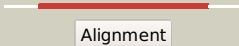



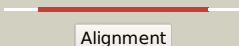

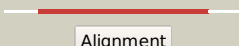

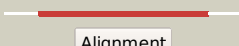

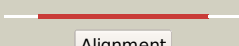

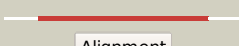








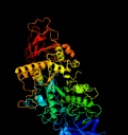




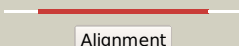
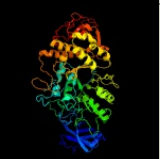
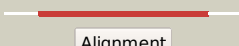
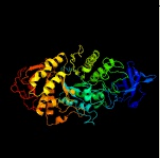
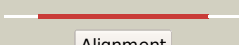
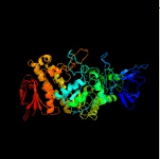
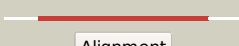


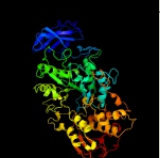

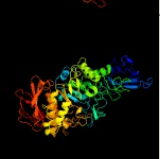

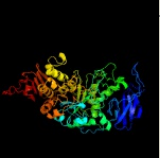
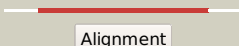


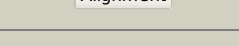
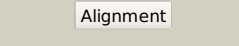


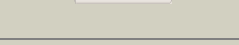


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1564c_(treX)_1769442_1771607
Date	Fri Aug 2 13:30:15 BST 2019
Unique Job ID	6dccc64ee3c9c343

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j7rA_	 Alignment		100.0	41	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: crystal structure of chlamydomonas reinhardtii isoamylase 1 (isa1)
2	c2vncB_	 Alignment		100.0	51	PDB header: hydrolase Chain: B: PDB Molecule: glycogen operon protein glgx; PDBTitle: crystal structure of glycogen debranching enzyme trex from2 sulfobolus solfataricus
3	c2wskA_	 Alignment		100.0	46	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
4	c1bf2A_	 Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
5	c2x4bA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: limit dextrinase; PDBTitle: barley limit dextrinase in complex with beta-cyclodextrin
6	c2fhfA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: crystal structure analysis of klebsiella pneumoniae pullulanase2 complexed with maltotetraose
7	c3wdjA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: type i pullulanase; PDBTitle: crystal structure of pullulanase complexed with maltotetraose from2 anoxybacillus sp. Im18-11
8	c2e8yA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: amylx protein; PDBTitle: crystal structure of pullulanase type i from bacillus subtilis str.2 168
9	c5wvtA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: catalytic mechanism, cyclodextrin inhibition, and allosteric2 regulation of paenibacillus barengoltzii pullulanase
10	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
11	c2ya1A_	 Alignment		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

12	c2wanA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
13	c2ya0A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
14	c5gquA_	 Alignment		100.0	19	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
15	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
16	c3amkA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
17	c3am1A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
18	c4bzyC_	 Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of human glycogen branching enzyme (gbe1)
19	c1m7xC_	 Alignment		100.0	19	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
20	c3m07A_	 Alignment		100.0	26	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	c2by0A_	 Alignment	not modelled	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
22	c1ehaA_	 Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase from2 sulfobolus solfataricus
23	c1ea9D_	 Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltodextrinase; PDBTitle: cyclomaltodextrinase
24	c1jibA_	 Alignment	not modelled	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.
25	c1gviA_	 Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
26	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 (tva1) mutant d356n/e396q complexed with p5, a3 pullulan model oligosaccharide
27	c5ot1A_	 Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase type ii, gh13 family; PDBTitle: the type iii pullulan hydrolase from thermococcus kodakarensis
28	d1bf2a3	 Alignment	not modelled	100.0	38	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

29	d2fhfa5	Alignment	not modelled	100.0	28	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
30	c4aeeA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of maltogenic amylase from s.marinus
31	c4aefB	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: neopullulanase (alpha-amylase ii); PDBTitle: the crystal structure of thermostable amylase from the pyrococcus
32	c3edeB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltodextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
33	c4u33F	Alignment	not modelled	100.0	16	PDB header: transferase Chain: F: PDB Molecule: alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase; PDBTitle: structure of mtb glge bound to maltose
34	c3czkA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-sucrose2 complex
35	c1jgiA	Alignment	not modelled	100.0	18	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
36	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
37	c3zoaB	Alignment	not modelled	100.0	19	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
38	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
39	c5x7uA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: trehalose synthase; PDBTitle: trehalose synthase from thermobaculum terrenum
40	c3ucqA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of amylsucrase from deinococcus geothermalis
41	c4tvuA	Alignment	not modelled	100.0	20	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
42	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)
43	c5ykbB	Alignment	not modelled	100.0	19	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
44	c1zjaB	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
45	c1uokA	Alignment	not modelled	100.0	20	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
46	c3a47A	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
47	c3k8kB	Alignment	not modelled	100.0	22	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
48	c5m99A	Alignment	not modelled	100.0	20	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
49	c1m53A	Alignment	not modelled	100.0	19	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
50	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
51	c4jclA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: cyclomaltodextrin glucanotransferase; PDBTitle: crystal structure of alpha-cgt from paenibacillus macerans at 1.72 angstrom resolution
52	d1g5aa2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
53	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 subtilis
						PDB header: transferase Chain: A: PDB Molecule: cvclomaltodextrin dlucanotransferase:

54	c3bmwA	Alignment	not modelled	100.0	19	PDBTitle: cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
55	c1qhoA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: amyp; PDBTitle: crystal structure of amyp in complex with maltose
56	c5h06C	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of an alpha-amylase from malbranchea cinnamomea
57	c3vm7A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 13; PDBTitle: crystal structure of bacillus licheniformis trehalose-6-phosphate2 hydrolase (trea)
58	c5brqA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: maltodextrin glycosyltransferase; PDBTitle: maltosyltransferase from thermotoga maritima
59	c1qjuA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of a noncanonic maltogenic alpha-amylase amyb from2 thermotoga neapolitana
60	c4gkIA	Alignment	not modelled	100.0	21	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
61	c1cygA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase
62	c5zcbA	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosyltransferase; PDBTitle: crystal structure of alpha-glucosyl transfer enzyme, xgta at 1.722 angstrom resolution
63	c6aaavA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: lmo0184 protein; PDBTitle: 1.8 angstrom crystal structure of listeria monocytogenes lmo01842 alpha-1,6-glucosidase
64	c5do8A	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,6-alpha-glucosidase; PDBTitle: structure of glucan-1,6-alpha-glucosidase from lactobacillus2 acidophilus ncfm
65	c4aieA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
66	c2z1kA	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: crystal structure of gamma-cgtase from alkalophilic bacillus clarkii2 at 1.65 angstrom resolution
67	c4jcmA	Alignment	not modelled	100.0	21	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
68	c5zxbB	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase a; PDBTitle: crystal structure of alpha-amylase from h.oreonii
69	c1wzaA	Alignment	not modelled	100.0	22	PDB header: hydrolase (o-glycosyl) Chain: A: PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
70	c2taaA	Alignment	not modelled	100.0	18	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
71	c2aaaA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
72	c2zidA	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
73	d1m7xa3	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
74	c2ze0A	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
75	d1gvia3	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
76	c3wy3A	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
77	d1j0ha3	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
78	d1wzla3	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
79	c1lwhA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
80	d1m53a2	Alignment	not modelled	100.0	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases

						Family: Amylase, catalytic domain
81	d1ea9c3	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
82	d1gjwa2	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
83	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
84	d2bhua3	Alignment	not modelled	100.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
85	d1lwha2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
86	d3bmva4	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
87	d2aaaa2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
88	d1csla4	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	d1pama4	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
90	d2guya2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	d1uoka2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
92	d1cgta4	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
93	d1qhoa4	Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	d1cyga4	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	d1eh9a3	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
96	d1h3ga3	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
97	c1jd7A	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of 2 pseudoalteromonas haloplanctis alpha-amylase
98	c1ud8A	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
99	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
100	d1wzaa2	Alignment	not modelled	100.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
101	c6gyaA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: a-amylase; PDBTitle: amylase in complex with branched ligand
102	c1e40A	Alignment	not modelled	100.0	17	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
103	c1hvxA	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearothermophilus alpha-amylase
104	c1jaeA	Alignment	not modelled	100.0	17	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
105	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 with 2 pseudo-maltonaose
106	d1ji1a3	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
107	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

108	c1bagA	Alignment	not modelled	100.0	19	PDB header: alpha-amylase Chain: A; PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
109	c2qpuB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
110	c3bpX	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
111	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
112	c5bn7A	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: maltodextrin glucosidase; PDBTitle: crystal structure of maltodextrin glucosidase from e.coli at 3.7 a2 resolution
113	d1r7aa2	Alignment	not modelled	100.0	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
114	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
115	c1jdaA	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
116	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
117	c1mwoA	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
118	d1avaa2	Alignment	not modelled	100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	d1ob0a2	Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
120	d1ua7a2	Alignment	not modelled	100.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain