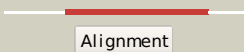
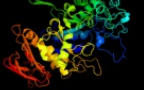
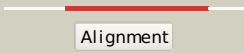







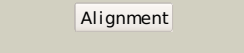

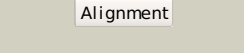

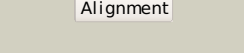



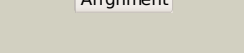

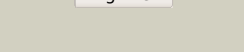












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3blpX_	 Alignment		100.0	16	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase
2	c1jaeA_	 Alignment		100.0	18	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
3	c1jd7A_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplantis alpha-amylase
4	c1tcmB_	 Alignment		100.0	15	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
5	c1qhoA_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
6	c1bagA_	 Alignment		100.0	21	PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
7	c3edeB_	 Alignment		100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltoextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
8	c3bmwA_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: cyclomaltoextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
9	c1cygA_	 Alignment		100.0	13	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
10	d1hx0a2	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
11	c1wpcA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose

12	d3dhpA2	Alignment		100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
13	c1ud8A_	Alignment		100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
14	c1jibA_	Alignment		100.0	15	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	d1jaea2	Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
16	c1gviA_	Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
17	d1g94a2	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
18	c1e40A_	Alignment		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
19	c1ea9D_	Alignment		100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltoextrinase; PDBTitle: cyclomaltoextrinase
20	c1hvxA_	Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearothermophilus alpha-amylase
21	c2d0gA_	Alignment	not modelled	100.0	14	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
22	c1mwoA_	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
23	c2aaaA_	Alignment	not modelled	100.0	17	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
24	c2wcsA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
25	c2taaA_	Alignment	not modelled	100.0	17	PDB header: hydrolase (o-glycosyl) Chain: A: PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
26	d1ua7a2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
27	c3bc9A_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: alpha-amylase b in complex with acarbose
28	c1jdaA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase

29	c2z1kA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
30	c2wskA	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
31	c1gcyA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
32	d1cgtA4	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
33	d3bmva4	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
34	c2qpuB	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
35	d1qhoa4	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
36	c1bf2A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
37	c3k8kB	Alignment	not modelled	100.0	18	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
38	c1m7xC	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
39	d1pama4	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
40	c1wzaA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase a; PDBTitle: crystal structure of alpha-amylase from h.orenii
41	d1cxlA4	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
42	c1jgiA	Alignment	not modelled	100.0	13	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
43	d1cyga4	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
44	c2wanA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
45	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
46	c2e8yA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: amyx protein; PDBTitle: crystal structure of pullulanase type i from bacillus subtilis str.2 168
47	d2aaaa2	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
48	c3amkA	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
49	c3dhuC	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus2 plantarum
50	d1wzla3	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
51	c3amIA	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
52	d1ob0a2	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
53	c1uokA	Alignment	not modelled	100.0	15	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
54	d2guya2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

55	c1m53A	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
56	c2ya0A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
57	c2ze0A	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
58	c3czkA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
59	d1ud2a2	Alignment	not modelled	100.0	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
60	c2ya1A	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
61	d1gcya2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
62	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
63	c3k1dA	Alignment	not modelled	100.0	15	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
64	c1zjaB	Alignment	not modelled	100.0	16	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
65	c3faxA	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein; PDBTitle: the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
66	d2gipa2	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
67	c3a47A	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
68	d1mxga2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
69	d1hvx2	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
70	d1h3ga3	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
71	d1gvia3	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
72	d1e43a2	Alignment	not modelled	100.0	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
73	c2fhfA	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
74	c2zidA	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
75	d1j0ha3	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
76	d2fhfa5	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
77	d1uoka2	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
78	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
79	d1m53a2	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
80	d1jila3	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
81	d2d3na2	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases

						Family: Amylase, catalytic domain
82	c3m07A_	Alignment	not modelled	100.0	18	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.
83	c1lwhA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
84	d1ea9c3	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
85	d1g5aa2	Alignment	not modelled	100.0	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
86	d1avaa2	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
87	c1ehaA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase2 from sulfobolus solfataricus
88	d1ht6a2	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	c2gdvA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: sucrose phosphorylase; PDBTitle: sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
90	d1bf2a3	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	c1gjuA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: maltodextrin glycosyltransferase; PDBTitle: maltosyltransferase from thermotoga maritima
92	d1wzaa2	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
93	c2dh3A_	Alignment	not modelled	100.0	17	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
94	d1lwha2	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	c2by0A_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
96	d1m7xa3	Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
97	d1eh9a3	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	d2bhua3	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
99	d1r7aa2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
100	d1gjwa2	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
101	c1iv8A_	Alignment	not modelled	100.0	14	PDB header: isomerase Chain: A: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: crystal structure of maltooligosyl trehalose synthase
102	c1bplB_	Alignment	not modelled	100.0	15	PDB header: glycosyltransferase Chain: B: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
103	c3hjeA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: 704aa long hypothetical glycosyltransferase; PDBTitle: crystal structure of sulfobolus tokodaii hypothetical2 maltooligosyl trehalose synthase
104	d1iv8a2	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
105	c1bplA_	Alignment	not modelled	99.9	12	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
106	c3aicC_	Alignment	not modelled	99.8	11	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase-si; PDBTitle: crystal structure of glucansucrase from streptococcus mutans
107	d1g94a1	Alignment	not modelled	99.5	28	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
108	d3dhpa1	Alignment	not modelled	99.5	19	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain

					Family: alpha-Amylases, C-terminal beta-sheet domain
109	dlhx0a1	Alignment	not modelled	99.5	20 Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
110	dlua7a1	Alignment	not modelled	99.5	28 Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
111	dljaea1	Alignment	not modelled	99.4	25 Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
112	c3hz3A	Alignment	not modelled	99.3	14 PDB header: transferase Chain: A: PDB Molecule: glucansucrase; PDBTitle: lactobacillus reuteri n-terminally truncated glucansucrase2 gtf180(d1025n)-sucrose complex
113	dlwzla2	Alignment	not modelled	99.1	18 Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
114	dljila2	Alignment	not modelled	99.1	14 Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
115	c3cc1B	Alignment	not modelled	98.7	12 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
116	dlqhoa3	Alignment	not modelled	98.6	15 Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
117	dlcgta3	Alignment	not modelled	98.6	18 Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
118	d2f2ha4	Alignment	not modelled	98.5	17 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: YicL catalytic domain-like
119	c3a5vA	Alignment	not modelled	98.5	14 PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of alpha-galactosidase i from mortierella vinacea
120	cluasA	Alignment	not modelled	98.4	17 PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of rice alpha-galactosidase