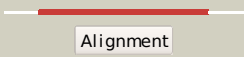

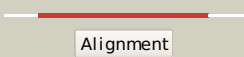

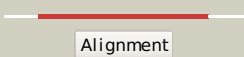

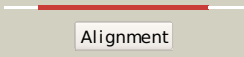

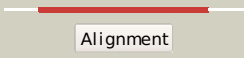

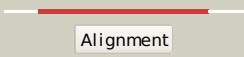

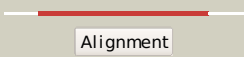

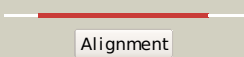

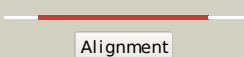

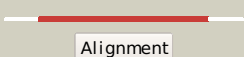

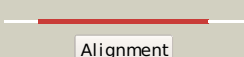



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1uokA_	 Alignment		100.0	45	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
2	c1m53A_	 Alignment		100.0	40	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
3	c1zjaB_	 Alignment		100.0	38	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
4	c3a47A_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
5	c2ze0A_	 Alignment		100.0	44	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
6	c2zidA_	 Alignment		100.0	44	PDB header: hydrolase Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
7	d1uoka2	 Alignment		100.0	48	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
8	d1m53a2	 Alignment		100.0	43	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
9	c3k8kB_	 Alignment		100.0	31	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
10	c1jgiA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of the active site mutant glu328gln of2 amylsucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
11	c1wzaA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase a; PDBTitle: crystal structure of alpha-amylase from h.orenii

12	c3edeB_	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltoextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
13	c3ucqA_	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of amylsucrase from deinococcus geothermalis
14	c1jibA_	Alignment		100.0	32	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.
15	c1gviA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
16	c3czkA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
17	c1ea9D_	Alignment		100.0	29	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltoextrinase; PDBTitle: cyclomaltoextrinase
18	c1lwhA_	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
19	c2d0gA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase i; PDBTitle: crystal structure of thermoactinomyces vulgaris r-47 alpha-2 amylase 1 (tva1) mutant d356n/e396q complexed with p5, a3 pullulan model oligosaccharide
20	c2wcsA_	Alignment		100.0	26	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	20	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
22	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
23	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
24	c1bf2A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
25	c3bmwA_	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: cyclomaltoextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanrobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
26	c1tcmB_	Alignment	not modelled	100.0	25	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
27	c1qhoA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
28	c1cygA_	Alignment	not modelled	100.0	25	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)

29	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
30	c2e8yA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: amylase protein; PDBTitle: crystal structure of pullulanase type i from bacillus subtilis str.2 168
31	c1m7xC_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
32	c2z1kA_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
33	c2vncB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: glycogen operon protein glgx; PDBTitle: crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
34	c3m07A_	Alignment	not modelled	100.0	20	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.
35	c3k1dA_	Alignment	not modelled	100.0	21	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
36	c2fhfA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
37	d1lwah2	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
38	d1wzaa2	Alignment	not modelled	100.0	33	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
39	c3amkA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
40	c2aaaA_	Alignment	not modelled	100.0	21	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
41	c2wanA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
42	d1g5aa2	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
43	d2fhfa5	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
44	c2taaA_	Alignment	not modelled	100.0	24	PDB header: hydrolase (o-glycosyl) Chain: A: PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
45	c3zt5D_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glge isoform 1 from streptomyces coelicolor with maltose2 bound
46	c2dh3A_	Alignment	not modelled	100.0	26	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
47	c3amlA_	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
48	c2gdvA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: sucrose phosphorylase; PDBTitle: sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
49	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
50	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
51	c2by0A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
52	d1gvia3	Alignment	not modelled	100.0	32	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
53	c1gjuA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: malto-dextrin glycosyltransferase; PDBTitle: maltosyltransferase from thermotoga maritima
54	d1cgta4	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
						Fold: TIM beta/alpha-barrel

55	d1wzla3	Alignment	not modelled	100.0	36	Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
56	d1pama4	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
57	d1h3ga3	Alignment	not modelled	100.0	28	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
58	d3bmva4	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
59	d1cxla4	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
60	d1qhoa4	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	c3dhuC_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus2 plantarum
62	d1ea9c3	Alignment	not modelled	100.0	32	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
63	d2guya2	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
64	d1bf2a3	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
65	d1j0ha3	Alignment	not modelled	100.0	33	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
66	d1cyga4	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
67	d1ji1a3	Alignment	not modelled	100.0	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
68	d2aaaa2	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
69	c2qpuB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
70	d1m7xa3	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
71	d2bhua3	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
72	c1e40A_	Alignment	not modelled	100.0	23	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
73	c1hvxA_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearothermophilus alpha-amylase
74	c1wpcA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltonaose
75	c1ud8A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amy38 with lithium ion
76	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
77	d1eh9a3	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
78	d1gjwa2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
79	d1r7aa2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
80	c1jaeA_	Alignment	not modelled	100.0	17	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
81	c3blpX_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase
82	c1jd7A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2

						pseudoalteromonas haloplantcis alpha-amylase
83	c1jdaA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
84	c1gcyA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
85	c3bc9A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: alpha-amylase b in complex with acarbose
86	d1avaa2	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
87	d1ob0a2	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
88	c1mw0A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
89	d1e43a2	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
90	d1ht6a2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	d2gjp2	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
92	d1ud2a2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
93	d1mxga2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	d1gcy2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	d1hvxa2	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
96	d2d3na2	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
97	d1ua7a2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	d1jaea2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
99	d1hx0a2	Alignment	not modelled	100.0	16	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	d3dhpa2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
102	c1iv8A_	Alignment	not modelled	100.0	23	PDB header: isomerase Chain: A: PDB Molecule: maltotigosyl trehalose synthase; PDBTitle: crystal structure of maltotigosyl trehalose synthase
103	c3hieA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: 704aa long hypothetical glycosyltransferase; PDBTitle: crystal structure of sulfobolus tokodaii hypothetical2 maltotigosyl trehalose synthase
104	c1bplB_	Alignment	not modelled	100.0	24	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	18	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
107	c3aicC_	Alignment	not modelled	99.5	21	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase-si; PDBTitle: crystal structure of glucansucrase from streptococcus mutans
108	d1uoka1	Alignment	not modelled	99.3	31	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
109	d1m53a1	Alignment	not modelled	99.3	23	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain

110	c2xn1B_	Alignment	not modelled	99.2	14	PDB header: hydrolase Chain: B: PDB Molecule: alpha-galactosidase; PDBTitle: structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
111	c3cc1B_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-n-acetyl galactosaminidase; PDBTitle: crystal structure of a putative alpha-n-acetyl galactosaminidase2 (bh1870) from bacillus halodurans c-125 at 2.00 a resolution
112	c3mi6A_	Alignment	not modelled	98.9	14	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.
113	c1uasA_	Alignment	not modelled	98.9	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of rice alpha-galactosidase
114	c2yfnA_	Alignment	not modelled	98.8	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase-sucrose kinase agask; PDBTitle: galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
115	d2f2ha4	Alignment	not modelled	98.7	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: YicI catalytic domain-like
116	d1eswa_	Alignment	not modelled	98.7	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
117	c3hz3A_	Alignment	not modelled	98.7	23	PDB header: transferase Chain: A: PDB Molecule: glucansucrase; PDBTitle: lactobacillus reuteri n-terminally truncated glucansucrase2_gtf180(d1025n)-sucrose complex
118	c3a5vA_	Alignment	not modelled	98.6	11	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of alpha-galactosidase i from mortierella vinacea
119	d1j0ha2	Alignment	not modelled	98.6	17	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
120	d1m7xa2	Alignment	not modelled	98.6	17	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain