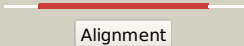

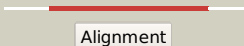

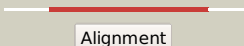







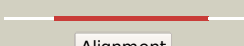




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1502_(-)_1692930_1693829
Date	Fri Aug 2 13:30:08 BST 2019
Unique Job ID	608e2017ec7b2963

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5muiA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> glycoside hydrolase bt_0996
2	<a href="#">c3r67A_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative glycosidase; <b>PDBTitle:</b> crystal structure of a putative glycosidase (bt_4094) from bacteroides2 thetaiotaomicron vpi-5482 at 2.30 a resolution
3	<a href="#">c5b0rA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> lin0857 protein; <b>PDBTitle:</b> beta-1,2-mannobiose phosphorylase from listeria innocua - beta-1,2-2 mannobiose complex
4	<a href="#">c3qc2A_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of a glycosyl hydrolase (bacova_03624) from2 bacteroides ovatus at 2.30 a resolution
5	<a href="#">d1vkda_</a>	 Alignment		100.0	16	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> TM1225-like predicted glycosylases
6	<a href="#">c4onzA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative glycoside hydrolase; <b>PDBTitle:</b> crystal structure of a putative glycoside hydrolase (bacova_02161)2 from bacteroides ovatus atcc 8483 at 1.85 a resolution
7	<a href="#">c3tawA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical glycoside hydrolase; <b>PDBTitle:</b> crystal structure of a putative glycoside hydrolase (bdj_3141) from2 parabacteroides distasonis atcc 8503 at 1.70 a resolution
8	<a href="#">c4udgB_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> uhgb_mp; <b>PDBTitle:</b> crystal structure of b-1,4-mannopyranosyl-chitobiose2 phosphorylase at 1.60 angstrom in complex with n-3 acetylglucosamine and inorganic phosphate
9	<a href="#">c5aydB_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-1,4-mannooligosaccharide phosphorylase; <b>PDBTitle:</b> crystal structure of ruminococcus albus beta-(1,4)-2 mannooigosaccharide phosphorylase (ramp2) in complexes with3 phosphate
10	<a href="#">c1yifC_</a>	 Alignment		100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> beta-1,4-xylosidase; <b>PDBTitle:</b> crystal structure of beta-1,4-xylosidase from bacillus subtilis, new2 york structural genomics consortium
11	<a href="#">c1yrzB_</a>	 Alignment		100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> xylan beta-1,4-xylosidase; <b>PDBTitle:</b> crystal structure of xylan beta-1,4-xylosidase from bacillus2 halodurans c-125

12	<a href="#">c5jzB</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> non-reducing end alpha-l-arabinofuranosidase bogh43b; <b>PDBTitle:</b> bacteroides ovatus xyloglucan pul gh43b
13	<a href="#">c2exiA</a>	Alignment		100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-d-xylosidase; <b>PDBTitle:</b> structure of the family43 beta-xylosidase d15g mutant from geobacillus2 stearothermophilus
14	<a href="#">c4u6dB</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical periplasmic protein; <b>PDBTitle:</b> zg3615, a family 117 glycoside hydrolase in complex with beta-3,6-2 anhydro-l-galactose
15	<a href="#">c5aycA</a>	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-o-beta-d-mannosyl-d-glucose phosphorylase; <b>PDBTitle:</b> crystal structure of ruminococcus albus 4-o-beta-d-mannosyl-d-glucose2 phosphorylase (ramp1) in complexes with sulfate and 4-o-beta-d-3 mannosyl-d-glucose
16	<a href="#">c4mlgF</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> structure of rs223-beta-xylosidase
17	<a href="#">d1y7ba2</a>	Alignment		100.0	9	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
18	<a href="#">c1yi7C</a>	Alignment		100.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-xylosidase, family 43 glycosyl hydrolase; <b>PDBTitle:</b> beta-d-xylosidase (selenomethionine) xynd from clostridium2 acetobutylicum
19	<a href="#">c5gIkB</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 43; <b>PDBTitle:</b> crystal structure of coxyl43, gh43 beta-xylosidase/alpha-2 arabinofuranosidase from a compost microbial metagenome, calcium-free3 form.
20	<a href="#">c5a8dA</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate binding family 6; <b>PDBTitle:</b> the high resolution structure of a novel alpha-l-arabinofuranosidase2 (ctgh43) from clostridium thermocellum atcc 27405
21	<a href="#">d1yifa2</a>	Alignment	not modelled	100.0	9	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
22	<a href="#">c5z5hA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase; <b>PDBTitle:</b> crystal structure of a thermostable glycoside hydrolase family 432 {beta}-1,4-xylosidase from geobacillus thermoleovorans it-08 in3 complex with d-xylose
23	<a href="#">d2exha2</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
24	<a href="#">d1wl7a1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
25	<a href="#">d1uyPa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> Glycosyl hydrolases family 32 N-terminal domain
26	<a href="#">c3c7hA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> crystal structure of glycoside hydrolase family 43 arabinoxylan2 arabinofuranohydrolase from bacillus subtilis in complex with axos-4-3 0.5.
27	<a href="#">c6ms3A</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 43; <b>PDBTitle:</b> crystal structure of the gh43 protein blxynb mutant (k247s) from2 bacillus licheniformis
28	<a href="#">c3watA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-o-beta-d-mannosyl-d-glucose phosphorylase; <b>PDBTitle:</b> crystal structure of 4-o-beta-d-mannosyl-d-glucose

						phosphorylase mgp2 complexed with man+glc
29	<a href="#">d1yrza2</a>	Alignment	not modelled	100.0	11	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
30	<a href="#">c4novA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xylosidase/arabinofuranosidase xsa43e; <b>PDBTitle:</b> xsa43e, a gh43 family enzyme from butyrivibrio proteoclasticus
31	<a href="#">c3qefB</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-xylosidase/alpha-l-arabinofuranosidase, gly43n; <b>PDBTitle:</b> the structure and function of an arabinan-specific alpha-1,2-arabinofuranosidase identified from screening the activities of 3 bacterial gh43 glycoside hydrolases
32	<a href="#">c4u6bC</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> conserved hypothetical lipoprotein; <b>PDBTitle:</b> zg3597, a family 117 glycoside hydrolase, produced by the marine2 bacterium zobellia galactanivorans
33	<a href="#">c3p2nB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3,6-anhydro-alpha-l-galactosidase; <b>PDBTitle:</b> discovery and structural characterization of a new glycoside hydrolase2 family abundant in coastal waters that was annotated as 'hypothetical3 protein'
34	<a href="#">c5ho0A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular arabinanase; <b>PDBTitle:</b> crystal structure of abna (closed conformation), a gh43 extracellular2 arabinanase from geobacillus stearothermophilus
35	<a href="#">c1w2tE</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> beta fructosidase; <b>PDBTitle:</b> beta-fructosidase from thermotoga maritima in complex with raffinose
36	<a href="#">c5joxA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> non-reducing end alpha-l-arabinofuranosidase bogh43a; <b>PDBTitle:</b> bacteroides ovatus xyloglucan pul gh43a in complex with aradnj
37	<a href="#">c4qqsB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase family 43; <b>PDBTitle:</b> crystal structure of a thermostable family-43 glycoside hydrolase
38	<a href="#">d1gyha</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
39	<a href="#">c3akqA</a>	Alignment	not modelled	99.9	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative secreted alpha l-arabinofuranosidase ii; <b>PDBTitle:</b> crystal structure of exo-1,5-alpha-l-arabinofuranosidase complexed2 with alpha-1,5-l-arabinofuranobiose
40	<a href="#">c3qz4B</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endo-1,4-beta-xylanase d; <b>PDBTitle:</b> crystal structure of an endo-1,4-beta-xylanase d (bt_3675) from2 bacteroides thetaiotaomicron vpi-5482 at 1.74 a resolution
41	<a href="#">c3r4zA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl hydrolase family 32, n terminal; <b>PDBTitle:</b> crystal structure of alpha-neoagarobiose hydrolase (alpha-nabh) in2 complex with alpha-d-galactopyranose from saccharophagus degradans 2-3 40
42	<a href="#">c3kstA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-xylanase (np_811807.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.70 a resolution
43	<a href="#">c3cpnA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylosidase, family 43 glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of beta-xylosidase, family 43 glycosyl2 hydrolase from clostridium acetobutylicum
44	<a href="#">c5m8bB</a>	Alignment	not modelled	99.9	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-l-arabinofuranosidase ii; <b>PDBTitle:</b> crystal structure of alpha-l-arabinofuranosidase from lactobacillus2 brevis
45	<a href="#">c3lv4B</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycoside hydrolase xyia; <b>PDBTitle:</b> crystal structure of the glycoside hydrolase, family 43 xyia protein2 from bacillus licheniformis. northeast structural genomics consortium3 target bir14.
46	<a href="#">c5c0pA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-arabinase; <b>PDBTitle:</b> the crystal structure of endo-arabinase from bacteroides2 thetaiotaomicron vpi-5482
47	<a href="#">d1uv4a1</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> alpha-L-arabinanase-like
48	<a href="#">c6n1bA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate-binding protein; <b>PDBTitle:</b> crystal structure of an n-acetylgalactosamine deacetylase from f.2 plautii in complex with blood group b trisaccharide
49	<a href="#">c4n2zA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gh62 arabinofuranosidase; <b>PDBTitle:</b> crystal structure of the alpha-l-arabinofuranosidase paabf62a from2 podospira anserina in complex with celotriose
50	<a href="#">c6r3uA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 32; <b>PDBTitle:</b> endo-levanase bt1760 mutant e221a from bacteroides thetaiotaomicron2 complexed with levantetraose
51	<a href="#">c5b6tB</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl hydrolase family 62 protein; <b>PDBTitle:</b> catalytic domain of coprinopsis cinerea gh62 alpha-l-2 arabinofuranosidase complexed with pb
52	<a href="#">c2niA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-fructofuranosidase;

52	<a href="#">c3vjaA</a>	Alignment	not modelled	99.9	10	<b>PDBTitle:</b> beta-fructofuranosidase from bifidobacterium longum - complex with2 fructose <b>PDB header:</b> hydrolase
53	<a href="#">c4n2rA</a>	Alignment	not modelled	99.9	13	<b>Chain:</b> A; <b>PDB Molecule:</b> alpha-l-arabinofuranosidase umabf62a; <b>PDBTitle:</b> crystal structure of the alpha-l-arabinofuranosidase umabf62a from2 ustilago maydis in complex with l-arabinofuranose
54	<a href="#">c5ubjA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-l-arabinofuranosidase axha-2; <b>PDBTitle:</b> structure of an alpha-l-arabinofuranosidase (gh62) from aspergillus2 nidulans
55	<a href="#">c6euiA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-glucanase; <b>PDBTitle:</b> the gh43, beta 1,3 galactosidase, bt3683 with galactose
56	<a href="#">c5msxA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative endo-1,4-beta-xylanase; <b>PDBTitle:</b> glycoside hydrolase bt_3662
57	<a href="#">c1y9gA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> exo-inulinase; <b>PDBTitle:</b> crystal structure of exo-inulinase from aspergillus awamori complexed2 with fructose
58	<a href="#">c3zxB</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> hiaxhd3; <b>PDBTitle:</b> engineering the active site of a gh43 glycoside hydrolase generates a2 biotechnologically significant enzyme that displays both endo-3 xylanase and exo-arabinofuranosidase activity
59	<a href="#">d1y4wa2</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> Glycosyl hydrolases family 32 N-terminal domain
60	<a href="#">c4pviA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> gh62 hydrolase; <b>PDBTitle:</b> crystal structure of gh62 hydrolase in complex with xylotriose
61	<a href="#">c3vt2B</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> ricin b lectin; <b>PDBTitle:</b> crystal structure of ct1,3gal43a in complex with isopropyl-beta-d-2 thiogalactoside
62	<a href="#">c2aezA</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> fructan 1-exohydrolase iia; <b>PDBTitle:</b> crystal structure of fructan 1-exohydrolase iia (e201q) from cichorium2 intybus in complex with 1-kestose
63	<a href="#">c4eqvA</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> invertase 2; <b>PDBTitle:</b> structure of saccharomyces cerevisiae invertase
64	<a href="#">c6eujC</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> beta-glucanase; <b>PDBTitle:</b> the gh43, beta 1,3 galactosidase, bt0265
65	<a href="#">c5flwB</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> exo-beta-1,3-galactanase; <b>PDBTitle:</b> crystal structure of putative exo-beta-1,3-galactanase from2 bifidobacterium bifidum s17
66	<a href="#">c2ac1A</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> invertase; <b>PDBTitle:</b> crystal structure of a cell-wall invertase from arabidopsis thaliana
67	<a href="#">c3sc7X</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> X; <b>PDB Molecule:</b> inulinase; <b>PDBTitle:</b> first crystal structure of an endo-inulinase, from aspergillus ficuum:2 structural analysis and comparison with other gh32 enzymes.
68	<a href="#">c3kf5A</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> invertase; <b>PDBTitle:</b> structure of invertase from schwanniomyces occidentalis
69	<a href="#">c3ugfB</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> sucrose:(sucrose/fructan) 6-fructosyltransferase; <b>PDBTitle:</b> crystal structure of a 6-sst/6-sft from pachysandra terminalis
70	<a href="#">c3nqhA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycosyl hydrolase; <b>PDBTitle:</b> crystal structure of a glycosyl hydrolase (bt_2959) from bacteroides2 thetaiotaomicron vpi-5482 at 2.11 a resolution
71	<a href="#">c5xh9A</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> extracellular invertase; <b>PDBTitle:</b> aspergillus kawachii beta-fructofuranosidase
72	<a href="#">c5fk8B</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-fructofuranosidase; <b>PDBTitle:</b> structure of d80a-fructofuranosidase from xanthophyllomyces2 dendrorhous complexed with neo-erlose
73	<a href="#">c4ffhA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> levan fructotransferase; <b>PDBTitle:</b> crystal structure of levan fructotransferase d54n mutant from2 arthrobacter ureafaciens in complex with sucrose
74	<a href="#">c4d47D</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> levansucrase; <b>PDBTitle:</b> x-ray structure of the levansucrase from erwinia amylovora
75	<a href="#">c3lemA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> fructosyltransferase; <b>PDBTitle:</b> crystal structure of fructosyltransferase (d191a) from a. japonicus in2 complex with nystose
76	<a href="#">c3bykA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> levansucrase; <b>PDBTitle:</b> crystal structure of b. subtilis levansucrase mutant d247a
77	<a href="#">d1oyga</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> Levansucrase

78	<a href="#">d2b4wa1</a>	Alignment	not modelled	99.2	8	<b>Fold:</b> 5-bladed beta-propeller <b>Superfamily:</b> Arabinanase/levansucrase/invertase <b>Family:</b> LmjF10.1260-like
79	<a href="#">c3vsrA</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-fructofuranosidase; <b>PDBTitle:</b> microbacterium saccharophilum k-1 beta-fructofuranosidase catalytic2 domain
80	<a href="#">c3wpzA</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-fructofuranosidase; <b>PDBTitle:</b> microbacterium saccharophilum k-1 beta-fructofuranosidase mutant2 t47s/s200t/f447p/f470y/p500s
81	<a href="#">c5hx0A</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein dfer_1899; <b>PDBTitle:</b> crystal structure of unknown function protein dfer_18992 from dyadobacter fermentans dsm 18053
82	<a href="#">c2yfrA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> levansucrase; <b>PDBTitle:</b> crystal structure of inulosucrase from lactobacillus2 johnsonii ncc533
83	<a href="#">c1w18A</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> levansucrase; <b>PDBTitle:</b> crystal structure of levansucrase from gluconacetobacter2 diazotrophicus
84	<a href="#">d1w8oa3</a>	Alignment	not modelled	98.5	13	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
85	<a href="#">c4fj6C</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> glycoside hydrolase family 33, candidate sialidase; <b>PDBTitle:</b> crystal structure of a glycoside hydrolase family 33, candidate2 sialidase (bdi_2946) from parabacteroides distasonis atcc 8503 at 3.190 a resolution
86	<a href="#">d1w0pa3</a>	Alignment	not modelled	98.3	13	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
87	<a href="#">d1n1ta2</a>	Alignment	not modelled	98.2	16	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
88	<a href="#">d3sila</a>	Alignment	not modelled	98.1	11	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
89	<a href="#">c3a72A</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> exo-arabinanase; <b>PDBTitle:</b> high resolution structure of penicillium chrysogenum alpha-l-2 arabinanase complexed with arabinobiose
90	<a href="#">c1n1vA</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> trypanosoma rangeli sialidase in complex with dana
91	<a href="#">c4bbwA</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> sialidase (neuraminidase); <b>PDBTitle:</b> the crystal structure of sialidase vpi 5482 (btsa) from bacteroides2 thetaiotaomicron
92	<a href="#">c2berA</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> bacterial sialidase; <b>PDBTitle:</b> y370g active site mutant of the sialidase from2 micromonospora viridifaciens in complex with beta-neu5ac3 (sialic acid).
93	<a href="#">c2w38A</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> crystal structure of the pseudaminidase from pseudomonas aeruginosa
94	<a href="#">c2vk7A</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> exo-alpha-sialidase; <b>PDBTitle:</b> the structure of clostridium perfringens nani sialidase and2 its catalytic intermediates
95	<a href="#">d2ah2a2</a>	Alignment	not modelled	97.4	14	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
96	<a href="#">c2xcyA</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> extracellular sialidase/neuraminidase, putative; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus sialidase
97	<a href="#">c2w5oA</a>	Alignment	not modelled	97.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> alpha-l-arabinofuranosidase; <b>PDBTitle:</b> complex structure of the gh93 alpha-l-arabinofuranosidase2 of fusarium graminearum with arabinobiose
98	<a href="#">c2jkbA</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> sialidase b; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae nanb in2 complex with 2,7-anhydro-neu5ac
99	<a href="#">d2slia2</a>	Alignment	not modelled	97.2	16	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
100	<a href="#">c4irtA</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative neuraminidase (bacova_03493) from2 bacteroides ovatus atcc 8483 at 1.74 a resolution
101	<a href="#">d1so7a</a>	Alignment	not modelled	97.1	11	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> Sialidases <b>Family:</b> Sialidases (neuraminidases)
102	<a href="#">c2w20B</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> sialidase a; <b>PDBTitle:</b> structure of the catalytic domain of the native nana2 sialidase from streptococcus pneumoniae
103	<a href="#">c2sliA</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> intramolecular trans-sialidase;

103	<a href="#">c23iiA_</a>	Alignment	not modelled	97.1	10	<b>PDB header:</b> leech intramolecular trans-sialidase complexed with 2,7-2 anhydro-neu5ac, the reaction product
104	<a href="#">c5mqrA_</a>	Alignment	not modelled	96.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-l-arabinobiosidase; <b>PDBTitle:</b> sialidase bt_1020
105	<a href="#">c4yw5A_</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> neuraminidase c; <b>PDBTitle:</b> crystal structure of streptococcus pneumoniae nanc, complex with2 oseltamivir carboxylate
106	<a href="#">c2vvzA_</a>	Alignment	not modelled	94.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sialidase a; <b>PDBTitle:</b> structure of the catalytic domain of streptococcus pneumoniae2 sialidase nana
107	<a href="#">c1w0pA_</a>	Alignment	not modelled	92.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> vibrio cholerae sialidase with alpha-2,6-sialyllactose
108	<a href="#">c1kitA_</a>	Alignment	not modelled	92.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sialidase; <b>PDBTitle:</b> vibrio cholerae neuraminidase
109	<a href="#">c4hbsA_</a>	Alignment	not modelled	89.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of a putative hydrolase (bacova_04882) from2 bacteroides ovatus atcc 8483 at 2.80 a resolution
110	<a href="#">c5uasA_</a>	Alignment	not modelled	55.1	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ulvanlyase-pl25; <b>PDBTitle:</b> structure of a new family of polysaccharide lyase pl25-ulvanlyase2 bound to -[glca(1-4)rha3s]-
111	<a href="#">c6bypA_</a>	Alignment	not modelled	24.7	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> short ulvan lyase; <b>PDBTitle:</b> structure of pl24 family polysaccharide lyase-lor107
112	<a href="#">c4ud1B_</a>	Alignment	not modelled	23.3	24	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> n protein; <b>PDBTitle:</b> structure of the n terminal domain of the mers cov nucleocapsid
113	<a href="#">c5n4kA_</a>	Alignment	not modelled	22.0	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoprotein; <b>PDBTitle:</b> n-terminal domain of a human coronavirus nl63 nucleocapsid protein