

















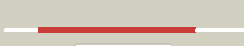
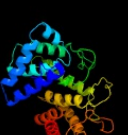




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0365c_(-)_443068_444198
Date	Tue Jul 23 14:50:43 BST 2019
Unique Job ID	9d79dcec81a6c92b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3k7xA_</a>	 Alignment		100.0	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin0763 protein; <b>PDBTitle:</b> crystal structure of the lin0763 protein from listeria innocua.2 northeast structural genomics consortium target lkr23.
2	<a href="#">c4c1sA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 76 mannosidase; <b>PDBTitle:</b> glycoside hydrolase family 76 (mannosidase) bt3792 from2 bacteroides thetaiotaomicron vpi-5482
3	<a href="#">c4bojC_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> alpha-1,6-mannanase; <b>PDBTitle:</b> crystal structure of bacillus circulans tn-31 aman6 in2 complex with mannobiose
4	<a href="#">c4mu9B_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 73; <b>PDBTitle:</b> crystal structure of a putative glycosylhydrolase (bt_3782) from2 bacteroides thetaiotaomicron vpi-5482 at 1.89 a resolution
5	<a href="#">c4v1sA_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-1,6-mannanase; <b>PDBTitle:</b> structure of the gh76 alpha-mannanase bt2949 from2 bacteroides thetaiotaomicron
6	<a href="#">d2d5ja1</a>	 Alignment		99.9	18	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Glycosyl Hydrolase Family 88
7	<a href="#">c2zzrA_</a>	 Alignment		99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> unsaturated glucuronyl hydrolase; <b>PDBTitle:</b> crystal structure of unsaturated glucuronyl hydrolase from2 streptococcus agalactiae
8	<a href="#">c3wiwA_</a>	 Alignment		99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase family 88; <b>PDBTitle:</b> crystal structure of unsaturated glucuronyl hydrolase specific for2 heparin
9	<a href="#">c4ce7B_</a>	 Alignment		99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> unsaturated 3s-rhamnoglycuronyl hydrolase; <b>PDBTitle:</b> crystal structure of a novel unsaturated beta-glucuronyl2 hydrolase enzyme, belonging to family gh105, involved in3 ulvan degradation
10	<a href="#">c4xuvB_</a>	 Alignment		99.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 105 protein; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase family 105 (gh105) enzyme2 from thielavia terrestris
11	<a href="#">c5zhhB_</a>	 Alignment		99.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> structure of cellobiose 2-epimerase from bacillus thermoamylovorans2 b4167

12	<a href="#">d1nc5a_</a>	Alignment		99.6	9	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Hypothetical protein YteR
13	<a href="#">c5x32B_</a>	Alignment		99.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acylglucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of d-mannose isomerase
14	<a href="#">c3gt5A_</a>	Alignment		99.6	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of an n-acetylglucosamine 2-epimerase family protein2 from xylella fastidiosa
15	<a href="#">c3wkgA_</a>	Alignment		99.6	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> crystal structure of cellobiose 2-epimerase in complex with2 glucosylmannose
16	<a href="#">c4wu0B_</a>	Alignment		99.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> similar to yter (bacilus subtilis); <b>PDBTitle:</b> structural analysis of c. acetobutylicum atcc 824 glycoside hydrolase2 from family 105
17	<a href="#">c5zigD_</a>	Alignment		99.5	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> the structure of cellobiose 2-epimerase from spirochaeta thermophila2 dsm 6192
18	<a href="#">c4z4IA_</a>	Alignment		99.5	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> crystal structure of cellobiose 2-epimerase from caldicellulosiruptor2 saccharolyticus dsm 8903
19	<a href="#">c5noaA_</a>	Alignment		99.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> family 88 glycosyl hydrolase; <b>PDBTitle:</b> polysaccharide lyase baccell_00875
20	<a href="#">c3vw5B_</a>	Alignment		99.4	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> cellobiose 2-epimerase; <b>PDBTitle:</b> crystal structure of sugar epimerase from ruminal bacterium
21	<a href="#">c3pmmA_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
22	<a href="#">c2gz6B_</a>	Alignment	not modelled	99.2	9	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetyl-d-glucosamine 2-epimerase; <b>PDBTitle:</b> crystal structure of anabaena sp. ch1 n-acetyl-d-glucosamine 2-2 epimerase at 2.0 a
23	<a href="#">c3k11A_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
24	<a href="#">c3wkaA_</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end beta-l-arabinofuranosidase; <b>PDBTitle:</b> crystal structure of gh127 beta-l-arabinofuranosidase hypba1 from2 bifidobacterium longum arabinose complex form
25	<a href="#">c4qk0C_</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gh127 beta-l-arabinofuranoside; <b>PDBTitle:</b> crystal structure of ara127n-se, a gh127 beta-l-arabinofuranosidase2 from geobacillus stearothermophilus t6
26	<a href="#">c5mqoA_</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end beta-l-arabinofuranosidase; <b>PDBTitle:</b> glycoside hydrolase bt_1003
27	<a href="#">c6ex6A_</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> six-hairpin glycosidase; <b>PDBTitle:</b> the gh127, beta-arabinofuranosidase, bt3674
28	<a href="#">c5opjA_</a>	Alianment	not modelled	98.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rhamnogalacturonan lyase;

						<b>PDBTitle:</b> rhamnogalacturonan lyase
29	<a href="#">d2afaa1</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> N-acylglucosamine (NAG) epimerase
30	<a href="#">d1fp3a_</a>	Alignment	not modelled	98.4	12	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> N-acylglucosamine (NAG) epimerase
31	<a href="#">c3h71C_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of endoglucanase-related protein from vibrio2 parahaemolyticus
32	<a href="#">c1ga2A_</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase 9g; <b>PDBTitle:</b> the crystal structure of endoglucanase 9g from clostridium2 cellulolyticum complexed with cellobiose
33	<a href="#">c4pw2A_</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-glucuronyl c5 epimerase b; <b>PDBTitle:</b> crystal structure of d-glucuronyl c5 epimerase
34	<a href="#">d1g87a1</a>	Alignment	not modelled	97.2	13	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
35	<a href="#">c5dgrB_</a>	Alignment	not modelled	97.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative endoglucanase-related protein; <b>PDBTitle:</b> crystal structure of gh9 exo-beta-d-glucosaminidase pbpra0520,2 glucosamine complex
36	<a href="#">c6gdtC_</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> carbohydrate <b>Chain:</b> C: <b>PDB Molecule:</b> endoglucanase-related protein; <b>PDBTitle:</b> crystal structure of exo-glucosidase/glucosaminidase vc0615 from2 vibrio cholerae
37	<a href="#">c2xfgA_</a>	Alignment	not modelled	96.9	14	<b>PDB header:</b> hydrolase/sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase 1; <b>PDBTitle:</b> reassembly and co-crystallization of a family 9 processive2 endoglucanase from separately expressed gh9 and cbm3c3 modules
38	<a href="#">c2yikA_</a>	Alignment	not modelled	96.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> catalytic domain of clostridium thermocellum celt
39	<a href="#">d1clca1</a>	Alignment	not modelled	96.8	14	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
40	<a href="#">c5u2oA_</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> j30 cch; <b>PDBTitle:</b> crystal structure of zn-binding triple mutant of gh family 92 endoglucanase j30
41	<a href="#">c4q88B_</a>	Alignment	not modelled	96.6	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> glycosyl hydrolase family 88 from bacteroides vulgatus
42	<a href="#">c5gxyA_</a>	Alignment	not modelled	96.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucanase; <b>PDBTitle:</b> crystal structure of endoglucanase celq from clostridium thermocellum2 complexed with cellobiose and tris
43	<a href="#">c1ut9A_</a>	Alignment	not modelled	96.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose 1,4-beta-cellobiosidase; <b>PDBTitle:</b> structural basis for the exocellulase activity of the2 cellobiohydrolase cbha from c. thermocellum
44	<a href="#">c3gzkA_</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulase; <b>PDBTitle:</b> structure of a. acidocaldarius cellulase cela
45	<a href="#">c1clcA_</a>	Alignment	not modelled	96.4	14	<b>PDB header:</b> glycosyl hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase celd; ec: 3.2.1.4; <b>PDBTitle:</b> three-dimensional structure of endoglucanase d at 1.92 angstroms resolution
46	<a href="#">c3x17B_</a>	Alignment	not modelled	96.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> crystal structure of metagenome-derived glycoside hydrolase family 92 endoglucanase
47	<a href="#">d1ks8a_</a>	Alignment	not modelled	96.3	9	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
48	<a href="#">d1ia6a_</a>	Alignment	not modelled	96.0	12	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
49	<a href="#">c6dhtA_</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xyloglucan-specific endo-beta-1,4-glucanase bogh9a; <b>PDBTitle:</b> bacteroides ovatus gh9 bacova_02649
50	<a href="#">c3wc3A_</a>	Alignment	not modelled	95.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1, 4-beta-glucanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-glucanase from eisenia fetida
51	<a href="#">d1tf4a1</a>	Alignment	not modelled	95.2	13	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
52	<a href="#">d1dl2a_</a>	Alignment	not modelled	95.1	12	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Seven-hairpin glycosidases <b>Family:</b> Class I alpha-1,2-mannosidase, catalytic domain
53	<a href="#">c5a29A_</a>	Alignment	not modelled	94.7	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolysaccharonate lyase; <b>PDBTitle:</b> family 2 pectate lyase from vibrio vulnificus
54	<a href="#">c1g6iA_</a>	Alignment	not modelled	94.5	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> class i alpha-1,2-mannosidase; <b>PDBTitle:</b> crystal structure of the yeast alpha-1,2-mannosidase with bound 1-2 deoxymannojirimycin at 1.59 a resolution

55	<a href="#">d1ut9a1</a>	Alignment	not modelled	93.9	11	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
56	<a href="#">d1nxca</a>	Alignment	not modelled	93.9	14	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Seven-hairpin glycosidases <b>Family:</b> Class I alpha-1,2-mannosidase, catalytic domain
57	<a href="#">c6fhnA</a>	Alignment	not modelled	93.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein; <b>PDBTitle:</b> structural dynamics and catalytic properties of a multi-modular2 xanthanase (pt derivative)
58	<a href="#">c2v8kA</a>	Alignment	not modelled	93.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pectate lyase; <b>PDBTitle:</b> structure of a family 2 pectate lyase in complex with trigalacturonic2 acid
59	<a href="#">c3a0oB</a>	Alignment	not modelled	92.9	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oligo alginate lyase; <b>PDBTitle:</b> crystal structure of alginate lyase from agrobacterium tumefaciens c58
60	<a href="#">c1x9dA</a>	Alignment	not modelled	92.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha- <b>PDBTitle:</b> crystal structure of human class i alpha-1,2-mannosidase in complex2 with thio-disaccharide substrate analogue
61	<a href="#">d1x9da1</a>	Alignment	not modelled	92.7	16	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Seven-hairpin glycosidases <b>Family:</b> Class I alpha-1,2-mannosidase, catalytic domain
62	<a href="#">c4zlgA</a>	Alignment	not modelled	89.0	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative b-glycan phosphorylase; <b>PDBTitle:</b> cellobionic acid phosphorylase - gluconic acid complex
63	<a href="#">d1kwfa</a>	Alignment	not modelled	88.3	14	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
64	<a href="#">c1js4B</a>	Alignment	not modelled	83.9	10	<b>PDB header:</b> glycosyl hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo/exocellulase e4; <b>PDBTitle:</b> endo/exocellulase:cellobiose from thermomonospora
65	<a href="#">d1wzza1</a>	Alignment	not modelled	83.7	15	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
66	<a href="#">d1hcua</a>	Alignment	not modelled	83.3	13	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Seven-hairpin glycosidases <b>Family:</b> Class I alpha-1,2-mannosidase, catalytic domain
67	<a href="#">c2fuqA</a>	Alignment	not modelled	81.8	8	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> heparinase ii protein; <b>PDBTitle:</b> crystal structure of heparinase ii
68	<a href="#">c1v7wA</a>	Alignment	not modelled	78.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> chitobiose phosphorylase; <b>PDBTitle:</b> crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcna2
69	<a href="#">c4ayqA</a>	Alignment	not modelled	77.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mannosyl-oligosaccharide 1,2-alpha-mannosidase; <b>PDBTitle:</b> structure of the gh47 processing alpha-1,2-mannosidase from2 caulobacter strain k31 in complex with mannoimidazole
70	<a href="#">c5czlA</a>	Alignment	not modelled	76.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucanase; <b>PDBTitle:</b> crystal structure of a novel gh8 endo-beta-1,4-glucanase from an2 achatina fulica gut metagenomic library
71	<a href="#">c3cihA</a>	Alignment	not modelled	75.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alpha-rhamnosidase; <b>PDBTitle:</b> crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron
72	<a href="#">c6fhjA</a>	Alignment	not modelled	71.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein,protein; <b>PDBTitle:</b> structural dynamics and catalytic properties of a multi-modular2 xanthanase, native.
73	<a href="#">c3qxqD</a>	Alignment	not modelled	68.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> structure of the bacterial cellulose synthase subunit z in complex2 with cellopentaose
74	<a href="#">c1krfA</a>	Alignment	not modelled	63.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mannosyl-oligosaccharide alpha-1,2-mannosidase; <b>PDBTitle:</b> structure of p. citrinum alpha 1,2-mannosidase reveals the basis for2 differences in specificity of the er and golgi class i enzymes
75	<a href="#">d2ri9a1</a>	Alignment	not modelled	63.1	16	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Seven-hairpin glycosidases <b>Family:</b> Class I alpha-1,2-mannosidase, catalytic domain
76	<a href="#">c3renB</a>	Alignment	not modelled	58.1	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase, family 8; <b>PDBTitle:</b> cpf_2247, a novel alpha-amylase from clostridium perfringens
77	<a href="#">c4xhcB</a>	Alignment	not modelled	56.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-l-rhamnosidase; <b>PDBTitle:</b> rhamnosidase from klebsiella oxytoca with rhamnose bound
78	<a href="#">c2cqtA</a>	Alignment	not modelled	52.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose phosphorylase; <b>PDBTitle:</b> crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
79	<a href="#">c3e6uA</a>	Alignment	not modelled	45.1	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> lanc-like protein 1; <b>PDBTitle:</b> crystal structure of human lanc1
80	<a href="#">c4ok2A</a>	Alignment	not modelled	45.1	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative alginate lyase;

						<b>PDBTitle:</b> crystal structure of alg17c mutant y258a
81	<a href="#">c5dztA_</a>	Alignment	not modelled	44.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> cylm; <b>PDBTitle:</b> crystal structure of class ii lanthipeptide synthetase cylm in complex2 with amp
82	<a href="#">c3htuE_</a>	Alignment	not modelled	37.7	11	<b>PDB header:</b> protein transport <b>Chain:</b> E; <b>PDB Molecule:</b> vacuolar protein-sorting-associated protein 25; <b>PDBTitle:</b> crystal structure of the human vps25-vps20 subcomplex
83	<a href="#">c5mqrA_</a>	Alignment	not modelled	37.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-l-arabinobiosidase; <b>PDBTitle:</b> sialidase bt_1020
84	<a href="#">c5x3aB_</a>	Alignment	not modelled	35.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glucanase; <b>PDBTitle:</b> apo structure of beta-1,3-1,4-glucanase from paenibacillus sp.x4
85	<a href="#">c4fnvA_</a>	Alignment	not modelled	32.8	8	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> heparinase iii protein, heparitin sulfate lyase; <b>PDBTitle:</b> crystal structure of heparinase iii
86	<a href="#">d1ulva1</a>	Alignment	not modelled	32.8	13	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Bacterial glucoamylase C-terminal domain-like
87	<a href="#">c5no8A_</a>	Alignment	not modelled	30.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> baccell_00875; <b>PDBTitle:</b> polysaccharide lyase baccell_00875
88	<a href="#">d1v5da_</a>	Alignment	not modelled	30.3	12	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
89	<a href="#">c3t33A_</a>	Alignment	not modelled	28.6	12	<b>PDB header:</b> signaling protein receptor <b>Chain:</b> A; <b>PDB Molecule:</b> g protein coupled receptor; <b>PDBTitle:</b> crystal structure of arabidopsis gcr2
90	<a href="#">c4q2bA_</a>	Alignment	not modelled	19.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endo-1,4-beta-d-glucanase; <b>PDBTitle:</b> the crystal structure of an endo-1,4-d-glucanase from pseudomonas2 putida kt2440
91	<a href="#">c3nfvA_</a>	Alignment	not modelled	18.8	11	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> alginate lyase; <b>PDBTitle:</b> crystal structure of an alginate lyase (bacova_01668) from bacteroides2 ovatus at 1.95 a resolution
92	<a href="#">c5cd2A_</a>	Alignment	not modelled	18.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endo-1,4-d-glucanase; <b>PDBTitle:</b> the crystal structure of endo-1,4-d-glucanase from vibrio fischeri2 es114
93	<a href="#">c2okxB_</a>	Alignment	not modelled	18.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> rhamnosidase b; <b>PDBTitle:</b> crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
94	<a href="#">c1xb4C_</a>	Alignment	not modelled	16.4	8	<b>PDB header:</b> unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> hypothetical 23.6 kda protein in yuh1-ura8 intergenic <b>PDBTitle:</b> crystal structure of subunit vps25 of the endosomal trafficking2 complex escrt-ii
95	<a href="#">d1xb4a2</a>	Alignment	not modelled	15.1	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Vacuolar sorting protein domain
96	<a href="#">d2g0da1</a>	Alignment	not modelled	14.5	9	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> LanC-like <b>Family:</b> LanC-like
97	<a href="#">c6m9sC_</a>	Alignment	not modelled	14.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> sznf; <b>PDBTitle:</b> crystal structure of semet sznf from streptomyces achromogenes var.2 streptozoticus nrri 2697
98	<a href="#">d1v7wa1</a>	Alignment	not modelled	13.8	15	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Glycosyltransferase family 36 C-terminal domain
99	<a href="#">d1vija4</a>	Alignment	not modelled	13.6	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Transglutaminase core