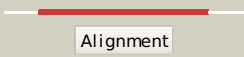

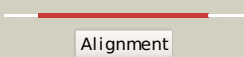

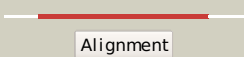

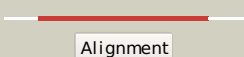

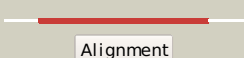

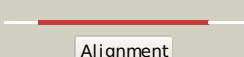

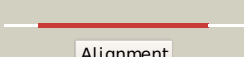

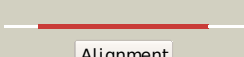

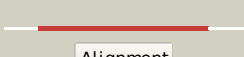

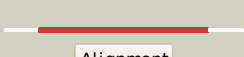














#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2xhyD_</a>	 Alignment		100.0	100	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase bgla; <b>PDBTitle:</b> crystal structure of e.coli bgla
2	<a href="#">c3pn8A_</a>	 Alignment		100.0	62	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phospho-beta-glucosidase; <b>PDBTitle:</b> the crystal structure of 6-phospho-beta-glucosidase from streptococcus2 mutans ua159
3	<a href="#">c3qomA_</a>	 Alignment		100.0	56	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase; <b>PDBTitle:</b> crystal structure of 6-phospho-beta-glucosidase from lactobacillus2 plantarum
4	<a href="#">d1qoxa_</a>	 Alignment		100.0	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
5	<a href="#">d2j78a1</a>	 Alignment		100.0	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
6	<a href="#">c3gnoA_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> os03g0212800 protein; <b>PDBTitle:</b> crystal structure of a rice os3bglu6 beta-glucosidase
7	<a href="#">c2dgaA_</a>	 Alignment		100.0	31	<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
8	<a href="#">c3ahxC_</a>	 Alignment		100.0	34	<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
9	<a href="#">c2rgmA_</a>	 Alignment		100.0	28	<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
10	<a href="#">c3fiyA_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of bglb
11	<a href="#">d1e4mm_</a>	 Alignment		100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase

12	<a href="#">dle4ia_</a>	Alignment		100.0	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
13	<a href="#">c2z1sA_</a>	Alignment		100.0	27	<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 complexed2 with cellotetraose
14	<a href="#">dlv08a_</a>	Alignment		100.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
15	<a href="#">dlgnxa_</a>	Alignment		100.0	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
16	<a href="#">c2jf7B_</a>	Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> strictosidine-o-beta-d-glucosidase; <b>PDBTitle:</b> structure of strictosidine glucosidase
17	<a href="#">dlpbga_</a>	Alignment		100.0	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
18	<a href="#">c2j75A_</a>	Alignment		100.0	33	<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 noeumycin
19	<a href="#">c3ptkB_</a>	Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase os4bglu12; <b>PDBTitle:</b> the crystal structure of rice (oryza sativa l.) os4bglu12
20	<a href="#">c3u57A_</a>	Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> raucaffricine-o-beta-d-glucosidase; <b>PDBTitle:</b> structures of alkaloid biosynthetic glucosidases decode substrate2 specificity
21	<a href="#">c3ai0A_</a>	Alignment	not modelled	100.0	29	<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
22	<a href="#">c1v02F_</a>	Alignment	not modelled	100.0	29	<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
23	<a href="#">dlcbga_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
24	<a href="#">dlv02a_</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
25	<a href="#">dlwcga1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
26	<a href="#">c2e3zB_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of intracellular family 1 beta-2 glucosidase bgl1a from the basidiomycete phanerochaete3 chrysosporium in substrate-free form
27	<a href="#">c2zoxA_</a>	Alignment	not modelled	100.0	29	<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
28	<a href="#">c3ahyD_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-glucosidase 2 from fungus trichoderma reesei2 in complex with tris

29	<a href="#">d1qvba</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
30	<a href="#">d1uwsa</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
31	<a href="#">d1ug6a</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
32	<a href="#">d1vffa1</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Family 1 of glycosyl hydrolase
33	<a href="#">c2cncA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoxylanase; <b>PDBTitle:</b> family 10 xylanase
34	<a href="#">d1xyza</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
35	<a href="#">c1xyzA</a>	Alignment	not modelled	100.0	18	<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
36	<a href="#">d1ur1a</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
37	<a href="#">d1v6ya</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
38	<a href="#">d1nq6a</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
39	<a href="#">d1fh9a</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
40	<a href="#">c3emzA</a>	Alignment	not modelled	100.0	15	<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 paenibacillus2 barcinonensis complexed with a conduramine derivative
41	<a href="#">d1vbua1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
42	<a href="#">d1kwga2</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
43	<a href="#">d1v6wa2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
44	<a href="#">d1v0la</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
45	<a href="#">c2jepB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xyloglucanase; <b>PDBTitle:</b> native family 5 xyloglucanase from paenibacillus pabuli
46	<a href="#">d1n82a</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
47	<a href="#">d1w32a</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
48	<a href="#">c2depA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable cellobiohydrolase; <b>PDBTitle:</b> crystal structure of xylanase b from clostridium2 stercorarium f9
49	<a href="#">c3ndyA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
50	<a href="#">d1ilwa</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
51	<a href="#">d1edga</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
52	<a href="#">d1bg4a</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
53	<a href="#">d1rh9a1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
54	<a href="#">d1w91a2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
55	<a href="#">c3aysA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> gh5 endoglucanase from a ruminal fungus in complex with cellotriose
						<b>Fold:</b> TIM beta/alpha-barrel

56	<a href="#">d1hjsa_</a>	Alignment	not modelled	99.9	14	<b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
57	<a href="#">d1hjqa_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
58	<a href="#">d1vjza_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
59	<a href="#">d1ta3b_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
60	<a href="#">d1tuxa_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
61	<a href="#">d1ceoa_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
62	<a href="#">c3mmwB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
63	<a href="#">c3ncoA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase fncel5a; <b>PDBTitle:</b> crystal structure of fncel5a from f. nodosum rt17-b1
64	<a href="#">d1us3a2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
65	<a href="#">c2fglA_</a>	Alignment	not modelled	99.9	22	<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 alkalophilic2 bacillus sp. ng-27
66	<a href="#">d1r85a_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
67	<a href="#">c3pzqA_</a>	Alignment	not modelled	99.9	15	<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
68	<a href="#">c1uz4A_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> man5a; <b>PDBTitle:</b> common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 itineraries for glucoside and mannoside hydrolysis
69	<a href="#">d1uuqa_</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
70	<a href="#">d1ur4a_</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
71	<a href="#">c2bs9B_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> native crystal structure of a gh39 beta-xylosidase xynb12 from geobacillus stearothermophilus
72	<a href="#">d1uhva2</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
73	<a href="#">d1foba_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
74	<a href="#">c3qr3B_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase eg-ii; <b>PDBTitle:</b> crystal structure of cel5a (eg2) from hypocrea jecorina (trichoderma2 reesei)
75	<a href="#">c3icgD_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endoglucanase d; <b>PDBTitle:</b> crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
76	<a href="#">c2oylB_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglycoceramidase ii; <b>PDBTitle:</b> endo-glycoceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
77	<a href="#">d1h1na_</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
78	<a href="#">c3l55B_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> b-1,4-endoglucanase/cellulase; <b>PDBTitle:</b> crystal structure of a putative beta-1,4-endoglucanase /2 cellulase from prevotella bryantii
79	<a href="#">c1uhvD_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> crystal structure of beta-d-xylosidase from2 thermoanaerobacterium saccharolyticum, a family 393 glycoside hydrolase
80	<a href="#">c1kwgA_</a>	Alignment	not modelled	99.7	14	<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
81	<a href="#">d2c0ha1</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases

					<b>Family:</b> beta-glycanases
82	<a href="#">d1bhga3</a>	Alignment	not modelled	99.7	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
83	<a href="#">d1ecea</a>	Alignment	not modelled	99.7	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
84	<a href="#">c1iszA</a>	Alignment	not modelled	99.7	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
85	<a href="#">c1bhgB</a>	Alignment	not modelled	99.6	18 <b>PDB header:</b> glycosidase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> human beta-glucuronidase at 2.6 a resolution
86	<a href="#">c2w5fB</a>	Alignment	not modelled	99.6	16 <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 the2 clostridium thermocellum n-terminal endo-1,4-beta-d-3 xylanase 10b (xyn10b) cbm22-1-gh10 modules complexed with4 xylohexaose
87	<a href="#">c2zunB</a>	Alignment	not modelled	99.6	12 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 458aa long hypothetical endo-1,4-beta-glucanase; <b>PDBTitle:</b> functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii
88	<a href="#">d1egza</a>	Alignment	not modelled	99.6	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
89	<a href="#">d1wkya2</a>	Alignment	not modelled	99.6	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
90	<a href="#">d1qnra</a>	Alignment	not modelled	99.6	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
91	<a href="#">c3lpgA</a>	Alignment	not modelled	99.6	18 <b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucuronidase; <b>PDBTitle:</b> structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3,2-dihydroquinolin-3-yl)methyl)urea
92	<a href="#">c3civA</a>	Alignment	not modelled	99.5	17 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-mannanase; <b>PDBTitle:</b> crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
93	<a href="#">d2pb1a1</a>	Alignment	not modelled	99.5	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
94	<a href="#">c3jugA</a>	Alignment	not modelled	99.5	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-mannanase; <b>PDBTitle:</b> crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
95	<a href="#">d1yq2a5</a>	Alignment	not modelled	99.5	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
96	<a href="#">c2cksB</a>	Alignment	not modelled	99.5	17 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase e-5; <b>PDBTitle:</b> x-ray crystal structure of the catalytic domain of2 thermobifida fusca endoglucanase cel5a (e5)
97	<a href="#">c3pzvB</a>	Alignment	not modelled	99.4	16 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> c2 crystal form of the endo-1,4-beta-glucanase from bacillus subtilis2 168
98	<a href="#">d1tg7a5</a>	Alignment	not modelled	99.4	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Glycosyl hydrolases family 35 catalytic domain
99	<a href="#">d1tvna1</a>	Alignment	not modelled	99.4	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
100	<a href="#">d1bqca</a>	Alignment	not modelled	99.4	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
101	<a href="#">d7a3ha</a>	Alignment	not modelled	99.4	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
102	<a href="#">d1h4pa</a>	Alignment	not modelled	99.4	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
103	<a href="#">c1us2A</a>	Alignment	not modelled	99.4	15 <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 in2 complex with xylopentaose
104	<a href="#">d1g01a</a>	Alignment	not modelled	99.3	12 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
105	<a href="#">c3cmgA</a>	Alignment	not modelled	99.3	19 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative beta-galactosidase; <b>PDBTitle:</b> crystal structure of putative beta-galactosidase from bacteroides2 fragilis
106	<a href="#">d1jz8a5</a>	Alignment	not modelled	99.3	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
107	<a href="#">c3fn9B</a>	Alignment	not modelled	99.3	16 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative beta-galactosidase; <b>PDBTitle:</b> crystal structure of putative beta-galactosidase from

					bacteroides2 fragilis
108	<a href="#">c1wkyA_</a>	Alignment	not modelled	99.1	15 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,4-mannanase; <b>PDBTitle:</b> crystal structure of alkaline mannanase from bacillus sp. strain jamb-2 602: catalytic domain and its carbohydrate binding module
109	<a href="#">c1j0yD_</a>	Alignment	not modelled	99.1	10 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-amylase; <b>PDBTitle:</b> beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
110	<a href="#">c2w62A_</a>	Alignment	not modelled	99.0	21 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycolipid-anchored surface protein 2; <b>PDBTitle:</b> saccharomyces cerevisiae gas2p in complex with2 laminaripectase
111	<a href="#">d1vema2</a>	Alignment	not modelled	98.9	11 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
112	<a href="#">c3u7vA_</a>	Alignment	not modelled	98.8	18 <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.
113	<a href="#">d2je8a5</a>	Alignment	not modelled	98.8	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
114	<a href="#">c2y8ka_</a>	Alignment	not modelled	98.7	16 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding family 6; <b>PDBTitle:</b> structure of ctgh5-cbm6, an arabinoxylan-specific xylanase.
115	<a href="#">c2vrqB_</a>	Alignment	not modelled	98.5	11 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-l-arabinofuranosidase; <b>PDBTitle:</b> structure of an inactive mutant of arabinofuranosidase from2 thermobacillus xylanilyticus in complex with a3 pentasaccharide
116	<a href="#">c3gm8A_</a>	Alignment	not modelled	98.5	21 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 2, candidate beta-glycosidase; <b>PDBTitle:</b> crystal structure of a beta-glycosidase from bacteroides vulgatus
117	<a href="#">d2cyga1</a>	Alignment	not modelled	98.5	11 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
118	<a href="#">c3thdD_</a>	Alignment	not modelled	98.4	15 <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
119	<a href="#">c3f55A_</a>	Alignment	not modelled	98.3	17 <b>PDB header:</b> hydrolase, allergen <b>Chain:</b> A: <b>PDB Molecule:</b> beta-1,3-glucanase; <b>PDBTitle:</b> crystal structure of the native endo beta-1,3-glucanase (hev b 2), a2 major allergen from hevea brasiliensis (space group p41)
120	<a href="#">c2wnwB_</a>	Alignment	not modelled	98.2	13 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> activated by transcription factor ssrb; <b>PDBTitle:</b> the crystal structure of srj from salmonella typhimurium