
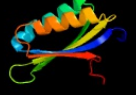













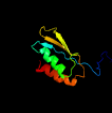
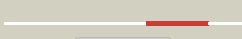







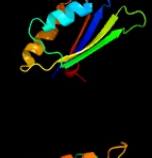

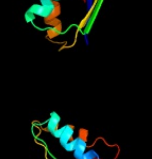



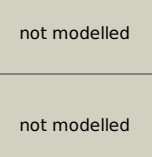


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1811_(mgtC)_2053450_2054154
 Date Fri Aug 2 13:30:42 BST 2019
 Unique Job ID c7ef0b31138e3b35

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lqjA_	 Alignment		99.5	100	PDB header: hydrolase Chain: A: PDB Molecule: mg2+ transport protein; PDBTitle: solution structure of the c-terminal domain of the mgtc protein from2 mycobacterium tuberculosis
2	c3ibwA_	 Alignment		97.2	19	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
3	d1u8sa2	 Alignment		96.2	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
4	c2lvwA_	 Alignment		95.4	14	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvN of the2 e.coli acetohydroxyacid synthase i (ahas i)
5	d1sc6a3	 Alignment		93.1	7	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
6	d1ygya3	 Alignment		93.1	6	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
7	c1y7pB_	 Alignment		92.9	5	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein af1403; PDBTitle: 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
8	d1phza1	 Alignment		92.7	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
9	d2qmwa2	 Alignment		92.6	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
10	c4lubA_	 Alignment		91.7	10	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
11	d2f1fa1	 Alignment		89.1	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: ilvH-like

12	c2fgcA_	Alignment		88.7	10	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
13	c2pnmA_	Alignment		88.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated
14	c2f1fA_	Alignment		87.0	14	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of acetoxyacid2 synthase isozyme iii from e. coli
15	d2fgca2	Alignment		86.6	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
16	d2pc6a2	Alignment		86.4	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
17	d1rwua_	Alignment		85.4	14	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
18	c1rwuA_	Alignment		85.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
19	d1zpv1	Alignment		84.8	10	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
20	c3mwbA_	Alignment		84.7	20	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
21	c2qmwA_	Alignment	not modelled	83.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
22	c2pc6C_	Alignment	not modelled	82.6	13	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
23	c5denA_	Alignment	not modelled	81.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
24	c6mk7A_	Alignment	not modelled	80.2	13	PDB header: membrane protein Chain: A: PDB Molecule: cell division protein ftsx; PDBTitle: solution structure of the large extracellular loop of ftsx in2 streptococcus pneumoniae
25	c5jk5A_	Alignment	not modelled	73.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex
26	c1ygyA_	Alignment	not modelled	72.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
27	c2mdaB_	Alignment	not modelled	70.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
28	c2qmvB_	Alignment	not modelled	64.9	12	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase;

28	c2qmxu	Alignment	not modelled	64.3	12	PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from <i>2 chlorobium tepidum</i> t1s PDB header: membrane protein
29	c4n8oA	Alignment	not modelled	64.3	21	Chain: A; PDB Molecule: cell division protein ftsx; PDBTitle: crystal structure of mycobacterial ftsx extracellular domain, bromide2 derivative
30	c4qo6A	Alignment	not modelled	50.8	17	PDB header: structural protein Chain: A; PDB Molecule: adenylate cyclase-like protein; PDBTitle: structural studies of cdsd, a structural protein of the type iii2 secretion system (tts) of <i>chlamydia trachomatis</i>
31	c3n0vD	Alignment	not modelled	47.0	2	PDB header: hydrolase Chain: D; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from <i>pseudomonas putida</i> kt2440 at 2.25 a resolution
32	c2yy3B	Alignment	not modelled	46.7	8	PDB header: translation Chain: B; PDB Molecule: elongation factor 1-beta; PDBTitle: crystal structure of translation elongation factor ef-1 beta from <i>2 pyrococcus horikoshii</i>
33	d2cg4a2	Alignment	not modelled	44.5	10	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
34	c3luyA	Alignment	not modelled	44.4	8	PDB header: isomerase Chain: A; PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from <i>bifidobacterium adolescentis</i>
35	c1u8sB	Alignment	not modelled	40.8	12	PDB header: transcription Chain: B; PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
36	d2cyya2	Alignment	not modelled	37.4	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
37	c4f3qA	Alignment	not modelled	34.7	16	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulatory protein cbu_1566; PDBTitle: structure of a yebc family protein (cbu_1566) from <i>coxiella burnetii</i>
38	d2joqa1	Alignment	not modelled	33.4	8	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: HP0495-like
39	c3k5pA	Alignment	not modelled	28.0	10	PDB header: oxidoreductase Chain: A; PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from <i>brucella melitensis</i>
40	d1u8sa1	Alignment	not modelled	27.5	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
41	c2bj3D	Alignment	not modelled	24.4	9	PDB header: transcription Chain: D; PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
42	c2ew9A	Alignment	not modelled	24.1	13	PDB header: hydrolase Chain: A; PDB Molecule: copper-transporting atpase 2; PDBTitle: solution structure of apowln5-6
43	d1kona	Alignment	not modelled	23.9	12	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
44	c2jsxA	Alignment	not modelled	23.7	11	PDB header: chaperone Chain: A; PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
45	c4g1uB	Alignment	not modelled	22.8	25	PDB header: transport protein/hydrolase Chain: B; PDB Molecule: hemin transport system permease protein hmuu; PDBTitle: x-ray structure of the bacterial heme transporter hmuuv from <i>yersinia2 pestis</i>
46	d1q5ya	Alignment	not modelled	21.1	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: Nickel responsive regulator NikR, C-terminal domain
47	c2nuuF	Alignment	not modelled	20.8	20	PDB header: transport protein/signaling protein Chain: F; PDB Molecule: ammonia channel; PDBTitle: regulating the escherichia coli ammonia channel: the crystal structure2 of the amtb-glnk complex
48	c1q5vB	Alignment	not modelled	19.5	10	PDB header: transcription Chain: B; PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
49	d1lfpA	Alignment	not modelled	18.3	9	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
50	c5a40C	Alignment	not modelled	18.1	15	PDB header: transport protein Chain: C; PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
51	d2nzca1	Alignment	not modelled	16.9	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: TM1266-like
52	c2ltmA	Alignment	not modelled	16.4	18	PDB header: electron transport Chain: A; PDB Molecule: nfu1 iron-sulfur cluster scaffold homolog, mitochondrial; PDBTitle: solution nmr structure of nfu1 iron-sulfur cluster scaffold homolog2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr2876b
53	c4czdD	Alignment	not modelled	16.2	6	PDB header: lyase Chain: D; PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with

						structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
54	c6hwhB_	Alignment	not modelled	15.1	11	PDB header: electron transport Chain: B; PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
55	c6p2rB_	Alignment	not modelled	14.7	10	PDB header: transferase Chain: B; PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
56	c2e1cA_	Alignment	not modelled	14.3	14	PDB header: transcription/dna Chain: A; PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
57	d1gh8a_	Alignment	not modelled	13.8	16	Fold: Ferredoxin-like Superfamily: eEF-1beta-like Family: eEF-1beta-like
58	c2k1hA_	Alignment	not modelled	13.5	15	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein ser13; PDBTitle: solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
59	c2mi2A_	Alignment	not modelled	13.3	16	PDB header: transport protein Chain: A; PDB Molecule: sec-independent protein translocase protein tatb; PDBTitle: solution structure of the e. coli tatb protein in dpc micelles
60	c2vbzA_	Alignment	not modelled	13.0	18	PDB header: dna-binding protein Chain: A; PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
61	c2dtjA_	Alignment	not modelled	13.0	7	PDB header: transferase Chain: A; PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
62	c4alzA_	Alignment	not modelled	12.8	11	PDB header: membrane protein Chain: A; PDB Molecule: yop proteins translocation protein d; PDBTitle: the yersinia t3ss basal body component yscd reveals a different2 structural periplasmic domain organization to known homologue prgh
63	d2ffma1	Alignment	not modelled	12.5	11	Fold: Hypothetical protein SAV1430 Superfamily: Hypothetical protein SAV1430 Family: Hypothetical protein SAV1430
64	c2cg4B_	Alignment	not modelled	12.2	11	PDB header: transcription Chain: B; PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
65	d1i1ga2	Alignment	not modelled	12.2	10	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
66	c6exxA_	Alignment	not modelled	12.2	9	PDB header: rna binding protein Chain: A; PDB Molecule: protein pes4; PDBTitle: crystal structure of pes4 rrm4
67	c3o1lB_	Alignment	not modelled	11.9	9	PDB header: hydrolase Chain: B; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
68	c5nwwA_	Alignment	not modelled	11.8	31	PDB header: viral protein Chain: A; PDB Molecule: scrfp-tag.gp41; PDBTitle: nmr assignment and structure of a peptide derived from the fusion2 peptide of hiv-1 gp41 in the presence of dodecylphosphocholine3 micelles
69	c6fu9A_	Alignment	not modelled	11.4	8	PDB header: antifungal protein Chain: A; PDB Molecule: nbs-lrr class disease resistance protein; PDBTitle: complex of rice blast (magnaporthe oryzae) effector protein avr-pikd2 with the hma domain of pikm-1 from rice (oryza sativa)
70	c5zneA_	Alignment	not modelled	10.6	11	PDB header: plant protein Chain: A; PDB Molecule: nbs-lrr type protein; PDBTitle: the crystal structure of immune receptor rga5a_s of resistance protein2 pia from rice (oryza sativa)
71	c3louB_	Alignment	not modelled	10.5	11	PDB header: hydrolase Chain: B; PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
72	d2guka1	Alignment	not modelled	10.2	23	Fold: PG1857-like Superfamily: PG1857-like Family: PG1857-like
73	d1lk5a2	Alignment	not modelled	9.6	20	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
74	c5svtA_	Alignment	not modelled	9.5	18	PDB header: membrane protein Chain: A; PDB Molecule: p2x purinoceptor 3; PDBTitle: anomalous cs+ signal reveals the site of na+ ion entry to the channel2 pore of the human p2x3 ion channel through the extracellular3 fenestrations
75	d2qifa1	Alignment	not modelled	9.5	25	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
76	c2e7xA_	Alignment	not modelled	9.3	15	PDB header: transcription regulator Chain: A; PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfolobus tokodaii 7 complexed with its cognate ligand
						PDB header: transport protein

77	c5a43B_	Alignment	not modelled	9.2	11	Chain: B: PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
78	d1o8ba2	Alignment	not modelled	8.6	15	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
79	c2ls4A_	Alignment	not modelled	8.4	28	PDB header: metal transport Chain: A: PDB Molecule: high affinity copper uptake protein 1; PDBTitle: 1h chemical shift assignments for the third transmembrane domain from2 the human copper transport 1
80	c6iu3A_	Alignment	not modelled	8.2	17	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
81	c2e1aD_	Alignment	not modelled	8.2	10	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
82	c3s1tB_	Alignment	not modelled	7.9	6	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: structure of the regulatory domain of aspartokinase (rv3709c; ak-beta)2 in complex with threonine from mycobacterium tuberculosis
83	d2bj7a2	Alignment	not modelled	7.9	10	Fold: Ferredoxin-like Superfamily: ACT-like Family: Nickel responsive regulator NikR, C-terminal domain
84	c5a6wA_	Alignment	not modelled	7.8	11	PDB header: antiviral protein Chain: A: PDB Molecule: resistance protein pikp-1; PDBTitle: complex of rice blast (magnaporthe oryzae) effector protein avr-pikd2 with the hma domain of pikp1 from rice (oryza sativa)
85	c2djwF_	Alignment	not modelled	7.8	10	PDB header: unknown function Chain: F: PDB Molecule: probable transcriptional regulator, asnc family; PDBTitle: crystal structure of ttha0845 from thermus thermophilus hb8
86	d1p6ta2	Alignment	not modelled	7.7	16	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
87	c2ga7A_	Alignment	not modelled	7.6	15	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein)
88	c2y3yC_	Alignment	not modelled	7.6	11	PDB header: transcription Chain: C: PDB Molecule: putative nickel-responsive regulator; PDBTitle: holo-ni(ii) hpnikr is a symmetric tetramer containing four canonic2 square-planar ni(ii) ions at physiological ph
89	c4k0eA_	Alignment	not modelled	7.6	12	PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
90	c2pjmA_	Alignment	not modelled	7.5	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
91	c5f1cA_	Alignment	not modelled	7.5	32	PDB header: membrane protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of an invertebrate p2x receptor from the gulf coast2 tick in the presence of atp and zn2+ ion at 2.9 angstroms
92	c1lk5C_	Alignment	not modelled	7.3	15	PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
93	c6cfwB_	Alignment	not modelled	7.2	14	PDB header: membrane protein Chain: B: PDB Molecule: monovalent cation/h+ antiporter subunit f; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
94	c2zbcH_	Alignment	not modelled	7.1	15	PDB header: transcription Chain: H: PDB Molecule: 83aa long hypothetical transcriptional regulator asnc; PDBTitle: crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfobolus tokodaii strain7.
95	c3nrbdD_	Alignment	not modelled	7.1	7	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
96	c2lj3mA_	Alignment	not modelled	7.0	16	PDB header: metal binding protein Chain: A: PDB Molecule: copper-ion-binding protein; PDBTitle: solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
97	c5o7jA_	Alignment	not modelled	6.8	30	PDB header: signaling protein Chain: A: PDB Molecule: histidine kinase; PDBTitle: structural insights into the periplasmic sensor domain of the gacs2 histidine kinase controlling biofilm formation in pseudomonas3 aeruginosa
98	c2crlA_	Alignment	not modelled	6.7	13	PDB header: chaperone Chain: A: PDB Molecule: copper chaperone for superoxide dismutase; PDBTitle: the apo form of hma domain of copper chaperone for2 superoxide dismutase
99	c2kncA_	Alignment	not modelled	6.6	11	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex