







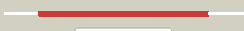








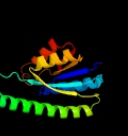






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2319c (-) _2591858_2592736
Date	Mon Aug 5 13:25:47 BST 2019
Unique Job ID	c455c4b517730a4d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3loqA_	 Alignment		100.0	16	PDB header: structure genomics, unknown function Chain: A; PDB Molecule: universal stress protein; PDBTitle: the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
2	c3olqA_	 Alignment		100.0	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: universal stress protein e; PDBTitle: the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
3	c3mt0A_	 Alignment		100.0	15	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
4	c4r2jA_	 Alignment		100.0	15	PDB header: metal binding protein, unknown function Chain: A; PDB Molecule: universal stress protein e; PDBTitle: crystal structure of ydaa (universal stress protein e) from salmonella2 typhimurium
5	c2jaxA_	 Alignment		100.0	22	PDB header: protein binding Chain: A; PDB Molecule: hypothetical protein tb31.7; PDBTitle: universal stress protein rv2623 from mycobaterium2 tuberculosis
6	c3ab8B_	 Alignment		100.0	19	PDB header: unknown function Chain: B; PDB Molecule: putative uncharacterized protein ttha0350; PDBTitle: crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
7	c3hgmD_	 Alignment		99.9	14	PDB header: signaling protein Chain: D; PDB Molecule: universal stress protein tead; PDBTitle: universal stress protein tead from the trap transporter teaabc of2 halomonas elongata
8	d2z3va1	 Alignment		99.9	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
9	c3s3tD_	 Alignment		99.9	15	PDB header: chaperone Chain: D; PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
10	c5ahwC_	 Alignment		99.9	19	PDB header: signaling protein Chain: C; PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein msmeg_3811 in2 complex with camp
11	c3dloC_	 Alignment		99.9	16	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus

12	d1mjha_	Alignment		99.9	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
13	d1tq8a_	Alignment		99.8	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
14	c3fg9B_	Alignment		99.8	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
15	c3fh0A_	Alignment		99.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative universal stress protein kpn_01444; PDBTitle: crystal structure of putative universal stress protein kpn_01444 -2 atpase
16	c4wnyA_	Alignment		99.8	14	PDB header: signaling protein Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei
17	c4r2IB_	Alignment		99.8	13	PDB header: unknown function Chain: B: PDB Molecule: universal stress protein f; PDBTitle: crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
18	d1jmva_	Alignment		99.8	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
19	d2gm3a1	Alignment		99.8	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
20	c2pfsA_	Alignment		99.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
21	c2dumD_	Alignment	not modelled	99.8	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0823; PDBTitle: crystal structure of hypothetical protein, ph0823
22	d1q77a_	Alignment	not modelled	99.7	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
23	c3idfA_	Alignment	not modelled	99.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: usp-like protein; PDBTitle: the crystal structure of a usp-like protein from wolinnella2 succinogenes to 2.0a
24	c4kpuB_	Alignment	not modelled	96.2	20	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
25	d1o94c_	Alignment	not modelled	94.8	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
26	c3g40A_	Alignment	not modelled	94.6	11	PDB header: transport protein Chain: A: PDB Molecule: na-k-cl cotransporter; PDBTitle: crystal structure of the cytoplasmic domain of a2 prokaryotic cation chloride cotransporter
27	d3clsc1	Alignment	not modelled	93.4	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
28	c5ol2E_	Alignment	not modelled	92.1	13	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa

						dehydrogenase2 complex from clostridium difficile
29	c6fahB	Alignment	not modelled	90.6	18	PDB header: flavoprotein Chain: B: PDB Molecule: caffel-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffel-coa2 reductase reaction
30	d1efpb	Alignment	not modelled	86.0	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
31	c5ow0B	Alignment	not modelled	85.9	19	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
32	c5gafi	Alignment	not modelled	83.8	13	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
33	c3a2kB	Alignment	not modelled	78.8	15	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
34	c4ltyD	Alignment	not modelled	77.9	12	PDB header: hydrolase Chain: D: PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
35	d1efvb	Alignment	not modelled	77.6	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
36	c2j289	Alignment	not modelled	77.5	15	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
37	c2ejbA	Alignment	not modelled	74.4	10	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
38	c1kh2D	Alignment	not modelled	73.1	18	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
39	c6eoaA	Alignment	not modelled	70.2	9	PDB header: flavoprotein Chain: A: PDB Molecule: phosphopantothenoilcysteine decarboxylase; PDBTitle: crystal structure of hal3 from cryptococcus neoformans
40	c2q8uA	Alignment	not modelled	69.4	17	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
41	c2e21A	Alignment	not modelled	68.5	15	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
42	c4mm1E	Alignment	not modelled	67.8	20	PDB header: transferase Chain: E: PDB Molecule: geranylgeranylglyceril phosphate synthase; PDBTitle: gggps from methanothermobacter thermautotrophicus
43	d1uf3a	Alignment	not modelled	66.4	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
44	d1ii7a	Alignment	not modelled	65.7	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
45	c3auzA	Alignment	not modelled	65.5	10	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
46	d1j20a1	Alignment	not modelled	63.0	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
47	c3qg5D	Alignment	not modelled	62.5	17	PDB header: hydrolase Chain: D: PDB Molecule: mre11; PDBTitle: the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
48	d1np7a2	Alignment	not modelled	62.2	12	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
49	c2xmoB	Alignment	not modelled	62.0	13	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
50	d2yvta1	Alignment	not modelled	61.3	26	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
51	c6jddA	Alignment	not modelled	56.9	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: cypemycin cysteine dehydrogenase (decarboxylating); PDBTitle: crystal structure of the cypemycin decarboxylase cypd.
52	c3av0A	Alignment	not modelled	56.8	6	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11-rad50 bound to atp s
53	c4fcxB	Alignment	not modelled	56.0	22	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad32; PDBTitle: s.pombe mre11 apoenzym
54	c2ze5A	Alignment	not modelled	55.8	13	PDB header: transferase Chain: A: PDB Molecule: isopentenyl transferase; PDBTitle: crystal structure of adenosine phosphate-isopentenyltransferase

55	c2iy3A	Alignment	not modelled	55.3	14	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal regognition particle
56	c6jlsA	Alignment	not modelled	54.9	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative flavoprotein decarboxylase; PDBTitle: crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
57	d1gsoa2	Alignment	not modelled	54.0	21	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
58	c3cvyA	Alignment	not modelled	53.0	12	PDB header: lyase/dna Chain: A: PDB Molecule: re11660p; PDBTitle: drosophila melanogaster (6-4) photolyase bound to repaired ds dna
59	c3dm5A	Alignment	not modelled	52.0	10	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
60	d1vbka1	Alignment	not modelled	50.9	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Thil-like
61	c4fbkB	Alignment	not modelled	49.4	22	PDB header: hydrolase, protein binding Chain: B: PDB Molecule: dna repair and telomere maintenance protein nbs1,dna repair PDBTitle: crystal structure of a covalently fused nbs1-mre11 complex with one2 manganese ion per active site
62	d2hy5a1	Alignment	not modelled	47.1	9	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
63	c2yxbA	Alignment	not modelled	46.4	12	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
64	d1wy5a1	Alignment	not modelled	46.0	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
65	d1nu0a	Alignment	not modelled	45.0	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
66	c3t1iC	Alignment	not modelled	44.8	20	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
67	c2j37W	Alignment	not modelled	44.7	11	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
68	c3vrhA	Alignment	not modelled	41.8	14	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
69	c2v3cC	Alignment	not modelled	37.8	16	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
70	c3vkbA	Alignment	not modelled	37.6	14	PDB header: transferase Chain: A: PDB Molecule: moeo5; PDBTitle: crystal structure of moeo5 soaked with fspp overnight
71	c3gndC	Alignment	not modelled	37.4	19	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
72	c4grdA	Alignment	not modelled	37.0	16	PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
73	d1sbza	Alignment	not modelled	35.3	12	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
74	c3pm6B	Alignment	not modelled	34.4	17	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
75	d2g0ta1	Alignment	not modelled	33.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	d1e0ta3	Alignment	not modelled	32.9	24	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
77	d1o4va	Alignment	not modelled	31.1	18	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
78	c5l3rC	Alignment	not modelled	30.9	13	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
79	c1qzwC	Alignment	not modelled	30.6	14	PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp

						and2 implications for inter-domain communication
80	c1qzuB_	Alignment	not modelled	30.4	13	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein mds018; PDBTitle: crystal structure of human phosphopantothencycysteine decarboxylase
81	c5ghaC_	Alignment	not modelled	29.8	26	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
82	c2p0yA_	Alignment	not modelled	29.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
83	c4r3uD_	Alignment	not modelled	29.6	10	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
84	d1pkla3	Alignment	not modelled	29.6	12	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
85	d2iela1	Alignment	not modelled	28.4	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
86	c3ib7A_	Alignment	not modelled	28.2	10	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
87	d2d1pa1	Alignment	not modelled	28.0	10	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
88	c4r81C_	Alignment	not modelled	27.8	8	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase; PDBTitle: nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis
89	c1s3mA_	Alignment	not modelled	27.5	14	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
90	d1s3la_	Alignment	not modelled	27.5	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
91	d1m7ja3	Alignment	not modelled	27.1	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
92	c2ppvA_	Alignment	not modelled	26.6	16	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
93	c4ykeA_	Alignment	not modelled	26.4	20	PDB header: hydrolase Chain: A: PDB Molecule: mre11; PDBTitle: crystal structure of eukaryotic mre11 catalytic domain from chaetomium2 thermophilum
94	d1xmpa_	Alignment	not modelled	26.4	13	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
95	c5ol2D_	Alignment	not modelled	25.6	17	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
96	d2p1ra1	Alignment	not modelled	25.6	24	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
97	c1ni5A_	Alignment	not modelled	23.1	14	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
98	d1to6a_	Alignment	not modelled	22.8	21	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
99	d1ni5a1	Alignment	not modelled	22.4	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
100	c2xrzA_	Alignment	not modelled	22.4	11	PDB header: lyase/dna Chain: A: PDB Molecule: deoxyribodipyrimidine photolyase; PDBTitle: x-ray structure of archaeal class ii cpd photolyase from2 methanosarcina mazei in complex with intact cpd-lesion
101	d1qzua_	Alignment	not modelled	21.7	13	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
102	d3bula2	Alignment	not modelled	21.2	9	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
103	c2pjuD_	Alignment	not modelled	21.1	14	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon regulatory protein2 prpr
104	c6qlgD_	Alignment	not modelled	20.6	13	PDB header: transferase Chain: D: PDB Molecule: flavin prenyltransferase pad1, mitochondrial; PDBTitle: crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate

105	c6ofuC_	Alignment	not modelled	20.1	15	PDB header: lyase Chain: C: PDB Molecule: ydji aldolase; PDBTitle: x-ray crystal structure of the ydji aldolase from escherichia coli k12
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