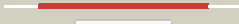



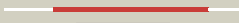



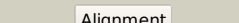

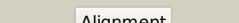

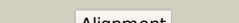









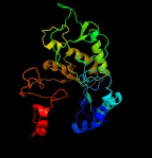




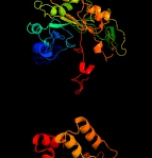

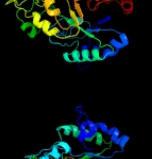
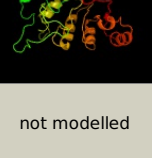


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1781c_malQ_2015309_2017483
Date	Fri Aug 2 13:30:39 BST 2019
Unique Job ID	fc57d31868153f08

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5b68A_	 Alignment		100.0	47	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of apo amylomaltase from corynebacterium glutamicum
2	c4s3rA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: amyloamaltase malq from escherichia coli in complex with the pseudo-2 heptasaccharide acarviosine-glucose-acarbose
3	d1x1na1	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
4	d1eswa_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
5	d1tz7a1	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
6	c4e2oA_	 Alignment		98.4	15	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
7	c3zt5D_	 Alignment		98.4	23	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glge isoform 1 from streptomyces coelicolor with maltose2 bound
8	d1ob0a2	 Alignment		98.3	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
9	c6gyaA_	 Alignment		98.3	24	PDB header: hydrolase Chain: A: PDB Molecule: a-amylase; PDBTitle: amylase in complex with branched ligand
10	c4u33F_	 Alignment		98.3	23	PDB header: transferase Chain: F: PDB Molecule: alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase; PDBTitle: structure of mtb glge bound to maltose
11	d1e43a2	 Alignment		98.1	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

12	c5do8A	Alignment		98.1	24	PDB header: hydrolase Chain: A: PDB Molecule: lmo0184 protein; PDBTitle: 1.8 angstrom crystal structure of listeria monocytogenes lmo01842 alpha-1,6-glucosidase
13	c1m53A	Alignment		98.1	18	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
14	c4gk1A	Alignment		98.1	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of a noncanonic maltogenic alpha-amylase amyb from2 thermotoga neapolitana
15	d1ht6a2	Alignment		98.0	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
16	d1uoka2	Alignment		98.0	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
17	c3a47A	Alignment		98.0	16	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
18	c5zxbB	Alignment		98.0	19	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
19	d1ua7a2	Alignment		97.9	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
20	d1lwaha2	Alignment		97.9	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
21	c1zjaB	Alignment	not modelled	97.9	22	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
22	d1ud2a2	Alignment	not modelled	97.9	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
23	c2wcsA	Alignment	not modelled	97.8	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
24	d1m53a2	Alignment	not modelled	97.8	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
25	d2gpa2	Alignment	not modelled	97.8	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
26	c1jdaA	Alignment	not modelled	97.7	19	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
27	c4aieA	Alignment	not modelled	97.7	24	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,6-alpha-glucosidase; PDBTitle: structure of glucan-1,6-alpha-glucosidase from lactobacillus2 acidophilus ncfm
28	d1gcya2	Alignment	not modelled	97.7	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
29	c5vkbB	Alignment	not modelled	97.7	24	PDB header: isomerase Chain: B: PDB Molecule: trehalose synthase;

29	c3ykbB	Alignment	not modelled	97.7	24	PDBTitle: the n253f mutant structure of trehalose synthase from deinococcus2 radiodurans reveals an open active-site conformation
30	c1uokA	Alignment	not modelled	97.7	19	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
31	d1bf2a3	Alignment	not modelled	97.7	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
32	c1wpcA	Alignment	not modelled	97.7	18	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaoase-producing amylase complexed with2 pseudo-maltonaoase
33	c5zcbA	Alignment	not modelled	97.6	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase
34	c1gcyA	Alignment	not modelled	97.6	21	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
35	c3dhuC	Alignment	not modelled	97.6	22	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus plantarum
36	d1gvia3	Alignment	not modelled	97.5	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
37	c1e40A	Alignment	not modelled	97.5	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
38	d2d3na2	Alignment	not modelled	97.5	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
39	c2dh3A	Alignment	not modelled	97.4	19	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
40	d1m7xa3	Alignment	not modelled	97.4	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
41	c2ze0A	Alignment	not modelled	97.3	23	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
42	c1ehaA	Alignment	not modelled	97.3	18	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase from2 sulfolobus solfataricus
43	c5brqA	Alignment	not modelled	97.3	21	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 13; PDBTitle: crystal structure of bacillus licheniformis trehalose-6-phosphate2 hydrolase (trea)
44	c1tcmB	Alignment	not modelled	97.3	19	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
45	d1j0ha3	Alignment	not modelled	97.3	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
46	c4tvuA	Alignment	not modelled	97.2	29	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
47	c1hvxA	Alignment	not modelled	97.2	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearothermophilus alpha-amylase
48	c3amkA	Alignment	not modelled	97.2	14	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
49	c2zidA	Alignment	not modelled	97.1	23	PDB header: hydrolase Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
50	c4mb1A	Alignment	not modelled	97.1	18	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase 1; PDBTitle: the structure of mall mutant enzyme g202p from bacillus subtilus
51	c4bzyC	Alignment	not modelled	97.1	18	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of human glycogen branching enzyme (gbe1)
52	c3uccqA	Alignment	not modelled	97.1	31	PDB header: transferase Chain: A: PDB Molecule: amylosucrase; PDBTitle: crystal structure of amylosucrase from deinococcus geothermalis
53	c1bf2A	Alignment	not modelled	97.1	14	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
54	d2guya2	Alignment	not modelled	97.1	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
55	d1eh9a3	Alignment	not modelled	97.1	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

56	c3am1A	Alignment	not modelled	97.1	18	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
57	d1hvxa2	Alignment	not modelled	97.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
58	c2qpuB	Alignment	not modelled	97.0	18	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
59	c3m07A	Alignment	not modelled	97.0	24	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.
60	c5h06C	Alignment	not modelled	96.9	21	PDB header: hydrolase Chain: C: PDB Molecule: amyp; PDBTitle: crystal structure of amyp in complex with maltose
61	c2taaA	Alignment	not modelled	96.8	27	PDB header: hydrolase (o-glycosyl) Chain: A: PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
62	d2bhua3	Alignment	not modelled	96.8	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
63	d1h3ga3	Alignment	not modelled	96.8	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
64	c5ot1A	Alignment	not modelled	96.8	21	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase type ii, gh13 family; PDBTitle: the type iii pullulan hydrolase from thermococcus kodakarensis
65	c2by0A	Alignment	not modelled	96.7	19	PDB header: hydrolase Chain: A: PDB Molecule: maltoooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
66	c1jgiA	Alignment	not modelled	96.6	24	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
67	c2wanA	Alignment	not modelled	96.5	17	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
68	c1qhoA	Alignment	not modelled	96.5	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
69	c3k1dA	Alignment	not modelled	96.5	19	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
70	d1cyga4	Alignment	not modelled	96.3	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
71	c2ya0A	Alignment	not modelled	96.3	11	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
72	c3edeB	Alignment	not modelled	96.3	24	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltodextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
73	c2ya1A	Alignment	not modelled	96.2	12	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: product complex of a multi-modular glycogen-degrading pneumococcal2 virulence factor spua
74	c1ud8A	Alignment	not modelled	96.0	17	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
75	c2z1kA	Alignment	not modelled	96.0	18	PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
76	c6irtA	Alignment	not modelled	95.9	22	PDB header: membrane protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: human lat1-4f2hc complex bound with bch
77	d3bmva4	Alignment	not modelled	95.9	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
78	c3wdjA	Alignment	not modelled	95.8	15	PDB header: hydrolase Chain: A: PDB Molecule: type i pullulanase; PDBTitle: crystal structure of pullulanase complexed with maltotetraose from2 anoxybacillus sp. Im18-11
79	c4aefB	Alignment	not modelled	95.7	20	PDB header: hydrolase Chain: B: PDB Molecule: neopullulanase (alpha-amylase ii); PDBTitle: the crystal structure of thermostable amylase from the pyrococcus
80	c5gquA	Alignment	not modelled	95.7	24	PDB header: transferase Chain: A: PDB Molecule: 1,4-alpha-glucan branching enzyme glgb; PDBTitle: crystal structure of branching enzyme from cyanothecae sp. atcc 51142
81	c2fhfA	Alignment	not modelled	95.6	24	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: crystal structure analysis of klebsiella pneumoniae pullulanase2 complexed with maltotetraose

82	d1pama4	Alignment	not modelled	95.6	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
83	c1ea9D	Alignment	not modelled	95.6	25	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltodextrinase; PDBTitle: cyclomaltodextrinase
84	c5wvtA	Alignment	not modelled	95.5	18	PDB header: hydrolase Chain: A: PDB Molecule: pulullanase; PDBTitle: catalytic mechanism, cyclodextrin inhibition, and allosteric2 regulation of paenibacillus barengoltzii pullulanase
85	c1wzaA	Alignment	not modelled	95.3	28	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase a; PDBTitle: crystal structure of alpha-amylase from h.oreonii
86	c1cygA	Alignment	not modelled	95.2	14	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
87	c1mwoA	Alignment	not modelled	95.2	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase; PDBTitle: crystal structure analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
88	c3bmwA	Alignment	not modelled	94.7	18	PDB header: transferase Chain: A: PDB Molecule: cyclomaltodextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
89	d1ea9c3	Alignment	not modelled	94.2	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
90	c1jibA	Alignment	not modelled	94.2	17	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.
91	c4jclA	Alignment	not modelled	94.2	13	PDB header: transferase Chain: A: PDB Molecule: cyclomaltodextrin glucanotransferase; PDBTitle: crystal structure of alpha-cgt from paenibacillus macerans at 1.72 angstrom resolution
92	c1lwhA	Alignment	not modelled	94.2	21	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
93	d1qhoa4	Alignment	not modelled	94.1	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	c3bc9A	Alignment	not modelled	94.1	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: alpha-amylase b in complex with acarbose
95	d1avaa2	Alignment	not modelled	94.0	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
96	c1bplA	Alignment	not modelled	93.9	15	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
97	c6aavA	Alignment	not modelled	93.6	22	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosyltransferase; PDBTitle: crystal structure of alpha-glucosyl transfer enzyme, xgta at 1.722 angstrom resolution
98	d1cxl4	Alignment	not modelled	93.6	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
99	d1gjwa2	Alignment	not modelled	93.5	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
100	c2gdvA	Alignment	not modelled	93.5	10	PDB header: transferase Chain: A: PDB Molecule: sucrose phosphorylase; PDBTitle: sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
101	c1gviA	Alignment	not modelled	93.4	18	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
102	c1bplB	Alignment	not modelled	93.0	15	PDB header: glycosyltransferase Chain: B: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
103	c2x4bA	Alignment	not modelled	92.8	17	PDB header: hydrolase Chain: A: PDB Molecule: limit dextrinase; PDBTitle: barley limit dextrinase in complex with beta-cyclodextrin
104	c1jd7A	Alignment	not modelled	92.3	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
105	c1qjuA	Alignment	not modelled	91.8	21	PDB header: transferase Chain: A: PDB Molecule: maltodextrin glycosyltransferase; PDBTitle: maltosyltransferase from thermotoga maritima
106	c3wy3A	Alignment	not modelled	91.5	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase mutant d202n in complex with2 glucose and glycerol
107	d2aaaa2	Alignment	not modelled	91.5	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
108	c3vm7A	Alignment	not modelled	91.4	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase;

108	c3vll7A	Alignment	not modelled	91.4	13	PDBTitle: structure of an alpha-amylase from malbranchea cinnamomea PDB header: transferase
109	c4jcmA	Alignment	not modelled	91.3	8	Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: crystal structure of gamma-cgtase from alkalophilic bacillus clarkii2 at 1.65 angstrom resolution
110	c3k8kB	Alignment	not modelled	91.0	25	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
111	c3zoaB	Alignment	not modelled	90.7	22	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
112	c5m99A	Alignment	not modelled	90.1	18	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
113	c2e8yA	Alignment	not modelled	90.0	14	PDB header: hydrolase Chain: A: PDB Molecule: amylx protein; PDBTitle: crystal structure of pullulanase type i from bacillus subtilis str.2 168
114	c5x7uA	Alignment	not modelled	89.9	23	PDB header: hydrolase Chain: A: PDB Molecule: trehalose synthase; PDBTitle: trehalose synthase from thermobaculum terrenum
115	c3czkA	Alignment	not modelled	89.9	18	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-sucrose2 complex
116	d1mxga2	Alignment	not modelled	89.5	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
117	d2fhfa5	Alignment	not modelled	89.4	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
118	d1r7aa2	Alignment	not modelled	89.0	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	c2aaaA	Alignment	not modelled	86.9	10	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
120	c1m7xC	Alignment	not modelled	86.8	17	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme