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Description	P75906
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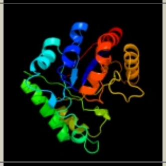
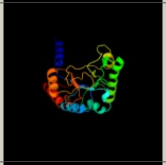
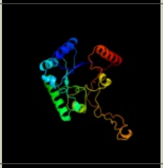
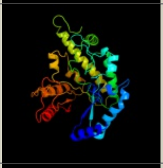
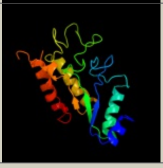
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2j13a1	Alignment		99.9	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
2	d2cc0a1	Alignment		99.9	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
3	d2iw0a1	Alignment		99.9	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
4	c1w17A_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
5	c2iw0A_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
6	d1ny1a_	Alignment		99.9	22	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
7	c2w3zA_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
8	d2c1ia1	Alignment		99.9	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
9	c2c1iA_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
10	c2vyoA_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
11	d2c71a1	Alignment		99.9	23	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase

12	c3rxzA_	Alignment		99.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**polysaccharide deacetylase; **PDBTitle:** crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
13	d1z7aa1	Alignment		99.7	11	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**PA1517-like
14	c3qbuD_	Alignment		99.7	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative peptidoglyacn deactelyase (hp0310) from2 helicobacter pylori
15	c3s6oD_	Alignment		99.7	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**polysaccharide deacetylase family protein; **PDBTitle:** crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
16	c1kwgA_	Alignment		99.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of thermus thermophilus a4 beta-galactosidase
17	d2nlya1	Alignment		99.4	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
18	d1kwga2	Alignment		98.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
19	d1k1xa3	Alignment		98.6	10	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**4-alpha-glucanotransferase, N-terminal domain
20	d1m7xa3	Alignment		98.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
21	c1m7xC_	Alignment	not modelled	98.5	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
22	c3bxwB_	Alignment	not modelled	98.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**chitinase domain-containing protein 1; **PDBTitle:** crystal structure of stabilin-1 interacting chitinase-like2 protein, si-clp
23	d1gvia3	Alignment	not modelled	98.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
24	d1j0ha3	Alignment	not modelled	98.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
25	d1ea9c3	Alignment	not modelled	98.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
26	c2xn1B_	Alignment	not modelled	98.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** structure of alpha-galactosidase from lactobacillus acidophilus ncfm2 with tris
27	d1avaa2	Alignment	not modelled	98.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
28	c2yfnA_	Alignment	not modelled	98.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase-sucrose kinase agask; **PDBTitle:** galactosidase domain of alpha-galactosidase-sucrose kinase,2 agask
						PDB header:glycosidase

29	c2aaaA_	Alignment	not modelled	98.2	11	**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
30	d1ht6a2	Alignment	not modelled	98.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
31	c3mi6A_	Alignment	not modelled	98.1	15	**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.
32	d1h3ga3	Alignment	not modelled	98.1	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
33	c3u7vA_	Alignment	not modelled	98.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
34	c1ehaA_	Alignment	not modelled	98.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyltrehalose trehalohydrolase; **PDBTitle:** crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
35	c1gviA_	Alignment	not modelled	98.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltogenic amylase; **PDBTitle:** thermus maltogenic amylase in complex with beta-cd
36	c3cz8A_	Alignment	not modelled	98.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sporulation-specific glycosylase ydhd; **PDBTitle:** crystal structure of putative sporulation-specific glycosylase ydhd2 from bacillus subtilis
37	c2vncB_	Alignment	not modelled	98.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
38	d1ob0a2	Alignment	not modelled	98.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
39	d1qhoa4	Alignment	not modelled	98.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
40	d1bf2a3	Alignment	not modelled	98.0	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
41	d1wzla3	Alignment	not modelled	98.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
42	d2d3na2	Alignment	not modelled	98.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
43	d2bhua3	Alignment	not modelled	98.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
44	c2e8yA_	Alignment	not modelled	98.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amyx protein; **PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168
45	d2fhfa5	Alignment	not modelled	98.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
46	c2zidA_	Alignment	not modelled	98.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dextran glucosidase; **PDBTitle:** crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
47	d2guya2	Alignment	not modelled	98.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
48	d1g5aa2	Alignment	not modelled	98.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
49	d2aaaa2	Alignment	not modelled	98.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	c1k1yA_	Alignment	not modelled	98.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
51	c3amkA_	Alignment	not modelled	98.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
52	c1lwhA_	Alignment	not modelled	97.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of t. maritima 4-alpha-glucanotransferase
53	c1jgiA_	Alignment	not modelled	97.9	18	**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
54	c2z1kA_	Alignment	not modelled	97.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**(neo)pullulanase; **PDBTitle:** crystal structure of ttha1563 from thermus thermophilus hb8
						PDB header:hydrolase

55	c3czkA_	Alignment	not modelled	97.9	12	**Chain:** A: **PDB Molecule:**sucrose hydrolase; **PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
56	c1tcmB_	Alignment	not modelled	97.9	11	**PDB header:**glycosyltransferase **Chain:** B: **PDB Molecule:**cyclodextrin glycosyltransferase; **PDBTitle:** cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
57	c3bmwA_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
58	d1cgta4	Alignment	not modelled	97.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
59	c1e40A_	Alignment	not modelled	97.9	15	**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
60	c2taaA_	Alignment	not modelled	97.9	9	**PDB header:**hydrolase (o-glycosyl) **Chain:** A: **PDB Molecule:**taka-amylase a; **PDBTitle:** structure and possible catalytic residues of taka-amylase a
61	c3edeB_	Alignment	not modelled	97.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
62	c1ea9D_	Alignment	not modelled	97.9	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** cyclomaltodextrinase
63	d1ud2a2	Alignment	not modelled	97.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
64	c1bf2A_	Alignment	not modelled	97.9	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
65	d1m53a2	Alignment	not modelled	97.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
66	d2gjpa2	Alignment	not modelled	97.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
67	d1gcya2	Alignment	not modelled	97.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
68	c2wanA_	Alignment	not modelled	97.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** pullulanase from bacillus acidopullulyticus
69	d1e43a2	Alignment	not modelled	97.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
70	d1uoka2	Alignment	not modelled	97.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
71	d1eh9a3	Alignment	not modelled	97.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
72	c3dhuC_	Alignment	not modelled	97.8	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
73	c1jibA_	Alignment	not modelled	97.8	12	**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.
74	c1cygA_	Alignment	not modelled	97.8	14	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**cyclodextrin glucanotransferase; **PDBTitle:** cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
75	c1ud8A_	Alignment	not modelled	97.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
76	c2wskA_	Alignment	not modelled	97.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycogen debranching enzyme; **PDBTitle:** crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
77	d1ua7a2	Alignment	not modelled	97.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
78	c2ya1A_	Alignment	not modelled	97.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
79	c3a47A_	Alignment	not modelled	97.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of isomaltase from saccharomyces cerevisiae
80	d1cyga4	Alignment	not modelled	97.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
81	d1lwha2	Alignment	not modelled	97.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

82	c3k1dA_	Alignment	not modelled	97.8	15	**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
83	c3amlA_	Alignment	not modelled	97.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
84	c1zjaB_	Alignment	not modelled	97.8	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**trehalulose synthase; **PDBTitle:** crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
85	d1cxla4	Alignment	not modelled	97.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
86	c1qhoA_	Alignment	not modelled	97.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
87	c1ll4A_	Alignment	not modelled	97.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase 1; **PDBTitle:** structure of c. immitis chitinase 1 complexed with2 allosamidin
88	c3ucqA_	Alignment	not modelled	97.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amylosucrase; **PDBTitle:** crystal structure of amylosucrase from deinococcus geothermalis
89	c2dh3A_	Alignment	not modelled	97.7	19	**PDB header:**transport protein, signaling protein **Chain:** A: **PDB Molecule:**4f2 cell-surface antigen heavy chain; **PDBTitle:** crystal structure of human ed-4f2hc
90	c3m07A_	Alignment	not modelled	97.7	15	**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.
91	c2by0A_	Alignment	not modelled	97.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase; **PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
92	c2wcsA_	Alignment	not modelled	97.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
93	c1uokA_	Alignment	not modelled	97.7	15	**PDB header:**glucosidase **Chain:** A: **PDB Molecule:**oligo-1,6-glucosidase; **PDBTitle:** crystal structure of b. cereus oligo-1,6-glucosidase
94	c2ze0A_	Alignment	not modelled	97.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase gsj
95	c1itxA_	Alignment	not modelled	97.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** catalytic domain of chitinase a1 from bacillus circulans wl-12
96	c1wpcA_	Alignment	not modelled	97.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltohexaosidase; **PDBTitle:** crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
97	c1gcyA_	Alignment	not modelled	97.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucan 1,4-alpha-maltotetrahydrolase; **PDBTitle:** high resolution crystal structure of maltotetraose-forming2 exo-amylase
98	c1jd7A_	Alignment	not modelled	97.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
99	c2x4bA_	Alignment	not modelled	97.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**limit dextrinase; **PDBTitle:** barley limit dextrinase in complex with beta-cyclodextrin
100	c1jneA_	Alignment	not modelled	97.7	14	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**imaginal disc growth factor-2; **PDBTitle:** crystal structure of imaginal disc growth factor-2
101	d1hvxa2	Alignment	not modelled	97.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
102	c2ya0A_	Alignment	not modelled	97.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase; **PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
103	d2b5dx2	Alignment	not modelled	97.6	12	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**AmyC N-terminal domain-like
104	c1jdaA_	Alignment	not modelled	97.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-alpha maltotetrahydrolase; **PDBTitle:** maltotetraose-forming exo-amylase
105	c1m53A_	Alignment	not modelled	97.6	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isomaltulose synthase; **PDBTitle:** crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
106	c1hjvA_	Alignment	not modelled	97.6	11	**PDB header:**lectin **Chain:** A: **PDB Molecule:**chitinase-3 like protein 1; **PDBTitle:** crystal structure of hcgp-39 in complex with chitin2 tetramer
107	c3faxA_	Alignment	not modelled	97.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reticulocyte binding protein; **PDBTitle:** the crystal structure of gbs pullulanase sap in complex with2 maltotetraose

108	c2qpuB_	Alignment	not modelled	97.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amylase type a isozyme; **PDBTitle:** sugar tongs mutant s378p in complex with acarbose
109	c1e9lA_	Alignment	not modelled	97.5	14	**PDB header:**macrophage secretory protein **Chain:** A: **PDB Molecule:**ym1 secretory protein; **PDBTitle:** the crystal structure of novel mammalian lectin ym12 suggests a saccharide binding site
110	c3zt5D_	Alignment	not modelled	97.5	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative glucanohydrolase pep1a; **PDBTitle:** glge isoform 1 from streptomyces coelicolor with maltose2 bound
111	c2b5dX_	Alignment	not modelled	97.4	12	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
112	c3chfA_	Alignment	not modelled	97.4	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of aspergillus fumigatus chitinase b1 in complex2 with tetrapeptide
113	c1wzaA_	Alignment	not modelled	97.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase a; **PDBTitle:** crystal structure of alpha-amylase from h.orenii
114	c1jaeA_	Alignment	not modelled	97.4	15	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
115	d1pama4	Alignment	not modelled	97.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
116	c1hvxA_	Alignment	not modelled	97.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** bacillus stearothermophilus alpha-amylase
117	d3bmva4	Alignment	not modelled	97.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
118	c1bagA_	Alignment	not modelled	97.3	8	**PDB header:**alpha-amylase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** alpha-amylase from bacillus subtilis complexed with2 maltopentaose
119	c2fhfA_	Alignment	not modelled	97.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pullulanase; **PDBTitle:** crystal structure analysis of klebsiella pneumoniae2 pullulanase complexed with maltotetraose
120	c3g6lA_	Alignment	not modelled	97.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** the crystal structure of a chitinase crchi1 from the nematophagous2 fungus clonostachys rosea