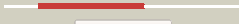



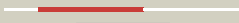






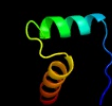
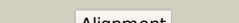




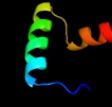






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2132_(-)_2393419_2393649
Date	Mon Aug 5 13:25:25 BST 2019
Unique Job ID	2a5e450db2a93f84

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bj3D_	 Alignment		95.3	23	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
2	c1q5vB_	 Alignment		94.5	29	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
3	d2h2ab1	 Alignment		93.1	31	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
4	c2ca9B_	 Alignment		93.1	26	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
5	d2bj7a1	 Alignment		92.5	21	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
6	d2h2aa1	 Alignment		92.3	31	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
7	c2k29A_	 Alignment		90.4	15	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
8	c5x3tA_	 Alignment		89.1	33	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapp26; PDBTitle: vappbc from mycobacterium tuberculosis
9	c4fxeB_	 Alignment		84.4	16	PDB header: toxin/toxin inhibitor Chain: B: PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
10	c1ea4K_	 Alignment		84.3	19	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
11	d2cpga_	 Alignment		84.3	19	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like

12	c6g1nB_	Alignment		79.0	18	PDB header: antitoxin Chain: B: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the burkholderia pseudomallei antitoxin hicb
13	c4q2uM_	Alignment		71.9	9	PDB header: toxin/toxin repressor Chain: M: PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
14	c6a6xC_	Alignment		67.8	25	PDB header: toxin Chain: C: PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex
15	c4pg8B_	Alignment		62.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of s. aureus homoserine dehydrogenase at pH8.5
16	c2k5jB_	Alignment		60.5	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
17	c3kk4B_	Alignment		60.0	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
18	c3do5A_	Alignment		57.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
19	c2ejwB_	Alignment		57.2	21	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8
20	c6dzsD_	Alignment		55.5	11	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
21	c3ingA_	Alignment	not modelled	54.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
22	c5yrzC_	Alignment	not modelled	53.2	16	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
23	c3mtjA_	Alignment	not modelled	50.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
24	c3c8mA_	Alignment	not modelled	49.2	7	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
25	d2bsqe1	Alignment	not modelled	47.5	13	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
26	c6geqD_	Alignment	not modelled	47.5	13	PDB header: dna binding protein Chain: D: PDB Molecule: pcf;f; PDBTitle: pcf;f from enterococcus faecalis pcf10
27	c2h1oH_	Alignment	not modelled	47.5	14	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
28	c4p7dA_	Alignment	not modelled	45.5	13	PDB header: toxin Chain: A: PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
						Fold: Ribbon-helix-helix

29	d1p94a_	Alignment	not modelled	39.4	15	Superfamily: Ribbon-helix-helix Family: CopG-like
30	c6a7vU_	Alignment	not modelled	36.0	31	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapb11; PDBTitle: crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
31	c4xb1B_	Alignment	not modelled	33.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 319aa long hypothetical homoserine dehydrogenase; PDBTitle: hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph
32	d1ebfa2	Alignment	not modelled	29.6	15	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
33	c6noyB_	Alignment	not modelled	23.2	24	PDB header: structural protein Chain: B: PDB Molecule: maintenance of carboxysome positioning b protein, mcsb; PDBTitle: structure of cyanothecce mcdb
34	c1y9qA_	Alignment	not modelled	19.5	28	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
35	c3wa8B_	Alignment	not modelled	18.9	23	PDB header: rna binding protein Chain: B: PDB Molecule: crispr-associated protein, cse2 family; PDBTitle: crystal structure of m. ruber casb
36	c5avoA_	Alignment	not modelled	17.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of the reduced form of homoserine dehydrogenase from2 sulfolobus tokodaii.
37	c2uwjE_	Alignment	not modelled	16.2	35	PDB header: chaperone Chain: E: PDB Molecule: type iii export protein psce; PDBTitle: structure of the heterotrimeric complex which regulates type iii2 secretion needle formation
38	c1ebuA_	Alignment	not modelled	16.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine
39	c2oa6B_	Alignment	not modelled	15.3	27	PDB header: lyase Chain: B: PDB Molecule: aristolochene synthase; PDBTitle: aristolochene synthase from aspergillus terreus complexed with2 pyrophosphate
40	c3v1vA_	Alignment	not modelled	14.9	5	PDB header: lyase Chain: A: PDB Molecule: 2-methylisoborneol synthase; PDBTitle: crystal structure of 2-methylisoborneol synthase from streptomyces2 coelicolor a3(2) in complex with mg2+ and geranyl-s-thiolodiphosphate
41	d1d0qa_	Alignment	not modelled	14.4	27	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
42	c1ueoA_	Alignment	not modelled	13.3	38	PDB header: antibiotic Chain: A: PDB Molecule: penaeidin-3a; PDBTitle: solution structure of the [t8a]-penaeidin-3
43	c5n07A_	Alignment	not modelled	12.0	18	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor nsrr; PDBTitle: structure of the [4fe-4s] form of the no response regulator nsrr
44	c4wwrE_	Alignment	not modelled	11.7	43	PDB header: transport protein Chain: E: PDB Molecule: large proline-rich protein bag6; PDBTitle: crystal structure of bag6-ubl4a dimerization domain
45	c2k5rA_	Alignment	not modelled	11.3	40	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein xf2673; PDBTitle: solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
46	c3v1xA_	Alignment	not modelled	11.0	5	PDB header: lyase Chain: A: PDB Molecule: 2-methylisoborneol synthase; PDBTitle: crystal structure of 2-methylisoborneol synthase from streptomyces2 coelicolor a3(2) in complex with mg2+ and 2-fluorogeranyl diphosphate
47	d1rfma_	Alignment	not modelled	10.9	3	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
48	c2e67D_	Alignment	not modelled	10.8	26	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein tthb029; PDBTitle: crystal structure of the hypothetical protein tthb029 from thermus2 thermophilus hb8
49	c6ajnF_	Alignment	not modelled	10.8	15	PDB header: toxin Chain: F: PDB Molecule: duf1778 domain-containing protein; PDBTitle: crystal structure of atar bound with accoa
50	d5easa2	Alignment	not modelled	10.7	15	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Terpenoid cyclase C-terminal domain
51	c5woqA_	Alignment	not modelled	10.0	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
52	c4b1vM_	Alignment	not modelled	9.9	40	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel-n domain bound to g-actin
53	c4b1vN_	Alignment	not modelled	9.9	40	PDB header: structural protein Chain: N: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel-n domain bound to g-actin
54	c6qtsC_	Alignment	not modelled	9.2	15	PDB header: transcription Chain: C: PDB Molecule: duf1778 domain-containing protein; PDBTitle: structure of the atat-atar complex bound dna PDB header: unknown function

55	c5g2fB_	Alignment	not modelled	9.1	29	Chain: B: PDB Molecule: type-iv like pilin ttha1222; PDBTitle: type iv-like competence pilin ttha1222 from thermus2 thermophilus
56	d1k25a1	Alignment	not modelled	9.0	24	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
57	c4mc8A_	Alignment	not modelled	8.9	32	PDB header: lyase Chain: A: PDB Molecule: putative sesquiterpene cyclase; PDBTitle: hedyacryol synthase in complex with hepes
58	d1pyya1	Alignment	not modelled	8.8	24	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
59	d1poia_	Alignment	not modelled	8.2	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
60	c5nx4A_	Alignment	not modelled	8.2	23	PDB header: ligase Chain: A: PDB Molecule: pentalenene synthase; PDBTitle: crystal structure of linalool/nerolidol synthase from streptomyces2 clavuligerus
61	c1nh2D_	Alignment	not modelled	8.2	25	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia small chain; PDBTitle: crystal structure of a yeast tfiia/tbp/dna complex
62	c1n20A_	Alignment	not modelled	8.0	31	PDB header: isomerase Chain: A: PDB Molecule: (+)-bornyl diphosphate synthase; PDBTitle: (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2,2,3-dihydrogeranyl diphosphate
63	c2eq8C_	Alignment	not modelled	7.9	27	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
64	c2mdvB_	Alignment	not modelled	7.9	16	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
65	c5i1uB_	Alignment	not modelled	7.8	23	PDB header: lyase Chain: B: PDB Molecule: germacradien-4-ol synthase; PDBTitle: crystal structure of germacradien-4-ol synthase from streptomyces2 citricolor
66	c2eq7C_	Alignment	not modelled	7.6	33	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
67	d1y9qa1	Alignment	not modelled	7.5	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
68	d1yqfa1	Alignment	not modelled	7.3	21	Fold: Mitochondrial glycoprotein MAM33-like Superfamily: Mitochondrial glycoprotein MAM33-like Family: Mitochondrial glycoprotein MAM33-like
69	c2ldja_	Alignment	not modelled	7.1	63	PDB header: de novo protein Chain: A: PDB Molecule: trp-cage mini-protein; PDBTitle: 1h chemical shift assignments and structure of trp-cage mini-protein2 with d-amino acid
70	c1nd9A_	Alignment	not modelled	7.1	25	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: solution structure of the n-terminal subdomain of2 translation initiation factor if2
71	d1nd9a_	Alignment	not modelled	7.1	25	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: N-terminal subdomain of bacterial translation initiation factor IF2
72	c5a0iA_	Alignment	not modelled	7.1	14	PDB header: lyase Chain: A: PDB Molecule: labdane-related diterpene synthase; PDBTitle: crystallographic structure of the bacterial labdane-related diterpene2 synthase lrdc in complex with mg and ppi at 2.57 a resolution.
73	c1nvpD_	Alignment	not modelled	6.9	29	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia gamma chain; PDBTitle: human tfiia/tbp/dna complex
74	c4b1uM_	Alignment	not modelled	6.9	40	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpel domain and rpel motif directed2 assemblies with g-actin reveal the molecular basis for actin binding3 cooperativity.
75	c4ypiA_	Alignment	not modelled	6.7	23	PDB header: rna binding protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35
76	d1q9ja2	Alignment	not modelled	6.6	19	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
77	c6m7fB_	Alignment	not modelled	6.6	22	PDB header: lyase Chain: B: PDB Molecule: cucumene synthase; PDBTitle: wild-type cucumene synthase
78	d1y9ba1	Alignment	not modelled	6.5	11	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VCA0319-like
79	d1zyba1	Alignment	not modelled	6.5	46	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
						PDB header: transferase Chain: A: PDB Molecule: lipoamide acyltransferase component of

80	c2cooA_	Alignment	not modelled	6.5	60	PDB header: solution structure of the e3 binding domain of 2 dihydrolipoamide branched chaintransacylase
81	c3jv1A_	Alignment	not modelled	6.1	16	PDB header: hydrolase Chain: A: PDB Molecule: p22 protein; PDBTitle: crystal structure of the trypanosoma brucei p22 protein
82	c6hs6E_	Alignment	not modelled	6.1	11	PDB header: transport protein Chain: E: PDB Molecule: type vi secretion protein impa; PDBTitle: c-terminal domain of the tssa component of the type vi secretion2 system from burkholderia cenocepacia
83	d1ps1a_	Alignment	not modelled	6.1	27	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Aristolochene/pentalenene synthase
84	c2lkyA_	Alignment	not modelled	6.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msmeq_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysm.17112.b
85	c6o7yA_	Alignment	not modelled	6.0	21	PDB header: rna binding protein Chain: A: PDB Molecule: putative eukaryotic translation initiation factor 4e type PDBTitle: trypanosoma cruzi eif4e5 translation initiation factor in complex with2 cap-4
86	c3uauA_	Alignment	not modelled	6.0	27	PDB header: cell adhesion Chain: A: PDB Molecule: surface-exposed lipoprotein; PDBTitle: crystal structure of the lipoprotein jlpa
87	c4zq8B_	Alignment	not modelled	5.9	18	PDB header: transferase Chain: B: PDB Molecule: isoprenoid synthase; PDBTitle: crystal structure of a terpene synthase from streptomyces lydicus,2 target efi-540129
88	c3dv0L_	Alignment	not modelled	5.9	13	PDB header: oxidoreductase/transferase Chain: I: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
89	c3qv0A_	Alignment	not modelled	5.9	11	PDB header: protein binding Chain: A: PDB Molecule: mitochondrial acidic protein mam33; PDBTitle: crystal structure of saccharomyces cerevisiae mam33
90	c4wxwxB_	Alignment	not modelled	5.5	21	PDB header: hydrolase, ligase Chain: B: PDB Molecule: v(d)j recombination-activating protein 1; PDBTitle: crystal structure of the core rag1/2 recombinase
91	d1nvpd1	Alignment	not modelled	5.4	31	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
92	c1w3dA_	Alignment	not modelled	5.3	13	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
93	c2bnoA_	Alignment	not modelled	5.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
94	d1w85j_	Alignment	not modelled	5.3	13	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
95	c6ehmB_	Alignment	not modelled	5.3	23	PDB header: virus like particle Chain: B: PDB Molecule: nucleoprotein; PDBTitle: model of the ebola virus nucleocapsid subunit from recombinant virus-2 like particles
96	c3n0fA_	Alignment	not modelled	5.3	14	PDB header: lyase Chain: A: PDB Molecule: isoprene synthase; PDBTitle: crystal structure of isoprene synthase from grey poplar leaves2 (populus x canescens)
97	c5f5mB_	Alignment	not modelled	5.3	31	PDB header: nuclear protein Chain: B: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of marburg virus nucleoprotein core domain
98	c6bqcA_	Alignment	not modelled	5.2	24	PDB header: transferase Chain: A: PDB Molecule: cyclopropane-fatty-acyl-phospholipid synthase; PDBTitle: cyclopropane fatty acid synthase from e. coli
99	c6egkB_	Alignment	not modelled	5.2	14	PDB header: lyase Chain: B: PDB Molecule: cucumene synthase; PDBTitle: t181n cucumene synthase