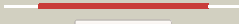


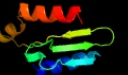
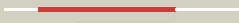
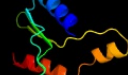





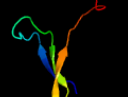










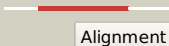

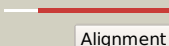

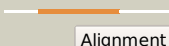



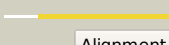

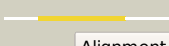

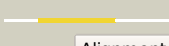

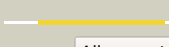

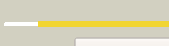

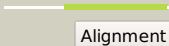
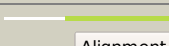
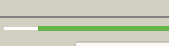

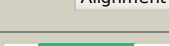
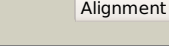
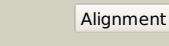
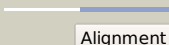


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2898c_(-)_3207952_3208338
Date	Thu Aug 8 16:20:05 BST 2019
Unique Job ID	24d28738c453183b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fovA_	 Alignment		100.0	41	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0102 protein rpa0323; PDBTitle: crystal structure of protein rpa0323 of unknown function from <i>Rhodospirillum rubrum</i>
2	d1gefa_	 Alignment		97.4	22	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
3	d1ob8a_	 Alignment		96.9	24	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
4	c2eo0A_	 Alignment		96.6	22	PDB header: dna binding protein Chain: A: PDB Molecule: hypothetical protein st1444; PDBTitle: crystal structure of holliday junction resolvase st1444
5	c2wj0B_	 Alignment		96.2	23	PDB header: hydrolase/dna Chain: B: PDB Molecule: archaeal hjc; PDBTitle: crystal structures of holliday junction resolvases from <i>Archaeoglobus fulgidus</i> bound to dna substrate
6	c5gkeB_	 Alignment		95.3	26	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
7	d1hh1a_	 Alignment		95.3	20	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like
8	c2vldA_	 Alignment		94.3	29	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease nucs; PDBTitle: crystal structure of a repair endonuclease from <i>Pyrococcus abyssi</i>
9	c4dapA_	 Alignment		94.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: sugar fermentation stimulation protein a; PDBTitle: the structure of <i>Escherichia coli</i> sfsa
10	c3dnxA_	 Alignment		93.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein spo1766; PDBTitle: spo1766 protein of unknown function from <i>Silicibacter pomeroyi</i>
11	d1y88a2	 Alignment		93.7	22	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: MRR-like

12	c1y88A_	 Alignment		93.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1548; PDBTitle: crystal structure of protein of unknown function af1548
13	c4davA_	 Alignment		91.2	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: sugar fermentation stimulation protein homolog; PDBTitle: the structure of pyrococcus furiosus sfsa in complex with dna
14	d2inba1	 Alignment		83.8	25	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: XisH-like
15	d2okfa1	 Alignment		81.9	23	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: XisH-like
16	c4qbnA_	 Alignment		79.9	19	PDB header: hydrolase Chain: A: PDB Molecule: nuclease; PDBTitle: vrr_nuc domain
17	d1xma_	 Alignment		78.4	27	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hypothetical protein VC1899
18	d1cw0a_	 Alignment		73.9	25	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
19	c4oc8A_	 Alignment		73.9	28	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease aspghi; PDBTitle: dna modification-dependent restriction endonuclease aspghi
20	d1m0da_	 Alignment		70.2	20	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
21	c4r8aF_	 Alignment	not modelled	68.5	29	PDB header: hydrolase/dna Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pafan1 - 5' flap dna complex
22	c4ribA_	 Alignment	not modelled	63.7	30	PDB header: hydrolase/dna Chain: A: PDB Molecule: fanconi-associated nuclease 1; PDBTitle: fan1 nuclease bound to 5' phosphorylated p(dt) single flap dna
23	c4qboA_	 Alignment	not modelled	58.0	21	PDB header: hydrolase Chain: A: PDB Molecule: nuclease; PDBTitle: vrr_nuc domain
24	c2ixsB_	 Alignment	not modelled	47.5	18	PDB header: hydrolase Chain: B: PDB Molecule: sdai restriction endonuclease; PDBTitle: structure of sdai restriction endonuclease
25	c4xqkB_	 Alignment	not modelled	45.4	25	PDB header: hydrolase/dna Chain: B: PDB Molecule: llabiii; PDBTitle: atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna
26	d1xdfa1	 Alignment	not modelled	42.5	12	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
27	c4onbA_	 Alignment	not modelled	26.6	15	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated exonuclease, cas4 family; PDBTitle: crystal structure of crispr-associated exonuclease (cas4 family) from2 pyrobaculum calidifontis jcm 11548
28	c2k7hA_	 Alignment	not modelled	25.5	10	PDB header: allergen Chain: A: PDB Molecule: stress-induced protein sam22; PDBTitle: nmr solution structure of soybean allergen gly m 4

29	d2o8ra3	Alignment	not modelled	25.2	44	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
30	c3bt3B	Alignment	not modelled	22.9	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: glyoxalase-related enzyme, arac type; PDBTitle: crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
31	c5jhfA	Alignment	not modelled	21.9	30	PDB header: protein transport Chain: A: PDB Molecule: klth0d11660p; PDBTitle: crystal structure of atg13(17br)-atg13(17lr)-atg17-atg29-atg31 complex
32	c4g6vE	Alignment	not modelled	21.7	19	PDB header: toxin Chain: E: PDB Molecule: adhesin/hemolysin; PDBTitle: cdia-ct/cdii toxin and immunity complex from burkholderia pseudomallei
33	c2o8rA	Alignment	not modelled	18.2	44	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from porphyromonas2 gingivalis
34	d2j9ga3	Alignment	not modelled	17.3	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
35	d1puza	Alignment	not modelled	17.3	55	Fold: YgfY-like Superfamily: YgfY-like Family: YgfY-like
36	d1vsra	Alignment	not modelled	17.1	26	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
37	d1icxa	Alignment	not modelled	16.9	12	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
38	c5jvvA	Alignment	not modelled	16.8	67	PDB header: transferase Chain: A: PDB Molecule: beta-1,3-glucosyltransferase; PDBTitle: crystal structure and characterization an elongating gh family 162 beta-1,3-glucosyltransferase
39	c1x6iB	Alignment	not modelled	16.5	64	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ygyf; PDBTitle: crystal structure of ygyf from escherichia coli
40	c2qv6D	Alignment	not modelled	15.9	11	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
41	c2jr5A	Alignment	not modelled	15.3	73	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0350 protein vc_2471; PDBTitle: solution structure of upf0350 protein vc_2471. northeast structural2 genomics target vcr36
42	c1gndA	Alignment	not modelled	14.5	15	PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform
43	d1iowa2	Alignment	not modelled	13.9	26	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
44	d2i7ra1	Alignment	not modelled	12.8	16	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Antibiotic resistance proteins
45	d2fiwa1	Alignment	not modelled	12.8	26	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
46	d2jfga1	Alignment	not modelled	12.2	30	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
47	c3g12A	Alignment	not modelled	12.1	15	PDB header: lyase Chain: A: PDB Molecule: putative lactoylglutathione lyase; PDBTitle: crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus
48	d1miau5	Alignment	not modelled	12.0	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
49	d1y0ka1	Alignment	not modelled	12.0	54	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: PA4535-like
50	d1w36b3	Alignment	not modelled	12.0	15	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
51	c3bpqD	Alignment	not modelled	11.8	25	PDB header: toxin Chain: D: PDB Molecule: toxin rele3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
52	d1kjqaz	Alignment	not modelled	11.4	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
53	d1e4ea2	Alignment	not modelled	11.3	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
54	c4ic1D	Alignment	not modelled	11.3	27	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of sso0001
55	c3g3oA	Alignment	not modelled	11.1	36	PDB header: biosynthetic protein Chain: A: PDB Molecule: vacuolar transporter chaperone 2; PDBTitle: crystal structure of the cytoplasmic tunnel domain in

					yeast2 vtc2p
56	c2duwA	Alignment	not modelled	10.7	15 PDB header: ligand binding protein Chain: A: PDB Molecule: putative coa-binding protein; PDBTitle: solution structure of putative coa-binding protein of2 klebsiella pneumoniae
57	c2cl2A	Alignment	not modelled	10.4	67 PDB header: hydrolase Chain: A: PDB Molecule: putative laminarinase; PDBTitle: endo-1,3(4)-beta-glucanase from phanerochaete chrysosporium, solved2 using native sulfur sad, exhibiting intact heptasaccharide3 glycosylation
58	c4hpgA	Alignment	not modelled	10.2	30 PDB header: protein transport Chain: A: PDB Molecule: atg29; PDBTitle: crystal structure of the atg17-atg31-atg29 complex
59	c4hpgD	Alignment	not modelled	10.2	30 PDB header: protein transport Chain: D: PDB Molecule: atg29; PDBTitle: crystal structure of the atg17-atg31-atg29 complex
60	d2ifaa1	Alignment	not modelled	9.8	17 Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
61	c3p1wA	Alignment	not modelled	9.6	28 PDB header: protein transport Chain: A: PDB Molecule: rabgdi protein; PDBTitle: crystal structure of rab gdi from plasmodium falciparum, pfl2060c
62	c3wdvB	Alignment	not modelled	9.6	50 PDB header: hydrolase Chain: B: PDB Molecule: beta-1,3-1,4-glucanase; PDBTitle: the complex structure of ptlc16a with cellotetraose
63	c3r23B	Alignment	not modelled	9.6	22 PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
64	c2mx0A	Alignment	not modelled	9.2	26 PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein hp_0268; PDBTitle: solution structure of hp0268 from helicobacter pylori
65	c1z8rA	Alignment	not modelled	8.9	25 PDB header: hydrolase Chain: A: PDB Molecule: coxsaackievirus b4 polyprotein; PDBTitle: 2a cysteine proteinase from human coxsackievirus b4 (strain2 jyb / benschoten / new york / 51)
66	c3kwaA	Alignment	not modelled	8.8	14 PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh dehydrogenase/nad(p)h nitroreductase; PDBTitle: crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
67	d1j6ua1	Alignment	not modelled	8.8	19 Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
68	d1iyb5	Alignment	not modelled	8.6	21 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
69	c2pvpB	Alignment	not modelled	8.5	10 PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
70	c2m5tA	Alignment	not modelled	8.2	25 PDB header: viral protein Chain: A: PDB Molecule: human rhinovirus 2a proteinase; PDBTitle: solution structure of the 2a proteinase from a common cold agent,2 human rhinovirus rv-c02, strain w12
71	c4eo3A	Alignment	not modelled	8.2	20 PDB header: oxidoreductase Chain: A: PDB Molecule: bacterioferritin comigratory protein/nadh dehydrogenase; PDBTitle: peroxiredoxin nitroreductase fusion enzyme
72	d2ayxa2	Alignment	not modelled	8.0	11 Fold: Flavodoxin-like Superfamily: CheY-like Family: RcsC linker domain-like
73	c3r6aB	Alignment	not modelled	7.9	15 PDB header: isomerase, lyase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein (hypothetical protein2 mm_3218) from methanosarcina mazei.
74	c6qb7A	Alignment	not modelled	7.8	28 PDB header: signaling protein Chain: A: PDB Molecule: btb/poz domain-containing protein kctd16; PDBTitle: structure of the h1 domain of human kctd16
75	c3ey5A	Alignment	not modelled	7.7	5 PDB header: transferase Chain: A: PDB Molecule: acetyltransferase-like, gnat family; PDBTitle: putative acetyltransferase from gnat family from bacteroides2 thetaiotaomicron.
76	d2hrva	Alignment	not modelled	7.7	17 Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
77	d3etja3	Alignment	not modelled	7.5	6 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
78	d1lfva	Alignment	not modelled	7.4	9 Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
79	c3h1tA	Alignment	not modelled	7.3	18 PDB header: hydrolase Chain: A: PDB Molecule: type i site-specific restriction-modification PDBTitle: the fragment structure of a putative hsdr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
80	d1cxa1	Alignment	not modelled	7.2	13 Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
					PDB header: hydrolase

81	c2iyeC_	Alignment	not modelled	7.2	28	Chain: C: PDB Molecule: copper-transporting atpase; PDBTitle: structure of catalytic cpx-atpase domain copb-b
82	d1fm4a_	Alignment	not modelled	7.1	15	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
83	c3cd1A_	Alignment	not modelled	7.1	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator aefr; PDBTitle: crystal structure of a tetr family transcriptional regulator from2 pseudomonas syringae pv. tomato str. dc3000
84	d1kqba_	Alignment	not modelled	7.0	9	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
85	c3g5oC_	Alignment	not modelled	7.0	20	PDB header: toxin/antitoxin Chain: C: PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
86	c6gq9A_	Alignment	not modelled	6.8	11	PDB header: allergen Chain: A: PDB Molecule: major allergen cor a 1.0401; PDBTitle: solution structure of the hazel allergen cor a 1.0401
87	d1jg5a_	Alignment	not modelled	6.8	31	Fold: GTP cyclohydrolase I feedback regulatory protein, GFRP Superfamily: GTP cyclohydrolase I feedback regulatory protein, GFRP Family: GTP cyclohydrolase I feedback regulatory protein, GFRP
88	c1wv9B_	Alignment	not modelled	6.8	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
89	c4g6xA_	Alignment	not modelled	6.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of glyoxalase/bleomycin resistance protein from2 catenulispora acidiphila.
90	d1qmra_	Alignment	not modelled	6.7	13	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
91	c3r3pB_	Alignment	not modelled	6.7	10	PDB header: hydrolase Chain: B: PDB Molecule: mobile intron protein; PDBTitle: homing endonuclease i-bth0305i catalytic domain
92	d1p3da1	Alignment	not modelled	6.7	24	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
93	d1o1xa_	Alignment	not modelled	6.6	19	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
94	c3zi1A_	Alignment	not modelled	6.6	21	PDB header: isomerase Chain: A: PDB Molecule: glyoxalase domain-containing protein 4; PDBTitle: crystal structure of human glyoxalase domain-containing protein 42 (glod4)
95	c2rk9B_	Alignment	not modelled	6.6	2	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily member from vibrio splendidus 12b01
96	d1p9oa_	Alignment	not modelled	6.4	20	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
97	c4kh8A_	Alignment	not modelled	6.3	40	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a lipocalin-like protein (ef0376) from2 enterococcus faecalis v583 at 1.60 a resolution
98	c3of4A_	Alignment	not modelled	6.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
99	c2mxqA_	Alignment	not modelled	6.2	67	PDB header: antimicrobial protein Chain: A: PDB Molecule: paneth cell-specific alpha-defensin 1; PDBTitle: the solution structure of defa1, a highly potent antimicrobial peptide2 from the horse