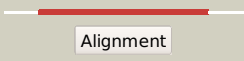

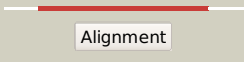
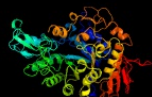
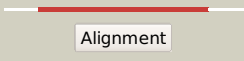

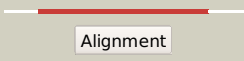

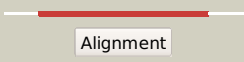

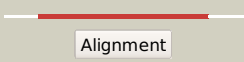

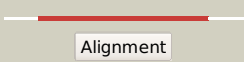

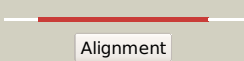

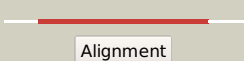

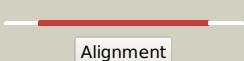

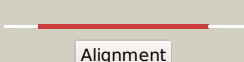



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2471_(aglA)_2773574_2775214
Date	Wed Aug 7 12:50:10 BST 2019
Unique Job ID	aeb01ba2fa641814

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6aavA_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosyltransferase; <b>PDBTitle:</b> crystal structure of alpha-glucosyl transfer enzyme, xgta at 1.722 angstrom resolution
2	<a href="#">c3a47A_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligo-1,6-glucosidase; <b>PDBTitle:</b> crystal structure of isomaltase from saccharomyces cerevisiae
3	<a href="#">c4mb1A_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligo-1,6-glucosidase 1; <b>PDBTitle:</b> the structure of mall mutant enzyme g202p from bacillus subtilus
4	<a href="#">c5do8A_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0184 protein; <b>PDBTitle:</b> 1.8 angstrom crystal structure of listeria monocytogenes lmo01842 alpha-1,6-glucosidase
5	<a href="#">c2zidA_</a>	 Alignment		100.0	34	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dextran glucosidase; <b>PDBTitle:</b> crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
6	<a href="#">c1uokA_</a>	 Alignment		100.0	30	<b>PDB header:</b> glucosidase <b>Chain:</b> A: <b>PDB Molecule:</b> oligo-1,6-glucosidase; <b>PDBTitle:</b> crystal structure of b. cereus oligo-1,6-glucosidase
7	<a href="#">c3wy3A_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase mutant d202n in complex with2 glucose and glycerol
8	<a href="#">c5zcbA_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase
9	<a href="#">c3zoaB_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose synthase/amilase tres; <b>PDBTitle:</b> the structure of trehalose synthase (tres) of mycobacterium2 smegmatis in complex with acarbose
10	<a href="#">c5brqA_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 13; <b>PDBTitle:</b> crystal structure of bacillus licheniformis trehalose-6-phosphate2 hydrolase (trea)
11	<a href="#">c4aieA_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucan 1,6-alpha-glucosidase; <b>PDBTitle:</b> structure of glucan-1,6-alpha-glucosidase from lactobacillus2 acidophilus ncfm

12	<a href="#">c1m53A_</a>	Alignment		100.0	34	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> isomaltulose synthase; <b>PDBTitle:</b> crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
13	<a href="#">d1m53a2</a>	Alignment		100.0	36	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
14	<a href="#">c1zjaB_</a>	Alignment		100.0	35	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> trehalulose synthase; <b>PDBTitle:</b> crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
15	<a href="#">c4tvuA_</a>	Alignment		100.0	33	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> crystal structure of trehalose synthase from deinococcus radiodurans2 reveals a closed conformation for catalysis of the intramolecular3 isomerization
16	<a href="#">c2ze0A_</a>	Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase gsj
17	<a href="#">d1uoka2</a>	Alignment		100.0	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
18	<a href="#">c5x7uA_</a>	Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> trehalose synthase from thermobaculum terrenum
19	<a href="#">c3k8kB_</a>	Alignment		100.0	27	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amylase, susg; <b>PDBTitle:</b> crystal structure of susg
20	<a href="#">c5ykbB_</a>	Alignment		100.0	33	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose synthase; <b>PDBTitle:</b> the n253f mutant structure of trehalose synthase from deinococcus2 radiodurans reveals an open active-site conformation
21	<a href="#">c4aeeA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase, catalytic region; <b>PDBTitle:</b> crystal structure of maltogenic amylase from s.marinus
22	<a href="#">c3edeB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclomaltodextrinase; <b>PDBTitle:</b> structural base for cyclodextrin hydrolysis
23	<a href="#">c1igiA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amylsucrase; <b>PDBTitle:</b> crystal structure of the active site mutant glu328gln of amylsucrase2 from neisseria polysaccharea in complex with the natural substrate3 sucrose
24	<a href="#">c5ot1A_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase type ii, gh13 family; <b>PDBTitle:</b> the type iii pullulan hydrolase from thermococcus kodakarensis
25	<a href="#">c1wzaA_</a>	Alignment	not modelled	100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase a; <b>PDBTitle:</b> crystal structure of alpha-amylase from h.oreonii
26	<a href="#">c5m99A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization
27	<a href="#">c1gviA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltogenic amylase; <b>PDBTitle:</b> thermus maltogenic amylase in complex with beta-cd
28	<a href="#">c1jibA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> neopullulanase; <b>PDBTitle:</b> complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a

					crystal soaked3 with maltohexaose.
29	<a href="#">c3ucqA</a>	Alignment	not modelled	100.0	28 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amylosucrase; <b>PDBTitle:</b> crystal structure of amylosucrase from deinococcus geothermalis
30	<a href="#">c3czkA</a>	Alignment	not modelled	100.0	24 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sucrose hydrolase; <b>PDBTitle:</b> crystal structure analysis of sucrose hydrolase(suh) e322q-sucrose2 complex
31	<a href="#">c1ea9D</a>	Alignment	not modelled	100.0	27 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cyclomaltodextrinase; <b>PDBTitle:</b> cyclomaltodextrinase
32	<a href="#">c4aefB</a>	Alignment	not modelled	100.0	27 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> neopullulanase (alpha-amylase ii); <b>PDBTitle:</b> the crystal structure of thermostable amylase from the pyrococcus
33	<a href="#">c1lwhA</a>	Alignment	not modelled	100.0	29 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-alpha-glucanotransferase; <b>PDBTitle:</b> crystal structure of t. maritima 4-alpha-glucanotransferase
34	<a href="#">c3m07A</a>	Alignment	not modelled	100.0	21 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative alpha amylase; <b>PDBTitle:</b> 1.4 angstrom resolution crystal structure of putative alpha amylase2 from salmonella typhimurium.
35	<a href="#">c2ya1A</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alkaline amylopullulanase; <b>PDBTitle:</b> product complex of a multi-modular glycogen-degrading pneumococcal2 virulence factor spua
36	<a href="#">c1tcmB</a>	Alignment	not modelled	100.0	27 <b>PDB header:</b> glycosyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclodextrin glycosyltransferase; <b>PDBTitle:</b> cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
37	<a href="#">c2wcsA</a>	Alignment	not modelled	100.0	32 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase, catalytic region; <b>PDBTitle:</b> crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
38	<a href="#">c5zxgB</a>	Alignment	not modelled	100.0	26 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic maltosyl-maltose hydrolase; <b>PDBTitle:</b> cyclic alpha-maltosyl-(1-->6)-maltose hydrolase from arthrobacter2 globiformis, ligand-free form
39	<a href="#">c3bmwA</a>	Alignment	not modelled	100.0	24 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclomaltodextrin glucanotransferase; <b>PDBTitle:</b> cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
40	<a href="#">c1qhoA</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
41	<a href="#">c3faxA</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> reticulocyte binding protein; <b>PDBTitle:</b> the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
42	<a href="#">c2d0gA</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase i; <b>PDBTitle:</b> crystal structure of thermoactinomyces vulgaris r-47 alpha-2 amylase 1 (tvai) mutant d356n/e396q complexed with p5, a3 pullulan model oligosaccharide
43	<a href="#">c1bf2A</a>	Alignment	not modelled	100.0	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> structure of pseudomonas isoamylase
44	<a href="#">c2z1kA</a>	Alignment	not modelled	100.0	29 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> (neo)pullulanase; <b>PDBTitle:</b> crystal structure of ttha1563 from thermus thermophilus hb8
45	<a href="#">d1wzaa2</a>	Alignment	not modelled	100.0	33 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
46	<a href="#">c2ya0A</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alkaline amylopullulanase; <b>PDBTitle:</b> catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
47	<a href="#">c4jcmA</a>	Alignment	not modelled	100.0	25 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclodextrin glucanotransferase; <b>PDBTitle:</b> crystal structure of gamma-cgtase from alkalophilic bacillus clarkii2 at 1.65 angstrom resolution
48	<a href="#">c1cygA</a>	Alignment	not modelled	100.0	26 <b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclodextrin glucanotransferase; <b>PDBTitle:</b> cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
49	<a href="#">c2vncB</a>	Alignment	not modelled	100.0	21 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycogen operon protein glgx; <b>PDBTitle:</b> crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
50	<a href="#">c4jclA</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclomaltodextrin glucanotransferase; <b>PDBTitle:</b> crystal structure of alpha-cgt from paenibacillus macerans at 1.72 angstrom resolution
51	<a href="#">d1lwha2</a>	Alignment	not modelled	100.0	31 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
52	<a href="#">c2gdvA</a>	Alignment	not modelled	100.0	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sucrose phosphorylase; <b>PDBTitle:</b> sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
53	<a href="#">c6irtA</a>	Alignment	not modelled	100.0	24 <b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4f2 cell-surface antigen heavy chain; <b>PDBTitle:</b> human lat1-4f2hc complex bound with bch
					<b>PDB header:</b> hydrolase

54	<a href="#">c3wdjA_</a>	Alignment	not modelled	100.0	22	<b>Chain:</b> A: <b>PDB Molecule:</b> type i pullulanase; <b>PDBTitle:</b> crystal structure of pullulanase complexed with maltotetraose from <i>Mycobacterium</i> sp. Im18-11
55	<a href="#">c4j7rA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> crystal structure of chlamydomonas reinhardtii isoamylase 1 (isa1)
56	<a href="#">c4e2oA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of alpha-amylase from <i>Geobacillus thermoleovorans</i> , 2 gta, complexed with acarbose
57	<a href="#">d2fhfa5</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
58	<a href="#">c5wvtA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase; <b>PDBTitle:</b> catalytic mechanism, cyclodextrin inhibition, and allosteric2 regulation of <i>Paenibacillus barengoltzii</i> pullulanase
59	<a href="#">c3vm7A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> structure of an alpha-amylase from <i>Malbranchea cinnamomea</i>
60	<a href="#">d1g5aa2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
61	<a href="#">c1ehaA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltrehalose trehalohydrolase; <b>PDBTitle:</b> crystal structure of glycosyltrehalose trehalohydrolase from <i>Mycobacterium solfataricus</i>
62	<a href="#">c4u33F_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase; <b>PDBTitle:</b> structure of mtb glge bound to maltose
63	<a href="#">c2x4bA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> limit dextrinase; <b>PDBTitle:</b> barley limit dextrinase in complex with beta-cyclodextrin
64	<a href="#">c2e8yA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amylx protein; <b>PDBTitle:</b> crystal structure of pullulanase type i from <i>Bacillus subtilis</i> str.2 168
65	<a href="#">c2wanA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase; <b>PDBTitle:</b> pullulanase from <i>Bacillus acidopullulyticus</i>
66	<a href="#">c3k1dA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha-glucan-branching enzyme; <b>PDBTitle:</b> crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from <i>Mycobacterium tuberculosis</i> h37rv
67	<a href="#">d1gvia3</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
68	<a href="#">d1wzla3</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
69	<a href="#">c3zt5D_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative glucanohydrolase pep1a; <b>PDBTitle:</b> glge isoform 1 from <i>Streptomyces coelicolor</i> with maltose2 bound
70	<a href="#">c2wskA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen debranching enzyme; <b>PDBTitle:</b> crystal structure of glycogen debranching enzyme glgx from <i>Escherichia coli</i> k-12
71	<a href="#">c2aaaA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> glycosidase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> calcium binding in alpha-amylases: an x-ray diffraction study at 2.12 angstroms resolution of two enzymes from <i>Aspergillus</i>
72	<a href="#">c2dh3A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transport protein, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4f2 cell-surface antigen heavy chain; <b>PDBTitle:</b> crystal structure of human ed-4f2hc
73	<a href="#">c2taaA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase (o-glycosyl) <b>Chain:</b> A: <b>PDB Molecule:</b> taka-amylase a; <b>PDBTitle:</b> structure and possible catalytic residues of taka-amylase a
74	<a href="#">c2fhfA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase; <b>PDBTitle:</b> crystal structure analysis of <i>Klebsiella pneumoniae</i> pullulanase2 complexed with maltotetraose
75	<a href="#">c1m7xC_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 1,4-alpha-glucan branching enzyme; <b>PDBTitle:</b> the x-ray crystallographic structure of branching enzyme
76	<a href="#">d1pama4</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
77	<a href="#">d3bmva4</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
78	<a href="#">c5gquA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha-glucan branching enzyme glgb; <b>PDBTitle:</b> crystal structure of branching enzyme from cyanobacterium sp. atcc 51142
79	<a href="#">d1cgta4</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
80	<a href="#">c2by0A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltooligosyltrehalose trehalohydrolase; <b>PDBTitle:</b> is radiation damage dependent on the dose-rate used

						during2 macromolecular crystallography data collection
81	<a href="#">c3am1A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> os06g0726400 protein; <b>PDBTitle:</b> structure of the starch branching enzyme i (bei) from oryza sativa l
82	<a href="#">d1cxl4</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
83	<a href="#">c3amkA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> os06g0726400 protein; <b>PDBTitle:</b> structure of the starch branching enzyme i (bei) from oryza sativa l
84	<a href="#">d1ea9c3</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
85	<a href="#">d1j0ha3</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
86	<a href="#">c5h06C_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> amyp; <b>PDBTitle:</b> crystal structure of amyp in complex with maltose
87	<a href="#">d1bf2a3</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
88	<a href="#">d1h3ga3</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
89	<a href="#">c4bzyC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 1,4-alpha-glucan-branching enzyme; <b>PDBTitle:</b> crystal structure of human glycogen branching enzyme (gbe1)
90	<a href="#">d2guya2</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
91	<a href="#">c1giuA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltodextrin glycosyltransferase; <b>PDBTitle:</b> maltosyltransferase from thermotoga maritima
92	<a href="#">d1qhoa4</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
93	<a href="#">d1ji1a3</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
94	<a href="#">c4gk1A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of a noncanonic maltogenic alpha-amylase amyb from2 thermotoga neapolitana
95	<a href="#">c2qpuB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amylase type a isozyme; <b>PDBTitle:</b> sugar tongs mutant s378p in complex with acarbose
96	<a href="#">d1cyga4</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
97	<a href="#">d2aaaa2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
98	<a href="#">c3dhuC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure of an alpha-amylase from lactobacillus plantarum
99	<a href="#">d2bhua3</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
100	<a href="#">d1m7xa3</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
101	<a href="#">d1eh9a3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
102	<a href="#">d1r7aa2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
103	<a href="#">d1gjwa2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
104	<a href="#">c1wpcA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucan 1,4-alpha-maltohexaosidase; <b>PDBTitle:</b> crystal structure of maltohexaoside-producing amylase complexed with2 pseudo-maltonaose
105	<a href="#">c1hvxA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> bacillus stearothermophilus alpha-amylase
106	<a href="#">c1ud8A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amylase; <b>PDBTitle:</b> crystal structure of amy38 with lithium ion
107	<a href="#">c1e40A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a



108	<a href="#">c6gyaA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> a-amylase; <b>PDBTitle:</b> amylase in complex with branched ligand
109	<a href="#">c5bn7A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> maltodextrin glucosidase; <b>PDBTitle:</b> crystal structure of maltodextrin glucosidase from e.coli at 3.7 a2 resolution
110	<a href="#">c1bagA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> alpha-amylase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase; <b>PDBTitle:</b> alpha-amylase from bacillus subtilis complexed with2 maltopentaose
111	<a href="#">c1gcyA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucan 1,4-alpha-maltotetrahydrolase; <b>PDBTitle:</b> high resolution crystal structure of maltotetraose-forming2 exo-amylase
112	<a href="#">c1jdaA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha maltotetrahydrolase; <b>PDBTitle:</b> maltotetraose-forming exo-amylase
113	<a href="#">c1jaeA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> glycosidase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> structure of tenebrio molitor larval alpha-amylase
114	<a href="#">c1jd7A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase; <b>PDBTitle:</b> crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
115	<a href="#">c3blpX_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> alpha-amylase 1; <b>PDBTitle:</b> role of aromatic residues in human salivary alpha-amylase
116	<a href="#">d1ob0a2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
117	<a href="#">d1avaa2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
118	<a href="#">c1mwoA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase; <b>PDBTitle:</b> crystal structure analysis of the hyperthermostable2 pyrocoocus woesei alpha-amylase
119	<a href="#">c3bc9A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha amylase, catalytic region; <b>PDBTitle:</b> alpha-amylase b in complex with acarbose
120	<a href="#">d1e43a2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain