

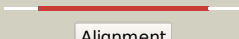

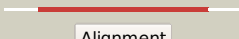


















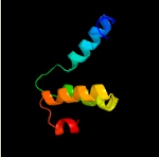




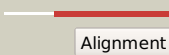
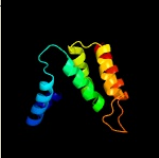
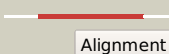

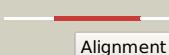

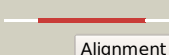




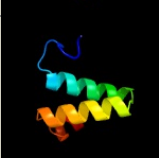

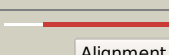

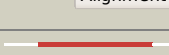
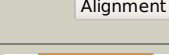
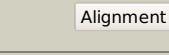
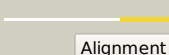



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0464c (-)_554316_554888
Date	Tue Jul 23 14:50:54 BST 2019
Unique Job ID	0c2d8a39cb871a4a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lvyB_	 Alignment		100.0	10	PDB header: lyase Chain: B; PDB Molecule: carboxymuconolactone decarboxylase family; PDBTitle: crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
2	d2oyoa1	 Alignment		100.0	20	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
3	d2prra1	 Alignment		100.0	17	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
4	c6ohiA_	 Alignment		100.0	14	PDB header: biosynthetic protein Chain: A; PDB Molecule: debrominase bmp8; PDBTitle: crystal structure of the debrominase bmp8 (apo)
5	d2pfxa1	 Alignment		100.0	16	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
6	c3c1B_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B; PDB Molecule: putative antioxidant defense protein mlr4105; PDBTitle: crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
7	d2o4da1	 Alignment		100.0	21	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
8	d2gmya1	 Alignment		100.0	16	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
9	d2ouwa1	 Alignment		99.9	26	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
10	c5dj4D_	 Alignment		99.8	20	PDB header: signaling protein Chain: D; PDB Molecule: sestrin-2; PDBTitle: leucine-bound sestrin2 from homo sapiens
11	c2qeua_	 Alignment		99.5	14	PDB header: lyase Chain: A; PDB Molecule: putative carboxymuconolactone decarboxylase; PDBTitle: crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution

12	c1p8cD_	 Alignment		99.4	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
13	c3beyC_	 Alignment		99.4	15	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved protein o27018; PDBTitle: crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
14	c5dipB_	 Alignment		99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase ahpd; PDBTitle: crystal structure of lpg0406 in reduced form from legionella2 pneumophila
15	d1vkea_	 Alignment		99.3	14	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
16	d2cwqa1	 Alignment		99.3	17	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
17	c3d7iB_	 Alignment		99.2	11	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family protein; PDBTitle: crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
18	d2q0ta1	 Alignment		99.1	10	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
19	d1vkeb_	 Alignment		99.1	16	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
20	d1knca_	 Alignment		99.1	20	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
21	c5gzxD_	 Alignment	not modelled	98.8	9	PDB header: hydrolase Chain: D: PDB Molecule: (r)-2-haloacid dehalogenase; PDBTitle: the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
22	c4g9qA_	 Alignment	not modelled	98.5	19	PDB header: lyase Chain: A: PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
23	d2af7a1	 Alignment	not modelled	98.0	21	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
24	c3bjxB_	 Alignment	not modelled	90.8	13	PDB header: hydrolase Chain: B: PDB Molecule: halocarboxylic acid dehalogenase dehi; PDBTitle: structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
25	c4n2xF_	 Alignment	not modelled	89.8	8	PDB header: hydrolase Chain: F: PDB Molecule: dl-2-haloacid dehalogenase; PDBTitle: crystal structure of dl-2-haloacid dehalogenase
26	d1a9xa1	 Alignment	not modelled	76.0	13	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
27	c6et8B_	 Alignment	not modelled	75.8	18	PDB header: protein binding Chain: B: PDB Molecule: albicidin resistance protein; PDBTitle: crystal structure of alba in complex with albicidin
28	c2ev2B_	 Alignment	not modelled	39.0	8	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the

						mycobacterial2 adenyl cyclase rv1264, at ph 8.5 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
29	d2p7vb1	Alignment	not modelled	38.0	10	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
30	d1khdA1	Alignment	not modelled	19.7	9	PDB header: transcription regulator Chain: A: PDB Molecule: protein sini; PDBTitle: solution structure of sini, antagonist to the master biofilm-regulator2 sinr in bacillus subtilis
31	c5tmxA	Alignment	not modelled	15.8	11	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
32	c2k9lA	Alignment	not modelled	14.3	11	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
33	c5dotA	Alignment	not modelled	13.8	11	PDB header: transport protein Chain: B: PDB Molecule: nucleoporin amo1; PDBTitle: crystal structure of chaetomium thermophilum gle1 ctd-nup42 gbm-ip62 complex
34	c6b4hB	Alignment	not modelled	13.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein-disulfide isomerase; PDBTitle: crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
35	c3gmfA	Alignment	not modelled	13.5	7	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of reduced dsba1 from neisseria2 meningitidis
36	c3dvwA	Alignment	not modelled	13.2	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
37	d1ku3a	Alignment	not modelled	12.9	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
38	d1jhfa1	Alignment	not modelled	12.5	29	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
39	d1v8ga1	Alignment	not modelled	11.9	11	PDB header: unknown function Chain: A: PDB Molecule: avh146; PDBTitle: crystal structure of phytophthora. sojae psr2
40	c5gncA	Alignment	not modelled	11.8	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
41	d1beda	Alignment	not modelled	11.7	8	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
42	c2k9mA	Alignment	not modelled	11.5	11	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
43	d1ngra	Alignment	not modelled	11.2	14	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
44	c3t72o	Alignment	not modelled	10.7	8	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of wolbachia pipientis alpha-dsba1 c97a/c146a
45	c3f4tA	Alignment	not modelled	10.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein dsba-like; PDBTitle: crystal structure of reduced dsbl
46	c3c7mB	Alignment	not modelled	10.5	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein of unknown function (duf1244); PDBTitle: crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
47	c3fybA	Alignment	not modelled	10.5	18	PDB header: transferase Chain: B: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: a single reactive noncanonical amino acid is able to dramatically2 stabilize protein structure
48	c6mtgB	Alignment	not modelled	10.4	9	PDB header: transcription, transferase Chain: X: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: x-ray crystal structure of escherichia coli sigma70 holoenzyme
49	c4iqcX	Alignment	not modelled	10.4	8	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
50	c1t3bA	Alignment	not modelled	10.4	33	PDB header: oxidoreductase Chain: E: PDB Molecule: putative thiol-disulfide isomerase or thioredoxin; PDBTitle: crystal structure of salmonella enterica serovar typhimurium srga
51	c3l9vE	Alignment	not modelled	9.8	11	PDB header: ligase Chain: C: PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
52	c5douC	Alignment	not modelled	9.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: rv2466c mediates the activation of tp053 to kill replicating
53	c4nxiB	Alignment	not modelled	9.6	18	

						and non-2 replicating mycobacterium tuberculosis
54	c3bcia_	Alignment	not modelled	9.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: disulfide bond protein a; PDBTitle: crystal structure of staphylococcus aureus dsba
55	d1t3ba1	Alignment	not modelled	9.4	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
56	c4npbA_	Alignment	not modelled	8.9	33	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide isomerase ii; PDBTitle: the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
57	c4p3yB_	Alignment	not modelled	8.7	14	PDB header: translation/oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: crystal structure of acinetobacter baumannii dsba in complex with ef-2 tu
58	d1ttva_	Alignment	not modelled	8.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
59	c2yx0A_	Alignment	not modelled	8.3	10	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
60	c4k2dA_	Alignment	not modelled	8.1	8	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein; PDBTitle: crystal structure of burkholderia pseudomallei dsba
61	c3thgA_	Alignment	not modelled	7.9	9	PDB header: protein binding Chain: A: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: crystal structure of the creosote rubisco activase c-domain
62	c3gl5A_	Alignment	not modelled	7.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dsba oxidoreductase sco1869; PDBTitle: crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
63	c5hfiA_	Alignment	not modelled	7.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein, cytosolic disulfide reductase PDBTitle: cytosolic disulfide reductase dsbm from pseudomonas aeruginosa with2 gsh
64	c4n30A_	Alignment	not modelled	7.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein disulfide isomerase; PDBTitle: crystal structure of pseudomonas aeruginosa dsba2
65	c2eq9C_	Alignment	not modelled	7.6	33	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
66	c1m6vE_	Alignment	not modelled	7.5	13	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
67	c6cy8B_	Alignment	not modelled	7.5	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: butyryl-coa dehydrogenase; PDBTitle: crystal structure of fad-dependent dehydrogenase
68	c1v57A_	Alignment	not modelled	7.4	25	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg; PDBTitle: crystal structure of the disulfide bond isomerase dsbg
69	c3h93A_	Alignment	not modelled	7.4	8	PDB header: transcription regulator Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of pseudomonas aeruginosa dsba
70	c4jhcC_	Alignment	not modelled	7.4	43	PDB header: translation Chain: C: PDB Molecule: sb:cb157 protein; PDBTitle: crystal structure of danio rerio slp1 in complex with slbp
71	c1a6bB_	Alignment	not modelled	7.3	33	PDB header: viral protein/dna Chain: B: PDB Molecule: zinc finger protein ncp10; PDBTitle: nmr structure of the complex between the zinc finger2 protein ncp10 of moloney murine leukemia virus and a3 sequence of the psi-packaging domain of hiv-1, 204 structures
72	c4jrrC_	Alignment	not modelled	7.2	8	PDB header: oxidoreductase Chain: C: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of disulfide bond oxidoreductase dsba1 from2 legionella pneumophila
73	d1abaa_	Alignment	not modelled	7.0	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
74	d2cyua1	Alignment	not modelled	6.9	44	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
75	c6hl2C_	Alignment	not modelled	6.8	17	PDB header: electron transport Chain: C: PDB Molecule: nadh-quinone oxidoreductase subunit e; PDBTitle: wild-type nuof from aquifex aeolicus - oxidized form
76	c1jzdA_	Alignment	not modelled	6.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
77	d1brwa1	Alignment	not modelled	6.8	12	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
						PDB header: hormone/growth factor receptor

78	c1yk0E_	Alignment	not modelled	6.5	50	Chain: E; PDB Molecule: atrial natriuretic factor; PDBTitle: structure of natriuretic peptide receptor-c complexed with atrial2 natriuretic peptide
79	c4ml1D_	Alignment	not modelled	6.5	17	PDB header: isomerase Chain: D; PDB Molecule: dsbp; PDBTitle: disulfide isomerase (dsbp) from multidrug resistance inca/c2 transferable plasmid in oxidized state (p212121 space group)
80	d1eeja1	Alignment	not modelled	6.5	33	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
81	d2o35a1	Alignment	not modelled	6.4	20	Fold: SMc04008-like Superfamily: SMc04008-like Family: SMc04008-like
82	c2o35A_	Alignment	not modelled	6.4	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein duf1244; PDBTitle: protein of unknown function (duf1244) from sinorhizobium meliloti
83	c2eq8C_	Alignment	not modelled	6.3	33	PDB header: oxidoreductase Chain: C; PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
84	c4xvwK_	Alignment	not modelled	6.3	17	PDB header: isomerase Chain: K; PDB Molecule: dsba-like protein; PDBTitle: crystal structure of proteus mirabilis scsc in a compact conformation
85	c3gv1A_	Alignment	not modelled	6.2	8	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: disulfide interchange protein; PDBTitle: crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
86	c3hd5A_	Alignment	not modelled	6.1	8	PDB header: oxidoreductase Chain: A; PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
87	c3ghaA_	Alignment	not modelled	6.1	7	PDB header: oxidoreductase Chain: A; PDB Molecule: disulfide bond formation protein d; PDBTitle: crystal structure of etda-treated bdbd (reduced)
88	c2in3A_	Alignment	not modelled	6.1	9	PDB header: isomerase Chain: A; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
89	d1u6pa_	Alignment	not modelled	5.9	33	Fold: Retrovirus zinc finger-like domains Superfamily: Retrovirus zinc finger-like domains Family: Retrovirus zinc finger-like domains
90	c4x2eA_	Alignment	not modelled	5.8	43	PDB header: transferase Chain: A; PDB Molecule: fic family protein putative filamentation induced by camp PDBTitle: clostridium difficile wild type fic protein
91	c2remB_	Alignment	not modelled	5.8	8	PDB header: oxidoreductase Chain: B; PDB Molecule: disulfide oxidoreductase; PDBTitle: crystal structure of oxidoreductase dsba from xylella fastidiosa
92	d1o17a1	Alignment	not modelled	5.8	11	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
93	c2imeA_	Alignment	not modelled	5.7	9	PDB header: transferase Chain: A; PDB Molecule: 2-hydroxychromene-2-carboxylate isomerase; PDBTitle: 2-hydroxychromene-2-carboxylate isomerase: a kappa class glutathione-2 s-transferase from pseudomonas putida
94	d1uoua1	Alignment	not modelled	5.7	18	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
95	c3feuA_	Alignment	not modelled	5.6	22	PDB header: oxidoreductase Chain: A; PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
96	c5hs9A_	Alignment	not modelled	5.5	10	PDB header: dna binding protein Chain: A; PDB Molecule: hth-type transcriptional regulator yodb; PDBTitle: crystal structure of the quinone-bound yodb from b. subtilis
97	d1fvka_	Alignment	not modelled	5.5	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
98	d2elca1	Alignment	not modelled	5.5	10	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
99	c6eezC_	Alignment	not modelled	5.3	14	PDB header: isomerase Chain: C; PDB Molecule: dsba-like disulfide oxidoreductase; PDBTitle: crystal structure of the thiol-disulfide exchange protein alpha-dsba22 from wolbachia pipientis