amkA	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
6	c4bzyC	 Alignment		100.0	27	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of human glycogen branching enzyme (gbe1)
7	c2e8yA	 Alignment		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
8	c3wdjA	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: type i pullulanase; PDBTitle: crystal structure of pullulanase complexed with maltotetraose from2 anoxybacillus sp. Im18-11
9	c4j7rA	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: crystal structure of chlamydomonas reinhardtii isoamylase 1 (isa1)
10	c1bf2A	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
11	c5wvtA	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: pulullanase; PDBTitle: catalytic mechanism, cyclodextrin inhibition, and allosteric2 regulation of paenibacillus barengoltzii pullulanase

12	c2fhfA_	Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: crystal structure analysis of klebsiella pneumoniae pullulanase2 complexed with maltotetraose
13	c3faxA_	Alignment		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
14	c2vncB_	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: glycogen operon protein glgx; PDBTitle: crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
15	c2ya0A_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
16	c2ya1A_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: product complex of a multi-modular glycogen-degrading pneumococcal2 virulence factor spua
17	c2x4bA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: limit dextrinase; PDBTitle: barley limit dextrinase in complex with beta-cyclodextrin
18	c2wanA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
19	c2by0A_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
20	c3m07A_	Alignment		100.0	25	PDB header: unknown function Chain: A: PDB Molecule: putative alpha amylase; PDBTitle: 1.4 angstrom resolution crystal structure of putative alpha amylase2 from salmonella typhimurium.
21	c2wskA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
22	c1ehaA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase from2 sulfolobus solfataricus
23	c4aeeA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of maltogenic amylase from s.marinus
24	c1ea9D_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltodextrinase; PDBTitle: cyclomaltodextrinase
25	c1gviA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
26	c1jibA_	Alignment	not modelled	100.0	19	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.
27	c4aefB_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: neopullulanase (alpha-amylase ii); PDBTitle: the crystal structure of thermostable amylase from the pyrococcus
28	c5ot1A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase type ii, gh13 family; PDBTitle: the type iii pullulan hydrolase from thermococcus kodakarensis

29	c2d0gA	Alignment	not modelled	100.0	17	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
30	d1m7xa3	Alignment	not modelled	100.0	58	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
31	c3edeB	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltodextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
32	c1jgiA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of the active site mutant glu328gln of amylsucrase2 from neisseria polysaccharea in complex with the natural substrate3 sucrose
33	c3czkA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-sucrose2 complex
34	c4e2oA	Alignment	not modelled	100.0	19	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of alpha-amylase from geobacillus thermoleovorans,2 gta, complexed with acarbose
35	c3ucqA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of amylsucrase from deinococcus geothermalis
36	c3zoaB	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: trehalose synthase/amylase tres; PDBTitle: the structure of trehalose synthase (tres) of mycobacterium2 smegmatis in complex with acarbose
37	c4tvuA	Alignment	not modelled	100.0	24	PDB header: isomerase Chain: A: PDB Molecule: trehalose synthase; PDBTitle: crystal structure of trehalose synthase from deinococcus radiodurans2 reveals a closed conformation for catalysis of the intramolecular3 isomerization
38	c5x7uA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: trehalose synthase; PDBTitle: trehalose synthase from thermobaculum terrenum
39	c5ykbB	Alignment	not modelled	100.0	25	PDB header: isomerase Chain: B: PDB Molecule: trehalose synthase; PDBTitle: the n253f mutant structure of trehalose synthase from deinococcus2 radiodurans reveals an open active-site conformation
40	c4u33F	Alignment	not modelled	100.0	21	PDB header: transferase Chain: F: PDB Molecule: alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase; PDBTitle: structure of mtb glge bound to maltose
41	c4mb1A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase 1; PDBTitle: the structure of mall mutant enzyme g202p from bacillus subtilus
42	c2wcsA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
43	c4gkIA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of a noncanonic maltogenic alpha-amylase amyb from2 thermotoga neapolitana
44	c3zt5D	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glge isoform 1 from streptomyces coelicolor with maltose2 bound
45	c3a47A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
46	c5do8A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: lmo0184 protein; PDBTitle: 1.8 angstrom crystal structure of listeria monocytogenes lmo01842 alpha-1,6-glucosidase
47	c1uokA	Alignment	not modelled	100.0	19	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
48	c1wzaA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase a; PDBTitle: crystal structure of alpha-amylase from h.orenii
49	c6aavA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosyltransferase; PDBTitle: crystal structure of alpha-glucosyl transfer enzyme, xgta at 1.722 angstrom resolution
50	c1zjaB	Alignment	not modelled	100.0	21	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	c5brgA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 13; PDBTitle: crystal structure of bacillus licheniformis trehalose-6-phosphate2 hydrolase (trea)
52	c5m99A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization
53	c5h06C	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: C: PDB Molecule: amyp; PDBTitle: crystal structure of amyp in complex with maltose
						PDB header: isomerase

54	c1m53A_	Alignment	not modelled	100.0	18	Chain: A; PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
55	c2aaaA_	Alignment	not modelled	100.0	22	PDB header: glycosidase Chain: A; PDB Molecule: alpha-amylase; PDBTitle: calcium binding in alpha-amylases: an x-ray diffraction study at 2.12 angstroms resolution of two enzymes from aspergillus
56	c2zidA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
57	c2ze0A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
58	c3wy3A_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase mutant d202n in complex with2 glucose and glycerol
59	c4aieA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A; PDB Molecule: glucan 1,6-alpha-glucosidase; PDBTitle: structure of glucan-1,6-alpha-glucosidase from lactobacillus2 acidophilus ncfm
60	d2fhfa5	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	d1bf2a3	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
62	c2z1kA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
63	c4jciA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A; PDB Molecule: cyclomaltodextrin glucanotransferase; PDBTitle: crystal structure of alpha-cgt from paenibacillus macerans at 1.72 angstrom resolution
64	c5zxbB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B; PDB Molecule: cyclic maltosyl-maltose hydrolase; PDBTitle: cyclic alpha-maltosyl-(1->6)-maltose hydrolase from arthrobacter2 globiformis, ligand-free form
65	c1tcmB_	Alignment	not modelled	100.0	19	PDB header: glycosyltransferase Chain: B; PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
66	c3vm7A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A; PDB Molecule: alpha-amylase; PDBTitle: structure of an alpha-amylase from malbranchea cinnamomea
67	d1g5aa2	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
68	c5zcbA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase
69	c3bmwA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A; PDB Molecule: cyclomaltodextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
70	c1qhoA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A; PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
71	c3k8kB_	Alignment	not modelled	100.0	23	PDB header: membrane protein Chain: B; PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
72	c3dhuC_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: C; PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus plantarum
73	c1ud8A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
74	c2taaA_	Alignment	not modelled	100.0	21	PDB header: hydrolase (o-glycosyl) Chain: A; PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
75	c1cygA_	Alignment	not modelled	100.0	18	PDB header: glycosyltransferase Chain: A; PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
76	c1wpcA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaoside-producing amylase complexed with2 pseudo-maltononase
77	c1e40A_	Alignment	not modelled	100.0	15	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
78	c4jcmA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A; PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: crystal structure of gamma-cgtase from alkalophilic bacillus clarkii2 at 1.65 angstrom resolution
79	c1jd7A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
						Fold: TIM beta/alpha-barrel

80	d2bhua3	Alignment	not modelled	100.0	27	Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
81	c1lwhA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
82	c1hvxA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearothermophilus alpha-amylase
83	c1gjuA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: maltodextrin glycosyltransferase; PDBTitle: maltosyltransferase from thermotoga maritima
84	c6gyaA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: a-amylase; PDBTitle: amylase in complex with branched ligand
85	c2dh3A	Alignment	not modelled	100.0	20	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
86	c1jaeA	Alignment	not modelled	100.0	21	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
87	d1wzla3	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
88	d1j0ha3	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	c3blpX	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase
90	d1eh9a3	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	d1gvia3	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
92	c1bagA	Alignment	not modelled	100.0	18	PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
93	d1m53a2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	d1uoka2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	d1pama4	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
96	d1ea9c3	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
97	d2aaaa2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	d1lwha2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
99	c6irtA	Alignment	not modelled	100.0	20	PDB header: membrane protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: human lat1-4f2hc complex bound with bch
100	d1h3ga3	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
101	c2qpuB	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
102	d3bmva4	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
103	d2guya2	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
104	d1csla4	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
105	d1gjwa2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
106	d1cyga4	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
107	d1qhoa4	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

108	c2gdvA	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: sucrose phosphorylase; PDBTitle: sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
109	d1cgta4	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
110	d1wzaa2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
111	c1gcyA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
112	d1ji1a3	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
113	c1jdaA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
114	c5bn7A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: maltodextrin glucosidase; PDBTitle: crystal structure of maltodextrin glucosidase from e.coli at 3.7 a2 resolution
115	c3bc9A	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: alpha-amylase b in complex with acarbose
116	c1mwoA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
117	d1hvxa2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
118	d1ud2a2	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	d1ob0a2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
120	d1e43a2	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain