

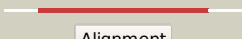













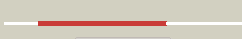





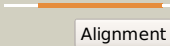

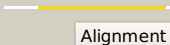

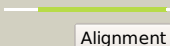

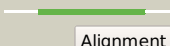



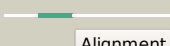
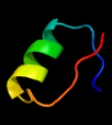
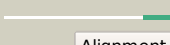

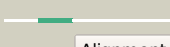
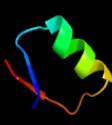
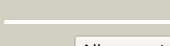

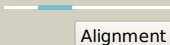


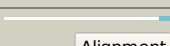
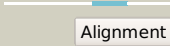
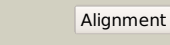
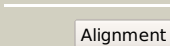
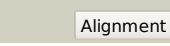


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3282_(maf)_3664216_3664884
Date	Thu Aug 8 16:20:49 BST 2019
Unique Job ID	66b0274915b810db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4oo0B_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: maf-like protein bca12394; PDBTitle: crystal structure of maf-like protein bcej2315_23540 from burkholderia2 cenocepacia
2	c4jhcA_	 Alignment		100.0	28	PDB header: cell cycle Chain: A: PDB Molecule: maf-like protein ycef; PDBTitle: crystal structure of the uncharacterized maf protein ycef from e. coli
3	d2amha1	 Alignment		100.0	18	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
4	d1ex2a_	 Alignment		100.0	28	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: Maf-like
5	c2p5xB_	 Alignment		100.0	28	PDB header: cell cycle Chain: B: PDB Molecule: n-acetylserotonin o-methyltransferase-like protein; PDBTitle: crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
6	c4p0eB_	 Alignment		100.0	29	PDB header: unknown function Chain: B: PDB Molecule: maf-like protein yhde; PDBTitle: yhde e33a (p212121 space group)
7	c4hebA_	 Alignment		100.0	26	PDB header: cell cycle Chain: A: PDB Molecule: septum formation protein maf; PDBTitle: the crystal structure of maf protein of bacillus subtilis
8	d2cara1	 Alignment		95.1	12	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
9	d1k7ka_	 Alignment		93.3	14	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
10	d1v7ra_	 Alignment		92.6	18	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
11	c3tquD_	 Alignment		86.8	17	PDB header: hydrolase Chain: D: PDB Molecule: non-canonical purine ntp pyrophosphatase; PDBTitle: structure of a ham1 protein from coxiella burnetii

12	d1vp2a_	 Alignment		81.3	17	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
13	d1b78a_	 Alignment		74.9	19	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
14	c4bnqA_	 Alignment		65.4	22	PDB header: hydrolase Chain: A: PDB Molecule: non-canonical purine ntp pyrophosphatase; PDBTitle: the structure of the staphylococcus aureus ham1 protein
15	c1x3lA_	 Alignment		54.1	12	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ph0495; PDBTitle: crystal structure of the ph0495 protein from pyrococcus horikoshii2 ot3
16	d1pdaa1	 Alignment		44.5	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
17	c2ypnA_	 Alignment		41.9	17	PDB header: transferase Chain: A: PDB Molecule: protein (hydroxymethylbilane synthase); PDBTitle: hydroxymethylbilane synthase
18	c4nmlA_	 Alignment		41.4	14	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: 2.60 angstrom resolution crystal structure of putative ribose 5-2 phosphate isomerase from toxoplasma gondii me49 in complex with dl-3 malic acid
19	c4mlqA_	 Alignment		40.6	21	PDB header: transferase Chain: A: PDB Molecule: porphobilinogen deaminase; PDBTitle: crystal structure of bacillus megaterium porphobilinogen deaminase
20	c3dv0l_	 Alignment		39.5	17	PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydrolypoyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
21	c3eq1A_	 Alignment	not modelled	38.5	21	PDB header: transferase Chain: A: PDB Molecule: porphobilinogen deaminase; PDBTitle: the crystal structure of human porphobilinogen deaminase at 2.8a resolution
22	d1w85j_	 Alignment	not modelled	35.5	17	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
23	c2db5A_	 Alignment	not modelled	34.5	19	PDB header: protein binding Chain: A: PDB Molecule: inad-like protein; PDBTitle: solution structure of the first pdz domain of inad-like2 protein
24	d1ydua1	 Alignment	not modelled	33.5	21	Fold: At5g01610-like Superfamily: At5g01610-like Family: At5g01610-like
25	c2o2tB_	 Alignment	not modelled	32.6	17	PDB header: structural protein Chain: B: PDB Molecule: multiple pdz domain protein; PDBTitle: the crystal structure of the 1st pdz domain of mpdz
26	d1rp5a2	 Alignment	not modelled	30.8	5	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
27	d1pyya2	 Alignment	not modelled	30.5	10	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
28	c2x0kB_	 Alignment	not modelled	29.5	20	PDB header: transferase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribf; PDBTitle: crystal structure of modular fad synthetase from2

						corynebacterium ammoniagenes
29	c3ouvA_	Alignment	not modelled	29.3	14	PDB header: transferase Chain: A: PDB Molecule: serine/threonine protein kinase; PDBTitle: semet derivative of I512m mutant of pasta domain 3 of mycobacterium2 tuberculosis pknb
30	c4htgA_	Alignment	not modelled	27.9	25	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: porphobilinogen deaminase, chloroplastic; PDBTitle: porphobilinogen deaminase from arabidopsis thaliana
31	d1pyya1	Alignment	not modelled	27.4	18	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
32	d1k25a2	Alignment	not modelled	27.4	7	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
33	c1w4kA_	Alignment	not modelled	26.4	21	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase e2; PDBTitle: peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
34	c4isdA_	Alignment	not modelled	26.2	22	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of glutathione transferase homolog from burkholderia2 gl bgr1, target efi-501803, with bound glutathione
35	c1zwvA_	Alignment	not modelled	25.8	17	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
36	c2e7kA_	Alignment	not modelled	25.8	18	PDB header: membrane protein Chain: A: PDB Molecule: maguk p55 subfamily member 2; PDBTitle: solution structure of the pdz domain from human maguk p552 subfamily member 2
37	c3op1A_	Alignment	not modelled	24.7	19	PDB header: transferase Chain: A: PDB Molecule: macrolide-efflux protein; PDBTitle: crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
38	d2b8na1	Alignment	not modelled	24.4	12	Fold: GckA/TtuD-like Superfamily: GckA/TtuD-like Family: GckA/TtuD-like
39	c2kz5A_	Alignment	not modelled	22.9	19	PDB header: transcription Chain: A: PDB Molecule: transcription factor nf-e2 45 kda subunit; PDBTitle: solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
40	c2mgvA_	Alignment	not modelled	21.7	29	PDB header: penicillin binding protein Chain: A: PDB Molecule: bifunctional membrane-associated penicillin-binding protein PDBTitle: nmr structure of pasta domain of pona2 from mycobacterium tuberculosis
41	c4qoyE_	Alignment	not modelled	21.3	24	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase PDBTitle: novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
42	c2eq7C_	Alignment	not modelled	21.0	31	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
43	d1sknp_	Alignment	not modelled	20.8	19	Fold: A DNA-binding domain in eukaryotic transcription factors Superfamily: A DNA-binding domain in eukaryotic transcription factors Family: A DNA-binding domain in eukaryotic transcription factors
44	c4tr1A_	Alignment	not modelled	20.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin 3; PDBTitle: crystal structure of gsh-bound cgrx2/c15s
45	d1k25a1	Alignment	not modelled	20.4	14	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
46	c2zc3F_	Alignment	not modelled	20.1	19	PDB header: biosynthetic protein Chain: F: PDB Molecule: penicillin-binding protein 2x; PDBTitle: penicillin-binding protein 2x (pbp 2x) acyl-enzyme complex2 (biapenem) from streptococcus pneumoniae
47	c6gyzB_	Alignment	not modelled	20.0	15	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus
48	c3i42A_	Alignment	not modelled	19.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey-like); PDBTitle: structure of response regulator receiver domain (chey-like) from2 methylobacillus flagellatus
49	c1w3dA_	Alignment	not modelled	18.6	17	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: nmr structure of the peripheral-subunit binding domain of bacillus2 stearothermophilus e2p
50	d1gh9a_	Alignment	not modelled	18.1	20	Fold: Rubredoxin-like Superfamily: Hypothetical protein MTH1184 Family: Hypothetical protein MTH1184
51	c2cooA_	Alignment	not modelled	18.1	17	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the e3 binding domain of2 dihydrolipamide branched chaintransacylase

52	d2fi0a1	Alignment	not modelled	17.7	15	Fold: SP0561-like Superfamily: SP0561-like Family: SP0561-like
53	d2eyqa2	Alignment	not modelled	17.7	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
54	d1y0ua_	Alignment	not modelled	17.2	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
55	c3eggC_	Alignment	not modelled	16.9	19	PDB header: hydrolase Chain: C: PDB Molecule: spinophilin; PDBTitle: crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
56	c3pdkB_	Alignment	not modelled	16.8	15	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
57	c2lz1A_	Alignment	not modelled	16.8	15	PDB header: transcription Chain: A: PDB Molecule: nuclear factor erythroid 2-related factor 2; PDBTitle: solution nmr structure of the dna-binding domain of human nf-e2-2 related factor 2, northeast structural genomics consortium (nesg)3 target hr3520o
58	d1t1va_	Alignment	not modelled	16.6	24	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: SH3BGR (SH3-binding, glutamic acid-rich protein-like)
59	d1w4ha1	Alignment	not modelled	16.2	24	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
60	c1x4pA_	Alignment	not modelled	15.7	33	PDB header: rna binding protein Chain: A: PDB Molecule: putative splicing factor, arginine/serine-rich PDBTitle: solution structure of surp domain in sfrs14 protei
61	d1e94a_	Alignment	not modelled	15.7	16	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
62	c5odhG_	Alignment	not modelled	15.3	20	PDB header: oxidoreductase Chain: G: PDB Molecule: heterodisulfide reductase, subunit a; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from 2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes
63	d1x4pa1	Alignment	not modelled	15.1	33	Fold: Surp module (SWAP domain) Superfamily: Surp module (SWAP domain) Family: Surp module (SWAP domain)
64	c2du4B_	Alignment	not modelled	14.9	15	PDB header: ligase/rna Chain: B: PDB Molecule: o-phosphoserine-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus o-phosphoserine-2 trna synthetase complexed with trnacys
65	d1p5dx2	Alignment	not modelled	14.7	20	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
66	c5w7IA_	Alignment	not modelled	14.6	17	PDB header: membrane protein Chain: A: PDB Molecule: n,n'-diacetylbacillosaminyl-1-phosphate transferase; PDBTitle: structure of campylobacter concisus pglc i57m/q175m variant
67	d2dl da2	Alignment	not modelled	14.5	19	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
68	c2du3A_	Alignment	not modelled	14.3	15	PDB header: ligase/rna Chain: A: PDB Molecule: o-phosphoserine-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus o-phosphoserine-2 trna synthetase complexed with trnacys and o-phosphoserine
69	c2eq9C_	Alignment	not modelled	14.2	17	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
70	d1nfpa_	Alignment	not modelled	13.9	16	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
71	d1zesa1	Alignment	not modelled	13.7	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
72	d2cyua1	Alignment	not modelled	13.7	24	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
73	c5n6yD_	Alignment	not modelled	13.6	38	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
74	c3zija_	Alignment	not modelled	13.5	9	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of the thioredoxin-like protein bc3987
75	c1nl3B_	Alignment	not modelled	13.2	13	PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase seca 1 subunit; PDBTitle: crystal structure of the seca protein translocation atpase2

						from mycobacterium tuberculosis in apo form
76	d1o8bb1	Alignment	not modelled	13.1	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
77	d1jqga2	Alignment	not modelled	12.9	25	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
78	c2ktaA	Alignment	not modelled	12.9	17	PDB header: hydrolase Chain: A: PDB Molecule: putative helicase; PDBTitle: solution nmr structure of a domain of protein a6ky75 from bacteroides2 vulgatus, northeast structural genomics target bvr106a
79	d1bala	Alignment	not modelled	12.6	24	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
80	c6a34B	Alignment	not modelled	12.4	22	PDB header: isomerase Chain: B: PDB Molecule: putative methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of 5-methylthioribose 1-phosphate isomerase from2 pyrococcus horikoshii ot3 - form i
81	c3ewlA	Alignment	not modelled	12.4	17	Chain: A: PDB Molecule: uncharacterized conserved protein bf1870; PDBTitle: crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
82	c2m8gX	Alignment	not modelled	12.3	17	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
83	d1etxa	Alignment	not modelled	12.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
84	c3juxA	Alignment	not modelled	11.7	21	PDB header: protein transport Chain: A: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the translocation atpase seca from thermotoga2 maritima
85	d1b65a	Alignment	not modelled	11.6	19	Fold: DmpA/ArgJ-like Superfamily: DmpA/ArgJ-like Family: DmpA-like
86	d1wh1a	Alignment	not modelled	11.5	22	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
87	d1k59a	Alignment	not modelled	10.9	37	Fold: RNase A-like Superfamily: RNase A-like Family: Ribonuclease A-like
88	c5t3uA	Alignment	not modelled	10.8	14	PDB header: transport protein Chain: A: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae
89	c4tkzA	Alignment	not modelled	10.6	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein gbs1890; PDBTitle: crystal structure of phosphotransferase system component eiia from2 streptococcus agalactiae
90	c2eq8C	Alignment	not modelled	10.5	21	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
91	c2jmkA	Alignment	not modelled	10.2	8	PDB header: protein binding Chain: A: PDB Molecule: hypothetical protein ta0956; PDBTitle: solution structure of ta0956
92	d1t9ka	Alignment	not modelled	10.2	30	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: lF2B-like
93	d1f2ea2	Alignment	not modelled	10.0	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
94	d1etob	Alignment	not modelled	9.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
95	d1qcza	Alignment	not modelled	9.9	13	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
96	c1w2wj	Alignment	not modelled	9.9	19	PDB header: isomerase Chain: J: PDB Molecule: 5-methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of yeast ypr118w, a methylthioribose-1-phosphate2 isomerase related to regulatory eif2b subunits
97	d1g3ka	Alignment	not modelled	9.9	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
98	c2vdaA	Alignment	not modelled	9.8	19	PDB header: protein transport Chain: A: PDB Molecule: translocase subunit seca; PDBTitle: solution structure of the seca-signal peptide complex
99	c3dinB	Alignment	not modelled	9.8	21	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: protein translocase subunit seca; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase