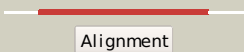

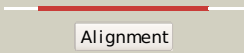







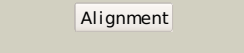

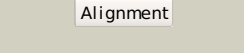
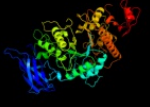
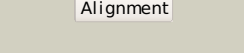



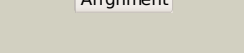

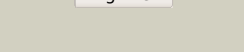



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2d0gA_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-amylase i; <b>PDBTitle:</b> crystal structure of thermoactinomyces vulgaris r-47 alpha-2 amylase 1 (tvai) mutant d356n/e396q complexed with p5, a3 pullulan model oligosaccharide
2	<a href="#">c1ea9D_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cyclomaltoextrinase; <b>PDBTitle:</b> cyclomaltoextrinase
3	<a href="#">c1gviA_</a>	 Alignment		100.0	31	<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
4	<a href="#">c1jibA_</a>	 Alignment		100.0	31	<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 maltotetraose.
5	<a href="#">c2e8yA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amyx protein; <b>PDBTitle:</b> crystal structure of pullulanase type i from bacillus subtilis str.2 168
6	<a href="#">c3edeB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cyclomaltoextrinase; <b>PDBTitle:</b> structural base for cyclodextrin hydrolysis
7	<a href="#">c3faxA_</a>	 Alignment		100.0	21	<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
8	<a href="#">c2wanA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase; <b>PDBTitle:</b> pullulanase from bacillus acidipullulyticus
9	<a href="#">c2ya0A_</a>	 Alignment		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-degrading2 pneumococcal virulence factor spua
10	<a href="#">c1bf2A_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> isoamylase; <b>PDBTitle:</b> structure of pseudomonas isoamylase
11	<a href="#">c2ya1A_</a>	 Alignment		100.0	21	<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-degrading2 pneumococcal virulence factor spua

12	<a href="#">c2vncB_</a>	Alignment		100.0	16	<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
13	<a href="#">c2wskA_</a>	Alignment		100.0	17	<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 from2 escherichia coli k-12
14	<a href="#">c2fhfA_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pullulanase; <b>PDBTitle:</b> crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
15	<a href="#">c2wcsA_</a>	Alignment		100.0	36	<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)
16	<a href="#">c2x4bA_</a>	Alignment		100.0	16	<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
17	<a href="#">c3m07A_</a>	Alignment		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 alpha2 amylase from salmonella typhi murium.
18	<a href="#">c3k1dA_</a>	Alignment		100.0	16	<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 mycobacterium3 tuberculosis h37rv
19	<a href="#">c1tcmB_</a>	Alignment		100.0	23	<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
20	<a href="#">c1m7xC_</a>	Alignment		100.0	16	<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
21	<a href="#">c3amkA_</a>	Alignment	not modelled	100.0	16	<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
22	<a href="#">c3bmwA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclomalto-dextrin glucanotransferase; <b>PDBTitle:</b> cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
23	<a href="#">c1qhoA_</a>	Alignment	not modelled	100.0	24	<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
24	<a href="#">c1cygA_</a>	Alignment	not modelled	100.0	23	<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)
25	<a href="#">c3amlA_</a>	Alignment	not modelled	100.0	14	<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
26	<a href="#">c2z1kA_</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> (neo)pullulanase; <b>PDBTitle:</b> crystal structure of tha1563 from thermus thermophilus hb8
27	<a href="#">dljila3</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
28	<a href="#">c2by0A_</a>	Alignment	not modelled	100.0	21	<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

29	<a href="#">c1ehaA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltrehalose trehalohydrolase; <b>PDBTitle:</b> crystal structure of glycosyltrehalose trehalohydrolase2 from sulfobolus solfataricus
30	<a href="#">c3k8kB</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-amylase, susg; <b>PDBTitle:</b> crystal structure of susg
31	<a href="#">d1gvia3</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
32	<a href="#">c2aaaA</a>	Alignment	not modelled	100.0	22	<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 diffraction2 study at 2.1 angstroms resolution of two enzymes from3 aspergillus
33	<a href="#">c3a47A</a>	Alignment	not modelled	100.0	21	<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
34	<a href="#">d1wzla3</a>	Alignment	not modelled	100.0	37	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
35	<a href="#">c1wzaA</a>	Alignment	not modelled	100.0	25	<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.orenii
36	<a href="#">c1jgiA</a>	Alignment	not modelled	100.0	23	<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 of2 amylsucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
37	<a href="#">c1m53A</a>	Alignment	not modelled	100.0	26	<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
38	<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
39	<a href="#">d1j0ha3</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
40	<a href="#">c1uoka</a>	Alignment	not modelled	100.0	24	<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
41	<a href="#">c3zt5D</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative glucanohydrolase pep1a; <b>PDBTitle:</b> glge isoform 1 from streptomyces coelicolor with maltose2 bound
42	<a href="#">d1ea9c3</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
43	<a href="#">c1zjaB</a>	Alignment	not modelled	100.0	26	<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)
44	<a href="#">c2zidA</a>	Alignment	not modelled	100.0	23	<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
45	<a href="#">c3ucqA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> amylsucrase; <b>PDBTitle:</b> crystal structure of amylsucrase from deinococcus geothermalis
46	<a href="#">c2ze0A</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase gsj
47	<a href="#">d3bmva4</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
48	<a href="#">c3czkA</a>	Alignment	not modelled	100.0	23	<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-2 sucrose complex
49	<a href="#">d1cgta4</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
50	<a href="#">d1pama4</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
51	<a href="#">d2aaaa2</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
52	<a href="#">c2gdvA</a>	Alignment	not modelled	100.0	17	<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="#">d2fhfa5</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
54	<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
55	<a href="#">d1ghoa4</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
56	<a href="#">d1h3ga3</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
57	<a href="#">c3dhuC</a>	Alignment	not modelled	100.0	21 <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 lactobacillus2 plantarum
58	<a href="#">d1csla4</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
59	<a href="#">c1gjuA</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> maltodextrin glycosyltransferase; <b>PDBTitle:</b> maltosyltransferase from thermotoga maritima
60	<a href="#">d1m53a2</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
61	<a href="#">d1cyga4</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
62	<a href="#">d1bf2a3</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
63	<a href="#">c1lwhA</a>	Alignment	not modelled	100.0	24 <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
64	<a href="#">d1uoka2</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
65	<a href="#">d1g5aa2</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
66	<a href="#">c2qpuB</a>	Alignment	not modelled	100.0	17 <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
67	<a href="#">d1wzaa2</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
68	<a href="#">c1hvxA</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> bacillus stearothermophilus alpha-amylase
69	<a href="#">c1ud8A</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amylase; <b>PDBTitle:</b> crystal structure of amyk38 with lithium ion
70	<a href="#">c2dh3A</a>	Alignment	not modelled	100.0	25 <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
71	<a href="#">c1wpcA</a>	Alignment	not modelled	100.0	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucan 1,4-alpha-maltohexaosidase; <b>PDBTitle:</b> crystal structure of maltohexaoase-producing amylase complexed with2 pseudo-maltononaoase
72	<a href="#">d1lwha2</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
73	<a href="#">c1e40A</a>	Alignment	not modelled	100.0	19 <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
74	<a href="#">d1gja2</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
75	<a href="#">d1m7xa3</a>	Alignment	not modelled	100.0	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
76	<a href="#">c1bagA</a>	Alignment	not modelled	100.0	14 <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
77	<a href="#">c1jaeA</a>	Alignment	not modelled	100.0	14 <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
78	<a href="#">c1gcyA</a>	Alignment	not modelled	100.0	16 <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
79	<a href="#">c1jd7A</a>	Alignment	not modelled	100.0	15 <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 of 2 pseudoalteromonas haloplantis alpha-amylase
80	<a href="#">d2bhua3</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
81	<a href="#">c1jdaA</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-alpha maltotetrahydrolase; <b>PDBTitle:</b> maltotetraose-forming exo-amylase
82	<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
83	<a href="#">d1eh9a3</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
84	<a href="#">d1r7aa2</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
85	<a href="#">c1mw0A_</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 analysis of the hyperthermostable2 pyrococcus woesei alpha-amylase
86	<a href="#">c3bc9A_</a>	Alignment	not modelled	100.0	19 <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
87	<a href="#">d1mxga2</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
88	<a href="#">d1avaa2</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
89	<a href="#">c1iv8A_</a>	Alignment	not modelled	100.0	22 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> maltooligosyl trehalose synthase; <b>PDBTitle:</b> crystal structure of maltooligosyl trehalose synthase
90	<a href="#">d1ht6a2</a>	Alignment	not modelled	100.0	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
91	<a href="#">d1gcya2</a>	Alignment	not modelled	100.0	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
92	<a href="#">d1ob0a2</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="#">d1ud2a2</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
94	<a href="#">d2gjpa2</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
95	<a href="#">d1hvxa2</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
96	<a href="#">d1e43a2</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
97	<a href="#">d1ua7a2</a>	Alignment	not modelled	100.0	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
98	<a href="#">d2d3na2</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
99	<a href="#">d1g94a2</a>	Alignment	not modelled	100.0	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
100	<a href="#">d1jaea2</a>	Alignment	not modelled	100.0	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
101	<a href="#">d1hx0a2</a>	Alignment	not modelled	100.0	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
102	<a href="#">d3dhpa2</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
103	<a href="#">c3hjeA_</a>	Alignment	not modelled	100.0	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 704aa long hypothetical glycosyltransferase; <b>PDBTitle:</b> crystal structure of sulfobolus tokodaii hypothetical2 maltooligosyl trehalose synthase
104	<a href="#">c1bplB_</a>	Alignment	not modelled	100.0	18 <b>PDB header:</b> glycosyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase; <b>PDBTitle:</b> glycosyltransferase
105	<a href="#">d1iv8a2</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
106	<a href="#">c1bplA_</a>	Alignment	not modelled	99.9	21 <b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,4-glucan-4-glucanohydrolase; <b>PDBTitle:</b> glycosyltransferase
107	<a href="#">c3aicC_</a>	Alignment	not modelled	99.7	19 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucosyltransferase-si; <b>PDBTitle:</b> crystal structure of glucansucrase from streptococcus mutans
108	<a href="#">c2yfnA_</a>	Alignment	not modelled	99.4	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase-sucrose kinase agask; <b>PDBTitle:</b> galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
109	<a href="#">c2xn1B_</a>	Alignment	not modelled	99.2	14 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> structure of alpha-galactosidase from lactobacillus

					acidophilus ncfm2 with tris
110	<a href="#">c3hz3A_</a>	Alignment	not modelled	99.2	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucansucrase; <b>PDBTitle:</b> lactobacillus reuteri n-terminally truncated glucansucrase2_gtf180(d1025n)-sucrose complex
111	<a href="#">c3mi6A_</a>	Alignment	not modelled	99.1	15 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target1br11.
112	<a href="#">d1ji1a1</a>	Alignment	not modelled	98.9	20 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
113	<a href="#">d1j0ha1</a>	Alignment	not modelled	98.8	23 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
114	<a href="#">d2fhfa1</a>	Alignment	not modelled	98.8	9 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
115	<a href="#">d1m7xa1</a>	Alignment	not modelled	98.7	11 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
116	<a href="#">d1ea9c1</a>	Alignment	not modelled	98.7	23 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
117	<a href="#">c3a5vA_</a>	Alignment	not modelled	98.7	14 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of alpha-galactosidase i from mortierella vinacea
118	<a href="#">c1uasA_</a>	Alignment	not modelled	98.7	13 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-galactosidase; <b>PDBTitle:</b> crystal structure of rice alpha-galactosidase
119	<a href="#">c3cc1B_</a>	Alignment	not modelled	98.7	13 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> crystal structure of a putative alpha-n-acetylgalactosaminidase2 (bh1870) from bacillus halodurans c-125 at 2.00 a resolution
120	<a href="#">d1wzla1</a>	Alignment	not modelled	98.7	20 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes