
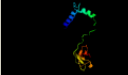



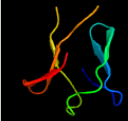



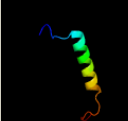



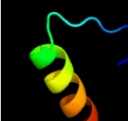

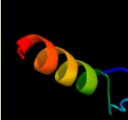





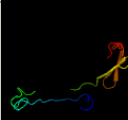
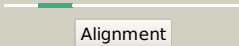
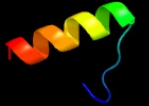

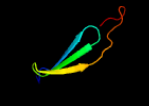


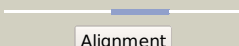
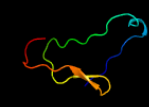
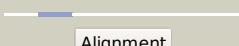

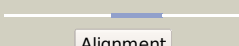

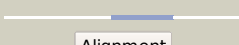
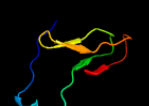
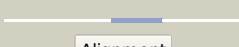
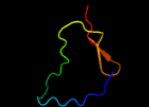



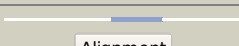

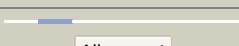
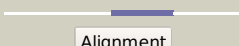





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3637_(-)_4076663_4077163
Date	Fri Aug 9 18:20:32 BST 2019
Unique Job ID	03259a8569d60b0a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fcyA_	 Alignment		98.8	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
2	c1bcoA_	 Alignment		98.1	11	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
3	d1bcoa1	 Alignment		96.4	17	Fold: mu transposase, C-terminal domain Superfamily: mu transposase, C-terminal domain Family: mu transposase, C-terminal domain
4	d1c6va_	 Alignment		74.4	25	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	d1bcoa2	 Alignment		68.9	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
6	c4uhpA_	 Alignment		56.9	39	PDB header: hydrolase Chain: A: PDB Molecule: large component of pyocin ap41; PDBTitle: crystal structure of the pyocin ap41 dnase-immunity complex
7	c4qkoH_	 Alignment		56.7	27	PDB header: antimicrobial protein Chain: H: PDB Molecule: pyocin-s2; PDBTitle: the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
8	d2jb0b1	 Alignment		56.3	23	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
9	c7ceiB_	 Alignment		55.0	28	PDB header: immune system Chain: B: PDB Molecule: protein (colicin e7 immunity protein); PDBTitle: the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
10	c3i3IA_	 Alignment		47.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
11	c3u1qB_	 Alignment		45.8	21	PDB header: peptidoglycan binding protein Chain: B: PDB Molecule: mycobacteria tuberculosis ld-transpeptidase type 2; PDBTitle: crystal structure of m. tuberculosis ld-transpeptidase type 2 with 2-2 mercaptoethanol

12	d2gykb1	 Alignment		40.4	23	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
13	c4jmxA	 Alignment		30.4	16	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable I,d-transpeptidase ldtA; PDBTitle: structure of Id transpeptidase ldtmt1 in complex with imipenem
14	c3dlrA	 Alignment		27.6	18	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv integrase
15	c6ed2A	 Alignment		27.3	24	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 2, tim barrel domain protein; PDBTitle: faecalibacterium prausnitzii beta-glucuronidase
16	c5ew5C	 Alignment		25.6	28	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
17	c3fn9B	 Alignment		25.1	16	PDB header: hydrolase Chain: B: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
18	c6ecaA	 Alignment		24.9	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucuronidase; PDBTitle: lactobacillus rhamnosus beta-glucuronidase
19	c6d1pB	 Alignment		24.1	14	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolases family 2, sugar binding domain protein; PDBTitle: apo structure of bacteroides uniformis beta-glucuronidase 3
20	c6mvgB	 Alignment		23.7	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucuronidase; PDBTitle: crystal structure of fmn-binding beta-glucuronidase from ruminococcus2 gnavus
21	c6dxuA	 Alignment	not modelled	21.9	19	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 2, tim barrel domain protein; PDBTitle: crystal structure of parabacteroides merdae beta-glucuronidase (gus)
22	c3cmgA	 Alignment	not modelled	21.2	19	PDB header: hydrolase Chain: A: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
23	c5ldrA	 Alignment	not modelled	21.1	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-d-galactosidase; PDBTitle: crystal structure of a cold-adapted dimeric beta-d-galactosidase from2 paracoccus sp. 32d strain in complex with galactose
24	c3bnwA	 Alignment	not modelled	20.7	9	PDB header: transferase Chain: A: PDB Molecule: riboflavin kinase, putative; PDBTitle: crystal structure of riboflavin kinase from trypanosoma brucei
25	c4jkmB	 Alignment	not modelled	19.5	13	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucuronidase; PDBTitle: crystal structure of clostridium perfringens beta-glucuronidase
26	c4ypjB	 Alignment	not modelled	18.6	14	PDB header: hydrolase Chain: B: PDB Molecule: beta galactosidase; PDBTitle: x-ray structure of the mutant of glycoside hydrolase
27	c6dxuB	 Alignment	not modelled	18.3	16	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 2, tim barrel domain protein; PDBTitle: crystal structure of parabacteroides merdae beta-glucuronidase (gus)
		 Alignment				PDB header: hydrolase

28	c5c70B_	Alignment	not modelled	17.4	22	Chain: B: PDB Molecule: glucuronidase; PDBTitle: the structure of aspergillus oryzae beta-glucuronidase
29	c5ag8A_	Alignment	not modelled	17.4	23	PDB header: hydrolase Chain: A: PDB Molecule: gingipain r2; PDBTitle: crystal structure of a mutant (665i6h) of the c-terminal2 domain of rgpb
30	c3djmA_	Alignment	not modelled	17.2	4	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein duf427; PDBTitle: crystal structure of a protein of unknown function from duf427 family2 (rsph17029_0682) from rhodobacter sphaeroides 2.4.1 at 2.51 a3 resolution
31	c4xvoB_	Alignment	not modelled	16.5	18	PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: l,d-transpeptidase from mycobacterium smegmatis
32	c5t9gD_	Alignment	not modelled	16.3	14	PDB header: hydrolase Chain: D: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bugh2cwt in complex with galactoisofagomine
33	c4cucA_	Alignment	not modelled	16.1	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: unravelling the multiple functions of the architecturally intricate2 streptococcus pneumoniae beta-galactosidase, bgaa.
34	c6d4oA_	Alignment	not modelled	15.9	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucuronidase; PDBTitle: eubacterium eligens beta-glucuronidase bound to an amoxapine-2 glucuronide conjugate
35	c5dmyA_	Alignment	not modelled	15.4	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: beta-galactosidase - construct 33-930
36	c2k0mA_	Alignment	not modelled	15.3	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the uncharacterized protein from2 rhodospirillum rubrum gene locus rru_a0810. northeast3 structural genomics target rrr43
37	c4k73A_	Alignment	not modelled	15.1	16	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: x-ray crystal structure of an l,d-transpeptidase from mycobacterium2 tuberculosis h37rv
38	c4jklA_	Alignment	not modelled	15.0	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucuronidase; PDBTitle: crystal structure of streptococcus agalactiae beta-glucuronidase in2 space group p21212
39	c5t98B_	Alignment	not modelled	14.9	22	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase; PDBTitle: crystal structure of bugh2awt
40	c3bgaB_	Alignment	not modelled	14.7	20	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482
41	c1psvA_	Alignment	not modelled	14.3	24	PDB header: designed peptide Chain: A: PDB Molecule: pda8d; PDBTitle: computationally designed peptide with a beta-beta-alpha2 fold selection, nmr, 32 structures
42	c3gm8A_	Alignment	not modelled	14.2	11	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 2, candidate beta-glycosidase; PDBTitle: crystal structure of a beta-glycosidase from bacteroides vulgatus
43	c5z19F_	Alignment	not modelled	13.4	16	PDB header: hydrolase Chain: F: PDB Molecule: beta-glucuronidase; PDBTitle: the crystal structure of ruminococcus gnavus beta-glucuronidase in2 complex with uronic isofagomine
44	d1jz8a3	Alignment	not modelled	13.4	18	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
45	c5i4rA_	Alignment	not modelled	12.4	40	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
46	d1fexa_	Alignment	not modelled	12.0	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
47	d1uwva1	Alignment	not modelled	11.8	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
48	c6ed1B_	Alignment	not modelled	11.5	22	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 2, sugar binding domain protein; PDBTitle: bacteroides dorei beta-glucuronidase
49	c6hpdA_	Alignment	not modelled	11.2	11	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase (gh2); PDBTitle: the structure of a beta-glucuronidase from glycoside hydrolase family2 2
50	d1yq2a3	Alignment	not modelled	11.2	19	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
51	c5z1bC_	Alignment	not modelled	11.1	18	PDB header: hydrolase Chain: C: PDB Molecule: glycosyl hydrolase family 2, tim barrel domain protein; PDBTitle: structure of bifidobacterium dentium beta-glucuronidase complexed with2 coumarin-3-o-glucuronide
52	d1zata1	Alignment	not modelled	11.0	15	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
53	c5mzyA_	Alignment	not modelled	11.0	9	PDB header: lyase Chain: A: PDB Molecule: glutaconate coa-transferase family, subunit a;

						PDBTitle: crystal structure of the decarboxylase aiba/aibb in complex with a2 possible transition state analog
54	c5n6uC	Alignment	not modelled	11.0	9	PDB header: hydrolase Chain: C: PDB Molecule: beta-mannosidase; PDBTitle: crystal structure of beta-d-mannosidase from dictyoglomus2 thermophilum.
55	d1yeza1	Alignment	not modelled	10.8	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
56	c4azzB	Alignment	not modelled	10.2	21	PDB header: hydrolase Chain: B: PDB Molecule: levanase; PDBTitle: carbohydrate binding module cbm66 from bacillus subtilis
57	d1g2913	Alignment	not modelled	10.1	16	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
58	c5uj6A	Alignment	not modelled	9.5	14	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolases family 2, sugar binding domain protein; PDBTitle: crystal structure of bacteroides uniformis beta-glucuronidase
59	d1vhea1	Alignment	not modelled	9.4	13	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Aminopeptidase/glucanase lid domain Family: Aminopeptidase/glucanase lid domain
60	c3lpgA	Alignment	not modelled	9.3	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: beta-glucuronidase; PDBTitle: structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3 2-dihydroquinolin-3-yl)methyl)urea
61	c1y8aA	Alignment	not modelled	8.6	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
62	c5nocA	Alignment	not modelled	8.6	25	PDB header: dna binding protein Chain: A: PDB Molecule: stage 0 sporulation protein j; PDBTitle: solution nmr structure of the c-terminal domain of parb (spo0j)
63	c2k6rA	Alignment	not modelled	8.3	16	PDB header: de novo protein Chain: A: PDB Molecule: full sequence design 1 synthetic superstable; PDBTitle: protein folding on a highly rugged landscape: experimental observation2 of glassy dynamics and structural frustration
64	c4lh9A	Alignment	not modelled	8.2	6	PDB header: transcription Chain: A: PDB Molecule: heterocyst differentiation control protein; PDBTitle: crystal structure of the refolded hood domain (asp256-gly295) of hetr
65	d1a1ua	Alignment	not modelled	8.0	29	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
66	c4z7aA	Alignment	not modelled	7.9	29	PDB header: transferase Chain: A: PDB Molecule: mycobacterium tuberculosis (3,3),d-transpeptidase type 5; PDBTitle: structural and biochemical characterization of a non-functionally2 redundant m. tuberculosis (3,3) l,d-transpeptidase, ldtmt5.
67	c3d8dA	Alignment	not modelled	7.7	8	PDB header: protein binding Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding family b member PDBTitle: crystal structure of the human fe65-ptb1 domain
68	d2gtad1	Alignment	not modelled	7.3	6	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
69	c5d55A	Alignment	not modelled	7.2	20	PDB header: cell adhesion Chain: A: PDB Molecule: hdab,hdaa (adhesin), hus-associated diffuse adherence; PDBTitle: crystal structure of the e. coli hda pilus minor tip subunit, hdab
70	d2grea1	Alignment	not modelled	7.1	13	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Aminopeptidase/glucanase lid domain Family: Aminopeptidase/glucanase lid domain
71	c3vxvA	Alignment	not modelled	6.7	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: methyl-cpg-binding domain protein 4; PDBTitle: crystal structure of methyl cpb binding domain of mbd4 in complex with2 the 5mcg/tg sequence
72	c3vynB	Alignment	not modelled	6.6	26	PDB header: transferase Chain: B: PDB Molecule: probable conserved lipoprotein lpps; PDBTitle: crystal structure of mycobacterium tuberculosis l,d-transpeptidase2 ldtmt2 n55 truncation mutant (residue 55-408)
73	c5m0rF	Alignment	not modelled	6.2	29	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
74	c6mvfA	Alignment	not modelled	6.1	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase/beta-glucuronidase; PDBTitle: crystal structure of fmn-binding beta-glucuronidase from2 facaelibacterium prausnitzii l2-6
75	d2nmla1	Alignment	not modelled	6.1	8	Fold: ERH-like Superfamily: ERH-like Family: ERH-like
76	c1fsdA	Alignment	not modelled	5.9	18	PDB header: novel sequence Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures
77	c1fsvA	Alignment	not modelled	5.9	18	PDB header: beta beta alpha motif Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif;

						PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif.2 nmr, minimized average structure
78	c2ksnA_	Alignment	not modelled	5.8	17	PDB header: signaling protein Chain: A; PDB Molecule: ubiquitin domain-containing protein 2; PDBTitle: solution structure of the n-terminal domain of dc-ubp/ubtd2
79	d2gtaa1	Alignment	not modelled	5.8	6	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
80	d1yvca1	Alignment	not modelled	5.8	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
81	c5z1vB_	Alignment	not modelled	5.7	22	PDB header: unknown function Chain: B; PDB Molecule: avrpib protein; PDBTitle: crystal structure of avrpib
82	d1y0ya1	Alignment	not modelled	5.7	13	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Aminopeptidase/glucanase lid domain Family: Aminopeptidase/glucanase lid domain
83	c4ndvB_	Alignment	not modelled	5.7	23	PDB header: sugar binding protein Chain: B; PDB Molecule: alpha-galactosyl-binding lectin; PDBTitle: crystal structure of l. decastes alpha-galactosyl-binding lectin in2 complex with globotriose
84	c2hkB_	Alignment	not modelled	5.6	15	PDB header: transferase Chain: B; PDB Molecule: l,d-transpeptidase; PDBTitle: crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
85	c2eqjA_	Alignment	not modelled	5.4	13	PDB header: transcription Chain: A; PDB Molecule: metal-response element-binding transcription PDBTitle: solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
86	c1fmeA_	Alignment	not modelled	5.3	18	PDB header: de novo protein Chain: A; PDB Molecule: fsd-ey peptide; PDBTitle: solution structure of fsd-ey, a novel peptide assuming a2 beta-beta-alpha fold
87	c3mxtA_	Alignment	not modelled	5.2	17	PDB header: ligase Chain: A; PDB Molecule: pantothenate synthetase; PDBTitle: crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
88	d1hs5a_	Alignment	not modelled	5.2	29	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
89	c2mqkA_	Alignment	not modelled	5.1	16	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase