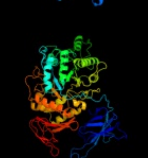


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wskA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
2	c2vncB_	 Alignment		100.0	43	PDB header: hydrolase Chain: B: PDB Molecule: glycogen operon protein glgx; PDBTitle: crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
3	c1bf2A_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
4	c2fhfA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
5	c2e8yA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: amyx protein; PDBTitle: crystal structure of pullulanase type i from bacillus subtilis str.2 168
6	c2x4bA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: limit dextrinase; PDBTitle: barley limit dextrinase in complex with beta-cyclodextrin
7	c2wanA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
8	c3faxA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein; PDBTitle: the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
9	c2ya1A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
10	c2ya0A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
11	c3k1dA_	 Alignment		100.0	23	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

12	c3amlA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
13	c3amkA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
14	c3m07A_	Alignment		100.0	27	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.
15	c1m7xC_	Alignment		100.0	21	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
16	c1ehaA_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
17	c2by0A_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
18	c1ea9D_	Alignment		100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltoextrinase; PDBTitle: cyclomaltoextrinase
19	c1jibA_	Alignment		100.0	22	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.
20	c1gviA_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
21	c2d0gA_	Alignment	not modelled	100.0	20	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	d2fhfa5	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
23	d1bf2a3	Alignment	not modelled	100.0	34	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
24	c3edeB_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltoextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
25	c3czkA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
26	c1jgiA_	Alignment	not modelled	100.0	20	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
27	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
28	c3bmwA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: cyclomaltoextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from

					thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
29	c2wcsA	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
30	c3k8kB	Alignment	not modelled	100.0	19 PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
31	c1tcmB	Alignment	not modelled	100.0	22 PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
32	c1qhoA	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
33	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)
34	c3a47A	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
35	c3uccqA	Alignment	not modelled	100.0	19 PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of amylsucrase from deinococcus geothermalis
36	c1m53A	Alignment	not modelled	100.0	20 PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
37	c1zjaB	Alignment	not modelled	100.0	23 PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
38	c1uokA	Alignment	not modelled	100.0	18 PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
39	c1wzaA	Alignment	not modelled	100.0	20 PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase a; PDBTitle: crystal structure of alpha-amylase from h.orenii
40	c1gjuA	Alignment	not modelled	100.0	20 PDB header: transferase Chain: A: PDB Molecule: maltoedextrin glycosyltransferase; PDBTitle: maltosyltransferase from thermotoga maritima
41	d1g5aa2	Alignment	not modelled	100.0	20 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
42	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
43	c2aaaA	Alignment	not modelled	100.0	15 PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: calcium binding in alpha-amylases: an x-ray diffraction2 study at 2.1 angstroms resolution of two enzymes from3 aspergillus
44	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
45	c2ze0A	Alignment	not modelled	100.0	17 PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
46	c2z1kA	Alignment	not modelled	100.0	21 PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of tha1563 from thermus thermophilus hb8
47	d3bmva4	Alignment	not modelled	100.0	17 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
48	d1m7xa3	Alignment	not modelled	100.0	21 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
49	d1gvia3	Alignment	not modelled	100.0	26 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
50	d1wzla3	Alignment	not modelled	100.0	25 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
51	d2bhua3	Alignment	not modelled	100.0	25 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
52	c3dhuC	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus2 plantarum
53	d1ea9c3	Alignment	not modelled	100.0	21 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
54	d1pama4	Alignment	not modelled	100.0	21 Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
					Fold: TIM beta/alpha-barrel

55	d1j0ha3	Alignment	not modelled	100.0	24	Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
56	c1lwhA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
57	d1csla4	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
58	d1m53a2	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
59	d1qhoa4	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
60	d2guya2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	d1cyga4	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
62	d2aaaa2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
63	d1cgta4	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
64	d1gja2	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
65	d1eh9a3	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
66	d1uoka2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
67	d1lwha2	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
68	d1h3ga3	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
69	c1bagA	Alignment	not modelled	100.0	16	PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
70	c1jaeA	Alignment	not modelled	100.0	16	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
71	d1wzaa2	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
72	c1ud8A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
73	c1e40A	Alignment	not modelled	100.0	19	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	c2gdvA	Alignment	not modelled	100.0	12	PDB header: transferase Chain: A: PDB Molecule: sucrose phosphorylase; PDBTitle: sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
75	c1hvxA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearotherophilus alpha-amylase
76	c2qpuB	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
77	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 haloplantis alpha-amylase
78	c3blpX	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase
79	c1wpcA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaoase-producing amylase complexed with2 pseudo-maltononaose
80	d1jila3	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
81	c2dh3A	Alignment	not modelled	100.0	18	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
82	c1gcvA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase;

82	c1gcya_	Alignment	not modelled	100.0	17	PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
83	c1jdaA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
84	d1r7aa2	Alignment	not modelled	100.0	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
85	c3bc9A_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: alpha-amylase b in complex with acarbose
86	c1mwoA_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
87	d1ua7a2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
88	d1gcya2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	d1avaa2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
90	d1e43a2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	d1ob0a2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
92	d2gjpa2	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
93	d1ud2a2	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	d1jaea2	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	d1hvxa2	Alignment	not modelled	100.0	20	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	d1g94a2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	d1ht6a2	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
99	d1mxga2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
100	d1hx0a2	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
101	d3dhp2	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
102	c1iv8A_	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: A: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: crystal structure of maltooligosyl trehalose synthase
103	c3hjeA_	Alignment	not modelled	100.0	20	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	14	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	25	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
107	d1bf2a1	Alignment	not modelled	99.9	34	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
108	d2fhfa1	Alignment	not modelled	99.8	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
109	d1m7xa1	Alignment	not modelled	99.7	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes

110	c3aicC_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: C: PDB Molecule: glucosyltransferase-si; PDBTitle: crystal structure of glucansucrase from streptococcus mutans
111	d2bhua1	Alignment	not modelled	99.6	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
112	d1eh9a1	Alignment	not modelled	99.6	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
113	c3hz3A_	Alignment	not modelled	99.2	14	PDB header: transferase Chain: A: PDB Molecule: glucansucrase; PDBTitle: lactobacillus reuteri n-terminally truncated glucansucrase2_gtf180(d1025n)-sucrose complex
114	c3lppA_	Alignment	not modelled	98.9	15	PDB header: hydrolase Chain: A: PDB Molecule: sucrase-isomaltase; PDBTitle: crystal complex of n-terminal sucrase-isomaltase with kotalanol
115	c2qmjA_	Alignment	not modelled	98.8	15	PDB header: hydrolase Chain: A: PDB Molecule: maltase-glucoamylase, intestinal; PDBTitle: crystal structure of the n-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
116	c3cc1B_	Alignment	not modelled	98.8	11	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-n-acetylglactosaminidase; PDBTitle: crystal structure of a putative alpha-n-acetylglactosaminidase2 (bh1870) from bacillus halodurans c-125 at 2.00 a resolution
117	d2f2ha4	Alignment	not modelled	98.8	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: YicI catalytic domain-like
118	d1eswa_	Alignment	not modelled	98.7	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	c3topA_	Alignment	not modelled	98.5	14	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: maltase-glucoamylase, intestinal; PDBTitle: crystal structure of the c-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
120	c2yfnA_	Alignment	not modelled	98.5	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase-sucrose kinase agask; PDBTitle: galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask