
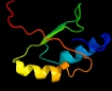





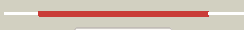












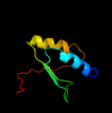


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2255A_(RVBD2255A)_2529104_2529322
Date	Mon Aug 5 13:25:39 BST 2019
Unique Job ID	389d1af49b1299b6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cg4a2	 Alignment		99.7	24	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
2	d2cyya2	 Alignment		99.7	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
3	d1i1ga2	 Alignment		99.7	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
4	c2djwF_	 Alignment		99.7	23	PDB header: unknown function Chain: F: PDB Molecule: probable transcriptional regulator, asnc family; PDBTitle: crystal structure of ttha0845 from thermus thermophilus hb8
5	d2cfxa2	 Alignment		99.7	19	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
6	c2zbcH_	 Alignment		99.7	13	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 sulfolobus tokodaii strain7.
7	c2e1aD_	 Alignment		99.6	19	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
8	c2cg4B_	 Alignment		99.5	24	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
9	c1i1gA_	 Alignment		99.5	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
10	c3i4pA_	 Alignment		99.5	21	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
11	c4pcqC_	 Alignment		99.5	24	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)

12	c2e1cA_	Alignment		99.5	21	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
13	c2e7xA_	Alignment		99.5	13	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
14	c2gqgB_	Alignment		99.5	24	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
15	c2p6tH_	Alignment		99.4	21	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
16	c2cfxD_	Alignment		99.4	20	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
17	c2dbbA_	Alignment		99.4	16	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
18	c2vbzA_	Alignment		99.4	25	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
19	c2ia0A_	Alignment		99.3	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
20	c4ch7A_	Alignment		99.2	6	PDB header: transcription Chain: A: PDB Molecule: nird-like protein; PDBTitle: crystal structure of the siroheme decarboxylase nirdl
21	c4czdD_	Alignment	not modelled	99.2	13	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.
22	c4czdA_	Alignment	not modelled	99.1	10	PDB header: lyase Chain: A: 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.
23	c2jxsA_	Alignment	not modelled	94.3	11	PDB header: chaperone Chain: A: PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
24	c3ibwA_	Alignment	not modelled	89.3	24	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
25	c4qo6A_	Alignment	not modelled	78.3	13	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 (ttss) of chlamydia trachomatis
26	c4n8oA_	Alignment	not modelled	76.2	7	PDB header: membrane protein Chain: A: PDB Molecule: cell division protein ftsx; PDBTitle: crystal structure of mycobacterial ftsx extracellular domain, bromide2 derivative
27	c6mk7A_	Alignment	not modelled	71.0	11	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
						PDB header: unknown function

28	c3bn7A_	Alignment	not modelled	65.6	20	Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (cc_2267) from <i>Caulobacter crescentus</i> cb15 at 1.64 Å resolution
29	c2a5hC_	Alignment	not modelled	64.8	17	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 Å x-ray crystal structure of lysine-2,3-aminomutase from <i>Clostridium subterminale</i> sb4, with Michaelis analog (l-α-lysine-3 external aldimine form of pyridoxal-5'-phosphate).
30	d1j5ya2	Alignment	not modelled	57.2	18	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain
31	d1q5ya_	Alignment	not modelled	51.9	7	Fold: Ferredoxin-like Superfamily: ACT-like Family: Nickel responsive regulator NikR, C-terminal domain
32	c1q5vB_	Alignment	not modelled	50.5	7	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
33	c2y3yC_	Alignment	not modelled	42.7	11	PDB header: transcription Chain: C: PDB Molecule: putative nickel-responsive regulator; PDBTitle: holo-ni(ii) hpnikr is a symmetric tetramer containing four canonical square-planar Ni(II) ions at physiological pH
34	c3bdeA_	Alignment	not modelled	41.6	13	PDB header: unknown function Chain: A: PDB Molecule: mll5499 protein; PDBTitle: crystal structure of a DabB family protein with a ferredoxin-like fold2 (mll5499) from <i>Mesorhizobium loti</i> maff303099 at 1.79 Å resolution
35	d1mlia_	Alignment	not modelled	41.4	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Muconalactone isomerase, MLI
36	d1uj4a2	Alignment	not modelled	39.7	19	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
37	d1o8ba2	Alignment	not modelled	39.6	11	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
38	d1lk5a2	Alignment	not modelled	39.1	11	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
39	c3znul_	Alignment	not modelled	38.4	16	PDB header: lyase Chain: I: PDB Molecule: 5-chloromuconolactone dehalogenase; PDBTitle: crystal structure of clcf in crystal form 2
40	c4wwsE_	Alignment	not modelled	38.2	10	PDB header: oxidoreductase Chain: E: PDB Molecule: putative heme-dependent peroxidase lmo2113; PDBTitle: structure of chlorite dismutase-like protein from <i>Listeria monocytogenes</i>
41	d1m0sa2	Alignment	not modelled	37.8	14	Fold: Ferredoxin-like Superfamily: D-ribose-5-phosphate isomerase (RpiA), lid domain Family: D-ribose-5-phosphate isomerase (RpiA), lid domain
42	c5a13J_	Alignment	not modelled	36.4	20	PDB header: oxidoreductase Chain: J: PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of chlorite dismutase from <i>Magnetospirillum</i> sp. in complex with thiocyanate
43	c2ca9B_	Alignment	not modelled	30.9	12	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from <i>Helicobacter pylori</i> in closed trans-2 conformation
44	d1rwua_	Alignment	not modelled	29.2	16	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
45	c1rwuA_	Alignment	not modelled	29.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybeD; PDBTitle: solution structure of conserved protein ybeD from <i>E. coli</i>
46	d2joqa1	Alignment	not modelled	28.3	6	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: HP0495-like
47	c2bj3D_	Alignment	not modelled	27.7	5	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr- <i>apo</i>
48	c3nn4C_	Alignment	not modelled	26.3	8	PDB header: oxidoreductase Chain: C: PDB Molecule: chlorite dismutase; PDBTitle: structure of chlorite dismutase from <i>Candidatus Nitrospira defluvii</i> 2 r173k mutant
49	c1lk5C_	Alignment	not modelled	25.5	11	PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from <i>Pyrococcus horikoshii</i>
50	c3l7oB_	Alignment	not modelled	24.9	11	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from <i>Streptococcus</i> 2 mutans ua159
51	c3kwmC_	Alignment	not modelled	23.9	11	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-isomerase a
52	c6j1kA_	Alignment	not modelled	23.6	17	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from <i>Ochrobactrum</i> 2 sp. csl1
53	c4gmkB_	Alignment	not modelled	21.8	11	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5-phosphate isomerase from

						the probiotic2 bacterium lactobacillus salivarius ucc118
54	c4x84C_	Alignment	not modelled	21.7	8	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
55	c1uj6A_	Alignment	not modelled	21.6	19	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
56	c2vxhF_	Alignment	not modelled	21.4	19	PDB header: oxidoreductase Chain: F: PDB Molecule: chlorite dismutase; PDBTitle: the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
57	c1lkzB_	Alignment	not modelled	21.0	11	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase a; PDBTitle: crystal structure of d-ribose-5-phosphate isomerase (rpiA) from2 escherichia coli.
58	c3u7jA_	Alignment	not modelled	20.3	14	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
59	c5y02D_	Alignment	not modelled	20.1	9	PDB header: lyase Chain: D: PDB Molecule: hydroxynitrile lyase; PDBTitle: c-terminal peptide depleted mutant of hydroxynitrile lyase from2 passiflora edulis (pehnl) bound with (r)-mandelonitrile
60	c6eepA_	Alignment	not modelled	19.3	14	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase from legionella2 pneumophila
61	c1m0sA_	Alignment	not modelled	19.1	14	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: northeast structural genomics consortium (nesg id ir21)
62	c1xtzA_	Alignment	not modelled	19.1	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
63	c2f8mB_	Alignment	not modelled	18.6	16	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
64	c5uf2A_	Alignment	not modelled	18.6	3	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5 phosphate isomerase a from neisseria2 gonorrhoeae
65	c3hheA_	Alignment	not modelled	17.4	8	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
66	c3sf5D_	Alignment	not modelled	17.4	11	PDB header: chaperone Chain: D: PDB Molecule: urease accessory protein ureh; PDBTitle: crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
67	d1uw4a_	Alignment	not modelled	16.8	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Smg-4/UPF3
68	c3qpiA_	Alignment	not modelled	16.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of dimeric chlorite dismutases from nitrobacter2 winogradskyi
69	c3bguA_	Alignment	not modelled	16.2	9	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein of unknown function; PDBTitle: crystal structure of a dimeric ferredoxin-like protein of unknown2 function (tfu_0763) from thermobifida fusca yx at 1.50 a resolution
70	d1sc6a3	Alignment	not modelled	15.7	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
71	d2nzca1	Alignment	not modelled	15.6	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: TM1266-like
72	d1rja_	Alignment	not modelled	15.1	8	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
73	d2bj7a2	Alignment	not modelled	14.9	5	Fold: Ferredoxin-like Superfamily: ACT-like Family: Nickel responsive regulator NikR, C-terminal domain
74	d1vdha_	Alignment	not modelled	14.0	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
75	c5z2vB_	Alignment	not modelled	13.6	17	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recr from pseudomonas aeruginosa pao1
76	d1t0tv_	Alignment	not modelled	12.9	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
77	c5zvqA_	Alignment	not modelled	12.2	19	PDB header: recombination Chain: A: PDB Molecule: recombination protein recr; PDBTitle: crystal structure of recombination mediator protein recr
78	d1vdda_	Alignment	not modelled	12.1	19	Fold: Recombination protein RecR Superfamily: Recombination protein RecR Family: Recombination protein RecR
79	c1vddC_	Alignment	not modelled	11.1	22	PDB header: recombination Chain: C: PDB Molecule: recombination protein recr;

						PDBTitle: crystal structure of recombinational repair protein recr
80	c2yadA_	Alignment	not modelled	11.1	21	PDB header: surfactant protein Chain: A; PDB Molecule: surfactant protein c brichos domain; PDBTitle: brichos domain of surfactant protein c precursor protein
81	c4nmIA_	Alignment	not modelled	11.1	22	PDB header: isomerase Chain: A; PDB Molecule: ribulose 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
82	c5yaaD_	Alignment	not modelled	10.8	17	PDB header: hydrolase Chain: D; PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 nyn domain from mus musculus
83	c5k8zB_	Alignment	not modelled	10.7	16	PDB header: oxidoreductase Chain: B; PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of dimeric chlorite dismutase from cyanosethec sp.2 pcc7425 (ph 8.5)
84	c2pbeA_	Alignment	not modelled	10.4	25	PDB header: transferase Chain: A; PDB Molecule: aminoglycoside 6-adenylyltransferase; PDBTitle: crystal structure of an aminoglycoside 6-adenylyltransferase2 from bacillus subtilis
85	d1pv8a_	Alignment	not modelled	9.9	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinic acid dehydratase, ALAD (porphobilinogen synthase)
86	c3dtzB_	Alignment	not modelled	9.4	15	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative chlorite dismutase ta0507; PDBTitle: crystal structure of putative chlorite dismutase ta0507
87	c2yadE_	Alignment	not modelled	9.1	26	PDB header: surfactant protein Chain: E; PDB Molecule: surfactant protein c brichos domain; PDBTitle: brichos domain of surfactant protein c precursor protein
88	c5nocA_	Alignment	not modelled	8.9	35	PDB header: dna binding protein Chain: A; PDB Molecule: stage 0 sporulation protein j; PDBTitle: solution nmr structure of the c-terminal domain of parb (spo0j)
89	c5lzh_	Alignment	not modelled	8.6	23	PDB header: lyase Chain: H; PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: pyrobaculum caldifontis 5-aminolaevulinic acid dehydratase
90	c3bb5B_	Alignment	not modelled	8.4	17	PDB header: unknown function Chain: B; PDB Molecule: stress responsive alpha-beta protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
91	d2pbea2	Alignment	not modelled	8.0	26	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: AadK N-terminal domain-like
92	c3ip1B_	Alignment	not modelled	7.8	16	PDB header: ligase Chain: B; PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
93	c3zmnA_	Alignment	not modelled	7.2	20	PDB header: viral protein Chain: A; PDB Molecule: vp17; PDBTitle: vp17, a capsid protein of bacteriophage p23-77
94	d2icya1	Alignment	not modelled	7.2	17	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
95	c2lqjA_	Alignment	not modelled	7.1	21	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
96	c2l2eA_	Alignment	not modelled	6.9	29	PDB header: metal binding protein Chain: A; PDB Molecule: calcium-binding protein ncs-1; PDBTitle: solution nmr structure of myristoylated ncs1p in apo form
97	d1f0la3	Alignment	not modelled	6.3	17	Fold: Toxins' membrane translocation domains Superfamily: Diphtheria toxin, middle domain Family: Diphtheria toxin, middle domain
98	c3g7sA_	Alignment	not modelled	6.1	21	PDB header: ligase Chain: A; PDB Molecule: long-chain-fatty-acid--coa ligase (fadd-1); PDBTitle: crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
99	d1q4ra_	Alignment	not modelled	5.9	6	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein