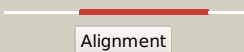

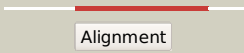


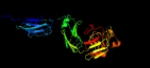
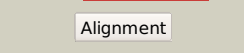



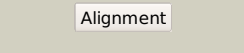

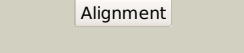



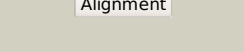

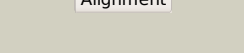
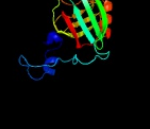
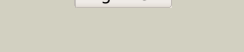




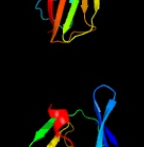


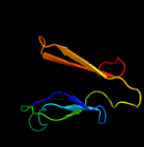
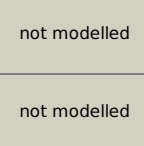


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0192 (-)_223562_224662
Date	Tue Jul 23 14:50:24 BST 2019
Unique Job ID	ee20a6df742d30d2

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3u1qB_	 Alignment		100.0	49	PDB header: peptidoglycan binding protein Chain: B: PDB Molecule: mycobacteria tuberculosis Id-transpeptidase type 2; PDBTitle: crystal structure of m. tuberculosis Id-transpeptidase type 2 with 2-2 mercaptoethanol
2	c3vynB_	 Alignment		100.0	49	PDB header: transferase Chain: B: PDB Molecule: probable conserved lipoprotein lpps; PDBTitle: crystal structure of mycobacterium tuberculosis I,d-transpeptidase2 ldtmt2 n55 truncation mutant (residue 55-408)
3	c4z7aA_	 Alignment		100.0	30	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) I,d-transpeptidase, ldtmt5.
4	c4xvoB_	 Alignment		100.0	44	PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: I,d-transpeptidase from mycobacterium smegmatis
5	c4jmxA_	 Alignment		100.0	45	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable I,d-transpeptidase ldtA; PDBTitle: structure of Id transpeptidase ldtmt1 in complex with imipenem
6	c4k73A_	 Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: x-ray crystal structure of an I,d-transpeptidase from mycobacterium2 tuberculosis h37rv
7	c2hklB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: l,d-transpeptidase; PDBTitle: crystal structure of enterococcus faecium I,d-2 transpeptidase c442s mutant
8	c5bmqA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of I,d-transpeptidase (yku) from stackebrandtia2 nassauensis
9	dlzata1	 Alignment		99.9	27	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
10	c1y7mB_	 Alignment		99.9	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14040; PDBTitle: crystal structure of the b. subtilis ykud protein at 2 a2 resolution
11	c4lzhA_	 Alignment		99.9	17	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: I,d-transpeptidase from klebsiella pneumoniae

12	d1y7ma1	Alignment		99.9	18	Fold: L,D-transpeptidase catalytic domain-like Superfamily: L,D-transpeptidase catalytic domain-like Family: L,D-transpeptidase catalytic domain-like
13	c4lpqA	Alignment		99.8	18	PDB header: transferase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of the l,d-transpeptidase (residues 123-326) from2 xylanimonas cellulositytica dsm 15894
14	c4y4vB	Alignment		99.8	16	PDB header: hydrolase Chain: B: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd6 in the d-ala-bound state
15	c4xxtA	Alignment		99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: fusion of predicted zn-dependent amidase/peptidase (cell PDBTitle: crystal structure of fused zn-dependent2 amidase/peptidase/peptodoglycan-binding domain-containing protein3 from clostridium acetobutylicum atcc 824
16	c4hu2A	Alignment		99.8	42	PDB header: unknown function Chain: A: PDB Molecule: probable conserved lipoprotein lpps; PDBTitle: crystal structure of ldtmt2, a l,d-transpeptidase from mycobacterium2 tuberculosis: domain a and b
17	c6ntwA	Alignment		99.2	13	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: probable l,d-transpeptidase yccb; PDBTitle: crystal structure of e. coli yccb
18	c3pe9D	Alignment		64.7	12	PDB header: unknown function Chain: D: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
19	d3btaa1	Alignment		58.3	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Clostridium neurotoxins, the second last domain
20	c4p9IA	Alignment		54.7	24	PDB header: transport protein Chain: A: PDB Molecule: ryanodine receptor 2; PDBTitle: crystal structure of mouse ryanodine receptor 2 spry2 domain (1080-2 1253) disease mutant a1107m
21	c3c12A	Alignment	not modelled	54.5	27	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal structure of flagd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
22	d1b09a	Alignment	not modelled	45.9	8	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Pentraxin (pentaxin)
23	d1uw6a	Alignment	not modelled	42.9	9	Fold: Nicotinic receptor ligand binding domain-like Superfamily: Nicotinic receptor ligand binding domain-like Family: Nicotinic receptor ligand binding domain-like
24	c4obiA	Alignment	not modelled	42.8	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1312 family protein (ef3258) from2 enterococcus faecalis v583 at 1.73 a resolution
25	d1a8da1	Alignment	not modelled	39.2	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Clostridium neurotoxins, the second last domain
26	d1cz5a1	Alignment	not modelled	39.1	14	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
27	c6er3B	Alignment	not modelled	39.0	14	PDB header: sugar binding protein Chain: B: PDB Molecule: bnr/asp-box repeat protein; PDBTitle: ruminococcus navus it-sialidase cbm40 bound to alpha2,3 sialyllactose PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
28	c1y5IA	Alignment	not modelled	38.5	16	Fold: Concanavalin A-like lectins/glucanases

29	d2sliA1	Alignment	not modelled	38.3	16	Superfamily: Concanavalin A-like lectins/glucanases Family: Leech intramolecular trans-sialidase, N-terminal domain
30	d1wjja_	Alignment	not modelled	37.6	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
31	c3flpJ_	Alignment	not modelled	36.6	17	PDB header: sugar binding protein Chain: J: PDB Molecule: sap-like pentraxin; PDBTitle: crystal structure of native heptameric sap-like pentraxin2 from limulus polyphemus
32	c2vu9A_	Alignment	not modelled	36.5	22	PDB header: hydrolase Chain: A: PDB Molecule: botulinum neurotoxin a heavy chain; PDBTitle: crystal structure of botulinum neurotoxin serotype a2 binding domain in complex with gt1b
33	c3pe9B_	Alignment	not modelled	35.9	12	PDB header: unknown function Chain: B: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
34	c1h5nC_	Alignment	not modelled	35.3	19	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
35	c4nl6C_	Alignment	not modelled	34.7	19	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
36	d2afja1	Alignment	not modelled	34.0	10	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: SPRY domain
37	c2vw9B_	Alignment	not modelled	33.8	15	PDB header: dna-binding protein Chain: B: PDB Molecule: single-stranded dna binding protein; PDBTitle: single stranded dna binding protein complex from2 helicobacter pylori
38	c2lojA_	Alignment	not modelled	33.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: solution nmr structure of tstm1273 from salmonella typhimurium lt2,2 nesg target stt322, csgid target idp01027 and oosp target tstm1273
39	c4zzkA_	Alignment	not modelled	32.7	23	PDB header: motor protein Chain: A: PDB Molecule: basal-body rod modification protein flgd; PDBTitle: crystal structure of truncated flgd (monoclinic form) from the human2 pathogen helicobacter pylori
40	c2jraB_	Alignment	not modelled	32.7	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein rpa2121; PDBTitle: a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
41	d1ogyA1	Alignment	not modelled	32.3	21	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
42	c2sliA_	Alignment	not modelled	31.9	26	PDB header: hydrolase Chain: A: PDB Molecule: intramolecular trans-sialidase; PDBTitle: leech intramolecular trans-sialidase complexed with 2,7-2 anhydro-neu5ac, the reaction product
43	d2r31a1	Alignment	not modelled	31.8	23	Fold: ATP12-like Superfamily: ATP12-like Family: ATP12-like
44	c3n7mA_	Alignment	not modelled	30.8	22	PDB header: toxin Chain: A: PDB Molecule: neurotoxin; PDBTitle: crystal structure of w1252a mutant of hcr d/c vpi 5995
45	c1eqqD_	Alignment	not modelled	30.5	15	PDB header: replication/rna Chain: D: PDB Molecule: single stranded dna binding protein; PDBTitle: single stranded dna binding protein and ssdna complex
46	c4qt6A_	Alignment	not modelled	29.8	27	PDB header: transport protein Chain: A: PDB Molecule: probable e3 ubiquitin-protein ligase herc1; PDBTitle: crystal structure of the spry domain of human herc1
47	c4dqaA_	Alignment	not modelled	29.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative carbohydrate binding protein2 (bacova_03559) from bacteroides ovatus atcc 8483 at 1.50 a resolution
48	c5kxiA_	Alignment	not modelled	29.1	25	PDB header: transport protein Chain: A: PDB Molecule: neuronal acetylcholine receptor subunit alpha-4; PDBTitle: x-ray structure of the human alpha4beta2 nicotinic receptor
49	d1saca_	Alignment	not modelled	28.7	8	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Pentraxin (pentraxin)
50	c6fvqE_	Alignment	not modelled	28.5	10	PDB header: membrane protein Chain: E: PDB Molecule: cys-loop ligand-gated ion channel; PDBTitle: the active form of a pentameric ion channel (stelic) gated by alkaline2 ph - r86a
51	c6hoxA_	Alignment	not modelled	28.4	11	PDB header: toxin Chain: A: PDB Molecule: binding domain (hc) of paraclostridial mosquitocidal PDBTitle: crystal structure of the binding domain of paraclostridial2 mosquitocidal protein 1
52	c5xgtA_	Alignment	not modelled	26.9	16	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of the n-terminal domain of staphylococcus aureus2 single-stranded dna-binding protein ssba at 1.82 angstrom resolution
53	c3sq9D_	Alignment	not modelled	26.0	10	PDB header: transport protein/receptor Chain: D: PDB Molecule: neuronal acetylcholine receptor subunit alpha-7, PDBTitle: crystal structures of the ligand binding domain of a pentameric alpha72 nicotinic receptor chimera

54	c2vxrA	Alignment	not modelled	25.8	19	PDB header: toxin Chain: A: PDB Molecule: botulinum neurotoxin type g; PDBTitle: crystal structure of the botulinum neurotoxin serotype g2 binding domain
55	d2piaa1	Alignment	not modelled	25.6	35	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
56	c3osvC	Alignment	not modelled	25.4	29	PDB header: structural protein Chain: C: PDB Molecule: flagellar basal-body rod modification protein flgd; PDBTitle: the crytsal structure of flgd from p. aeruginosa
57	c5gqoB	Alignment	not modelled	25.4	32	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein; PDBTitle: structure of the second single stranded dna binding protein (ssbb)2 from mycobacterium smegmatis
58	d1f00i2	Alignment	not modelled	25.0	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
59	c3lgjA	Alignment	not modelled	25.0	21	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
60	c5jiaH	Alignment	not modelled	24.9	23	PDB header: ran-binding protein Chain: H: PDB Molecule: ran-binding protein 10; PDBTitle: the crystal structure of ius-spry domain from ranbp10
61	c5ch7E	Alignment	not modelled	24.6	18	PDB header: oxidoreductase Chain: E: PDB Molecule: dms0 reductase family type ii enzyme, molybdopterin PDBTitle: crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
62	c6rteB	Alignment	not modelled	24.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
63	c1z9fA	Alignment	not modelled	23.6	20	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
64	d1lka	Alignment	not modelled	23.5	32	Fold: Head-binding domain of phage P22 tailspike protein Superfamily: Head-binding domain of phage P22 tailspike protein Family: Head-binding domain of phage P22 tailspike protein
65	d1y5ia1	Alignment	not modelled	22.5	22	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
66	c4p9jC	Alignment	not modelled	22.2	22	PDB header: transport protein Chain: C: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of rabbit ryanodine receptor 1 spry2 domain (1070-2 1246)
67	c5odnG	Alignment	not modelled	22.1	8	PDB header: dna binding protein Chain: G: PDB Molecule: single-stranded dna-binding protein; PDBTitle: salinibacter ruber single-strand binding protein
68	c1cz5A	Alignment	not modelled	21.9	14	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
69	c3oggA	Alignment	not modelled	21.9	15	PDB header: toxin Chain: A: PDB Molecule: botulinum neurotoxin type d; PDBTitle: crystal structure of the receptor binding domain of botulinum2 neurotoxin d
70	c3fugA	Alignment	not modelled	21.5	19	PDB header: toxin Chain: A: PDB Molecule: bont/f (neurotoxin type f); PDBTitle: glycosylated sv2 and gangliosides as dual receptors for2 botulinum neurotoxin serotype f
71	c3pgzB	Alignment	not modelled	20.7	10	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of a single strand binding protein (ssb) from2 bartonella henselae
72	d3ulla	Alignment	not modelled	20.1	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
73	d2iv2x1	Alignment	not modelled	19.7	17	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
74	c2bg9A	Alignment	not modelled	19.5	22	PDB header: ion channel/receptor Chain: A: PDB Molecule: acetylcholine receptor protein, alpha chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
75	c4aaq5A	Alignment	not modelled	19.5	22	PDB header: membrane protein Chain: A: PDB Molecule: acetylcholine receptor subunit alpha; PDBTitle: gating movement in acetylcholine receptor analysed by time-resolved2 electron cryo-microscopy (closed class)
76	c1dfcB	Alignment	not modelled	19.4	9	PDB header: structural protein Chain: B: PDB Molecule: fascin; PDBTitle: crystal structure of human fascin, an actin-crosslinking protein
77	d1qvca	Alignment	not modelled	19.2	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
78	c1qvcA	Alignment	not modelled	19.2	16	PDB header: dna binding protein Chain: A: PDB Molecule: single stranded dna binding protein monomer; PDBTitle: crystal structure analysis of single stranded dna binding protein2 (ssb) from e.coli
79	d1eyga	Alignment	not modelled	19.1	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins

					Family: Single strand DNA-binding domain, SSB
80	d2in5a1	Alignment	not modelled	19.0	29 Fold: YmcC-like Superfamily: YmcC-like Family: YmcC-like
81	d2fnja1	Alignment	not modelled	19.0	10 Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: SPRY domain
82	d2fb5a1	Alignment	not modelled	19.0	22 Fold: Yojj-like Superfamily: Yojj-like Family: Yojj-like
83	c5fraD_	Alignment	not modelled	18.6	23 PDB header: sugar binding protein Chain: D: PDB Molecule: sialidase; PDBTitle: cbm40_cpf0721-6'sl
84	c5c33B_	Alignment	not modelled	17.9	14 PDB header: contractile protein Chain: B: PDB Molecule: ryanodine receptor 2; PDBTitle: crystal structure of mouse ryanodine receptor 2 spry1 domain
85	c2bg9B_	Alignment	not modelled	17.9	11 PDB header: ion channel/receptor Chain: B: PDB Molecule: acetylcholine receptor protein, beta chain; PDBTitle: refined structure of the nicotinic acetylcholine receptor2 at 4a resolution.
86	d1ccza2	Alignment	not modelled	17.7	8 Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C2 set domains
87	d1epwa1	Alignment	not modelled	17.7	15 Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Clostridium neurotoxins, the second last domain
88	c1ue7A_	Alignment	not modelled	17.2	20 PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis
89	c2vkyB_	Alignment	not modelled	17.0	32 PDB header: viral protein Chain: B: PDB Molecule: tail protein, piigcn4; PDBTitle: headbinding domain of phage p22 tailspike c-terminally fused to2 isoleucine zipper piigcn4 (chimera i)
90	c2g8yB_	Alignment	not modelled	16.9	12 PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
91	c2kppA_	Alignment	not modelled	16.8	23 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0431 protein; PDBTitle: solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
92	c5t5iL_	Alignment	not modelled	16.7	28 PDB header: oxidoreductase Chain: L: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdd; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
93	d2jioa1	Alignment	not modelled	16.7	16 Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
94	d1h0ha1	Alignment	not modelled	16.5	19 Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
95	c4owtB_	Alignment	not modelled	16.4	22 PDB header: dna binding protein Chain: B: PDB Molecule: soos complex subunit b1; PDBTitle: structural basis of soos1 complex assembly
96	c6hinA_	Alignment	not modelled	16.3	13 PDB header: membrane protein Chain: A: PDB Molecule: 5-hydroxytryptamine receptor 3a; PDBTitle: mouse serotonin 5-ht3 receptor, serotonin-bound, f conformation
97	c1mp9B_	Alignment	not modelled	16.2	24 PDB header: dna binding protein Chain: B: PDB Molecule: tata-binding protein; PDBTitle: tbp from a mesothermophilic archaeon, sulfolobus acidocaldarius
98	c2v73B_	Alignment	not modelled	16.0	14 PDB header: sugar-binding protein Chain: B: PDB Molecule: putative exo-alpha-sialidase; PDBTitle: the structure of the family 40 cbm from c. perfringens nanj2 in complex with a sialic acid containing molecule
99	c3eivB_	Alignment	not modelled	15.8	15 PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein 2; PDBTitle: crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor