Phyre2

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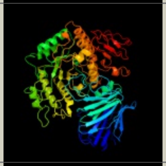
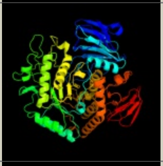
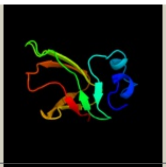
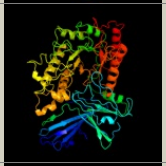
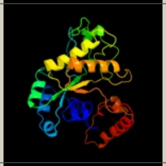
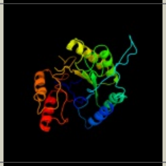
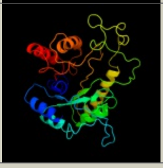
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lppA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrase-isomaltase; **PDBTitle:** crystal complex of n-terminal sucrase-isomaltase with kotalanol
2	c2qmjA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltase-glucoamylase, intestinal; **PDBTitle:** crystal structure of the n-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
3	c3topA_	Alignment		100.0	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**maltase-glucoamylase, intestinal; **PDBTitle:** crystal structure of the c-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
4	c1xsiF_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative family 31 glucosidase yici; **PDBTitle:** structure of a family 31 alpha glycosidase
5	c2xvgA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha xylosidase; **PDBTitle:** crystal structure of alpha-xylosidase (gh31) from2 cellvibrio japonicus
6	c2g3nA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of the sulfolobus solfataricus alpha-2 glucosidase mala in complex with beta-octyl-glucopyranoside
7	c3ffjA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase (family 31); **PDBTitle:** the crystal structure of the glycosyl hydrolase (family 31) from2 ruminococcus obeum atcc 29174
8	c2x2iB_	Alignment		100.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-1,4-glucan lyase isozyme 1; **PDBTitle:** crystal structure of the gracilariopsis lemaneiformis alpha-2 1,4-glucan lyase with acarbose
9	d2f2ha4	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
10	c1zy9A_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase (ec 3.2.1.22) (melibiase)2 (tm1192) from thermotoga maritima at 2.34 a resolution
11	c2yfnA_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask

12	d2f2ha3	Alignment		100.0	34	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**Putative glucosidase YicI, domain 3
13	d2f2ha2	Alignment		100.0	15	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**YicI N-terminal domain-like
14	c2xn1B_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
15	d1zy9a2	Alignment		99.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
16	c3mi6A_	Alignment		99.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
17	c3cc1B_	Alignment		99.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-n-acetylgalactosaminidase; **PDBTitle:** crystal structure of a putative alpha-n-acetylgalactosaminidase2 (bh1870) from bacillus halodurans c-125 at 2.00 a resolution
18	d1uasa2	Alignment		99.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
19	c1uasA_	Alignment		99.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of rice alpha-galactosidase
20	d1szna2	Alignment		99.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
21	c2wskA_	Alignment	not modelled	99.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycogen debranching enzyme; **PDBTitle:** crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
22	c3a5vA_	Alignment	not modelled	99.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase i from mortierella vinacea
23	c3lrmB_	Alignment	not modelled	99.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase 1; **PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
24	c3dhuC_	Alignment	not modelled	99.2	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
25	c3a23A_	Alignment	not modelled	99.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase; **PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
26	d1r46a2	Alignment	not modelled	99.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
27	c1t0oA_	Alignment	not modelled	99.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
28	c1r46B_	Alignment	not modelled	99.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase a; **PDBTitle:** structure of human alpha-galactosidase
						Fold:TIM beta/alpha-barrel

29	d1ktba2	Alignment	not modelled	98.9	19	**Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
30	c1gviA_	Alignment	not modelled	98.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
31	c1ktbA_	Alignment	not modelled	98.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** the structure of alpha-n-acetylgalactosaminidase
32	c1ea9D_	Alignment	not modelled	98.5	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
33	d1gvia3	Alignment	not modelled	98.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
34	c3a47A_	Alignment	not modelled	98.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
35	d1j0ha3	Alignment	not modelled	98.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
36	d1ea9c3	Alignment	not modelled	98.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
37	d1m53a2	Alignment	not modelled	98.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
38	c1uokA_	Alignment	not modelled	98.2	13	**PDB header:**glucosidase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of b. cereus oligo-1,6-glucosidase
39	c1jibA_	Alignment	not modelled	98.2	13	**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.
40	c2ze0A_	Alignment	not modelled	98.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
41	d1uoka2	Alignment	not modelled	98.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
42	c1bagA_	Alignment	not modelled	98.2	10	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
43	c1m53A_	Alignment	not modelled	98.2	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
44	c2wanA_	Alignment	not modelled	98.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
45	c1zjaB_	Alignment	not modelled	98.2	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
46	c1gcyA_	Alignment	not modelled	98.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
47	c2zidA_	Alignment	not modelled	98.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dextran glucosidase; **PDBTitle:** crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
48	c2aaaA_	Alignment	not modelled	98.1	14	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** calcium binding in alpha-amylases: an x-ray diffraction2 study at 2.1 angstroms resolution of two enzymes from3 aspergillus
49	d2bhua3	Alignment	not modelled	98.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	d1h3ga3	Alignment	not modelled	98.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
51	c1lwhA_	Alignment	not modelled	98.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
52	c3edeB_	Alignment	not modelled	98.0	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
53	d2aaaa2	Alignment	not modelled	97.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
54	d1m7xa3	Alignment	not modelled	97.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
55	c1wzaA_	Alignment	not modelled	97.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase a; **PDBTitle:** crystal structure of alpha-amylase from h.orenii

56	d1lwha2	Alignment	not modelled	97.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
57	c3czkA_	Alignment	not modelled	97.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
58	d1eh9a3	Alignment	not modelled	97.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
59	c1ehaA_	Alignment	not modelled	97.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
60	d1bf2a3	Alignment	not modelled	97.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
61	c2wcsA_	Alignment	not modelled	97.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
62	c3faxA_	Alignment	not modelled	97.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
63	c2e8yA_	Alignment	not modelled	97.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
64	c2qpuB_	Alignment	not modelled	97.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme; **PDBTitle:** sugar tongs mutant s378p in complex with acarbose
65	d1ht6a2	Alignment	not modelled	97.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
66	c3k1dA_	Alignment	not modelled	97.8	14	**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
67	d1avaa2	Alignment	not modelled	97.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	c1bf2A_	Alignment	not modelled	97.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
69	c1jdaA_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
70	d1wzla3	Alignment	not modelled	97.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
71	d2guya2	Alignment	not modelled	97.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
72	c2vncB_	Alignment	not modelled	97.8	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
73	c2taaA_	Alignment	not modelled	97.8	11	**PDB header:**hydrolase (o-glycosyl) **Chain:** A: **PDB Molecule:**taka-amylase a; **PDBTitle:** structure and possible catalytic residues of taka-amylase a
74	d1qhoa4	Alignment	not modelled	97.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
75	c2z1kA_	Alignment	not modelled	97.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
76	c2by0A_	Alignment	not modelled	97.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
77	d1gcya2	Alignment	not modelled	97.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
78	d1ua7a2	Alignment	not modelled	97.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
79	c3m07A_	Alignment	not modelled	97.7	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative alpha amylase; **PDBTitle:** 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium.
80	c1tcmB_	Alignment	not modelled	97.7	18	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
81	c1cygA_	Alignment	not modelled	97.7	15	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
82	c2ya0A_	Alignment	not modelled	97.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-

						degrading2 pneumococcal virulence factor spua
83	d1g5aa2	Alignment	not modelled	97.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
84	c3ucqA_	Alignment	not modelled	97.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis
85	c3amkA_	Alignment	not modelled	97.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
86	d1wzaa2	Alignment	not modelled	97.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
87	c3zt5D_	Alignment	not modelled	97.6	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucanohydrolase pep1a; **PDBTitle:** glge isoform 1 from streptomyces coelicolor with maltose2 bound
88	c1qhoA_	Alignment	not modelled	97.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
89	c1jaeA_	Alignment	not modelled	97.6	13	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
90	c2x4bA_	Alignment	not modelled	97.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin
91	c2d0gA_	Alignment	not modelled	97.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase i; **PDBTitle:** crystal structure of thermoactinomyces vulgaris r-47 alpha-2 amylase 1 (tvai) mutant d356n/e396q complexed with p5, a3 pullulan model oligosaccharide
92	c1m7xC_	Alignment	not modelled	97.5	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
93	c2ya1A_	Alignment	not modelled	97.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
94	d1jaea2	Alignment	not modelled	97.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
95	c2dh3A_	Alignment	not modelled	97.5	15	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
96	d3bmva4	Alignment	not modelled	97.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
97	c1e40A_	Alignment	not modelled	97.3	16	**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
98	c1jgiA_	Alignment	not modelled	97.3	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of the active site mutant glu328gln of2 amylosucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
99	d1pama4	Alignment	not modelled	97.2	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
100	c1jd7A_	Alignment	not modelled	97.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
101	c3bmwA_	Alignment	not modelled	97.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
102	d3dhpa2	Alignment	not modelled	97.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
103	d1cyga4	Alignment	not modelled	97.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
104	c1hvxA_	Alignment	not modelled	97.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** bacillus stearothermophilus alpha-amylase
105	c3amlA_	Alignment	not modelled	97.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
106	c1wpcA_	Alignment	not modelled	97.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltohexaosidase; **PDBTitle:** crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
107	d1cxla4	Alignment	not modelled	97.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
108	d1hx0a2	Alignment	not modelled	97.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases

						Family: Amylase, catalytic domain
109	d2fhfa5	Alignment	not modelled	97.1	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
110	c1ud8A_	Alignment	not modelled	97.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
111	d1cgta4	Alignment	not modelled	97.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
112	c3blpX_	Alignment	not modelled	96.9	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
113	c2fhfA_	Alignment	not modelled	96.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
114	d1hvxa2	Alignment	not modelled	96.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
115	d1ud2a2	Alignment	not modelled	96.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	d1ob0a2	Alignment	not modelled	96.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
117	d1e43a2	Alignment	not modelled	96.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
118	c1gjuA_	Alignment	not modelled	96.6	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltodextrin glycosyltransferase; **PDBTitle:** maltosyltransferase from thermotoga maritima
119	c3bc9A_	Alignment	not modelled	96.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** alpha-amylase b in complex with acarbose
120	d1g94a2	Alignment	not modelled	96.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain