






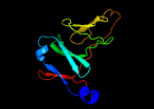



Phyre2

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Description	RVBD3526 (-)_3962618_3963778
Date	Fri Aug 9 18:20:20 BST 2019
Unique Job ID	6ea3a1d5878e5277

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zylA_	Alignment		100.0	100	PDB header: oxidoreductase Chain: A: PDB Molecule: possible oxidoreductase; PDBTitle: crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
2	c4qdfA_	Alignment		100.0	62	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: 3-ketosteroid 9alpha-hydroxylase oxygenase; PDBTitle: crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
3	c4qdfB_	Alignment		100.0	61	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: 3-ketosteroid 9alpha-hydroxylase oxygenase; PDBTitle: crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
4	c3gteB_	Alignment		100.0	17	PDB header: electron transport, oxidoreductase Chain: B: PDB Molecule: ddmc; PDBTitle: crystal structure of dicamba monooxygenase with non-heme iron
5	c3gkqB_	Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: terminal oxygenase component of carbazole 1,9a-dioxygenase; PDBTitle: terminal oxygenase of carbazole 1,9a-dioxygenase from novosphingobium2 sp. ka1
6	c3vcaA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ring-hydroxylating dioxygenase; PDBTitle: quaternary ammonium oxidative demethylation: x-ray crystallographic,2 resonance raman and uv-visible spectroscopic analysis of a rieske-3 type demethylase
7	c2de7B_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: terminal oxygenase component of carbazole; PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
8	c3n0qA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative aromatic-ring hydroxylating dioxygenase; PDBTitle: crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution
9	c3gcfC_	Alignment		100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: terminal oxygenase component of carbazole 1,9a- PDBTitle: terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioides aromaticivorans ic177
10	c1z01D_	Alignment		100.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase PDBTitle: 2-oxoquinoline 8-monooxygenase component: active site modulation by2 rieske-[2fe-2s] center oxidation/reduction
11	c1uljA_	Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: biphenyl dioxygenase large subunit; PDBTitle: biphenyl dioxygenase (bpha1a2) in complex with the substrate

12	c1wqlA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-sulfur protein large subunit of cumene dioxygenase; PDBTitle: cumene dioxygenase (cuma1a2) from pseudomonas fluorescens ip01
13	c2b1xE_	Alignment		100.0	15	PDB header: oxidoreductase Chain: E: PDB Molecule: naphthalene dioxygenase large subunit; PDBTitle: crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp.
14	c2hmnA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: naphthalene 1,2-dioxygenase alpha subunit; PDBTitle: crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene.
15	c2gbxE_	Alignment		100.0	16	PDB header: oxidoreductase Chain: E: PDB Molecule: biphenyl 2,3-dioxygenase alpha subunit; PDBTitle: crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
16	d1wqla1	Alignment		100.0	23	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
17	d1ulia1	Alignment		100.0	18	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
18	d1z0ia1	Alignment		100.0	17	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
19	d2b1xa1	Alignment		100.0	19	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
20	d2de6a1	Alignment		100.0	18	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
21	d1o7na1	Alignment	not modelled	100.0	21	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
22	d2bmoa1	Alignment	not modelled	100.0	20	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
23	c3d89A_	Alignment	not modelled	99.9	20	PDB header: electron transport Chain: A: PDB Molecule: rieske domain-containing protein; PDBTitle: crystal structure of a soluble rieske ferredoxin from mus musculus
24	c2de7E_	Alignment	not modelled	99.9	24	PDB header: oxidoreductase Chain: E: PDB Molecule: ferredoxin component of carbazole; PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
25	c3dqyA_	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene 1,2-dioxygenase system ferredoxin PDBTitle: crystal structure of toluene 2,3-dioxygenase ferredoxin
26	d1fqta_	Alignment	not modelled	99.9	23	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
27	c4aivA_	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nitrite reductase [nad(p)h] small subunit nird; PDBTitle: crystal structure of putative nadh-dependent nitrite reductase small2 subunit from mycobacterium tuberculosis
28	d1vm9a_	Alignment	not modelled	99.9	21	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
						Fold: ISP domain

29	d2jzaa1	Alignment	not modelled	99.9	19	Superfamily: ISP domain Family: NirD-like
30	d3c0da1	Alignment	not modelled	99.9	14	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
31	c3gceA	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin component of carbazole 1,9a- PDBTitle: ferredoxin of carbazole 1,9a-dioxygenase from nocardiooides2 aromaticivorans ic177
32	d2jo6a1	Alignment	not modelled	99.8	16	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
33	c2i7fB	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin component of dioxygenase; PDBTitle: sphingomonas yanoikuyae b1 ferredoxin
34	c2qpzA	Alignment	not modelled	99.8	24	PDB header: metal binding protein Chain: A: PDB Molecule: naphthalene 1,2-dioxygenase system ferredoxin PDBTitle: naphthalene 1,2-dioxygenase rieske ferredoxin
35	c5cxmC	Alignment	not modelled	99.8	18	PDB header: metal binding protein Chain: C: PDB Molecule: cytochrome b6/f complex iron-sulfur subunit; PDBTitle: crystal structure of the cyanobacterial plasma membrane rieske protein2 petc3 from synechocystis pcc 6803
36	d1rfsa	Alignment	not modelled	99.6	16	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
37	d1q90c	Alignment	not modelled	99.6	17	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
38	d3cx5e1	Alignment	not modelled	99.6	20	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
39	c4aayH	Alignment	not modelled	99.5	22	PDB header: oxidoreductase Chain: H: PDB Molecule: arob; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
40	d1g8kb	Alignment	not modelled	99.5	19	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
41	d1riea	Alignment	not modelled	99.5	26	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
42	d2e74d1	Alignment	not modelled	99.4	15	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
43	c2nvgA	Alignment	not modelled	99.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: soluble domain of rieske iron sulfur protein.
44	d1nyka	Alignment	not modelled	99.2	24	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
45	c2e76D	Alignment	not modelled	99.1	15	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
46	c2fyuE	Alignment	not modelled	98.9	21	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
47	c2fynO	Alignment	not modelled	98.9	22	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
48	c1p84E	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
49	d1z01a2	Alignment	not modelled	98.7	11	Fold: TBP-like Superfamily: Bet v1-like Family: Ring hydroxylating alpha subunit catalytic domain
50	d2b1xa2	Alignment	not modelled	98.5	11	Fold: TBP-like Superfamily: Bet v1-like Family: Ring hydroxylating alpha subunit catalytic domain
51	d2bmoa2	Alignment	not modelled	98.4	16	Fold: TBP-like Superfamily: Bet v1-like Family: Ring hydroxylating alpha subunit catalytic domain
52	d1wqla2	Alignment	not modelled	98.3	14	Fold: TBP-like Superfamily: Bet v1-like Family: Ring hydroxylating alpha subunit catalytic domain
53	d1ulia2	Alignment	not modelled	98.3	16	Fold: TBP-like Superfamily: Bet v1-like Family: Ring hydroxylating alpha subunit catalytic domain
54	d1o7na2	Alignment	not modelled	98.2	17	Fold: TBP-like Superfamily: Bet v1-like Family: Ring hydroxylating alpha subunit catalytic domain
						PDB header: electron transport

55	c6hwhB	Alignment	not modelled	97.9	23	Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
56	d1jm1a	Alignment	not modelled	97.7	29	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
57	d2de6a2	Alignment	not modelled	97.5	18	Fold: TBP-like Superfamily: Bet v1-like Family: Ring hydroxylating alpha subunit catalytic domain
58	c6fo2R	Alignment	not modelled	96.4	22	PDB header: membrane protein Chain: R: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: cryoem structure of bovine cytochrome bc1 with no ligand bound
59	c5xyil	Alignment	not modelled	64.1	19	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8; PDBTitle: small subunit of trichomonas vaginalis ribosome
60	c2ba1B	Alignment	not modelled	50.2	17	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
61	c5xxul	Alignment	not modelled	39.4	18	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein es8; PDBTitle: small subunit of toxoplasma gondii ribosome
62	c6oawA	Alignment	not modelled	37.8	20	PDB header: immune system Chain: A: PDB Molecule: wyl1; PDBTitle: crystal structure of a crispr cas-related protein
63	c1dvaX	Alignment	not modelled	36.3	83	PDB header: hydrolase/hydrolase inhibitor Chain: X: PDB Molecule: peptide e-76; PDBTitle: crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
64	c1dvaY	Alignment	not modelled	36.3	83	PDB header: hydrolase/hydrolase inhibitor Chain: Y: PDB Molecule: peptide e-76; PDBTitle: crystal structure of the complex between the peptide exosite inhibitor2 e-76 and coagulation factor viia
65	c3ky7A	Alignment	not modelled	33.7	16	PDB header: transferase Chain: A: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
66	c3j3al	Alignment	not modelled	30.5	24	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8; PDBTitle: structure of the human 40s ribosomal proteins
67	c2z0rA	Alignment	not modelled	29.5	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha0547; PDBTitle: crystal structure of hypothetical protein ttha0547
68	d1p9pa	Alignment	not modelled	26.3	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: tRNA(m1G37)-methyltransferase TrmD
69	c3k2tA	Alignment	not modelled	25.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
70	c2kppA	Alignment	not modelled	25.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0431 protein; PDBTitle: solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
71	c2xzn2	Alignment	not modelled	24.7	21	PDB header: ribosome Chain: 2: PDB Molecule: 40s ribosomal protein s8; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
72	c5x2dA	Alignment	not modelled	23.4	11	PDB header: cell adhesion Chain: A: PDB Molecule: tegumental protein 20.8 kda; PDBTitle: crystal structure of dlc like domain of cstal3 (83-177aa)
73	d1w44a	Alignment	not modelled	22.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
74	c3j20R	Alignment	not modelled	22.6	60	PDB header: ribosome Chain: R: PDB Molecule: 30s ribosomal protein s17p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
75	c3j38I	Alignment	not modelled	22.0	24	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
76	c1ph4A	Alignment	not modelled	21.8	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggtttggcg
77	c1jb7A	Alignment	not modelled	21.8	18	PDB header: dna-binding protein/dna Chain: A: PDB Molecule: telomere-binding protein alpha subunit; PDBTitle: dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
78	c4b6aR	Alignment	not modelled	21.7	8	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l19-b; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
79	c4ifdl	Alignment	not modelled	21.0	16	PDB header: hydrolase/rna Chain: I: PDB Molecule: exosome complex component csl4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
						PDB header: ribosome

80	c3izbP_	Alignment	not modelled	20.5	60	Chain: P; PDB Molecule: 40s ribosomal protein rps11 (s17p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
81	c2w3nA_	Alignment	not modelled	20.2	13	PDB header: lyase Chain: A; PDB Molecule: carbonic anhydrase 2; PDBTitle: structure and inhibition of the co2-sensing carbonic anhydrase can22 from the pathogenic fungus cryptococcus neoformans
82	c3iz6P_	Alignment	not modelled	20.1	60	PDB header: ribosome Chain: P; PDB Molecule: 40s ribosomal protein s11 (s17p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
83	d2ivxa2	Alignment	not modelled	19.7	20	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
84	c4nooA_	Alignment	not modelled	19.6	17	PDB header: immune system Chain: A; PDB Molecule: vgrg protein; PDBTitle: molecular mechanism for self-protection against type vi secretion2 system in vibrio cholerae
85	c6bo0A_	Alignment	not modelled	18.8	0	PDB header: oxidoreductase Chain: A; PDB Molecule: mdba protein; PDBTitle: mdba protein, a thiol-disulfide oxidoreductase from corynebacterium2 matruchotii
86	c6gcsM_	Alignment	not modelled	18.7	25	PDB header: oxidoreductase Chain: M; PDB Molecule: numm subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
87	c3j3aL_	Alignment	not modelled	18.3	60	PDB header: ribosome Chain: L; PDB Molecule: 40s ribosomal protein s11; PDBTitle: structure of the human 40s ribosomal proteins
88	c3u5gL_	Alignment	not modelled	18.1	60	PDB header: ribosome Chain: L; PDB Molecule: 40s ribosomal protein s11-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
89	c3b99B_	Alignment	not modelled	18.0	28	PDB header: isomerase Chain: B; PDB Molecule: prostaglandin i2 synthase; PDBTitle: crystal structure of zebrafish prostacyclin synthase (cytochrome p4502 8a1) in complex with substrate analog u51605
90	c1dfcB_	Alignment	not modelled	17.8	13	PDB header: structural protein Chain: B; PDB Molecule: fascin; PDBTitle: crystal structure of human fascin, an actin-crosslinking protein
91	c3zeyE_	Alignment	not modelled	17.5	60	PDB header: ribosome Chain: E; PDB Molecule: 40s ribosomal proteins s11, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
92	c2c3yA_	Alignment	not modelled	17.5	27	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
93	c5xyiL_	Alignment	not modelled	17.4	60	PDB header: ribosome Chain: L; PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome
94	c3zf7T_	Alignment	not modelled	17.4	8	PDB header: ribosome Chain: T; PDB Molecule: 60s ribosomal protein l19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
95	c2xznoQ_	Alignment	not modelled	17.3	60	PDB header: ribosome Chain: Q; PDB Molecule: ribosomal protein s17 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
96	c4abol_	Alignment	not modelled	16.3	11	PDB header: structural protein Chain: I; PDB Molecule: microtubule integrity protein mal3; PDBTitle: mal3 ch domain homology model and mammalian tubulin (2xrp) docked into2 the 8.6-angstrom cryo-em map of mal3-gtppgamas-microtubules
97	c3j39R_	Alignment	not modelled	15.9	9	PDB header: ribosome Chain: R; PDB Molecule: 60s ribosomal protein l19; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
98	d2c42a2	Alignment	not modelled	15.8	27	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
99	c6b4iD_	Alignment	not modelled	15.4	19	PDB header: transport protein Chain: D; PDB Molecule: nucleoporin like 2; PDBTitle: crystal structure of human gle1 ctd-nup42 gbm-ddx19b(adp) complex