








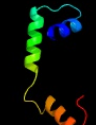





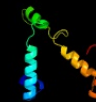





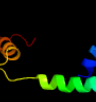


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2410c_(-)_2707343_2708320
Date	Wed Aug 7 12:50:03 BST 2019
Unique Job ID	d8931172364ea092

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3bgea1	 Alignment		86.2	15	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
2	d3ctda1	 Alignment		77.7	17	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
3	c3ctdB_	 Alignment		68.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative atpase, aaa family; PDBTitle: crystal structure of a putative aaa family atpase from prochlorococcus2 marinus subsp. pastoris
4	c3pvsA_	 Alignment		56.8	14	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
5	c2r26C_	 Alignment		44.4	10	PDB header: transferase Chain: C: PDB Molecule: citrate synthase; PDBTitle: the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum
6	d1a59a_	 Alignment		44.1	12	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
7	d2r9ga1	 Alignment		42.2	21	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
8	d1ioma_	 Alignment		33.9	9	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
9	c5an6A_	 Alignment		33.2	15	PDB header: dna binding protein Chain: A: PDB Molecule: crispr-associated protein, csm2 family; PDBTitle: crystal structure of thermotoga maritima csm2
10	c6jdxC_	 Alignment		31.4	38	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of acric2 dimer in complex with partial nme1cas92 preprocessed with protease alpha-chymotrypsin
11	d1csca_	 Alignment		26.7	6	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase

12	c4wlpB_	Alignment		24.0	22	PDB header: protein binding Chain: B: PDB Molecule: nuclear factor related to kappa-b-binding protein; PDBTitle: crystal structure of uch37-nfrkb inhibited deubiquitylating complex
13	c2ibpB_	Alignment		23.2	9	PDB header: transferase Chain: B: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from pyrobaculum aerophilum
14	d1xmec1	Alignment		22.2	38	Fold: Single transmembrane helix Superfamily: Bacterial ba3 type cytochrome c oxidase subunit IIa Family: Bacterial ba3 type cytochrome c oxidase subunit IIa
15	c3bvdC_	Alignment		22.2	38	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome c oxidase polypeptide 2a; PDBTitle: structure of surface-engineered cytochrome ba3 oxidase from thermus2 thermophilus under xenon pressure, 100psi 5min
16	c2c6xA_	Alignment		21.6	8	PDB header: transferase Chain: A: PDB Molecule: citrate synthase 1; PDBTitle: structure of bacillus subtilis citrate synthase
17	c6j9mF_	Alignment		19.2	38	PDB header: hydrolase/hydrolase inhibitor Chain: F: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: nmebh+acriic2
18	c6j9mA_	Alignment		17.2	38	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: nmebh+acriic2
19	c2x11A_	Alignment		17.1	24	PDB header: translation Chain: A: PDB Molecule: arginine attenuator peptide; PDBTitle: structural basis of translational stalling by human cytomegalovirus2 (hcmv) and fungal arginine attenuator peptide (aap)
20	c3i6xC_	Alignment		16.1	18	PDB header: calmodulin-binding, membrane protein Chain: C: PDB Molecule: ras gtpase-activating-like protein iqgap1; PDBTitle: crystal structure of the calponin homology domain of iqgap1
21	c3o8jH_	Alignment	not modelled	15.2	5	PDB header: transferase Chain: H: PDB Molecule: 2-methylcitrate synthase; PDBTitle: crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
22	d1o7xa_	Alignment	not modelled	14.0	13	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
23	c3izcN_	Alignment	not modelled	11.8	18	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein rpl14 (I14e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
24	c6musB_	Alignment	not modelled	11.7	12	PDB header: rna binding protein/rna Chain: B: PDB Molecule: uncharacterized protein csm2; PDBTitle: cryo-em structure of larger csm-crrna-target rna ternary complex in2 type iii-a crispr-cas system
25	c5lcyD_	Alignment	not modelled	11.6	13	PDB header: transcription Chain: D: PDB Molecule: frmr; PDBTitle: formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
26	c3o0kB_	Alignment	not modelled	11.2	7	PDB header: oxidoreductase Chain: B: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo/keto reductase from brucella melitensis
27	c5lbnD_	Alignment	not modelled	10.4	10	PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor frmr; PDBTitle: the asymmetric tetrameric structure of the formaldehyde sensing2 transcriptional repressor frmr from escherichia coli
28	c1vgpA_	Alignment	not modelled	10.3	9	PDB header: transferase Chain: A: PDB Molecule: 373aa long hypothetical citrate synthase; PDBTitle: crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
						PDB header: transferase

29	c3hwkE	Alignment	not modelled	10.2	4	Chain: E: PDB Molecule: methylcitrate synthase; PDBTitle: crystal structure of methylcitrate synthase from mycobacterium2 tuberculosis
30	d2ezha	Alignment	not modelled	10.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
31	c3b3dA	Alignment	not modelled	10.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: putative morphine dehydrogenase; PDBTitle: b.subtilis ytbpe
32	c2bp1C	Alignment	not modelled	9.9	7	PDB header: oxidoreductase Chain: C: PDB Molecule: aflatoxin b1 aldehyde reductase member 2; PDBTitle: structure of the aflatoxin aldehyde reductase in complex with nadph
33	d1kvka2	Alignment	not modelled	9.9	15	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
34	c3npdA	Alignment	not modelled	9.9	36	PDB header: unknown function Chain: A: PDB Molecule: putative secreted protein; PDBTitle: crystal structure of a putative secreted protein (pa3611) from2 pseudomonas aeruginosa at 1.60 a resolution
35	c6abxA	Alignment	not modelled	9.8	13	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase (msed_1522) from metallosphaera2 sedula in complex with citrate
36	c2rr8A	Alignment	not modelled	9.6	17	PDB header: protein binding Chain: A: PDB Molecule: iqgap1 protein; PDBTitle: solution structure of calponin homology domain of iqgap1
37	c2I9uB	Alignment	not modelled	9.4	83	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbB-3; PDBTitle: spatial structure of dimeric erbB3 transmembrane domain
38	c2I9uA	Alignment	not modelled	9.4	83	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-3; PDBTitle: spatial structure of dimeric erbB3 transmembrane domain
39	c2yleA	Alignment	not modelled	9.2	13	PDB header: actin-binding protein Chain: A: PDB Molecule: protein spire homolog 1; PDBTitle: crystal structure of the human spir-1 kind fsi domain in2 complex with the fsi peptide
40	c4m1pA	Alignment	not modelled	9.0	16	PDB header: transcription repressor Chain: A: PDB Molecule: copper-sensitive operon repressor (csor); PDBTitle: crystal structure of the copper-sensing repressor csor with cu(i) from2 geobacillus thermodenitrificans ng80-2
41	c1vgmB	Alignment	not modelled	9.0	10	PDB header: transferase Chain: B: PDB Molecule: 378aa long hypothetical citrate synthase; PDBTitle: crystal structure of an isozyme of citrate synthase from sulfolobus2 tokodaii strain7
42	c2vohB	Alignment	not modelled	9.0	21	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2 homologous antagonist/killer; PDBTitle: structure of mouse a1 bound to the bak bh3-domain
43	c5jioI	Alignment	not modelled	8.8	12	PDB header: transport protein Chain: I: PDB Molecule: nuclear pore complex protein nup93; PDBTitle: alternative composite structure of the inner ring of the human nuclear2 pore complex (16 copies of nup188, 16 copies of nup205)
44	c5fmtB	Alignment	not modelled	8.7	15	PDB header: protein transport Chain: B: PDB Molecule: flagellar associated protein; PDBTitle: crift54 ch-domain
45	c4xghA	Alignment	not modelled	8.7	13	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: x-ray crystal structure of citrate synthase from burkholderia2 thailandensis
46	c3ci9B	Alignment	not modelled	8.6	16	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
47	c1ezeA	Alignment	not modelled	8.6	38	PDB header: transferase inhibitor Chain: A: PDB Molecule: cholesteryl ester transferase inhibitor protein; PDBTitle: structural studies of a baboon (papio sp.) plasma protein2 inhibitor of cholesteryl ester transferase.
48	c5uqqD	Alignment	not modelled	8.3	5	PDB header: transferase Chain: D: PDB Molecule: 2-methylcitrate synthase, mitochondrial; PDBTitle: crystal structure of 2-methylcitrate synthase from aspergillus2 fumigatus
49	c3njcA	Alignment	not modelled	8.2	40	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yslb protein; PDBTitle: crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460.
50	c3eevC	Alignment	not modelled	8.2	15	PDB header: transferase Chain: C: PDB Molecule: chloramphenicol acetyltransferase; PDBTitle: crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
51	c1vbjB	Alignment	not modelled	8.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f synthase; PDBTitle: the crystal structure of prostaglandin f synthase from trypanosoma2 brucei
52	d1k3pa	Alignment	not modelled	7.9	12	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
53	c6e3yE	Alignment	not modelled	7.8	29	PDB header: signaling protein Chain: E: PDB Molecule: receptor activity-modifying protein 1; PDBTitle: cryo-em structure of the active, gs-protein complexed, human cgrp2 receptor
54	c4fziA	Alignment	not modelled	7.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f synthase; PDBTitle: crystal structure of prostaglandin f synthase from

						trypanosoma cruzi
55	c4q3mF_	Alignment	not modelled	7.6	7	PDB header: hydrolase Chain: F: PDB Molecule: mgs-m4; PDBTitle: crystal structure of mgs-m4, an aldo-keto reductase enzyme from a2 medee basin deep-sea metagenome library
56	c1uvqC_	Alignment	not modelled	7.6	35	PDB header: immune system Chain: C: PDB Molecule: orexin; PDBTitle: crystal structure of hla-dq0602 in complex with a2 hypocretin peptide
57	c3v0tA_	Alignment	not modelled	7.6	8	PDB header: oxidoreductase Chain: A: PDB Molecule: perakine reductase; PDBTitle: crystal structure of perakine reductase, founder member of a novel akr2 subfamily with unique conformational changes during nadph binding
58	c3n2tA_	Alignment	not modelled	7.2	3	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
59	c3n8uB_	Alignment	not modelled	7.1	25	PDB header: hydrolase Chain: B: PDB Molecule: imelysin peptidase; PDBTitle: crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution
60	c5hb3A_	Alignment	not modelled	7.1	6	PDB header: transport protein Chain: A: PDB Molecule: nucleoporin nic96; PDBTitle: crystal structure of chaetomium thermophilum nic96 sol-nup53 complex
61	d1hw6a_	Alignment	not modelled	7.0	7	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
62	c5kzfj_	Alignment	not modelled	6.8	19	PDB header: hydrolase Chain: J: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
63	d1hnra_	Alignment	not modelled	6.8	17	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
64	c1wynA_	Alignment	not modelled	6.7	15	PDB header: structural protein Chain: A: PDB Molecule: calponin-2; PDBTitle: solution structure of the ch domain of human calponin-2
65	c6hxiD_	Alignment	not modelled	6.7	11	PDB header: lyase Chain: D: PDB Molecule: succinyl-coa ligase (adp-forming) subunit alpha; PDBTitle: structure of atp citrate lyase from methanotrix soehngenii in complex2 with citrate and coenzyme a
66	c5svaT_	Alignment	not modelled	6.7	17	PDB header: transcription, transferase/dna Chain: T: PDB Molecule: mediator of rna polymerase ii transcription subunit 4; PDBTitle: mediator-rna polymerase ii pre-initiation complex
67	c3tqgA_	Alignment	not modelled	6.6	8	PDB header: transferase Chain: A: PDB Molecule: 2-methylcitrate synthase; PDBTitle: structure of the 2-methylcitrate synthase (prpc) from coxiella2 burnetii
68	d2al6a2	Alignment	not modelled	6.5	16	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Third domain of FERM
69	d1iv8a2	Alignment	not modelled	6.3	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
70	c3iabB_	Alignment	not modelled	6.3	15	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonucleases p/mrp protein subunit pop7; PDBTitle: crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
71	c6gu1B_	Alignment	not modelled	6.2	16	PDB header: unknown function Chain: B: PDB Molecule: secreted rxlr effector peptide protein, putative; PDBTitle: sfi3 effector protein from the oomycete plant pathogen phytophthora2 infestans
72	d2ctsa_	Alignment	not modelled	6.2	8	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
73	c4ufcA_	Alignment	not modelled	6.2	45	PDB header: hydrolase Chain: A: PDB Molecule: gh95; PDBTitle: crystal structure of the gh95 enzyme bacova_03438
74	d2cpta1	Alignment	not modelled	6.2	24	Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
75	c1wypA_	Alignment	not modelled	6.2	6	PDB header: structural protein Chain: A: PDB Molecule: calponin 1; PDBTitle: solution structure of the ch domain of human calponin 1
76	d1pyfa_	Alignment	not modelled	6.2	17	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
77	c6mbcB_	Alignment	not modelled	6.0	25	PDB header: apoptosis Chain: B: PDB Molecule: df4; PDBTitle: human bfl-1 in complex with the designed peptide df4
78	c2v6xA_	Alignment	not modelled	6.0	25	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: structural insight into the interaction between esct-iii and vps4
79	c3jz0B_	Alignment	not modelled	6.0	11	PDB header: transferase/antibiotic Chain: B: PDB Molecule: lincosamide nucleotidyltransferase; PDBTitle: linb complexed with clindamycin and ampcpp
						Fold: Profilin-like

80	d1ioua_	Alignment	not modelled	5.9	21	Superfamily: SNARE-like Family: Synatpobrevin N-terminal domain
81	c2nupC_	Alignment	not modelled	5.9	14	PDB header: protein transport Chain: C: PDB Molecule: vesicle-trafficking protein sec22b; PDBTitle: crystal structure of the human sec23a/24a heterodimer, complexed with2 the snare protein sec22b
82	c3egdC_	Alignment	not modelled	5.9	14	PDB header: protein transport Chain: C: PDB Molecule: vesicle-trafficking protein sec22b; PDBTitle: crystal structure of the mammalian copii-coat protein sec23a/24a2 complexed with the snare protein sec22 and bound to the transport3 signal sequence of vesicular stomatitis virus glycoprotein
83	c2eiuE_	Alignment	not modelled	5.9	56	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: hypothetical protein aq_1627; PDBTitle: crystal structure of a putative protein (aq1627) from aquifex aeolicus
84	d1ji8a_	Alignment	not modelled	5.9	11	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
85	c6mp2B_	Alignment	not modelled	5.8	6	PDB header: hydrolase Chain: B: PDB Molecule: blman5b; PDBTitle: crystal structure of blman5b solved by siras
86	c3erpA_	Alignment	not modelled	5.8	7	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
87	c4wghA_	Alignment	not modelled	5.8	28	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde reductase; PDBTitle: crystal structure of aldo/keto reductase from klebsiella pneumoniae in2 complex with nadp and acetate at 1.8 a resolution
88	c5w8sA_	Alignment	not modelled	5.7	9	PDB header: transferase Chain: A: PDB Molecule: lipid-a-disaccharide synthase; PDBTitle: lipid a disaccharide synthase (lpxb)-7 solubilizing mutations
89	d1ur3m_	Alignment	not modelled	5.7	9	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
90	c1vw4d_	Alignment	not modelled	5.6	26	PDB header: ribosome Chain: D: PDB Molecule: PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
91	c2bbrA_	Alignment	not modelled	5.6	43	PDB header: viral protein Chain: A: PDB Molecule: viral casp8 and fadd-like apoptosis regulator; PDBTitle: crystal structure of mc159 reveals molecular mechanism of2 disc assembly and vflip inhibition
92	c3k7bA_	Alignment	not modelled	5.6	44	PDB header: viral protein Chain: A: PDB Molecule: protein a33; PDBTitle: the structure of the poxvirus a33 protein reveals a dimer of unique c-2 type lectin-like domains.
93	d2jq9a1	Alignment	not modelled	5.6	27	Fold: Spectrin repeat-like Superfamily: MIT domain Family: MIT domain
94	d1ifqa_	Alignment	not modelled	5.6	14	Fold: Profilin-like Superfamily: SNARE-like Family: Synatpobrevin N-terminal domain
95	c3qbrY_	Alignment	not modelled	5.6	16	PDB header: apoptosis Chain: Y: PDB Molecule: bcl-2 homologous antagonist/killer; PDBTitle: bakbh3 in complex with sj a
96	c5vwwB_	Alignment	not modelled	5.6	24	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-bh3 - cubic
97	c5ua4B_	Alignment	not modelled	5.5	20	PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist; PDBTitle: crystal structure of a179l:bid bh3 complex
98	c5vwwC_	Alignment	not modelled	5.5	24	PDB header: apoptosis Chain: C: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-rt - tetragonal
99	d2bgca1	Alignment	not modelled	5.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like