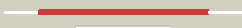



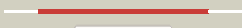














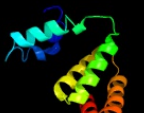




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1767 (-) _2000081_2000440
Date	Fri Aug 2 13:30:37 BST 2019
Unique Job ID	2bbe2a88176144c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5dipB_	 Alignment		99.9	37	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxide reductase ahpd; PDBTitle: crystal structure of lpg0406 in reduced form from legionella2 pneumophila
2	c1p8cD_	 Alignment		99.9	25	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of tm1620 (apc4843) from thermotoga2 maritima
3	c2qeuA_	 Alignment		99.9	23	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
4	d1vkea_	 Alignment		99.9	25	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
5	c3d7iB_	 Alignment		99.9	22	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
6	d2cwqa1	 Alignment		99.9	22	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
7	d1vkeb_	 Alignment		99.9	31	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
8	c3beyC_	 Alignment		99.8	30	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
9	d2q0ta1	 Alignment		99.8	19	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
10	d2af7a1	 Alignment		99.8	23	Fold: AhpD-like Superfamily: AhpD-like Family: CMD-like
11	d2ouwa1	 Alignment		99.8	25	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like

12	c4g9qA_	Alignment		99.7	18	PDB header: lyase Chain: A: PDB Molecule: 4-carboxymuconolactone decarboxylase; PDBTitle: crystal structure of a 4-carboxymuconolactone decarboxylase
13	d1knca_	Alignment		99.7	17	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
14	c6ohiA_	Alignment		99.5	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: debrominase bmp8; PDBTitle: crystal structure of the debrominase bmp8 (apo)
15	d2pfxa1	Alignment		99.4	20	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
16	c3lvyB_	Alignment		99.3	24	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family; PDBTitle: crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
17	c3c1lB_	Alignment		99.3	14	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
18	d2prra1	Alignment		99.3	19	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
19	d2gmya1	Alignment		99.2	20	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
20	d2oyoal	Alignment		99.2	20	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
21	d2o4da1	Alignment	not modelled	99.2	32	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
22	c5dj4D_	Alignment	not modelled	98.5	20	PDB header: signaling protein Chain: D: PDB Molecule: sestrin-2; PDBTitle: leucine-bound sestrin2 from homo sapiens
23	c5gzxD_	Alignment	not modelled	98.2	20	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
24	d1otva_	Alignment	not modelled	34.5	10	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: PqqC-like
25	d2p7vb1	Alignment	not modelled	28.5	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
26	c5l87A_	Alignment	not modelled	27.7	24	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiases.
27	c3ff5B_	Alignment	not modelled	27.5	22	PDB header: protein transport Chain: B: PDB Molecule: peroxisomal biogenesis factor 14; PDBTitle: crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
28	c1x3wB_	Alignment	not modelled	25.0	24	PDB header: hydrolase Chain: B: PDB Molecule: uv excision repair protein rad23; PDBTitle: structure of a peptide:n-glycanase-rad23 complex
						PDB header: signaling protein

29	c5aonB	Alignment	not modelled	25.0	26	Chain: B: PDB Molecule: peroxin 14; PDBTitle: crystal structure of the conserved n-terminal domain of2 pex14 from trypanosoma brucei
30	c3bjxB	Alignment	not modelled	23.5	22	PDB header: hydrolase Chain: B: PDB Molecule: halocarboxylic acid dehalogenase dehi; PDBTitle: structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
31	c2iosA	Alignment	not modelled	19.5	10	PDB header: antitumor protein Chain: A: PDB Molecule: programmed cell death 4, pdcd4; PDBTitle: crystal structure of the c-terminal ma3 domain of pdcd42 (mouse); form 3
32	d2itba1	Alignment	not modelled	19.0	18	Fold: Ferritin-like Superfamily: Ferritin-like Family: MiaE-like
33	d1p4wa	Alignment	not modelled	18.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
34	c4wv4A	Alignment	not modelled	17.9	16	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 10; PDBTitle: heterodimer of taf8/taf10
35	c2k9lA	Alignment	not modelled	17.9	13	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
36	c2w85A	Alignment	not modelled	17.6	20	PDB header: protein transport Chain: A: PDB Molecule: peroxisomal membrane anchor protein pex14; PDBTitle: structure of pex14 in complex with pex19
37	c2hl7A	Alignment	not modelled	17.6	9	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
38	c5thA	Alignment	not modelled	16.0	19	PDB header: chaperone Chain: A: PDB Molecule: c-terminal spycatcher fusion of wildtype zebrafish tnf PDBTitle: heterodimeric spycatcher/spytag-fused zebrafish trap1 in atp/adp-2 hybrid state
39	c5tmxA	Alignment	not modelled	15.8	15	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
40	d1tueb	Alignment	not modelled	15.5	9	Fold: E2 regulatory, transactivation domain Superfamily: E2 regulatory, transactivation domain Family: E2 regulatory, transactivation domain
41	c5mqfT	Alignment	not modelled	14.8	18	PDB header: splicing Chain: T: PDB Molecule: pre-mrna-splicing factor cwc22 homolog; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
42	d1x9na1	Alignment	not modelled	14.8	15	Fold: ATP-dependent DNA ligase DNA-binding domain Superfamily: ATP-dependent DNA ligase DNA-binding domain Family: ATP-dependent DNA ligase DNA-binding domain
43	c1qaxA	Alignment	not modelled	14.4	28	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (3-hydroxy-3-methylglutaryl-coenzyme a reductase); PDBTitle: ternary complex of pseudomonas mevalonii hmg-coa reductase with hmg-2 coa and nad+
44	c2k9mA	Alignment	not modelled	14.2	13	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: structure of the core binding domain of sigma54
45	c2qsfX	Alignment	not modelled	13.4	12	PDB header: dna binding protein Chain: X: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of the rad4-rad23 complex
46	c2kw0A	Alignment	not modelled	13.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from escherichia.coli
47	c1t3qD	Alignment	not modelled	12.4	24	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
48	c4j0bB	Alignment	not modelled	12.3	19	PDB header: chaperone Chain: B: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: structure of mitochondrial hsp90 (trap1) with adp-bef3
49	c5y6qA	Alignment	not modelled	12.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase small subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
50	c4c9bB	Alignment	not modelled	12.0	13	PDB header: splicing Chain: B: PDB Molecule: pre-mrna-splicing factor cwc22 homolog; PDBTitle: crystal structure of eif4aiii-cwc22 complex
51	c4zohC	Alignment	not modelled	11.9	23	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase iron-sulfur subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
52	c6et8B	Alignment	not modelled	11.8	17	PDB header: protein binding Chain: B: PDB Molecule: albicidin resistance protein; PDBTitle: crystal structure of alba in complex with albicidin
53	c4r33A	Alignment	not modelled	11.8	16	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
54	c5lj3H	Alignment	not modelled	11.6	14	PDB header: splicing Chain: H: PDB Molecule: cwc22; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching

55	c3t72o	Alignment	not modelled	11.2	7	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
56	d2nna1	Alignment	not modelled	11.1	7	Fold: E2 regulatory, transactivation domain Superfamily: E2 regulatory, transactivation domain Family: E2 regulatory, transactivation domain
57	c3o4B	Alignment	not modelled	10.9	15	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
58	d1su3a1	Alignment	not modelled	10.9	7	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
59	d1khd1	Alignment	not modelled	10.6	13	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
60	c3df0C	Alignment	not modelled	10.5	15	PDB header: hydrolase Chain: C: PDB Molecule: calpastatin; PDBTitle: calcium-dependent complex between m-calpain and calpastatin
61	c1ffuA	Alignment	not modelled	10.3	17	PDB header: hydrolase Chain: A: PDB Molecule: cuts, iron-sulfur protein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
62	c2dvwB	Alignment	not modelled	10.2	12	PDB header: cell cycle/protein-binding Chain: B: PDB Molecule: 26s protease regulatory subunit 6b; PDBTitle: structure of the oncoprotein gankyrin in complex with s62 atpase of the 26s proteasome
63	d2f05a1	Alignment	not modelled	10.0	8	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
64	d1dxsa	Alignment	not modelled	9.9	13	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
65	c2q0oA	Alignment	not modelled	9.8	22	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
66	c3cixA	Alignment	not modelled	9.6	17	PDB header: adomet binding protein Chain: A: PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
67	c1yh1A	Alignment	not modelled	9.6	17	PDB header: transferase Chain: A: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: structure of the complex of trypanosoma cruzi farnesyl diphosphate2 synthase with risedronate, dmapp and mg+2
68	d1a9xa1	Alignment	not modelled	9.5	28	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
69	c4ipeA	Alignment	not modelled	9.5	19	PDB header: chaperone Chain: A: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: crystal structure of mitochondrial hsp90 (trap1) with amppnp
70	c4wxcC	Alignment	not modelled	9.1	20	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
71	d1rcwa	Alignment	not modelled	9.1	15	Fold: Heme oxygenase-like Superfamily: Heme oxygenase-like Family: PqqC-like
72	d1s5qb	Alignment	not modelled	8.7	12	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
73	d1uoua1	Alignment	not modelled	8.7	13	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
74	c2ekkA	Alignment	not modelled	8.3	30	PDB header: protein binding Chain: A: PDB Molecule: uba domain from e3 ubiquitin-protein ligase PDBTitle: solution structure of ruh-074, a human uba domain
75	c4dt1A	Alignment	not modelled	8.2	25	PDB header: dna binding protein Chain: A: PDB Molecule: chromosome segregation in meiosis protein 2; PDBTitle: crystal structure of the psy3-csm2 complex
76	c4onsC	Alignment	not modelled	8.0	16	PDB header: cell adhesion Chain: C: PDB Molecule: catenin alpha-2; PDBTitle: structural and thermodynamic characterization of cadherin-beta-2 catenin-alpha-catenin complex formation
77	d1ku3a	Alignment	not modelled	7.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
78	c2diiA	Alignment	not modelled	7.7	15	PDB header: transcription Chain: A: PDB Molecule: tfiih basal transcription factor complex p62 PDBTitle: solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit

79	c3h20A_	Alignment	not modelled	7.7	17	PDB header: replication Chain: A: PDB Molecule: replication protein b; PDBTitle: crystal structure of primase repb'
80	d1v97a1	Alignment	not modelled	7.6	17	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
81	c6fkgC_	Alignment	not modelled	7.6	25	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
82	d3bula1	Alignment	not modelled	7.5	14	Fold: Methionine synthase domain-like Superfamily: Methionine synthase domain Family: Methionine synthase domain
83	d1slma1	Alignment	not modelled	7.2	16	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
84	d1dgja1	Alignment	not modelled	7.2	11	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
85	c4oogA_	Alignment	not modelled	7.2	11	PDB header: hydrolase/rna Chain: A: PDB Molecule: ribonuclease 3; PDBTitle: crystal structure of yeast rnaase iii (rnt1p) complexed with the2 product of dsrna processing
86	c2k53A_	Alignment	not modelled	7.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a3dk08 protein; PDBTitle: nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
87	c5ux1D_	Alignment	not modelled	6.9	9	PDB header: lyase Chain: D: PDB Molecule: trna-(ms2)io(6)a)-hydroxylase-like; PDBTitle: protein 43 with aldehyde deformylating oxygenase activity from2 synechococcus
88	c5xf9G_	Alignment	not modelled	6.9	14	PDB header: oxidoreductase Chain: G: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
89	c4xlqB_	Alignment	not modelled	6.8	17	PDB header: hydrolase Chain: B: PDB Molecule: structure-specific endonuclease subunit slx4; PDBTitle: c. glabrata slx1 in complex with slx4ccd.
90	c2llwA_	Alignment	not modelled	6.8	17	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein sti1; PDBTitle: solution structure of the yeast sti1 dp2 domain
91	c4lqxB_	Alignment	not modelled	6.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: tena/thi-4 domain-containing protein; PDBTitle: crystal structure of a tena/thi-4 domain-containing protein (sso2700)2 from sulfobolus solfataricus p2 at 2.34 a resolution
92	d1qaxa2	Alignment	not modelled	6.6	31	Fold: Substrate-binding domain of HMG-CoA reductase Superfamily: Substrate-binding domain of HMG-CoA reductase Family: Substrate-binding domain of HMG-CoA reductase
93	d1jroa1	Alignment	not modelled	6.5	13	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
94	c2kztA_	Alignment	not modelled	6.4	23	PDB header: apoptosis Chain: A: PDB Molecule: programmed cell death protein 4; PDBTitle: structure of the tandem ma-3 region of pdcd4
95	c2qsgX_	Alignment	not modelled	6.4	24	PDB header: dna binding protein/dna Chain: X: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of rad4-rad23 bound to a uv-damaged dna
96	c5odiE_	Alignment	not modelled	6.3	18	PDB header: oxidoreductase Chain: E: PDB Molecule: methyl-viologen reducing hydrogenase, subunit g; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus cocrystallized with com-sh
97	c5ui5I_	Alignment	not modelled	6.2	13	PDB header: transcription/dna Chain: I: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: crystal structure of aquifex aeolicus sigman bound to promoter dna
98	d1yt3a2	Alignment	not modelled	6.2	9	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
99	c3c19A_	Alignment	not modelled	6.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mk0293; PDBTitle: crystal structure of protein mk0293 from methanopyrus kandleri av19