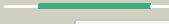

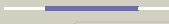
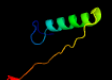
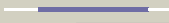
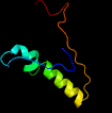

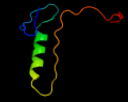

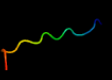

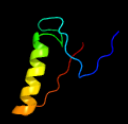
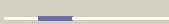




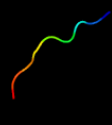






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1508A (-) _1699872_1700234
Date	Fri Aug 2 13:30:09 BST 2019
Unique Job ID	0715edf99f984630

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rfxB_	 Alignment		42.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: uronate dehydrogenase; PDBTitle: crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
2	d1i24a_	 Alignment		16.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
3	c1z7eC_	 Alignment		14.5	17	PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna
4	c1z45A_	 Alignment		14.5	9	PDB header: isomerase Chain: A: PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae3 complexed with nad, udp-glucose, and galactose
5	c6ckgA_	 Alignment		14.4	43	PDB header: transferase Chain: A: PDB Molecule: d-glycerate 3-kinase; PDBTitle: d-glycerate 3-kinase from cryptococcus neoformans var. grubii serotype2 a (h99 / atcc 208821 / cbs 10515 / fgsc 9487)
6	c3ay3C_	 Alignment		11.7	11	PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
7	c1n7gB_	 Alignment		11.1	74	PDB header: lyase Chain: B: PDB Molecule: gdp-d-mannose-4,6-dehydratase; PDBTitle: crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
8	d1lodfa_	 Alignment		9.2	43	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
9	c2z0lA_	 Alignment		8.7	56	PDB header: replication Chain: A: PDB Molecule: early antigen protein d; PDBTitle: crystal structure of ebv-dna polymerase accessory protein2 bmr1
10	c6j9nB_	 Alignment		8.4	56	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: acriic3; PDBTitle: nmehnh+acriic3
11	c6bwcA_	 Alignment		8.1	39	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysaccharide biosynthesis protein capd; PDBTitle: x-ray structure of pen from bacillus thuringiensis

12	c4lk3A_	Alignment		8.0	56	PDB header: lyase Chain: A: PDB Molecule: udp-glucuronic acid decarboxylase 1; PDBTitle: crystal structure of human udp-xylose synthase r236a substitution
13	d1rpna_	Alignment		8.0	72	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
14	c2q1wC_	Alignment		7.8	47	PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
15	c3ha2B_	Alignment		7.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-quinone reductase; PDBTitle: crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
16	d2cuqa1	Alignment		7.3	30	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
17	c5if3B_	Alignment		7.3	44	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: crystal structure of a short-chain dehydrogenase/reductase sdr from2 burkholderia vietnamiensis
18	d1n7ha_	Alignment		7.2	78	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
19	c2qx7A_	Alignment		6.6	39	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
20	c1jmtB_	Alignment		6.6	67	PDB header: rna binding protein Chain: B: PDB Molecule: splicing factor u2af 65 kda subunit; PDBTitle: x-ray structure of a core u2af65/u2af35 heterodimer
21	c2hvpA_	Alignment	not modelled	6.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
22	c2z1mC_	Alignment	not modelled	6.4	83	PDB header: lyase Chain: C: PDB Molecule: gdp-d-mannose dehydratase; PDBTitle: crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
23	c3slgB_	Alignment	not modelled	6.3	44	PDB header: transferase Chain: B: PDB Molecule: pbpg3 protein; PDBTitle: crystal structure of pbpg3 protein from burkholderia pseudomallei
24	c4r1sB_	Alignment	not modelled	6.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: cinnamoyl coa reductase; PDBTitle: crystal structure of petunia hybrida cinnamoyl-coa reductase
25	d1qpma_	Alignment	not modelled	6.1	62	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
26	c4rgiA_	Alignment	not modelled	6.1	60	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ktsc domain protein ypo2434 from yersinia pestis
27	c2iodD_	Alignment	not modelled	6.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydroflavonol 4-reductase; PDBTitle: binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
28	d1db3a_	Alignment	not modelled	6.0	78	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

29	d1gy8a_	Alignment	not modelled	5.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
30	d1rkxa_	Alignment	not modelled	5.9	44	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
31	c2zklA_	Alignment	not modelled	5.6	18	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
32	d1gega_	Alignment	not modelled	5.4	39	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
33	c4fquF_	Alignment	not modelled	5.4	33	PDB header: oxidoreductase Chain: F: PDB Molecule: putative glutathione transferase; PDBTitle: glutathionyl-hydroquinone reductase pcpf of sphingobium2 chlorophenicum
34	d1t2aa_	Alignment	not modelled	5.3	74	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
35	c1t2aC_	Alignment	not modelled	5.3	74	PDB header: structural genomics,lyase Chain: C: PDB Molecule: gdp-mannose 4,6 dehydratase; PDBTitle: crystal structure of human gdp-d-mannose 4,6-dehydratase
36	d1tnsa_	Alignment	not modelled	5.3	46	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
37	c4lvuB_	Alignment	not modelled	5.2	28	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia thailandensis
38	d1sr8a_	Alignment	not modelled	5.2	38	Fold: CbiD-like Superfamily: CbiD-like Family: CbiD-like
39	c3ak4C_	Alignment	not modelled	5.2	26	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-dependent quinuclidinone reductase; PDBTitle: crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
40	c3gquA_	Alignment	not modelled	5.2	36	PDB header: rna binding protein Chain: A: PDB Molecule: nop5p protein; PDBTitle: pyrococcus horikoshii nop5 rna binding domain
41	c6nrcC_	Alignment	not modelled	5.2	32	PDB header: oxidoreductase Chain: C: PDB Molecule: 3-oxoacyl-acyl reductase fabg; PDBTitle: putative short-chain dehydrogenase/reductase (sdr) from acinetobacter2 baumannii
42	c1yvWD_	Alignment	not modelled	5.1	27	PDB header: hydrolase Chain: D: PDB Molecule: phosphoribosyl-atp pyrophosphatase; PDBTitle: crystal structure of phosphoribosyl-atp2 pyrophosphohydrolase from bacillus cereus. nesgc target3 bcr13.
43	d1yvwa1	Alignment	not modelled	5.1	27	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: HisE-like (PRA-PH)