














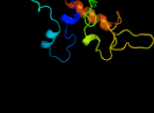








# Phyre2

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Description	RVBD1006_(-)_1123718_1125421
Date	Wed Jul 31 22:05:07 BST 2019
Unique Job ID	8a1d9f9a243a227a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4uozC_</a>	 Alignment		99.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> beta-(1,6)-galactosidase from bifidobacterium animalis subsp. lactis2 bl-04 nucleophile mutant e324a in complex with galactose
2	<a href="#">c4ojyA_</a>	 Alignment		99.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> 3d structure of the e323a catalytic mutant of gan42b, a gh42 beta-2 galactosidase from g. stearothermophilus
3	<a href="#">c4uzsB_</a>	 Alignment		99.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of bifidobacterium bifidum beta-galactosidase
4	<a href="#">c1kwgA_</a>	 Alignment		99.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of thermus thermophilus a4 beta-galactosidase
5	<a href="#">c5e9aB_</a>	 Alignment		99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure analysis of the cold-adamped beta-galactosidase from2 rahnella sp. r3
6	<a href="#">c3ttsD_</a>	 Alignment		99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of beta-galactosidase from bacillus circulans sp.2 alkalophilus
7	<a href="#">c5xb7E_</a>	 Alignment		99.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> gh42 alpha-l-arabinopyranosidase from bifidobacterium animalis subsp.2 lactis bl-04
8	<a href="#">c5gslB_</a>	 Alignment		99.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 778aa long hypothetical beta-galactosidase; <b>PDBTitle:</b> glycoside hydrolase a
9	<a href="#">c3u7vA_</a>	 Alignment		98.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
10	<a href="#">c4d1iB_</a>	 Alignment		98.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase, putative, bg135a; <b>PDBTitle:</b> the structure of the gh35 beta-galactosidase bg135a from2 cellvibrio japonicus
11	<a href="#">d1kwga2</a>	 Alignment		98.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain

12	<a href="#">c5gsmB_</a>	Alignment		98.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-beta-d-glucosaminidase; <b>PDBTitle:</b> glycoside hydrolase b with product
13	<a href="#">d1n82a_</a>	Alignment		98.6	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
14	<a href="#">d1us3a2</a>	Alignment		98.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
15	<a href="#">c1j0yD_</a>	Alignment		98.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-amylase; <b>PDBTitle:</b> beta-amylase from bacillus cereus var. mycooides in complex2 with glucose
16	<a href="#">c6fheA_</a>	Alignment		98.5	19	<b>PDB header:</b> artificial enzyme <b>Chain:</b> A: <b>PDB Molecule:</b> synthetic construct; <b>PDBTitle:</b> highly active enzymes by automated modular backbone assembly and2 sequence design
17	<a href="#">c4xx6A_</a>	Alignment		98.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of a glycosylated endo-beta-1,4-xylanase (glycoside2 hydrolase family 10/gh10) enzyme from gloeophyllum trabeum
18	<a href="#">d1l1wa_</a>	Alignment		98.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
19	<a href="#">d1v0la_</a>	Alignment		98.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
20	<a href="#">c3vocA_</a>	Alignment		98.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta/alpha-amylase; <b>PDBTitle:</b> crystal structure of the catalytic domain of beta-amylase from2 paenibacillus polymyxa
21	<a href="#">c6gvbC_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> exo-beta-1,4-mannosidase; <b>PDBTitle:</b> crystal structure of cutibacterium acnes exo-beta-1,4-mannosidase
22	<a href="#">c4l4oA_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> the crystal structure of cbxyn10b in native form
23	<a href="#">c4e8cA_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase, family 35; <b>PDBTitle:</b> crystal structure of streptococcal beta-galactosidase in complex with2 galactose
24	<a href="#">c2depA_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable celoxylanase; <b>PDBTitle:</b> crystal structure of xylanase b from clostridium stercoararium f9
25	<a href="#">c5mrjA_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-xylanase-like protein from2 acremonium chrysogenum
26	<a href="#">d1ta3b_</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
27	<a href="#">c3d3aA_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
28	<a href="#">c6mp2B_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> blman5b; <b>PDBTitle:</b> crystal structure of blman5b solved by siras
						<b>PDB header:</b> hydrolase

29	<a href="#">c6q8nB_</a>	Alignment	not modelled	98.3	17	<b>Chain:</b> B: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> gh10 endo-xylanase in complex with xylobiose epoxide inhibitor
30	<a href="#">c3thdD_</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
31	<a href="#">d1v6ya_</a>	Alignment	not modelled	98.3	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
32	<a href="#">c5ofIA_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 48; <b>PDBTitle:</b> crystal structure of cbxyn10c variant e140q/e248q complexed with2 celohexaose
33	<a href="#">d1ur1a_</a>	Alignment	not modelled	98.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
34	<a href="#">c2cncA_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoxylanase; <b>PDBTitle:</b> family 10 xylanase
35	<a href="#">c1us2A_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-xylanase; <b>PDBTitle:</b> xylanase10c (mutant e385a) from cellvibrio japonicus in complex with2 xylopentaose
36	<a href="#">c3rdkB_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> protein crystal structure of xylanase a1 of paenibacillus sp. jdr-2
37	<a href="#">d1fh9a_</a>	Alignment	not modelled	98.2	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
38	<a href="#">c3u7bB_</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> a new crystal structure of a fusarium oxysporum gh10 xylanase reveals2 the presence of an extended loop on top of the catalytic cleft
39	<a href="#">c4madA_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of beta-galactosidase c (bgac) from bacillus2 circulans atcc 31382
40	<a href="#">c3w26A_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 10; <b>PDBTitle:</b> the high-resolution crystal structure of tsxyla, intracellular2 xylanase from /thermoanaerobacterium saccharolyticum jw/sl-ys485/:3 the complex of the e146a mutant with xylotriose
41	<a href="#">c5xzoA_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of gh10 xylanase xyl10c from bispora. sp mey-1
42	<a href="#">c5bx9A_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pslg; <b>PDBTitle:</b> structure of pslg from pseudomonas aeruginosa
43	<a href="#">c3emzA_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> crystal structure of xylanase xynb from paenibacillus barcinonensis2 complexed with a conduramine derivative
44	<a href="#">c4pmuD_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endo-1,4-beta-xylanase a; <b>PDBTitle:</b> crystal structure of a novel reducing-end xylose-releasing exo-2 oligoxylanase (xyna) belonging to gh10 family (space group p1211)
45	<a href="#">d1vbua1</a>	Alignment	not modelled	98.1	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
46	<a href="#">c4pmyB_</a>	Alignment	not modelled	98.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xylanase; <b>PDBTitle:</b> crystal structure of gh10 endo-b-1,4-xylanase (xynb) from xanthomonas2 axonopodis pv citri complexed with xylose
47	<a href="#">c6fhfA_</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> artificial enzyme <b>Chain:</b> A: <b>PDB Molecule:</b> design; <b>PDBTitle:</b> highly active enzymes by automated modular backbone assembly and2 sequence design
48	<a href="#">c1xyzA_</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> 1,4-beta-d-xylan-xylanohydrolase; <b>PDBTitle:</b> a common protein fold and similar active site in two2 distinct families of beta-glycanases
49	<a href="#">d1xyza_</a>	Alignment	not modelled	98.1	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
50	<a href="#">d1bg4a_</a>	Alignment	not modelled	98.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
51	<a href="#">c5m0kB_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-xylanase from cellulomonas2 flavigena
52	<a href="#">c4w8IB_</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-1,4-beta-xylanase c; <b>PDBTitle:</b> structure of gh10 from paenibacillus barcinonensis
53	<a href="#">c4f8xA_</a>	Alignment	not modelled	98.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> penicillium canescens endo-1,4-beta-xylanase xyle
54	<a href="#">d1nq6a_</a>	Alignment	not modelled	98.1	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases

55	<a href="#">d1tuxa_</a>	Alignment	not modelled	98.1	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
56	<a href="#">c2fglA_</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline thermostable endoxylanase; <b>PDBTitle:</b> an alkali thermostable f/10 xylanase from alkalophilic bacillus sp.2 ng-27
57	<a href="#">c3ogrA_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> complex structure of beta-galactosidase from trichoderma reesei with2 galactose
58	<a href="#">c4xv0A_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of an endo-beta-1,4-xylanase (glycoside hydrolase2 family 10/gh10) enzyme from trichoderma reesei
59	<a href="#">c4k68B_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gh10 xylanase; <b>PDBTitle:</b> structure of a novel gh10 endoxylanase retrieved from sugarcane soil2 metagenome
60	<a href="#">d1vema2</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
61	<a href="#">c6eonA_</a>	Alignment	not modelled	98.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> galactanase bt0290
62	<a href="#">d1v6wa2</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
63	<a href="#">c3wugA_</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase a; <b>PDBTitle:</b> the mutant crystal structure of b-1,4-xylanase (xynas9_v43p/g44e) with2 xylobiose from streptomyces sp. 9
64	<a href="#">d1r85a_</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
65	<a href="#">c1iszA_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-d-xylanase; <b>PDBTitle:</b> crystal structure of xylanase from streptomyces2 olivaceoviridis e-86 complexed with galactose
66	<a href="#">c4hu8A_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh10 xylanase; <b>PDBTitle:</b> crystal structure of a bacterial ig-like domain containing gh102 xylanase from termite gut
67	<a href="#">c3w5gB_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> crystal structure of tomato beta-galactosidase 4 in complex with2 galactose
68	<a href="#">c1xc6A_</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> native structure of beta-galactosidase from penicillium sp. in complex2 with galactose
69	<a href="#">c5d4yA_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xylanase; <b>PDBTitle:</b> a psychrophilic glycoside hydrolase family 10 endo-beta-1,4-xylanase
70	<a href="#">c5ccuA_</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted endoglycosylceramidase; <b>PDBTitle:</b> crystal structure of endoglycosylceramidase i from rhodococcus equi
71	<a href="#">c2w5fB_</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-1,4-beta-xylanase y; <b>PDBTitle:</b> high resolution crystallographic structure of the clostridium2 thermocellum n-terminal endo-1,4-beta-d-xylanase 10b (xyn10b) cbm22-3 1- gh10 modules complexed with xylohexaose
72	<a href="#">d1tg7a5</a>	Alignment	not modelled	97.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Glycosyl hydrolases family 35 catalytic domain
73	<a href="#">c5jvkB_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structural insights into a family 39 glycoside hydrolase from the gut2 symbiont bacteroides cellulosilyticus wh2.
74	<a href="#">c2oylB_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglycosylceramidase ii; <b>PDBTitle:</b> endo-glycosylceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
75	<a href="#">d1w32a_</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
76	<a href="#">c4ee9A_</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of the rbcel1 endo-1,4-glucanase
77	<a href="#">c6ierA_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase 1317; <b>PDBTitle:</b> apo structure of a beta-glucosidase 1317
78	<a href="#">c5dt5E_</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of the gh1 beta-glucosidase from exiguobacterium2 antarcticum b7 in space group p21
79	<a href="#">c2xfyA_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-amylase; <b>PDBTitle:</b> crystal structure of barley beta-amylase complexed with alpha-2 cyclodextrin
80	<a href="#">c3ta9B_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 1; <b>PDBTitle:</b> beta-glucosidase a from the halothermophile h. orenii

81	<a href="#">d1wdpa1</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
82	<a href="#">d1b1ya_</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
83	<a href="#">c2z1sA_</a>	Alignment	not modelled	97.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase b; <b>PDBTitle:</b> beta-glucosidase b from paenibacillus polymyxa complexed with2 cellotetraose
84	<a href="#">d1fa2a_</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
85	<a href="#">d1vffa1</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
86	<a href="#">c5ns6C_</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-glucosidase bglm-g1 from marine metagenome
87	<a href="#">c4r27B_</a>	Alignment	not modelled	96.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase; <b>PDBTitle:</b> crystal structure of beta-glycosidase bgl167
88	<a href="#">d1rh9a1</a>	Alignment	not modelled	96.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
89	<a href="#">c3w53A_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of psychrophilic beta-glucosidase bglu from2 micrococcus antarcticus
90	<a href="#">d1gnxa_</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
91	<a href="#">c5xgzA_</a>	Alignment	not modelled	96.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glycosidase; <b>PDBTitle:</b> metagenomic glucose-tolerant glycosidase
92	<a href="#">d1h4pa_</a>	Alignment	not modelled	96.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
93	<a href="#">c2j75A_</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase a; <b>PDBTitle:</b> beta-glucosidase from thermotoga maritima in complex with2 noeuromycin
94	<a href="#">c4im4F_</a>	Alignment	not modelled	96.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> endoglucanase e; <b>PDBTitle:</b> multifunctional cellulase, xylanase, mannanase
95	<a href="#">d1ug6a_</a>	Alignment	not modelled	96.7	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
96	<a href="#">c5ogzB_</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase a; <b>PDBTitle:</b> crystal structure of ruminiclostridium thermocellum beta-glucosidase a
97	<a href="#">d1pbga_</a>	Alignment	not modelled	96.6	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
98	<a href="#">d1e4ia_</a>	Alignment	not modelled	96.6	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
99	<a href="#">c5yj7C_</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> glycoside hydrolase; <b>PDBTitle:</b> structural insight into the beta-gh1 glucosidase bglN1 from oleaginous2 microalgae nannochloropsis
100	<a href="#">c5yhsB_</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvylated beta-d-galactosidase; <b>PDBTitle:</b> pyruvylated beta-d-galactosidase from bacillus sp. hma207, apo form
101	<a href="#">c4w7wA_</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> high-resolution structure of xacel5a in complex with cellopentaose
102	<a href="#">c3ahxC_</a>	Alignment	not modelled	96.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-glucosidase a; <b>PDBTitle:</b> crystal structure of beta-glucosidase a from bacterium clostridium2 cellulovorans
103	<a href="#">c3ai0A_</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-glucosidase from termite neotermes2 koshunensis in complex with para-nitrophenyl-beta-d-glucopyranoside
104	<a href="#">c5wkaC_</a>	Alignment	not modelled	96.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of a gh1 beta-glucosidase retrieved from microbial2 metagenome of poraque amazon lake
105	<a href="#">c2zoxA_</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cytosolic beta-glucosidase; <b>PDBTitle:</b> crystal structure of the covalent intermediate of human cytosolic2 beta-glucosidase
106	<a href="#">c3pzqA_</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family <b>PDBTitle:</b> structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol

107	<a href="#">d1qoxa_</a>	Alignment	not modelled	96.4	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
108	<a href="#">c4jhoA_</a>	Alignment	not modelled	96.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannosidase/beta-glucosidase; <b>PDBTitle:</b> structural analysis and insights into glycon specificity of the rice2 gh1 os7bglu26 beta-d-mannosidase
109	<a href="#">c4aweA_</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-d-1,4-mannanase; <b>PDBTitle:</b> the crystal structure of chrysonilia sitophila endo-beta-d-2 1,4-mannanase
110	<a href="#">c6gpaA_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> carbohydrate <b>Chain:</b> A: <b>PDB Molecule:</b> arabinogalactan endo-beta-1,4-galactanase; <b>PDBTitle:</b> beta-1,4-galactanase from bacteroides thetaiotaomicron with galactose
111	<a href="#">d1hjsa_</a>	Alignment	not modelled	96.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
112	<a href="#">d1vjza_</a>	Alignment	not modelled	96.3	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
113	<a href="#">c3wh5A_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of gh1 beta-glucosidase td2f2
114	<a href="#">c2l0dA_</a>	Alignment	not modelled	96.1	22	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein; <b>PDBTitle:</b> solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
115	<a href="#">c2dgaA_</a>	Alignment	not modelled	96.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of hexameric beta-glucosidase in wheat
116	<a href="#">c5hosA_</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> crystal structure of the endo-beta-1,4-glucanase xac0029 from2 xanthomonas axonopodis pv. citri
117	<a href="#">d1v08a_</a>	Alignment	not modelled	96.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
118	<a href="#">c2rgmA_</a>	Alignment	not modelled	95.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> rice bglu1 beta-glucosidase, a plant exoglucanase/beta-glucosidase
119	<a href="#">c3wh9A_</a>	Alignment	not modelled	95.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-mannanase; <b>PDBTitle:</b> the ligand-free structure of manbk from aspergillus niger bk01
120	<a href="#">c1v02F_</a>	Alignment	not modelled	95.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> dhurrinase; <b>PDBTitle:</b> crystal structure of the sorghum bicolor dhurrinase 1