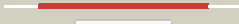



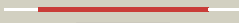












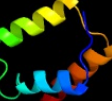




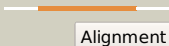

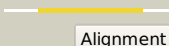

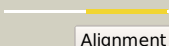

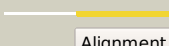

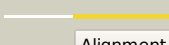



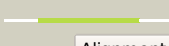





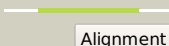
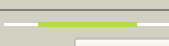
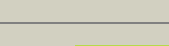
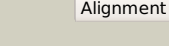


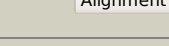
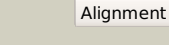


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0543c (-)_635576_635878
Date	Fri Jul 26 01:50:09 BST 2019
Unique Job ID	309e8b8df9bda11a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kvcA_	 Alignment		100.0	99	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
2	c2lkyA_	 Alignment		100.0	61	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
3	c3ol4B_	 Alignment		100.0	41	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
4	c2m0nA_	 Alignment		100.0	42	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
5	d1khda1	 Alignment		91.2	14	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
6	d1o17a1	 Alignment		90.5	12	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
7	d1v8ga1	 Alignment		88.1	16	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
8	d2tpta1	 Alignment		87.9	13	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
9	d1uoua1	 Alignment		87.2	19	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
10	d1brwa1	 Alignment		86.5	14	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
11	d1qksa1	 Alignment		81.3	21	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase

12	d1hj3a1	 Alignment		80.5	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
13	d1e2rb1	 Alignment		73.8	21	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
14	c5tdyD	 Alignment		73.7	17	PDB header: motor protein Chain: D: PDB Molecule: flagellar motor switch protein flig; PDBTitle: structure of cofolded flifc:flign complex from thermotoga maritima
15	c1o17A	 Alignment		71.5	13	PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyl-transferase (trpd)
16	c4hkmA	 Alignment		70.4	12	PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure of an anthranilate phosphoribosyltransferase (target2 id nysgrc-016600) from xanthomonas campestris
17	c2dsjA	 Alignment		66.7	12	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
18	d1nira1	 Alignment		64.4	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
19	d1ng6a	 Alignment		64.0	17	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/YqeY domain
20	d1h9xa1	 Alignment		63.9	24	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
21	d1hzua1	 Alignment	not modelled	63.7	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
22	c3mk7F	 Alignment	not modelled	63.7	21	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
23	c1khdD	 Alignment	not modelled	63.6	11	PDB header: transferase Chain: D: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.9 resolution3 (current name, pectobacterium carotovorum)
24	c6f6jC	 Alignment	not modelled	62.7	32	PDB header: oxidoreductase Chain: C: PDB Molecule: l-lysine 3-hydroxylase; PDBTitle: crystal structure of the fe(ii)/alpha-ketoglutarate dependent2 dioxygenase kdo1 with fe(ii)/succinate/(3s)-3-hydroxy-l-lysine
25	c2gbbA	 Alignment	not modelled	62.2	22	PDB header: isomerase Chain: A: PDB Molecule: putative chorismate mutase; PDBTitle: crystal structure of secreted chorismate mutase from yersinia pestis
26	c4ga5H	 Alignment	not modelled	62.1	17	PDB header: transferase Chain: H: PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
27	c3h5gA	 Alignment	not modelled	54.7	10	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
28	c2zyuA	 Alignment	not modelled	53.5	26	PDB header: oxygen binding, transport protein Chain: A: PDB Molecule: cytochrome c552;

28	c2zxyA	Alignment	not modelled	53.5	20	PDBTitle: crystal structure of cytochrome c555 from aquifex aeolicus PDB header: transferase
29	c1brwB	Alignment	not modelled	52.9	13	Chain: B; PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
30	c2j0fC	Alignment	not modelled	51.3	18	PDB header: transferase Chain: C; PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
31	c1v8gB	Alignment	not modelled	48.6	16	PDB header: transferase Chain: B; PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
32	c6paxA	Alignment	not modelled	48.4	21	PDB header: gene regulation/dna Chain: A; PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
33	c1otpA	Alignment	not modelled	47.7	16	PDB header: phosphorylase Chain: A; PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
34	c3hjiA	Alignment	not modelled	47.4	18	PDB header: proton transport Chain: A; PDB Molecule: flagellar motor switch protein flig; PDBTitle: the structure of full-length flig from aquifex aeolicus
35	c1vquB	Alignment	not modelled	47.1	11	PDB header: transferase Chain: B; PDB Molecule: anthranilate phosphoribosyltransferase 2; PDBTitle: crystal structure of anthranilate phosphoribosyltransferase 22 (17130499) from nostoc sp. at 1.85 a resolution
36	c2bpgB	Alignment	not modelled	45.5	17	PDB header: transferase Chain: B; PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
37	c5wujB	Alignment	not modelled	44.0	20	PDB header: motor protein Chain: B; PDB Molecule: flagellar motor switch protein flig; PDBTitle: crystal structure of flif-flig complex from h. pylori
38	c6ge2A	Alignment	not modelled	40.5	32	PDB header: hormone Chain: A; PDB Molecule: exendin-4; PDBTitle: exendin-4 based dual glp-1/glucagon receptor agonist
39	d1dy7b1	Alignment	not modelled	39.9	24	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
40	c1zswA	Alignment	not modelled	38.2	11	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: glyoxalase family protein; PDBTitle: crystal structure of bacillus cereus metallo protein from glyoxalase2 family
41	c4gtnA	Alignment	not modelled	37.8	13	PDB header: transferase Chain: A; PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi
42	c1h1oA	Alignment	not modelled	36.5	20	PDB header: electron transport Chain: A; PDB Molecule: cytochrome c-552; PDBTitle: acidithiobacillus ferrooxidans cytochrome c4 structure2 supports a complex-induced tuning of electron transfer
43	c2m29A	Alignment	not modelled	35.9	13	PDB header: metal binding protein Chain: A; PDB Molecule: calcium-binding protein 4; PDBTitle: nmr structure of ca2+ bound cabb4 n-domain
44	c5nofB	Alignment	not modelled	34.7	20	PDB header: transferase Chain: B; PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyltransferase from thermococcus kodakaraensis
45	c1jrjA	Alignment	not modelled	34.7	32	PDB header: hormone/growth factor Chain: A; PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
46	d1zswa2	Alignment	not modelled	33.4	11	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: BC1024-like
47	c2zmeD	Alignment	not modelled	32.8	33	PDB header: protein transport Chain: D; PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
48	c3oajA	Alignment	not modelled	32.1	31	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative ring-cleaving dioxygenase mhqo; PDBTitle: crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
49	c5mxzA	Alignment	not modelled	32.0	31	PDB header: electron transport Chain: A; PDB Molecule: cytochrome c-552 ks_3358; PDBTitle: kustc0563 y40f mutant
50	c3cuqD	Alignment	not modelled	32.0	33	PDB header: protein transport Chain: D; PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
51	c5j1bB	Alignment	not modelled	31.9	18	PDB header: signaling protein Chain: B; PDB Molecule: cell wall assembly regulator smi1; PDBTitle: structure of the core domaine of knr4, an intrinsically disordered2 protein from saccharomyces cerevisiae - wt.
52	c1wvoA	Alignment	not modelled	30.9	39	PDB header: transferase Chain: A; PDB Molecule: sialic acid synthase; PDBTitle: solution structure of rsgi ruh-029, an antifreeze protein2 like domain in human n-acetylneuraminic acid phosphate3 synthase gene.

53	c4muoB_	Alignment	not modelled	30.7	11	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein ybib; PDBTitle: the trpd2 enzyme from e.coli: ybib
54	c3g6iA_	Alignment	not modelled	30.5	35	PDB header: unknown function Chain: A: PDB Molecule: putative outer membrane protein, part of carbohydrate PDBTitle: crystal structure of an outer membrane protein, part of a putative2 carbohydrate binding complex (bt_1022) from bacteroides3 thetaiotaomicron vpi-5482 at 1.93 a resolution
55	c2xtsD_	Alignment	not modelled	30.3	24	PDB header: oxidoreductase/electron transport Chain: D: PDB Molecule: cytochrome c; PDBTitle: crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
56	d1h1oa1_	Alignment	not modelled	29.5	13	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
57	c1c8aA_	Alignment	not modelled	28.8	22	PDB header: antifreeze protein Chain: A: PDB Molecule: protein (antifreeze protein type iii); PDBTitle: nmr structure of intramolecular dimer antifreeze protein2 rd3, 40 sa structures
58	c3ecjC_	Alignment	not modelled	28.8	23	PDB header: oxidoreductase Chain: C: PDB Molecule: protein (homoprotocatechuate 2,3-dioxygenase); PDBTitle: structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
59	d1c75a_	Alignment	not modelled	28.3	26	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
60	d1c8aa2_	Alignment	not modelled	27.9	22	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
61	d3nlaa_	Alignment	not modelled	27.6	22	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
62	c6hwhj_	Alignment	not modelled	27.3	26	PDB header: electron transport Chain: J: PDB Molecule: co-purified unknown peptide built as polyala; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
63	c5xj0Y_	Alignment	not modelled	27.2	22	PDB header: transferase/transcription Chain: Y: PDB Molecule: gp76; PDBTitle: t. thermophilus rna polymerase holoenzyme bound with gp39 and gp76
64	c5n1tB_	Alignment	not modelled	26.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
65	d1fcdc1_	Alignment	not modelled	25.8	10	Fold: Cytochrome c Superfamily: Cytochrome c Family: Two-domain cytochrome c
66	c3omeE_	Alignment	not modelled	25.8	15	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
67	d1dvha_	Alignment	not modelled	25.5	21	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
68	d1xb4a1_	Alignment	not modelled	24.6	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
69	d1a56a_	Alignment	not modelled	23.6	19	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
70	c4pwaA_	Alignment	not modelled	23.6	21	PDB header: electron transport Chain: A: PDB Molecule: putative cytochrome c; PDBTitle: crystal structure of the c-type cytochrome soru from sinorhizobium2 meliloti
71	c1rz4A_	Alignment	not modelled	23.4	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit 11; PDBTitle: crystal structure of human eif3k
72	d1kx7a_	Alignment	not modelled	22.7	16	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
73	c3uc9A_	Alignment	not modelled	22.6	14	PDB header: recombination Chain: A: PDB Molecule: increased recombination centers protein 6; PDBTitle: crystal structure of yeast irc6p - a novel type of conserved clathrin2 accessory protein
74	c4j20B_	Alignment	not modelled	22.6	11	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c-555; PDBTitle: x-ray structure of the cytochrome c-554 from chlorobaculum tepidum
75	c3elkA_	Alignment	not modelled	22.4	7	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator ta0346; PDBTitle: crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum
76	c2k7ba_	Alignment	not modelled	22.3	13	PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein 1; PDBTitle: nmr structure of mg2+-bound cabp1 n-domain
77	d1opsa_	Alignment	not modelled	22.3	22	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
						PDB header: protein transport

78	c2x49A_	Alignment	not modelled	21.5	16	Chain: A: PDB Molecule: invasion protein inva; PDBTitle: crystal structure of the c-terminal domain of inva
79	c3gr0D_	Alignment	not modelled	21.2	31	PDB header: membrane protein Chain: D: PDB Molecule: protein prgh; PDBTitle: periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
80	c6adqC_	Alignment	not modelled	21.1	26	PDB header: electron transport Chain: C: PDB Molecule: cytochrome bc1 complex cytochrome c subunit; PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
81	c2v7sA_	Alignment	not modelled	20.9	15	PDB header: unknown function Chain: A: PDB Molecule: probable conserved lipoprotein lppa; PDBTitle: crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
82	d2pq3a1	Alignment	not modelled	20.9	13	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
83	d1luca_	Alignment	not modelled	20.7	22	Fold: beta-clip Superfamily: AFP III-like domain Family: AFP III-like domain
84	c6faqA_	Alignment	not modelled	20.3	8	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding protein; PDBTitle: structure of h. salinarum rosr (vng0258) grown from kbr
85	c4a5pC_	Alignment	not modelled	20.3	17	PDB header: protein transport Chain: C: PDB Molecule: protein mxia; PDBTitle: structure of the shigella flexneri mxia protein
86	c3ek7A_	Alignment	not modelled	20.2	20	PDB header: fluorescent protein Chain: A: PDB Molecule: myosin light chain kinase, green fluorescent protein, PDBTitle: calcium-saturated gcamp2 dimer
87	c3deeA_	Alignment	not modelled	20.2	12	PDB header: transcription Chain: A: PDB Molecule: putative regulatory protein; PDBTitle: crystal structure of a putative regulatory protein involved in2 transcription (ngo1945) from neisseria gonorrhoeae fa 1090 at 2.25 a3 resolution
88	c3kblA_	Alignment	not modelled	19.9	36	PDB header: protein binding Chain: A: PDB Molecule: female germline-specific tumor suppressor gld-1; PDBTitle: crystal structure of the gld-1 homodimerization domain from2 caenorhabditis elegans n169a mutant at 2.28 a resolution
89	c2zszW_	Alignment	not modelled	19.8	20	PDB header: electron transport Chain: W: PDB Molecule: PDBTitle: crystal structure of cytochrome c554 from vibrio2 parahaemolyticus strain rimd2210633
90	d1q0oa2	Alignment	not modelled	19.5	9	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases
91	c2wl9A_	Alignment	not modelled	19.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: catechol 2,3-dioxygenase; PDBTitle: crystal structure of catechol 2,3-dioxygenase
92	c3u0kA_	Alignment	not modelled	19.2	13	PDB header: fluorescent protein Chain: A: PDB Molecule: rcamp; PDBTitle: crystal structure of the genetically encoded calcium indicator rcamp
93	c4esbA_	Alignment	not modelled	19.1	4	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, padr family; PDBTitle: crystal structure of padr-like transcriptional regulator (bc4206) from2 bacillus cereus strain atcc 14579
94	d2c8sa1	Alignment	not modelled	19.0	19	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
95	d1cc5a_	Alignment	not modelled	18.7	36	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
96	c4xxlA_	Alignment	not modelled	18.7	9	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c class i; PDBTitle: crystal structure of class 1 cytochrome mtd from sideroxydans2 lithotrophicus es-1
97	c2dkjB_	Alignment	not modelled	18.6	17	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of t.th.hb8 serine hydroxymethyltransferase
98	c5znhA_	Alignment	not modelled	18.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: catechol 2,3-dioxygenase, extradiol protein; PDBTitle: catechol 2,3-dioxygenase with 4-methyl catechol from diaphorobacter sp2 ds2
99	d1mpya1	Alignment	not modelled	18.2	13	Fold: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Superfamily: Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase Family: Extradiol dioxygenases