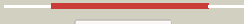



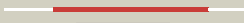





















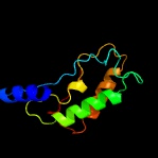






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0062_(celA1)_65549_66691
Date	Tue Jul 23 14:50:09 BST 2019
Unique Job ID	ecd200071223270d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uoza_	 Alignment		100.0	99	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
2	c5xyhA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: cbsa; PDBTitle: crystal structure of catalytic domain of 1,4-beta-cellobiosidase2 (cbsa) from xanthomonas oryzae pv. oryzae
3	c3vohA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: cellobiohydrolase; PDBTitle: cccl6a catalytic domain complexed with cellobiose
4	d1qjwa_	 Alignment		100.0	30	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
5	c5xczA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: glucanase; PDBTitle: structure of the cellobiohydrolase cel6a from phanerochaete2 chrysosporium in complex with cellobiose at 2.1 angstrom
6	d1oc7a_	 Alignment		100.0	30	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
7	d1dysa_	 Alignment		100.0	30	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
8	c3a64A_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: cellobiohydrolase; PDBTitle: crystal structure of cccl6c, a glycoside hydrolase family 62 enzyme, from coprinopsis cinerea
9	c4b4fB_	 Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,4-exocellulase; PDBTitle: thermobifida fusca cel6b(e3) co-crystallized with cellobiose
10	c5jx6C_	 Alignment		100.0	31	PDB header: hydrolase Chain: C: PDB Molecule: glucanase; PDBTitle: gh6 orpinomyces sp. y102 enzyme
11	c6faoA_	 Alignment		100.0	48	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 6; PDBTitle: discovery and characterization of a thermostable gh6 endoglucanase2 from a compost metagenome

12	d2bodx1	Alignment		100.0	43	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
13	c4w86B	Alignment		61.6	11	PDB header: hydrolase Chain: B: PDB Molecule: xyloglucan-specific endo-beta-1,4-glucanase; PDBTitle: crystal structure of xeg5a, a gh5 xyloglucan-specific endo-beta-1,4-2 glucanase from ruminal metagenomic library, in complex with glucose3 and tris
14	c4w7wA	Alignment		56.5	12	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: high-resolution structure of xacel5a in complex with cellopentaose
15	c3w0kA	Alignment		50.9	14	PDB header: hydrolase Chain: A: PDB Molecule: bifunctional endomannanase/endoglucanase; PDBTitle: crystal structure of a glycoside hydrolase
16	c4lx4D	Alignment		50.1	10	PDB header: hydrolase Chain: D: PDB Molecule: endoglucanase(endo-1,4-beta-glucanase)protein; PDBTitle: crystal structure determination of pseudomonas stutzeri endoglucanase2 cel5a using a twinned data set
17	c5tnvA	Alignment		47.2	13	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family protein 2; PDBTitle: crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
18	c3ne8A	Alignment		46.1	19	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
19	c4ee9A	Alignment		43.7	8	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of the rbcel1 endo-1,4-glucanase
20	c3u7bB	Alignment		40.4	20	PDB header: hydrolase Chain: B: PDB Molecule: endo-1,4-beta-xylanase; PDBTitle: a new crystal structure of a fusarium oxysporum gh10 xylanase reveals2 the presence of an extended loop on top of the catalytic cleft
21	d1d8wa	Alignment	not modelled	39.1	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: L-rhamnose isomerase
22	d2pw4a1	Alignment	not modelled	37.2	50	Fold: jann2411-like Superfamily: jann2411-like Family: jann2411-like
23	d1tz9a	Alignment	not modelled	36.7	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
24	d3byqa1	Alignment	not modelled	35.5	35	Fold: Bacillus chorismate mutase-like Superfamily: BB2672-like Family: BB2672-like
25	d2pb1a1	Alignment	not modelled	35.2	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
26	c3obeB	Alignment	not modelled	33.8	7	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
27	c3ndyA	Alignment	not modelled	33.4	10	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase d; PDBTitle: the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
28	c4nf7A	Alignment	not modelled	33.3	9	PDB header: hydrolase Chain: A: PDB Molecule: endo-1,4-beta-glucanase cel5c; PDBTitle: crystal structure of the gh5 family catalytic domain of endo-1,4-beta-2 glucanase cel5c from butyrivibrio proteoclasticus.

29	c5w7dA_	Alignment	not modelled	31.4	21	PDB header: hydrolase Chain: A: PDB Molecule: acyloxyacyl hydrolase; PDBTitle: murine acyloxyacyl hydrolase (aoah), s262a mutant
30	d1bxbA_	Alignment	not modelled	30.6	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
31	c4yztA_	Alignment	not modelled	30.2	11	PDB header: hydrolase Chain: A: PDB Molecule: cellulose hydrolase; PDBTitle: crystal structure of a tri-modular gh5 (subfamily 4) endo-beta-1, 4-2 glucanase from bacillus licheniformis complexed with cellotetraose
32	c3vniC_	Alignment	not modelled	29.9	10	PDB header: isomerase Chain: C: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
33	c5c5gA_	Alignment	not modelled	29.8	15	PDB header: hydrolase Chain: A: PDB Molecule: spherulin-4; PDBTitle: crystal structure of aspergillus clavatus sph3
34	c2qtpA_	Alignment	not modelled	29.6	36	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1185 family protein (spo0826) from2 silicibacter pomeroyi dss-3 at 2.10 a resolution
35	d2qtpa1	Alignment	not modelled	29.6	36	Fold: Bacillus chorismate mutase-like Superfamily: BB2672-like Family: BB2672-like
36	d1vjza_	Alignment	not modelled	29.1	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
37	c4m6iA_	Alignment	not modelled	28.5	33	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan amidase rv3717; PDBTitle: structure of the reduced, zn-bound form of mycobacterium tuberculosis2 peptidoglycan amidase rv3717
38	c3anyB_	Alignment	not modelled	27.4	28	PDB header: lyase Chain: B: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
39	c3absD_	Alignment	not modelled	27.4	28	PDB header: lyase Chain: D: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
40	c5gnnA_	Alignment	not modelled	27.3	25	PDB header: lipid binding protein Chain: A: PDB Molecule: lipid binding protein; PDBTitle: crystal structure of lipid binding protein nakanori at 1.6a
41	c3qxbB_	Alignment	not modelled	24.9	10	PDB header: isomerase Chain: B: PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
42	c6gl2A_	Alignment	not modelled	23.9	8	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase, family gh5; PDBTitle: structure of zngengagh5_4 wild type at 1.2 angstrom resolution
43	c4eisA_	Alignment	not modelled	23.5	28	PDB header: oxidoreductase Chain: A: PDB Molecule: polysaccharide monooxygenase-3; PDBTitle: structural basis for substrate targeting and catalysis by fungal2 polysaccharide monooxygenases (pmo-3)
44	c3kctB_	Alignment	not modelled	23.0	15	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
45	c3p14C_	Alignment	not modelled	22.5	13	PDB header: isomerase Chain: C: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
46	c5hosA_	Alignment	not modelled	22.2	10	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of the endo-beta-1,4-glucanase xac0029 from2 xanthomonas axonopodis pv. citri
47	c2zunB_	Alignment	not modelled	21.1	12	PDB header: hydrolase Chain: B: PDB Molecule: 458aa long hypothetical endo-1,4-beta-glucanase; PDBTitle: functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii
48	c5hmqE_	Alignment	not modelled	20.5	21	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
49	c4d7uB_	Alignment	not modelled	19.2	39	PDB header: oxidoreductase Chain: B: PDB Molecule: endoglucanase ii; PDBTitle: the structure of the catalytic domain of nclpmo9c from the filamentous2 fungus neurospora crassa
50	c4eirB_	Alignment	not modelled	19.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: polysaccharide monooxygenase-2; PDBTitle: structural basis for substrate targeting and catalysis by fungal2 polysaccharide monooxygenases (pmo-2)
51	c4htyA_	Alignment	not modelled	18.9	12	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of a metagenome-derived cellulase cel5a
52	c3qayC_	Alignment	not modelled	17.9	23	PDB header: lyase Chain: C: PDB Molecule: endolysin; PDBTitle: catalytic domain of cd27l endolysin targeting clostridia difficile
53	d1hjja_	Alignment	not modelled	17.9	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases

						Family: beta-glycanases
54	c2dfxl	Alignment	not modelled	17.4	18	PDB header: hydrolase Chain: I; PDB Molecule: colicin-e5 immunity protein; PDBTitle: crystal structure of the carboxy terminal domain of colicin2 e5 complexed with its inhibitor
55	c4ntqB	Alignment	not modelled	17.2	23	PDB header: toxin Chain: B; PDB Molecule: ecl cdii; PDBTitle: cdia-ct/cdii toxin and immunity complex from enterobacter cloacae
56	d1ecea	Alignment	not modelled	17.0	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
57	c5a94B	Alignment	not modelled	16.8	15	PDB header: hydrolase Chain: B; PDB Molecule: putative retaining b-glycosidase; PDBTitle: crystal structure of beta-glucanase sdgluc5_26a from saccharophagus2 degradans in complex with tetrasaccharide a, form 1
58	c2hk1D	Alignment	not modelled	16.2	11	PDB header: isomerase Chain: D; PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of 2 d-fructose
59	d1xima	Alignment	not modelled	15.9	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
60	c4r14B	Alignment	not modelled	15.7	19	PDB header: hydrolase Chain: B; PDB Molecule: gtp cyclohydrolase-2; PDBTitle: crystal structure of gtp cyclohydrolase ii from helicobacter pylori2 26695
61	c5emiA	Alignment	not modelled	15.6	13	PDB header: hydrolase Chain: A; PDB Molecule: cell wall hydrolase/autolysin; PDBTitle: n-acetylmuramoyl-l-alanine amidase amic2 of nostoc punctiforme
62	d2ifxa1	Alignment	not modelled	15.4	55	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Mmll-like
63	c5dcjA	Alignment	not modelled	15.4	22	PDB header: transferase Chain: A; PDB Molecule: osmolarity sensor protein envz; PDBTitle: structure of the envz periplasmic domain with chaps reveals the 2 mechanism of porin inactivation by bile salts
64	c3zmrA	Alignment	not modelled	15.3	11	PDB header: hydrolase Chain: A; PDB Molecule: cellulase (glycosyl hydrolase family 5); PDBTitle: bacteroides ovatus gh5 xyloglucanase in complex with a xxxg2 heptasaccharide
65	c5nltD	Alignment	not modelled	15.1	33	PDB header: oxidoreductase Chain: D; PDB Molecule: cvaa9a; PDBTitle: cvaa9a
66	c4b5qA	Alignment	not modelled	15.0	28	PDB header: hydrolase Chain: A; PDB Molecule: glycoside hydrolase family 61 protein d; PDBTitle: the lytic polysaccharide monoxygenase gh61d structure from the 2 basidiomycota fungus phanerochaete chrysosporium
67	c2rngA	Alignment	not modelled	14.9	40	PDB header: antimicrobial protein Chain: A; PDB Molecule: big defensin; PDBTitle: solution structure of big defensin
68	d1bqca	Alignment	not modelled	14.7	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
69	c3aysA	Alignment	not modelled	14.6	13	PDB header: hydrolase Chain: A; PDB Molecule: endoglucanase; PDBTitle: gh5 endoglucanase from a ruminal fungus in complex with cellotriose
70	c5aciA	Alignment	not modelled	14.5	39	PDB header: oxidoreductase Chain: A; PDB Molecule: lytic polysaccharide monoxygenase; PDBTitle: x-ray structure of lpmo
71	c4binA	Alignment	not modelled	14.3	31	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylmuramoyl-l-alanine amidase amic; PDBTitle: crystal structure of the e. coli n-acetylmuramoyl-l-alanine amidase2 amic
72	d1edga	Alignment	not modelled	14.3	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
73	c2yetB	Alignment	not modelled	14.1	22	PDB header: hydrolase Chain: B; PDB Molecule: gh61 isozyme a; PDBTitle: thermoascus gh61 isozyme a
74	c5fohA	Alignment	not modelled	13.9	33	PDB header: oxidoreductase Chain: A; PDB Molecule: polysaccharide monoxygenase; PDBTitle: crystal structure of the catalytic domain of nclpmo9a
75	d1vpxa	Alignment	not modelled	13.8	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
76	d1ffvb2	Alignment	not modelled	13.3	14	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
77	c3ejaB	Alignment	not modelled	13.1	25	PDB header: unknown function Chain: B; PDB Molecule: protein gh61e; PDBTitle: magnesium-bound glycoside hydrolase 61 isoform e from thielavia2 terrestris
78	c2e12B	Alignment	not modelled	13.1	36	PDB header: translation Chain: B; PDB Molecule: hypothetical protein xcc3642; PDBTitle: the crystal structure of xc5848 from xanthomonas campestris2 adopting a novel variant of sm-like motif
79	c4tufC	Alignment	not modelled	13.0	12	PDB header: hydrolase Chain: C; PDB Molecule: major extracellular endoglucanase; PDBTitle: catalytic domain of the major endoglucanase from xanthomonas2 campestris pv. campestris

80	d1sqwa1	Alignment	not modelled	12.9	44	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
81	c5o2xA	Alignment	not modelled	12.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: glycoside hydrolase family 61; PDBTitle: extended catalytic domain of h. jecorina lpmo9a a.k.a eg4
82	c4x0vH	Alignment	not modelled	12.5	11	PDB header: hydrolase Chain: H: PDB Molecule: beta-1,3-1,4-glucanase; PDBTitle: structure of a gh5 family lichenase from caldicellulosiruptor sp. f32
83	d2djka1	Alignment	not modelled	12.2	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: PDI-like
84	c2j8fA	Alignment	not modelled	12.1	24	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of the modular cpl-1 endolysin complexed with a2 peptidoglycan analogue (e94q mutant in complex with a disaccharide-3 pentapeptide)
85	c3bj5A	Alignment	not modelled	12.0	10	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase; PDBTitle: alternative conformations of the x region of human protein disulphide-2 isomerase modulate exposure of the substrate binding b' domain
86	d1xova2	Alignment	not modelled	11.5	30	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: N-acetylmuramoyl-L-alanine amidase-like
87	c5fipA	Alignment	not modelled	11.4	9	PDB header: hydrolase Chain: A: PDB Molecule: gh5 cellulase; PDBTitle: discovery and characterization of a novel thermostable and2 highly halotolerant gh5 cellulase from an icelandic hot3 spring isolate
88	c3hynA	Alignment	not modelled	11.2	16	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein; PDBTitle: crystal structure of a putative signal transduction protein2 (eubrec_0645) from eubacterium rectale atcc 33656 at 1.20 a3 resolution
89	c4k3zA	Alignment	not modelled	10.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: d-erythrulose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrulose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
90	d1bxca	Alignment	not modelled	10.9	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
91	d1x3ha2	Alignment	not modelled	10.8	10	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
92	c3wugA	Alignment	not modelled	10.8	12	PDB header: hydrolase Chain: A: PDB Molecule: endo-1,4-beta-xylanase a; PDBTitle: the mutant crystal structure of b-1,4-xylanase (xynas9_v43p/g44e) with2 xylobiose from streptomyces sp. 9
93	c4rn7A	Alignment	not modelled	10.8	40	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of n-acetylmuramoyl-l-alanine amidase from2 clostridium difficile 630
94	c2qw5B	Alignment	not modelled	10.6	11	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
95	c5dlcC	Alignment	not modelled	10.4	18	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
96	d1s99a	Alignment	not modelled	10.3	33	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: Putative thiamin/HMP-binding protein YkoF
97	c3qr3B	Alignment	not modelled	10.0	11	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase eg-ii; PDBTitle: crystal structure of cel5a (eg2) from hypocrea jecorina (trichoderma2 reesei)
98	c3excX	Alignment	not modelled	10.0	22	PDB header: hydrolase Chain: X: PDB Molecule: uncharacterized protein; PDBTitle: structure of the rna'se sso8090 from sulfolobus solfataricus
99	c2inrA	Alignment	not modelled	9.8	11	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 4 subunit a; PDBTitle: crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (gria) from staphylococcus aureus