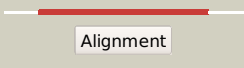

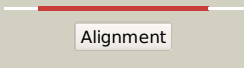

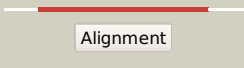

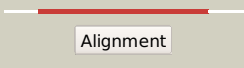

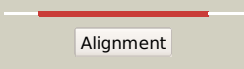

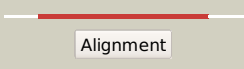

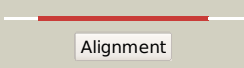
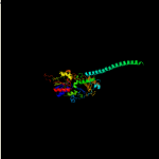
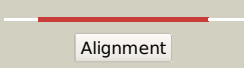
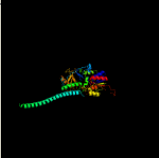
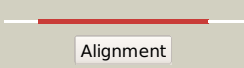

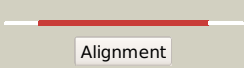

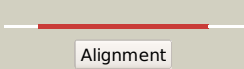








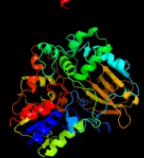



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1432_(-)_1609855_1611276
Date	Wed Jul 31 22:05:54 BST 2019
Unique Job ID	c65667766762aa36

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4repA_</a>			100.0	17	<b>PDB header:</b> oxidoreductase, flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-carotene desaturase; <b>PDBTitle:</b> crystal structure of gamma-carotenoid desaturase
2	<a href="#">c5mogB_</a>			100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-tocopherol methyltransferase; <b>PDBTitle:</b> oryza sativa phytoene desaturase inhibited by norflurazon
3	<a href="#">c1s3bB_</a>			100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase [flavin-containing] b; <b>PDBTitle:</b> crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan
4	<a href="#">c4i58A_</a>			100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexylamine oxidase; <b>PDBTitle:</b> cyclohexylamine oxidase from brevibacterium oxydans ih-35a
5	<a href="#">c3we0A_</a>			100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase/monooxygenase; <b>PDBTitle:</b> l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813
6	<a href="#">c2hkoA_</a>			100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1
7	<a href="#">c2v1dA_</a>			100.0	15	<b>PDB header:</b> oxidoreductase/repressor <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> structural basis of lsd1-corest selectivity in histone h32 recognition
8	<a href="#">c2xagA_</a>			100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
9	<a href="#">c4gutA_</a>			100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1b; <b>PDBTitle:</b> crystal structure of lsd1-npac
10	<a href="#">c4iv9B_</a>			100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan 2-monooxygenase; <b>PDBTitle:</b> structure of the flavoprotein tryptophan-2-monooxygenase
11	<a href="#">c3x0vA_</a>			100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine oxidase; <b>PDBTitle:</b> structure of l-lysine oxidase

12	<a href="#">c3rhaA_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putrescine oxidase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from arthrobacter aurescens
13	<a href="#">c5ttkB_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase; <b>PDBTitle:</b> crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida
14	<a href="#">c2ivdA_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase; <b>PDBTitle:</b> structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
15	<a href="#">c5mbxA_</a>	Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal n(1)-acetyl-spermine/spermidine oxidase; <b>PDBTitle:</b> crystal structure of reduced murine n1-acetylpolyamine oxidase in2 complex with n1-acetylspermine
16	<a href="#">c1f8sA_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
17	<a href="#">c6cr0A_</a>	Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-6-hydroxynicotine oxidase; <b>PDBTitle:</b> 1.55 a resolution structure of (s)-6-hydroxynicotine oxidase from2 shinella hzn7
18	<a href="#">c3bnuA_</a>	Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyamine oxidase fms1; <b>PDBTitle:</b> crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine
19	<a href="#">c2vvlD_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> monoamine oxidase n; <b>PDBTitle:</b> the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
20	<a href="#">c2yg4B_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putrescine oxidase; <b>PDBTitle:</b> structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine
21	<a href="#">c3ka7A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from methanosarcina2 mazi. northeast structural genomics consortium target id3 mar208
22	<a href="#">c1sezA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase, mitochondrial; <b>PDBTitle:</b> crystal structure of protoporphyrinogen ix oxidase
23	<a href="#">c1h83A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyamine oxidase; <b>PDBTitle:</b> structure of polyamine oxidase in complex with2 1,8-diaminooctane
24	<a href="#">c3nksA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase; <b>PDBTitle:</b> structure of human protoporphyrinogen ix oxidase
25	<a href="#">c3k7tB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-hydroxy-l-nicotine oxidase; <b>PDBTitle:</b> crystal structure of apo-form 6-hydroxy-l-nicotine oxidase, crystal2 form p3121
26	<a href="#">c2jb1B_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
27	<a href="#">c4dshB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of reduced udp-galactopyranose mutase
28	<a href="#">c3uteB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex

29	<a href="#">c3i6dA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase; <b>PDBTitle:</b> crystal structure of ppo from bacillus subtilis with af
30	<a href="#">c3lovA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protoporphyrinogen oxidase; <b>PDBTitle:</b> crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution
31	<a href="#">c4dgcA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phytoene dehydrogenase; <b>PDBTitle:</b> crystal structure of phytoene desaturase crti from pantoea ananatis
32	<a href="#">c5g3sB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-tryptophan oxidase vioa; <b>PDBTitle:</b> the structure of the l-tryptophan oxidase vioa from chromobacterium2 violaceum - samarium derivative
33	<a href="#">c1i8tB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> strcuture of udp-galactopyranose mutase from e.coli
34	<a href="#">c2bi8A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad
35	<a href="#">c1txR</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> transferase/protein binding <b>Chain:</b> R: <b>PDB Molecule:</b> rab escort protein 1; <b>PDBTitle:</b> structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid
36	<a href="#">c2yr6A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pro-enzyme of l-phenylalanine oxidase; <b>PDBTitle:</b> crystal structure of l-phenylalanine oxidase from psuedomonas sp.p501
37	<a href="#">c1v0jB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> udp-galactopyranose mutase from mycobacterium tuberculosis
38	<a href="#">c3hdql</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> I: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate
39	<a href="#">c4mo2A</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of udp-n-acetylgalactopyranose mutase from2 campylobacter jejuni
40	<a href="#">c2b9yA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminooxidase; <b>PDBTitle:</b> crystal structure of cla-producing fatty acid isomerase2 from p. acnes
41	<a href="#">d1o5wa1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
42	<a href="#">d2dw4a2</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
43	<a href="#">c3nrrA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf1083; <b>PDBTitle:</b> crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223
44	<a href="#">d2v5za1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
45	<a href="#">c6fjhB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> lkce; <b>PDBTitle:</b> crystal structure of the seleniated lkce from streptomyces rochei
46	<a href="#">c6c87A</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> rab gdp dissociation inhibitor alpha; <b>PDBTitle:</b> crystal structure of rab gdp dissociation inhibitor alpha from2 naegleria fowleri
47	<a href="#">d1reoal</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
48	<a href="#">d2iida1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
49	<a href="#">c1gndA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> gtpase activation <b>Chain:</b> A: <b>PDB Molecule:</b> guanine nucleotide dissociation inhibitor; <b>PDBTitle:</b> guanine nucleotide dissociation inhibitor, alpha-isoform
50	<a href="#">c3cpiH</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> rab gdp-dissociation inhibitor; <b>PDBTitle:</b> crystal structure of yeast rab-gdi
51	<a href="#">c3qj4A</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renalase; <b>PDBTitle:</b> crystal structure of human renalase (isoform 1)
52	<a href="#">d1b5qa1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
53	<a href="#">c2e1mA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
54	<a href="#">d1d5ta1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
55	<a href="#">c2p1wA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> rabgdi protein;

55	<a href="#">c3p1wA</a>	Alignment	not modelled	99.8	13	<b>PDBTitle:</b> crystal structure of rab gdi from plasmodium falciparum, pfl2060c
56	<a href="#">d1vg0a1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
57	<a href="#">d2bcgg1</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
58	<a href="#">c3nlcA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein vp0956; <b>PDBTitle:</b> crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
59	<a href="#">d1seza1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
60	<a href="#">c1yvvB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase, flavin-containing; <b>PDBTitle:</b> x-ray structure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
61	<a href="#">d1i8ta1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
62	<a href="#">d2ivda1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
63	<a href="#">d2bi7a1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
64	<a href="#">c1coyA</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> oxidoreductase(oxygen receptor) <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> crystal structure of cholesterol oxidase complexed with a steroid2 substrate. implications for fad dependent alcohol oxidases
65	<a href="#">c4ia6B</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> myosin-crossreactive antigen; <b>PDBTitle:</b> hydratase from lactobacillus acidophilus in a ligand bound form (la2 lah)
66	<a href="#">c6a2uD</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> signaling protein/oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glucose dehydrogenase; <b>PDBTitle:</b> crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
67	<a href="#">c2gewA</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cholesterol oxidase; <b>PDBTitle:</b> atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
68	<a href="#">c1pj6A</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethylglycine oxidase; <b>PDBTitle:</b> crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
69	<a href="#">c3axbA</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix
70	<a href="#">c4xwzA</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl amine:oxygen oxidoreductase; <b>PDBTitle:</b> the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadoriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine
71	<a href="#">c3atrA</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved archaeal protein; <b>PDBTitle:</b> geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
72	<a href="#">c3djeA</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl amine: oxygen oxidoreductase; <b>PDBTitle:</b> crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
73	<a href="#">c2i0zA</a>	Alignment	not modelled	99.2	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(fad)-utilizing dehydrogenases; <b>PDBTitle:</b> crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases
74	<a href="#">c5twcA</a>	Alignment	not modelled	99.2	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> oxidoreductase iruo in the oxidized form
75	<a href="#">c4cnjD</a>	Alignment	not modelled	99.2	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> l-aminoacetone oxidase from streptococcus oligofermentans2 belongs to a new 3-domain family of bacterial flavoproteins
76	<a href="#">c2eq7B</a>	Alignment	not modelled	99.2	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e3 component; <b>PDBTitle:</b> crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
77	<a href="#">c4at2A</a>	Alignment	not modelled	99.2	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketosteroid-delta4-5alpha-dehydrogenase; <b>PDBTitle:</b> the crystal structure of 3-ketosteroid-delta4-(5alpha)-2 dehydrogenase from rhodococcus jostii rha1 in complex3 with 4-androstene-3,17- dione
78	<a href="#">c1ps9A</a>	Alignment	not modelled	99.2	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
79	<a href="#">c2gqfA</a>	Alignment	not modelled	99.2	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hi0933; <b>PDBTitle:</b> crystal structure of flavoprotein hi0933 from haemophilus

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80	<a href="#">c3ab1B_</a>	Alignment	not modelled	99.2	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin nadp+ oxidoreductase
81	<a href="#">c1ojtA_</a>	Alignment	not modelled	99.2	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
82	<a href="#">c2c3dB_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxopropyl-com reductase; <b>PDBTitle:</b> 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
83	<a href="#">c3urhB_</a>	Alignment	not modelled	99.1	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
84	<a href="#">c5nmwA_</a>	Alignment	not modelled	99.1	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
85	<a href="#">c2qaeA_</a>	Alignment	not modelled	99.1	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
86	<a href="#">c2q0lA_</a>	Alignment	not modelled	99.1	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
87	<a href="#">d2bs2a2</a>	Alignment	not modelled	99.1	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
88	<a href="#">c1dxlC_</a>	Alignment	not modelled	99.1	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
89	<a href="#">c5odhG_</a>	Alignment	not modelled	99.1	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> heterodisulfide reductase, subunit a; <b>PDBTitle:</b> heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes
90	<a href="#">c4usqA_</a>	Alignment	not modelled	99.1	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of flavin-containing monooxygenase from2 cellvibrio sp. br
91	<a href="#">c3l8kB_</a>	Alignment	not modelled	99.1	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoyl dehydrogenase from sulfolobus2 solfataricus
92	<a href="#">c1xdiA_</a>	Alignment	not modelled	99.1	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rv3303c-lpda; <b>PDBTitle:</b> crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
93	<a href="#">c4jdrB_</a>	Alignment	not modelled	99.1	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli
94	<a href="#">d2i0za1</a>	Alignment	not modelled	99.1	38	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
95	<a href="#">c6garB_</a>	Alignment	not modelled	99.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
96	<a href="#">c1zmcG_</a>	Alignment	not modelled	99.1	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
97	<a href="#">c4usrA_</a>	Alignment	not modelled	99.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> structure of flavin-containing monooxygenase from2 pseudomonas stutzeri nf13
98	<a href="#">c1x31A_</a>	Alignment	not modelled	99.1	49	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcosine oxidase alpha subunit; <b>PDBTitle:</b> crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
99	<a href="#">c4c3yF_</a>	Alignment	not modelled	99.1	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 3-ketosteroid dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-ketosteroid delta1-dehydrogenase from2 rhodococcus erythropolis sq1 in complex with 1,4-androstadiene-3,17-3 dione
100	<a href="#">c5fjnB_</a>	Alignment	not modelled	99.1	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid deaminase; <b>PDBTitle:</b> structure of l-amino acid deaminase from proteus myxofaciens2 in complex with anthranilate
101	<a href="#">c2a87A_</a>	Alignment	not modelled	99.1	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of m. tuberculosis thioredoxin reductase
102	<a href="#">c2gmhA_</a>	Alignment	not modelled	99.1	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein-ubiquinone <b>PDBTitle:</b> structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
103	<a href="#">d3coxa1</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
104	<a href="#">c3v76A_</a>	Alignment	not modelled	99.1	29	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> flavoprotein; <b>PDBTitle:</b> the crystal structure of a flavoprotein from sinorhizobium



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105	<a href="#">c3jskN_</a>	Alignment	not modelled	99.1	44	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> N: <b>PDB Molecule:</b> cypbp37 protein; <b>PDBTitle:</b> thiazole synthase from neurospora crassa
106	<a href="#">c1v59B_</a>	Alignment	not modelled	99.1	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
107	<a href="#">c5xhuA_</a>	Alignment	not modelled	99.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ycgf from bacillus subtilis
108	<a href="#">c4jnaA_</a>	Alignment	not modelled	99.1	29	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> deph; <b>PDBTitle:</b> crystal structure of the deph complex with dimethyl-fk228
109	<a href="#">c4b1bB_</a>	Alignment	not modelled	99.1	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom
110	<a href="#">c4a9wB_</a>	Alignment	not modelled	99.1	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> flavin-containing monooxygenase from stentrophomonas maltophilia
111	<a href="#">c1djnB_</a>	Alignment	not modelled	99.1	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
112	<a href="#">c6de6B_</a>	Alignment	not modelled	99.1	49	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> 2.1 a resolution structure of histamine dehydrogenase from rhizobium2 sp. 4-9
113	<a href="#">c5hxfF_</a>	Alignment	not modelled	99.1	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> l-amino acid deaminase; <b>PDBTitle:</b> l-amino acid deaminase from proteus vulgaris
114	<a href="#">c6qkgB_</a>	Alignment	not modelled	99.1	45	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
115	<a href="#">c3lzxB_</a>	Alignment	not modelled	99.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase 2; <b>PDBTitle:</b> crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
116	<a href="#">c3fbsB_</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
117	<a href="#">d1neka2</a>	Alignment	not modelled	99.1	30	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
118	<a href="#">c1zkgA_</a>	Alignment	not modelled	99.1	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of mouse thioredoxin reductase type 2
119	<a href="#">c3dqzA_</a>	Alignment	not modelled	99.1	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
120	<a href="#">c5glgA_</a>	Alignment	not modelled	99.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase 2; <b>PDBTitle:</b> the novel function of osm1 under anaerobic condition in the er was2 revealed by crystal structure of osm1, a soluble fumarate reductase3 in yeast