



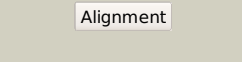


Phyre2

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 Description RVBD1563c_(treY)_1767141_1769438
 Date Fri Aug 2 13:30:15 BST 2019
 Unique Job ID 198ff193eb0bf36f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zcrB_	 Alignment		100.0	36	PDB header: hydrolase Chain: B: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: dsm5389 glycosyltrehalose synthase
2	c3hjeA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: 704aa long hypothetical glycosyltransferase; PDBTitle: crystal structure of sulfolobus tokodaii hypothetical maltooligosyl2 trehalose synthase
3	d1iv8a2	 Alignment		100.0	34	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
4	c1iv8A_	 Alignment		100.0	34	PDB header: isomerase Chain: A: PDB Molecule: maltooligosyl trehalose synthase; PDBTitle: crystal structure of maltooligosyl trehalose synthase
5	c5ot1A_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase type ii, gh13 family; PDBTitle: the type iii pullulan hydrolase from thermococcus kodakarensis
6	c1gviA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
7	c4aeeA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of maltogenic amylase from s.marinus
8	c1ea9D_	 Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltodextrinase; PDBTitle: cyclomaltodextrinase
9	c1jibA_	 Alignment		100.0	31	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.
10	c3edeB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltodextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
11	c4aefB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: neopullulanase (alpha-amylase ii); PDBTitle: the crystal structure of thermostable amylase from the pyrococcus

12	c1tcmB_	Alignment		100.0	24	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
13	c2z1kA_	Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
14	c2wcsA_	Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
15	c2d0gA_	Alignment		100.0	27	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
16	c5zxbB_	Alignment		100.0	26	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
17	c1qhoA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
18	c2gdvA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: sucrose phosphorylase; PDBTitle: sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
19	d1gvia3	Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
20	c3bmwA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: cyclomaltodextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
21	c1cygA_	Alignment	not modelled	100.0	31	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
22	c4jcmA_	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: crystal structure of gamma-cgtase from alkaliphilic bacillus clarkii2 at 1.65 angstrom resolution
23	c4jclA_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: cyclomaltodextrin glucanotransferase; PDBTitle: crystal structure of alpha-cgt from paenibacillus macerans at 1.72 angstrom resolution
24	c3vm7A_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of an alpha-amylase from malbranchea cinnamomea
25	c2qpuB_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
26	c4u33F_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: F: PDB Molecule: alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase; PDBTitle: structure of mtb glge bound to maltose
27	c3ucqA_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: amylosucrase; PDBTitle: crystal structure of amylosucrase from deinococcus geothermalis
28	c3zt5D_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glge isoform 1 from streptomyces coelicolor with maltose2 bound
						Fold: TIM beta/alpha-barrel

29	d1j0ha3	Alignment	not modelled	100.0	29	Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
30	d1wzla3	Alignment	not modelled	100.0	34	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
31	c2aaaA	Alignment	not modelled	100.0	26	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
32	c1wzaA	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase a; PDBTitle: crystal structure of alpha-amylase from h.oreonii
33	c1m53A	Alignment	not modelled	100.0	21	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
34	c4e2oA	Alignment	not modelled	100.0	29	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	c2taaA	Alignment	not modelled	100.0	23	PDB header: hydrolase (o-glycosyl) Chain: A: PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
36	d2guya2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
37	d1pama4	Alignment	not modelled	100.0	32	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
38	d1cgtA4	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
39	d3bmva4	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
40	c3k8kB	Alignment	not modelled	100.0	25	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
41	d2aaaa2	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
42	d1qhoa4	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
43	c4gkIA	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of a noncanonic maltogenic alpha-amylase amyb from2 thermotoga neapolitana
44	d1cxa4	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
45	d1cyga4	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
46	c1lwhA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
47	c1jaeA	Alignment	not modelled	100.0	20	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
48	c5wvtA	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: catalytic mechanism, cyclodextrin inhibition, and allosteric2 regulation of paenibacillus barengoltzii pullulanase
49	c3wdjA	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: type i pullulanase; PDBTitle: crystal structure of pullulanase complexed with maltotetraose from2 anoxybacillus sp. lm18-11
50	d1ea9c3	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
51	c1jgiA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: amylосуcrase; PDBTitle: crystal structure of the active site mutant glu328gln of amylосуcrase2 from neisseria polysaccharea in complex with the natural substrate3 sucrose
52	c2wskA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
53	d1j1a3	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
54	d1m53a2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
55	d1g5aa2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

56	c1m7xC	Alignment	not modelled	100.0	22	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
57	c2wanA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
58	d1uoka2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
59	c3faxA	Alignment	not modelled	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
60	c3dhuC	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus plantarum
61	c5m99A	Alignment	not modelled	100.0	25	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
62	c3zoaB	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: trehalose synthase/amyase tres; PDBTitle: the structure of trehalose synthase (tres) of mycobacterium2 smegmatis in complex with acarbose
63	c3k1dA	Alignment	not modelled	100.0	25	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	c3czkA	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-sucrose2 complex
65	d1m7xa3	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
66	d1h3ga3	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
67	c4tvuA	Alignment	not modelled	100.0	26	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
68	d1r7aa2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
69	d1ob0a2	Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
70	c5h06C	Alignment	not modelled	100.0	32	PDB header: hydrolase Chain: C: PDB Molecule: amyp; PDBTitle: crystal structure of amyp in complex with maltose
71	c1wpcA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaoside-producing amylase complexed with2 pseudo-maltonaose
72	c5gquA	Alignment	not modelled	100.0	22	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
73	c5x7uA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: trehalose synthase; PDBTitle: trehalose synthase from thermobaculum terrenum
74	c3a47A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
75	d1hvxa2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
76	c4aieA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,6-alpha-glucosidase; PDBTitle: structure of glucan-1,6-alpha-glucosidase from lactobacillus2 acidophilus ncfm
77	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
78	c1jdaA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
79	c2zidA	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
80	d1ud2a2	Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
81	d1gcya2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

82	d1ht6a2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
83	c1ud8A	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
84	c1uokA	Alignment	not modelled	100.0	23	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
85	d2d3na2	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
86	d1lwha2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
87	c5do8A	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: lmo0184 protein; PDBTitle: 1.8 angstrom crystal structure of listeria monocytogenes lmo01842 alpha-1,6-glucosidase
88	c4mb1A	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase 1; PDBTitle: the structure of mall mutant enzyme g202p from bacillus subtilus
89	d2gja2	Alignment	not modelled	100.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
90	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)
91	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
92	c1jd7A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
93	c5brqA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 13; PDBTitle: crystal structure of bacillus licheniformis trehalose-6-phosphate2 hydrolase (trea)
94	c1hvxA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearothermophilus alpha-amylase
95	c2ze0A	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
96	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
97	c2dh3A	Alignment	not modelled	100.0	25	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
98	c6gyaA	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: a-amylase; PDBTitle: amylase in complex with branched ligand
99	d1e43a2	Alignment	not modelled	100.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
100	c1ehaA	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase from2 sulfolobus solfataricus
101	c3wy3A	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase mutant d202n in complex with2 glucose and glycerol
102	d1avaa2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
103	c5zcbA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase
104	c3m07A	Alignment	not modelled	100.0	21	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.
105	c5ykbB	Alignment	not modelled	100.0	27	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
106	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
107	d1wzaa2	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
108	c2ya1A	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: product complex of a multi-modular glycogen-degrading pneumococcal2 virulence factor spua

109	c1gjuA	Alignment	not modelled	100.0	29	PDB header: transferase Chain: A: PDB Molecule: maltodextrin glycosyltransferase; PDBTitle: maltosyltransferase from thermotoga maritima
110	d1g94a2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
111	d1ua7a2	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
112	c4bzyC	Alignment	not modelled	100.0	22	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of human glycogen branching enzyme (gbe1)
113	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
114	c1bf2A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
115	c2ya0A	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
116	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
117	d2fhfa5	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
118	d2bhua3	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	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
120	d1eh9a3	Alignment	not modelled	100.0	30	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain