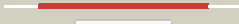



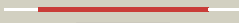












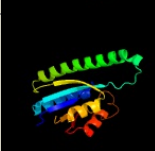

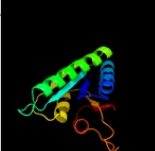




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1996 (-)_2239012_2239965
Date	Mon Aug 5 13:25:10 BST 2019
Unique Job ID	e77c0a698a116ef9

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jaxA_	 Alignment		100.0	50	PDB header: protein binding Chain: A: PDB Molecule: hypothetical protein tb31.7; PDBTitle: universal stress protein rv2623 from mycobacterium2 tuberculosis
2	c3olqA_	 Alignment		100.0	12	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	c3loqA_	 Alignment		100.0	22	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
4	c3mt0A_	 Alignment		100.0	17	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
5	c3ab8B_	 Alignment		100.0	20	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.
6	c4r2jA_	 Alignment		100.0	14	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
7	d1tq8a_	 Alignment		99.8	37	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
8	c5ahwC_	 Alignment		99.8	23	PDB header: signaling protein Chain: C: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein msmeg_3811 in2 complex with camp
9	c3s3tD_	 Alignment		99.8	19	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
10	c3dloC_	 Alignment		99.8	25	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
11	c3fh0A_	 Alignment		99.8	37	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

12	c3hgmD_	Alignment		99.8	24	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
13	d2z3va1	Alignment		99.8	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
14	d1mjha_	Alignment		99.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
15	d2gm3a1	Alignment		99.8	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
16	c4wnyA_	Alignment		99.7	22	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	c3fg9B_	Alignment		99.7	18	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
18	c4r2IB_	Alignment		99.7	24	PDB header: unknown function Chain: B: PDB Molecule: universal stress protein f; PDBTitle: crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
19	c2dumD_	Alignment		99.7	16	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0823; PDBTitle: crystal structure of hypothetical protein, ph0823
20	d1jmva_	Alignment		99.7	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
21	c2pfsA_	Alignment	not modelled	99.6	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
22	c3idfA_	Alignment	not modelled	99.6	18	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
23	d1q77a_	Alignment	not modelled	99.6	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
24	c3g40A_	Alignment	not modelled	94.0	10	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
25	c6eoaA_	Alignment	not modelled	76.7	23	PDB header: flavoprotein Chain: A: PDB Molecule: phosphopantothencysteine decarboxylase; PDBTitle: crystal structure of hal3 from cryptococcus neoformans
26	c4kpuB_	Alignment	not modelled	69.3	19	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
27	c3a2kB_	Alignment	not modelled	66.8	18	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
28	c6qlgD_	Alignment	not modelled	65.8	20	PDB header: transferase Chain: D: PDB Molecule: flavin prenyltransferase pad1, mitochondrial;

						PDBTitle: crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate
29	d1sbza_	Alignment	not modelled	63.7	21	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
30	c6jlsA_	Alignment	not modelled	62.5	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative flavoprotein decarboxylase; PDBTitle: crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
31	c5ol2E_	Alignment	not modelled	61.4	15	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
32	c4r3uD_	Alignment	not modelled	58.9	14	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
33	c4n7bA_	Alignment	not modelled	58.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: lytb; PDBTitle: structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
34	c3zquA_	Alignment	not modelled	56.9	9	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
35	d2ajta2	Alignment	not modelled	55.8	5	Fold: Fucl/AraA N-terminal and middle domains Superfamily: Fucl/AraA N-terminal and middle domains Family: AraA N-terminal and middle domain-like
36	c1kh2D_	Alignment	not modelled	52.4	12	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
37	c3dnfB_	Alignment	not modelled	50.5	9	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
38	c5ow0B_	Alignment	not modelled	48.1	18	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
39	c2ppvA_	Alignment	not modelled	46.8	21	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
40	d1p3y1_	Alignment	not modelled	45.5	21	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
41	c1ni5A_	Alignment	not modelled	44.6	26	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
42	c2e21A_	Alignment	not modelled	43.0	5	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
43	c2p0yA_	Alignment	not modelled	40.5	24	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
44	d1owla2	Alignment	not modelled	38.4	15	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
45	c4rheB_	Alignment	not modelled	36.3	16	PDB header: lyase Chain: B: PDB Molecule: 3-octaprenyl-4-hydroxybenzoate carboxylase; PDBTitle: crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
46	d2hzba1	Alignment	not modelled	36.3	19	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
47	c2xrzA_	Alignment	not modelled	35.8	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
48	d1m7ja3	Alignment	not modelled	34.1	17	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: D-aminoacylase, catalytic domain
49	c6fkxD_	Alignment	not modelled	33.8	17	PDB header: hydrolase Chain: D: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of an acetyl xylan esterase from a desert metagenome
50	c6fahB_	Alignment	not modelled	33.4	19	PDB header: flavoprotein Chain: B: PDB Molecule: caffeyl-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
51	c3s40C_	Alignment	not modelled	33.0	14	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
52	c2eibA_	Alignment	not modelled	32.9	9	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase;

52	c2cjuA	Alignment	not modelled	32.5	9	PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
53	c2hxgB	Alignment	not modelled	32.3	5	PDB header: isomerase Chain: B: PDB Molecule: l-arabinose isomerase; PDBTitle: crystal structure of mn2+ bound ecai
54	d1qzua	Alignment	not modelled	32.3	21	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
55	d1np7a2	Alignment	not modelled	32.0	10	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
56	c5h75B	Alignment	not modelled	31.7	20	PDB header: lyase Chain: B: PDB Molecule: mersacidin decarboxylase,immunoglobulin g-binding protein PDBTitle: crystal structure of the mrsd-protein a fusion protein
57	c4r1oF	Alignment	not modelled	31.7	8	PDB header: isomerase Chain: F: PDB Molecule: l-arabinose isomerase; PDBTitle: crystal structure of thermophilic geobacillus kaustophilus l-arabinose2 isomerase
58	c3fcyB	Alignment	not modelled	31.3	13	PDB header: hydrolase Chain: B: PDB Molecule: xylan esterase 1; PDBTitle: crystal structure of acetyl xylan esterase 1 from2 thermoanaerobacterium sp. jw/sl ys485
59	d1g5qa	Alignment	not modelled	30.7	6	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
60	c1qzuB	Alignment	not modelled	30.2	21	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein mds018; PDBTitle: crystal structure of human phosphopantothenoylcysteine decarboxylase
61	c3mveB	Alignment	not modelled	30.1	21	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
62	d1j20a1	Alignment	not modelled	29.1	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
63	c2yxba	Alignment	not modelled	29.0	11	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	d1mvla	Alignment	not modelled	28.3	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
65	c1mvla	Alignment	not modelled	28.3	12	PDB header: lyase Chain: A: PDB Molecule: ppc decarboxylase athal3a; PDBTitle: ppc decarboxylase mutant c175s
66	d1xrsa	Alignment	not modelled	28.2	13	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: D-lysine 5,6-aminomutase alpha subunit, KamD
67	d1o94c	Alignment	not modelled	26.6	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
68	c2fzvc	Alignment	not modelled	26.5	16	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative arsenical resistance protein; PDBTitle: crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
69	c3vrhA	Alignment	not modelled	26.3	15	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
70	c3urkA	Alignment	not modelled	24.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: isph in complex with propynyl diphosphate (1061)
71	c3ke8A	Alignment	not modelled	24.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: crystal structure of isph:hmbpp-complex
72	d1ni5a1	Alignment	not modelled	24.4	26	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
73	d3clsd1	Alignment	not modelled	24.4	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
74	c2q0xA	Alignment	not modelled	23.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: alpha/beta hydrolase fold protein of unknown function
75	d2j07a2	Alignment	not modelled	22.6	15	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
76	c2j289	Alignment	not modelled	22.5	10	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
77	c2vefB	Alignment	not modelled	22.3	8	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
78	c4n7a	Alignment	not modelled	22.0	13	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase;

78	c81zpa_	Alignment	not modelled	22.0	13	PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
79	d1vlqa_	Alignment	not modelled	20.5	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetyl xylan esterase-like
80	c1o94D_	Alignment	not modelled	20.4	17	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
81	c2nz2A_	Alignment	not modelled	19.6	10	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
82	c5ghaC_	Alignment	not modelled	19.5	12	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
83	d2g0ta1	Alignment	not modelled	18.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
84	c1vl2C_	Alignment	not modelled	18.3	9	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
85	d3clsc1	Alignment	not modelled	18.0	22	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
86	d1to6a_	Alignment	not modelled	17.9	21	Fold: Glycerate kinase I Superfamily: Glycerate kinase I Family: Glycerate kinase I
87	d1p5dx1	Alignment	not modelled	17.6	19	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
88	c3llcA_	Alignment	not modelled	17.2	30	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
89	c1w2wj_	Alignment	not modelled	17.0	9	PDB header: isomerase Chain: J: PDB Molecule: 5-methylthioribose-1-phosphate isomerase; PDBTitle: crystal structure of yeast ypr118w, a methylthioribose-1-phosphate2 isomerase related to regulatory eif2b subunits
90	c3qjgD_	Alignment	not modelled	16.7	13	PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from staphylococcus aureus
91	c3mcuF_	Alignment	not modelled	16.7	22	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
92	c2j4dA_	Alignment	not modelled	16.5	13	PDB header: dna binding protein Chain: A: PDB Molecule: cryptochrome dash; PDBTitle: cryptochrome 3 from arabidopsis thaliana
93	c6jddA_	Alignment	not modelled	16.3	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: cypemycin cysteine dehydrogenase (decarboxylating); PDBTitle: crystal structure of the cypemycin decarboxylase cypd.
94	d2jbwa1	Alignment	not modelled	16.0	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
95	c2qs9A_	Alignment	not modelled	15.9	15	PDB header: structural protein Chain: A: PDB Molecule: retinoblastoma-binding protein 9; PDBTitle: crystal structure of the human retinoblastoma-binding2 protein 9 (rbbp-9). nesg target hr2978
96	d1s5pa_	Alignment	not modelled	15.5	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
97	c3c04A_	Alignment	not modelled	15.4	19	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
98	c4ao6A_	Alignment	not modelled	15.3	14	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: native structure of a novel cold-adapted esterase from an2 arctic intertidal metagenomic library
99	c5gafi_	Alignment	not modelled	15.1	13	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp