

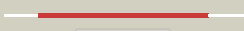
























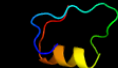

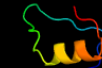



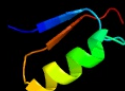



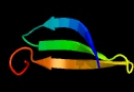



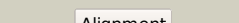

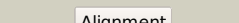






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2817c_(-)_3123977_3124993
Date	Wed Aug 7 12:50:48 BST 2019
Unique Job ID	6a663b52a2aec3cc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lfxE_	 Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: E; PDB Molecule: uncharacterized protein; PDBTitle: structure of tm1797, a cas1 protein from thermotoga maritima
2	c4n06A_	 Alignment		100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: crispr-associated endonuclease cas1 1; PDBTitle: crystal structure of cas1 from archaeoglobus fulgidus and its2 nucleolytic activity
3	c2yzsB_	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of uncharacterized conserved protein from aquifex2 aeolicus
4	c3pv9D_	 Alignment		100.0	18	PDB header: immune system Chain: D; PDB Molecule: putative uncharacterized protein ph1245; PDBTitle: structure of ph1245, a cas1 from pyrococcus horikoshii
5	c4w8kB_	 Alignment		100.0	15	PDB header: viral protein Chain: B; PDB Molecule: cas1 protein; PDBTitle: crystal structure of a putative cas1 enzyme from vibrio phage icp1
6	c5xvnL_	 Alignment		100.0	20	PDB header: immune system Chain: L; PDB Molecule: crispr-associated endonuclease cas1; PDBTitle: e. far cas1-cas2/prespacer binary complex
7	c4zkjA_	 Alignment		100.0	17	PDB header: unknown function Chain: A; PDB Molecule: crispr-associated protein cas1; PDBTitle: crystal structure of crispr-associated protein
8	c5fclD_	 Alignment		100.0	12	PDB header: dna binding protein Chain: D; PDB Molecule: crispr-associated endonuclease cas1; PDBTitle: crystal structure of cas1 from pectobacterium atrosepticum
9	c3godA_	 Alignment		100.0	14	PDB header: immune system Chain: A; PDB Molecule: cas1; PDBTitle: structural basis for dnase activity of a conserved protein2 implicated in crispr-mediated antiviral defense
10	c4p6iD_	 Alignment		100.0	15	PDB header: hydrolase Chain: D; PDB Molecule: crispr-associated endonuclease cas1; PDBTitle: crystal structure of the cas1-cas2 complex from escherichia coli
11	c3nkdB_	 Alignment		100.0	14	PDB header: immune system Chain: B; PDB Molecule: crispr-associated protein cas1; PDBTitle: structure of crisp-associated protein cas1 from escherichia coli str.2 k-12

12	c3nkeA	 Alignment		100.0	16	PDB header: immune system Chain: A; PDB Molecule: protein ygbt; PDBTitle: high resolution structure of the c-terminal domain crisp-associated2 protein cas1 from escherichia coli str. k-12
13	d1p3da1	 Alignment		66.9	13	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
14	d2jfga1	 Alignment		65.0	13	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
15	d1j6ua1	 Alignment		60.4	16	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
16	c5nc8B	 Alignment		58.7	3	PDB header: transport protein Chain: B; PDB Molecule: potassium efflux system protein; PDBTitle: shewanella denitrificans kef ctd in amp bound form
17	c3fwzA	 Alignment		55.3	13	PDB header: membrane protein Chain: A; PDB Molecule: inner membrane protein ybal; PDBTitle: crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
18	c3e6mD	 Alignment		53.3	13	PDB header: transcription regulator Chain: D; PDB Molecule: marr family transcriptional regulator; PDBTitle: the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
19	c2hbpA	 Alignment		46.7	13	PDB header: endocytosis, protein binding Chain: A; PDB Molecule: cytoskeleton assembly control protein sla1; PDBTitle: solution structure of sla1 homology domain 1
20	d2hmva1	 Alignment		46.6	6	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
21	d1lssa	 Alignment	not modelled	46.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
22	c2g1uA	 Alignment	not modelled	44.8	9	PDB header: transport protein Chain: A; PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
23	c4kbfF	 Alignment	not modelled	42.4	14	PDB header: transcription/replication Chain: F; PDB Molecule: uncharacterized protein pob3n; PDBTitle: structure of the spt16d pob3n heterodimer
24	c5z2fA	 Alignment	not modelled	42.4	17	PDB header: oxidoreductase Chain: A; PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporsarcina2 sp. tg-14
25	c3l4bG	 Alignment	not modelled	39.8	19	PDB header: transport protein Chain: G; PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
26	c5xg7A	 Alignment	not modelled	39.3	8	PDB header: sugar binding protein Chain: A; PDB Molecule: galactoside-binding soluble lectin 13; PDBTitle: galectin-13/placental protein 13 crystal structure
27	d1ld1a	 Alignment	not modelled	38.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
28	c3kc2A	 Alignment	not modelled	38.3	17	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae

29	c4kzkA	Alignment	not modelled	37.4	3	PDB header: sugar binding protein Chain: A: PDB Molecule: l-arabinose abc transporter, periplasmic l-arabinose- PDBTitle: the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis
30	d1lcla	Alignment	not modelled	36.8	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
31	c4j7cA	Alignment	not modelled	36.8	6	PDB header: transport protein Chain: A: PDB Molecule: ktr system potassium uptake protein a; PDBTitle: ktrab potassium transporter from bacillus subtilis
32	d2loja1	Alignment	not modelled	36.4	15	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: DRTGG domain
33	c2ea1B	Alignment	not modelled	36.2	15	PDB header: sugar binding protein Chain: B: PDB Molecule: galectin-9; PDBTitle: crystal structure of human galectin-9 n-terminal crd in complex with2 forssman pentasaccharide
34	c3lh1A	Alignment	not modelled	36.0	13	PDB header: hydrolase Chain: A: PDB Molecule: putative agmatinase; PDBTitle: crystal structure of a putative agmatinase from clostridium difficile
35	c2yxsA	Alignment	not modelled	34.4	13	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin-8 variant; PDBTitle: crystal structure of n-terminal domain of human galectin-8 with d-2 lactose
36	c4xrfA	Alignment	not modelled	34.2	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of mepr like protein complexed with pseudoligands
37	c6e20B	Alignment	not modelled	33.7	15	PDB header: sugar binding protein Chain: B: PDB Molecule: galectin; PDBTitle: crystal structure of the dario rerio galectin-1-l2
38	c3llvA	Alignment	not modelled	33.5	6	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
39	c2ymzF	Alignment	not modelled	33.0	13	PDB header: sugar binding protein Chain: F: PDB Molecule: galectin 2; PDBTitle: crystal structure of chicken galectin 2
40	c5ugjC	Alignment	not modelled	32.3	22	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
41	c3vv1B	Alignment	not modelled	32.3	10	PDB header: sugar binding protein Chain: B: PDB Molecule: protein lec-6; PDBTitle: crystal structure of caenorhabditis elegans galectin lec-6
42	d1woha	Alignment	not modelled	32.0	10	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
43	d1a2za	Alignment	not modelled	31.7	11	Fold: Phosphorylase/hydrolase-like Superfamily: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) Family: Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
44	d2gala	Alignment	not modelled	30.1	10	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
45	c3eywA	Alignment	not modelled	29.6	10	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
46	c2d61X	Alignment	not modelled	29.2	18	PDB header: sugar binding protein Chain: X: PDB Molecule: lectin, galactose binding, soluble 9; PDBTitle: crystal structure of mouse galectin-9 n-terminal crd2 (crystal form 2)
47	d1is3a	Alignment	not modelled	29.2	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
48	d2uubb1	Alignment	not modelled	26.7	14	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
49	c3nv4A	Alignment	not modelled	26.2	13	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin 9 short isoform variant; PDBTitle: crystal structure of human galectin-9 c-terminal crd in complex with2 sialyllactose
50	c2dycA	Alignment	not modelled	25.8	8	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin-4; PDBTitle: crystal structure of the n-terminal domain of mouse galectin-4
51	c3wb9A	Alignment	not modelled	25.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: diaminopimelate dehydrogenase; PDBTitle: crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
52	d2nn8a1	Alignment	not modelled	25.6	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
53	d1euca1	Alignment	not modelled	25.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
						PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transporter, substrate-

54	c4wzzA	Alignment	not modelled	25.2	11	binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
55	c4f3yA	Alignment	not modelled	25.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
56	c3nixF	Alignment	not modelled	24.8	9	PDB header: oxidoreductase Chain: F: PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
57	c3nipB	Alignment	not modelled	24.2	17	PDB header: hydrolase Chain: B: PDB Molecule: 3-guanidinopropionase; PDBTitle: crystal structure of pseudomonas aeruginosa guanidinopropionase2 complexed with 1,6-diaminohexane
58	c4gvlB	Alignment	not modelled	24.0	8	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: crystal structure of the gsuk rck domain
59	c4ywjB	Alignment	not modelled	23.2	28	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
60	c3rysA	Alignment	not modelled	23.2	8	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase 1; PDBTitle: the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
61	c5kt0A	Alignment	not modelled	22.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anaabaena variabilis.
62	c3bioB	Alignment	not modelled	22.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
63	c4dz4D	Alignment	not modelled	22.5	14	PDB header: hydrolase Chain: D: PDB Molecule: agmatinase; PDBTitle: x-ray crystal structure of a hypothetical agmatinase from burkholderia2 thailandensis
64	d1xfka	Alignment	not modelled	22.2	20	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
65	d1c1la	Alignment	not modelled	22.1	18	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
66	c4hl0B	Alignment	not modelled	22.0	15	PDB header: sugar binding protein Chain: B: PDB Molecule: galectin; PDBTitle: crystal structure of full-length toxascaris leonina galectin
67	c4rxuA	Alignment	not modelled	21.7	3	PDB header: transport protein Chain: A: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
68	c3jw4C	Alignment	not modelled	21.6	14	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, marr/emrr family; PDBTitle: the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
69	d1oi7a1	Alignment	not modelled	21.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
70	c4j0eB	Alignment	not modelled	21.4	8	PDB header: oxidoreductase Chain: B: PDB Molecule: probable 3-hydroxyacyl-coa dehydrogenase f54c8.1; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase from2 caenorhadbitis elegans in p1 space group
71	d1ko7a1	Alignment	not modelled	21.3	9	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phoshatase HprK N-terminal domain
72	c3k6jA	Alignment	not modelled	21.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: protein f01g10.3, confirmed by transcript evidence; PDBTitle: crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
73	c3m1rF	Alignment	not modelled	20.8	17	PDB header: hydrolase Chain: F: PDB Molecule: formimidoylglutamase; PDBTitle: the crystal structure of formimidoylglutamase from bacillus2 subtilis subsp. subtilis str. 168
74	d2aeba1	Alignment	not modelled	20.8	10	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
75	c3ff4A	Alignment	not modelled	20.6	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
76	d1hlca	Alignment	not modelled	20.3	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
77	d1a9xa4	Alignment	not modelled	20.3	6	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
78	c5zeeA	Alignment	not modelled	20.3	19	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: arginase; PDBTitle: crystal structure of entamoeba histolytica arginase in

						complex with 2 n(omega)-hydroxy-l-arginine (noha) at 1.74 a
79	c1jrxA_	Alignment	not modelled	19.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
80	c3wudA_	Alignment	not modelled	19.9	13	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin; PDBTitle: x-ray crystal structure of xenopus laevis galectin-ib
81	c3b9cB_	Alignment	not modelled	19.9	21	PDB header: unknown function Chain: B: PDB Molecule: hspc159; PDBTitle: crystal structure of human grp crd
82	d1gq6a_	Alignment	not modelled	19.7	6	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
83	c5tenH_	Alignment	not modelled	19.4	22	PDB header: oxidoreductase Chain: H: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
84	c3uugB_	Alignment	not modelled	18.9	3	PDB header: sugar binding protein Chain: B: PDB Molecule: multiple sugar-binding periplasmic receptor chve; PDBTitle: crystal structure of the periplasmic sugar binding protein chve
85	c1j6uA_	Alignment	not modelled	18.9	10	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
86	d1pq3a_	Alignment	not modelled	18.6	13	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
87	d1qmja_	Alignment	not modelled	18.4	21	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
88	d2d59a1	Alignment	not modelled	18.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
89	c1s3bB_	Alignment	not modelled	18.1	8	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase [flavin-containing] b; PDBTitle: crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
90	d1zhva2	Alignment	not modelled	18.1	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
91	c6aioA_	Alignment	not modelled	17.9	13	PDB header: flavoprotein Chain: A: PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monooxygenase pnpa from2 pseudomonas putida dll-e4
92	c3bchA_	Alignment	not modelled	17.8	8	PDB header: cell adhesion, ribosomal protein Chain: A: PDB Molecule: 40s ribosomal protein sa; PDBTitle: crystal structure of the human laminin receptor precursor
93	d1w6na_	Alignment	not modelled	17.6	16	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
94	c5j97B_	Alignment	not modelled	17.5	8	PDB header: rna binding protein Chain: B: PDB Molecule: caprin-2; PDBTitle: dimerization domain of cytoplasmic activation/proliferation-associated2 protein-2 (caprin-2)
95	c6nr2C_	Alignment	not modelled	17.3	12	PDB header: transport protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
96	c6nr2D_	Alignment	not modelled	17.3	12	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
97	c6nr2B_	Alignment	not modelled	17.3	12	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
98	c6nr2A_	Alignment	not modelled	17.3	12	PDB header: transport protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of the trpm8 ion channel in complex with the menthol2 analog ws-12 and pi(4,5)p2
99	c1x50A_	Alignment	not modelled	17.3	16	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin-4; PDBTitle: solution structure of the c-terminal gal-bind lectin domain2 from human galectin-4