

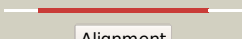













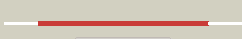







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0237_(lpq)_287186_288352
Date	Tue Jul 23 14:50:29 BST 2019
Unique Job ID	f3644ff8447354f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bmxB_	 Alignment		100.0	33	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase (ybbd) from bacillus subtilis
2	c3sqjB_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3; PDBTitle: crystal structure of glycoside hydrolase from synechococcus
3	c4yyfC_	 Alignment		100.0	73	PDB header: hydrolase Chain: C: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of a glycosyl hydrolase of gh3 family member2 from [mycobacterium smegmatis str. mc2 155
4	c4zm6A_	 Alignment		100.0	32	PDB header: hydrolase, transferase Chain: A: PDB Molecule: n-acetyl-beta-d glucosaminidase; PDBTitle: a unique gcn5-related glucosamine n-acetyltransferase region exist in2 the fungal multi-domain gh3 beta-n-acetylglucosaminidase
5	c3lk6A_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: lipoprotein ybbd; PDBTitle: beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
6	c5jp0A_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase bogh3b; PDBTitle: bacteroides ovatus xyloglucan pul gh3b with bound glucose
7	c5vqdA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucoside phosphorylase bglx; PDBTitle: beta-glucoside phosphorylase bglx
8	c5m6gA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure glucan 1,4-beta-glucosidase from saccharopolyspora2 erythraea
9	c5bu9B_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from beutenbergia2 cavernae dsm 12333
10	c3f93D_	 Alignment		100.0	21	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of exo-1,3/1,4-beta-glucanase (exop) from2 pseudoalteromonas sp. bb1
11	c5z87B_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: emgh1; PDBTitle: structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus

12	c5yotB_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: isoprimeverose-producing enzyme; PDBTitle: isoprimeverose-producing enzyme from aspergillus oryzae in complex2 with isoprimeverose
13	d1x38a1	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
14	c1ex1A_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: protein (beta-d-glucan exohydrolase isoenzyme exo1); PDBTitle: beta-d-glucan exohydrolase from barley
15	c3u48A_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: jmb19063; PDBTitle: from soil to structure: a novel dimeric family 3-beta-glucosidase2 isolated from compost using metagenomic analysis
16	c4zo9B_	Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: lin1840 protein; PDBTitle: crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose
17	c5z9sB_	Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3 protein; PDBTitle: functional and structural characterization of a beta-glucosidase2 involved in saponin metabolism from intestinal bacteria
18	c5tf0B_	Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3 n-terminal domain protein; PDBTitle: crystal structure of glycosyl hydrolase family 3 n-terminal domain2 protein from bacteroides intestinalis
19	c3wo8B_	Alignment		100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylglucosaminidase; PDBTitle: crystal structure of the beta-n-acetylglucosaminidase from thermotoga2 maritima
20	c5bzaA_	Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of cbsa from thermotoga neapolitana
21	c5iobC_	Alignment	not modelled	100.0	41	PDB header: hydrolase Chain: C: PDB Molecule: beta-glucosidase-related glycosidases; PDBTitle: crystal structure of beta-n-acetylglucosaminidase-like protein from2 corynebacterium glutamicum
22	c6q7jB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: exo-1,4-beta-xylosidase xlnD; PDBTitle: gh3 exo-beta-xylosidase (xlnD) in complex with xylobiose aziridine2 activity based probe
23	c4iidB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase 1; PDBTitle: crystal structure of beta-glucosidase 1 from aspergillus aculeatus in2 complex with 1-deoxynojirimycin
24	c5nbsA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structural studies of a glycoside hydrolase family 3 beta-glucosidase2 from the model fungus neurospora crassa
25	c5a7mA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylosidase; PDBTitle: the structure of hypocrea jecorina beta-xylosidase xyl3a (bx11)
26	c3zz1A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-d-glucoside glucohydrolase; PDBTitle: crystal structure of a glycoside hydrolase family 3 beta-glucosidase,2 bgl1 from hypocrea jecorina at 2.1a resolution.
27	c4d0jD_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of glycoside hydrolase family 3 beta-2 glucosidase cel3a from the moderately thermophilic fungus3 rasamsonia emersonii
28	c4g6cA_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase 1; PDBTitle: crystal structure of beta-hexosaminidase 1 from

						burkholderia2 cenocepacia j2315
29	c2x41A_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana in2 complex with glucose
30	c3tevA_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hyrolase, family 3; PDBTitle: the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
31	c5wabD_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
32	c5wabC_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: C: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
33	c4i3gB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
34	c4gvgB_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of salmonella typhimurium family 3 glycoside2 hydrolase (nagz)
35	c3ac0B_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
36	c5g1mA_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of nagz from pseudomonas aeruginosa
37	d1tr9a_	Alignment	not modelled	100.0	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: NagZ-like
38	c5wvpA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: expression, characterization and crystal structure of a novel beta-2 glucosidase from paenibacillus barengoltzii
39	c5k6A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: b-glucosidase; PDBTitle: structure of a gh3 b-glucosidase from cow rumen metagenome
40	d1o4ua1	Alignment	not modelled	76.7	26	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
41	c4ce4S_	Alignment	not modelled	65.4	22	PDB header: ribosome Chain: S: PDB Molecule: mrp18; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
42	d2p12a1	Alignment	not modelled	62.3	16	Fold: FomD barrel-like Superfamily: FomD-like Family: FomD-like
43	d2gycm1	Alignment	not modelled	62.0	20	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
44	d1pv8a_	Alignment	not modelled	58.5	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
45	c2htmB_	Alignment	not modelled	54.2	21	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
46	c1o4uA_	Alignment	not modelled	50.9	26	PDB header: transferase Chain: A: PDB Molecule: type ii quinolic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
47	c4n6eA_	Alignment	not modelled	44.3	23	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
48	d2vcha1	Alignment	not modelled	41.5	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
49	c3bboQ_	Alignment	not modelled	41.4	17	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein l18; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
50	c5nlmB_	Alignment	not modelled	41.4	15	PDB header: transferase Chain: B: PDB Molecule: indoxyl udp-glucosyltransferase; PDBTitle: complex between a udp-glucosyltransferase from polygonum tinctorium2 capable of glucosylating indoxyl and indoxyl sulfate
51	d1d2da_	Alignment	not modelled	39.1	20	Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: a tRNA synthase domain
52	d1xm3a_	Alignment	not modelled	37.9	26	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
53	c2djvA_	Alignment	not modelled	37.2	17	PDB header: protein binding Chain: A: PDB Molecule: methionyl-trna synthetase; PDBTitle: solution structures of the whep-trs domain of human2 methionyl-trna synthetase
						Fold: S15/NS1 RNA-binding domain

54	d1fyja_	Alignment	not modelled	36.7	27	Superfamily: S15/NS1 RNA-binding domain Family: a tRNA synthase domain
55	c4v19S_	Alignment	not modelled	34.5	18	PDB header: ribosome Chain: S: PDB Molecule: mitoribosomal protein ul18m, mrpl18; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
56	c3wdjA_	Alignment	not modelled	33.4	21	PDB header: hydrolase Chain: A: PDB Molecule: type i pullulanase; PDBTitle: crystal structure of pullulanase complexed with maltotetraose from <i>2 anoxybacillus sp. Im18-11</i>
57	c2jtxA_	Alignment	not modelled	31.9	27	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor iie subunit PDBTitle: nmr structure of the tfiie-alpha carboxyl terminus
58	c2rngA_	Alignment	not modelled	29.7	27	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor iie subunit PDBTitle: solution structure of the c-terminal acidic domain of tfiie2 alpha
59	c1x59A_	Alignment	not modelled	29.3	11	PDB header: protein binding Chain: A: PDB Molecule: histidyl-trna synthetase; PDBTitle: solution structures of the whep-trs domain of human2 histidyl-trna synthetase
60	c6jtdB_	Alignment	not modelled	28.3	19	PDB header: transferase Chain: B: PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccg1 in complex with udp
61	d2c1xa1	Alignment	not modelled	27.0	7	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
62	c4a3uB_	Alignment	not modelled	26.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh\;flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from <i>zymomonas mobilis2 (ncr)</i>
63	c2cosa_	Alignment	not modelled	25.4	26	PDB header: transferase Chain: A: PDB Molecule: serine/threonine protein kinase lats2; PDBTitle: solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
64	d1r6ta1	Alignment	not modelled	24.8	23	Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: a tRNA synthase domain
65	d1yxva1	Alignment	not modelled	24.3	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
66	d1vhna_	Alignment	not modelled	24.0	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
67	c2e8yA_	Alignment	not modelled	23.1	29	PDB header: hydrolase Chain: A: PDB Molecule: amyx protein; PDBTitle: crystal structure of pullulanase type i from <i>bacillus subtilis str.2 168</i>
68	c5v2ka_	Alignment	not modelled	22.9	11	PDB header: transferase Chain: A: PDB Molecule: udp-glycosyltransferase 74f2; PDBTitle: crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid
69	d1ovya_	Alignment	not modelled	22.7	19	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
70	c1w1nA_	Alignment	not modelled	22.2	7	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol 3-kinase tor1; PDBTitle: the solution structure of the fatc domain of the protein kinase tor12 from yeast
71	c2ya0A_	Alignment	not modelled	21.3	23	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
72	d1k3ka_	Alignment	not modelled	21.0	33	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
73	c3wc4A_	Alignment	not modelled	20.7	5	PDB header: transferase Chain: A: PDB Molecule: udp-glucose:anthocyanidin 3-o-glucosyltransferase; PDBTitle: crystal structure of udp-glucose: anthocyanidin 3-o-2 glucosyltransferase from <i>clitoria ternatea</i>
74	c3j3vO_	Alignment	not modelled	20.3	18	PDB header: ribosome Chain: O: PDB Molecule: 50s ribosomal protein l18; PDBTitle: atomic model of the immature 50s subunit from <i>bacillus subtilis (state2 i-a)</i>
75	d2odfa1	Alignment	not modelled	19.8	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: FGase-like
76	c2y69X_	Alignment	not modelled	19.7	22	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 7b; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
77	d1v54k_	Alignment	not modelled	19.7	22	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIb Family: Mitochondrial cytochrome c oxidase subunit VIIb
78	c2kitA_	Alignment	not modelled	19.2	7	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase tor1; PDBTitle: the solution structure of the reduced yeast tor1 fatc domain bound to2 dpc micelles at 298k
79	d2acva1	Alignment	not modelled	18.5	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
80	c1iq8B_	Alignment	not modelled	18.1	12	PDB header: transferase Chain: B: PDB Molecule: archaeosine trna-guanine transglycosylase;

						PDBTitle: crystal structure of archaeosine trna-guanine transglycosylase from2 pyrococcus horikoshii
81	c4j7rA_	Alignment	not modelled	18.1	14	PDB header: hydrolase Chain: A; PDB Molecule: isoamylase; PDBTitle: crystal structure of chlamydomonas reinhardtii isoamylase 1 (isa1)
82	c5emiA_	Alignment	not modelled	17.6	15	PDB header: hydrolase Chain: A; PDB Molecule: cell wall hydrolase/autolysin; PDBTitle: n-acetylmuramoyl-l-alanine amidase amic2 of nostoc punctiforme
83	d2pq6a1	Alignment	not modelled	17.5	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
84	c2wanA_	Alignment	not modelled	17.2	18	PDB header: hydrolase Chain: A; PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
85	c4jicB_	Alignment	not modelled	16.7	11	PDB header: oxidoreductase Chain: B; PDB Molecule: gtn reductase; PDBTitle: glycerol trinitrate reductase nera from agrobacterium radiobacter
86	c3hbjA_	Alignment	not modelled	16.5	11	PDB header: transferase Chain: A; PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
87	c3atyA_	Alignment	not modelled	16.1	13	PDB header: oxidoreductase Chain: A; PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tcoye
88	c3w1hB_	Alignment	not modelled	16.1	17	PDB header: transferase Chain: B; PDB Molecule: l-seryl-trna(sec) selenium transferase; PDBTitle: crystal structure of the selenocysteine synthase sela from aquifex2 aeolicus
89	c4binA_	Alignment	not modelled	15.9	21	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
90	c6ei9A_	Alignment	not modelled	15.9	15	PDB header: flavoprotein Chain: A; PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
91	c2qlcC_	Alignment	not modelled	15.5	13	PDB header: dna binding protein Chain: C; PDB Molecule: dna repair protein radc homolog; PDBTitle: the crystal structure of dna repair protein radc from chlorobium2 tepidum t1s
92	c5tmdA_	Alignment	not modelled	14.5	16	PDB header: transferase Chain: A; PDB Molecule: glycosyltransferase, os79; PDBTitle: crystal structure of os79 from o. sativa in complex with u2f and2 trichothecene.
93	c2h90A_	Alignment	not modelled	14.5	18	PDB header: oxidoreductase Chain: A; PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
94	d1ulza2	Alignment	not modelled	14.4	18	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
95	c3ht4B_	Alignment	not modelled	14.1	23	PDB header: lyase Chain: B; PDB Molecule: aluminum resistance protein; PDBTitle: crystal structure of the q81a77_baccr protein from bacillus cereus.2 northeast structural genomics consortium target bcr213
96	c5o60P_	Alignment	not modelled	14.1	16	PDB header: ribosome Chain: P; PDB Molecule: 50s ribosomal protein l18; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
97	d1gwja_	Alignment	not modelled	13.9	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
98	d1n82a_	Alignment	not modelled	13.9	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
99	c5hssA_	Alignment	not modelled	13.9	11	PDB header: lyase Chain: A; PDB Molecule: linalool dehydratase/isomerase; PDBTitle: linalool dehydratase/isomerase: ldi with monoterpene substrate