


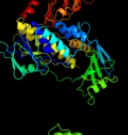

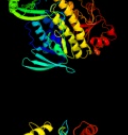



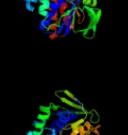












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2qa2A_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide oxygenase cab; <b>PDBTitle:</b> crystal structure of cab, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
2	<a href="#">c1pn0A_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenol 2-monooxygenase; <b>PDBTitle:</b> phenol hydroxylase from trichosporon cutaneum
3	<a href="#">c3fmwC_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxygenase; <b>PDBTitle:</b> the crystal structure of mtmoiv, a baeyer-villiger2 monooxygenase from the mithramycin biosynthetic pathway in3 streptomyces argillaceus.
4	<a href="#">c2dkhA_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxybenzoate hydroxylase; <b>PDBTitle:</b> crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate
5	<a href="#">c3ihgA_</a>	Alignment		100.0	23	<b>PDB header:</b> flavoprotein, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rdme; <b>PDBTitle:</b> crystal structure of a ternary complex of aklavinone-112 hydroxylase with fad and aklavinone
6	<a href="#">c2r0gB_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> reb; <b>PDBTitle:</b> chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
7	<a href="#">c1phhA_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> p-hydroxybenzoate hydroxylase; <b>PDBTitle:</b> crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate
8	<a href="#">c2bryA_</a>	Alignment		100.0	17	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> nedd9 interacting protein with calponin homology <b>PDBTitle:</b> crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
9	<a href="#">c3e1tA_</a>	Alignment		100.0	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> halogenase; <b>PDBTitle:</b> structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases
10	<a href="#">c2rgjA_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> crystal structure of flavin-containing monooxygenase phzs
11	<a href="#">d1k0ia1</a>	Alignment		100.0	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

12	<a href="#">c3nixF</a>	Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> flavoprotein/dehydrogenase; <b>PDBTitle:</b> crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43.
13	<a href="#">c3i3lA</a>	Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkylhalidase cmls; <b>PDBTitle:</b> crystal structure of cmls, a flavin-dependent halogenase
14	<a href="#">c3gmbB</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-methyl-3-hydroxypyridine-5-carboxylic acid <b>PDBTitle:</b> crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic2 acid oxygenase
15	<a href="#">c3allA</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; <b>PDBTitle:</b> crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
16	<a href="#">c2x3nA</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable fad-dependent monooxygenase; <b>PDBTitle:</b> crystal structure of pqsI, a probable fad-dependent2 monooxygenase from pseudomonas aeruginosa
17	<a href="#">d1pn0a1</a>	Alignment		100.0	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
18	<a href="#">d3c96a1</a>	Alignment		100.0	25	<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
19	<a href="#">c3c4aA</a>	Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tryptophan hydroxylase viod; <b>PDBTitle:</b> crystal structure of viod hydroxylase in complex with fad2 from chromobacterium violaceum. northeast structural3 genomics consortium target cvr158
20	<a href="#">c2xdoC</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetx2 protein; <b>PDBTitle:</b> structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
21	<a href="#">c3cgvA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> geranylgeranyl reductase related protein; <b>PDBTitle:</b> crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution
22	<a href="#">c2vouA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,6-dihydroxypyridine hydroxylase; <b>PDBTitle:</b> structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
23	<a href="#">c3atrA</a>	Alignment	not modelled	100.0	15	<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
24	<a href="#">c3ihmB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> styrene monooxygenase a; <b>PDBTitle:</b> structure of the oxygenase component of a pseudomonas styrene2 monooxygenase
25	<a href="#">d2voua1</a>	Alignment	not modelled	100.0	25	<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
26	<a href="#">c2ardA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase prna; <b>PDBTitle:</b> the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
27	<a href="#">c2pyxA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> crystal structure of tryptophan halogenase (yp_750003.1) from2 shewanella frigidimarina ncimb 400 at 1.50 a resolution
28	<a href="#">c2weuD</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> antifungal protein <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan 5-halogenase; <b>PDBTitle:</b> crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan

29	<a href="#">c2e4gB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> biosynthetic protein, flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> rebh with bound l-trp
30	<a href="#">d2gmha1</a>	Alignment	not modelled	100.0	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
31	<a href="#">c2gmhA_</a>	Alignment	not modelled	100.0	13	<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
32	<a href="#">c3nrnA_</a>	Alignment	not modelled	99.9	16	<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
33	<a href="#">c1yvVB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine oxidase, flavin-containing; <b>PDBTitle:</b> x-ray structurure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
34	<a href="#">c3nyeA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-arginine dehydrogenase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
35	<a href="#">c3da1A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
36	<a href="#">c1y56B_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sarcosine oxidase; <b>PDBTitle:</b> crystal structure of l-proline dehydrogenase from p.horikoshii
37	<a href="#">c3qj4A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renalase; <b>PDBTitle:</b> crystal structure of human renalase (isoform 1)
38	<a href="#">d2ivda1</a>	Alignment	not modelled	99.6	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
39	<a href="#">c3ka7A_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from methanosarcina2 mazel. northeast structural genomics consortium target id3 mar208
40	<a href="#">c1ryiB_</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycine oxidase; <b>PDBTitle:</b> structure of glycine oxidase with bound inhibitor glycolate
41	<a href="#">d1reoa1</a>	Alignment	not modelled	99.5	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
42	<a href="#">d2gqfa1</a>	Alignment	not modelled	99.5	19	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
43	<a href="#">c2gahB_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> heterotetrameric sarcosine oxidase beta-subunit; <b>PDBTitle:</b> heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution
44	<a href="#">c1ltxR_</a>	Alignment	not modelled	99.5	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 rab2 geranylgeranyl transferase and isoprenoid
45	<a href="#">c3bhkA_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monomeric sarcosine oxidase; <b>PDBTitle:</b> crystal structure of r49k mutant of monomeric sarcosine oxidase2 crystallized in phosphate as precipitant
46	<a href="#">c2olnA_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nikd protein; <b>PDBTitle:</b> nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution
47	<a href="#">c2r4iA_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aerobic glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
48	<a href="#">c2vvlD_</a>	Alignment	not modelled	99.5	11	<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.
49	<a href="#">d1b5qa1</a>	Alignment	not modelled	99.4	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
50	<a href="#">c3dmeB_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved exported protein; <b>PDBTitle:</b> crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141
51	<a href="#">c3ps9A_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna 5-methylaminomethyl-2-thiouridine biosynthesis <b>PDBTitle:</b> crystal structure of mnmC from e. coli
52	<a href="#">c2q7vA_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans thioredoxin2 reductase
53	<a href="#">c3i6dA_</a>	Alignment	not modelled	99.4	13	<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

54	<a href="#">d2iida1</a>	Alignment	not modelled	99.4	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
55	<a href="#">c3f8rD_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase (trxb-3); <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
56	<a href="#">c3ab1B_</a>	Alignment	not modelled	99.4	14	<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
57	<a href="#">c2ivdA_</a>	Alignment	not modelled	99.4	15	<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
58	<a href="#">d1jnra2</a>	Alignment	not modelled	99.4	13	<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
59	<a href="#">d1pn0a2</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
60	<a href="#">c1pj6A_</a>	Alignment	not modelled	99.4	14	<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
61	<a href="#">d1w4xa1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
62	<a href="#">d1kf6a2</a>	Alignment	not modelled	99.4	15	<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
63	<a href="#">c3djeA_</a>	Alignment	not modelled	99.4	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
64	<a href="#">c3pvcA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna 5-methylaminomethyl-2-thiouridine biosynthesis <b>PDBTitle:</b> crystal structure of apo mnmC from yersinia pestis
65	<a href="#">c2zxiC_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> fad-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> structure of aquifex aeolicus gida in the form ii crystal
66	<a href="#">c3cesB_</a>	Alignment	not modelled	99.3	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of e.coli mnmG (gida), a highly-conserved trna2 modifying enzyme
67	<a href="#">c2rgoA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
68	<a href="#">d2bs2a2</a>	Alignment	not modelled	99.3	16	<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
69	<a href="#">c3k7tB_</a>	Alignment	not modelled	99.3	13	<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,2 crystal form p3121
70	<a href="#">c3jskN_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> N: <b>PDB Molecule:</b> cybbp37 protein; <b>PDBTitle:</b> thiazole synthase from neurospora crassa
71	<a href="#">d2i0za1</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
72	<a href="#">d1neka2</a>	Alignment	not modelled	99.3	11	<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
73	<a href="#">c1s3bB_</a>	Alignment	not modelled	99.3	16	<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
74	<a href="#">d1qo8a2</a>	Alignment	not modelled	99.3	15	<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
75	<a href="#">d1rp0a1</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Thi4-like
76	<a href="#">c1f8sA_</a>	Alignment	not modelled	99.3	15	<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.
77	<a href="#">c1c0ia_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-amino acid oxidase; <b>PDBTitle:</b> crystal structure of d-amino acid oxidase in complex with2 two anthranilate molecules
78	<a href="#">c2rghA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase

79	<a href="#">c2zbwA</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
80	<a href="#">c3g05B</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of n-terminal domain (2-550) of e.coli mnmg
81	<a href="#">c1yq4A</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> avian respiratory complex ii with 3-nitropropionate and ubiquinone
82	<a href="#">c3dgzA</a>	Alignment	not modelled	99.2	14	<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
83	<a href="#">c3lzxB</a>	Alignment	not modelled	99.2	17	<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)
84	<a href="#">c3cp8C</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from chlorobium tepidum
85	<a href="#">c3h8lA</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> the first x-ray structure of a sulfide:quinone2 oxidoreductase: insights into sulfide oxidation mechanism
86	<a href="#">d1ryia1</a>	Alignment	not modelled	99.2	13	<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
87	<a href="#">d1y0pa2</a>	Alignment	not modelled	99.2	18	<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="#">c1zkqA</a>	Alignment	not modelled	99.2	14	<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
89	<a href="#">c1d4cB</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c fumarate reductase; <b>PDBTitle:</b> crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
90	<a href="#">c1jrxA</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c; <b>PDBTitle:</b> crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
91	<a href="#">c1f6mF</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
92	<a href="#">d2gf3a1</a>	Alignment	not modelled	99.2	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
93	<a href="#">d1d4ca2</a>	Alignment	not modelled	99.2	14	<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
94	<a href="#">c3gwdA</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase; <b>PDBTitle:</b> closed crystal structure of cyclohexanone monooxygenase
95	<a href="#">d1pj5a2</a>	Alignment	not modelled	99.2	16	<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
96	<a href="#">c2acza</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
97	<a href="#">c1qo8A</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c3 fumarate reductase; <b>PDBTitle:</b> the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
98	<a href="#">c1sezA</a>	Alignment	not modelled	99.1	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
99	<a href="#">d1o5wa1</a>	Alignment	not modelled	99.1	23	<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
100	<a href="#">c3lovA</a>	Alignment	not modelled	99.1	16	<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
101	<a href="#">c1w4xA</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> oxygenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetone monooxygenase; <b>PDBTitle:</b> phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
102	<a href="#">c3p4rM</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit; <b>PDBTitle:</b> crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
103	<a href="#">d2gjc1</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Thi4-like

104	<a href="#">c1kf6A_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase flavoprotein; <b>PDBTitle:</b> e. coli quinol-fumarate reductase with bound inhibitor hqno
105	<a href="#">d2qv8a1</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
106	<a href="#">c1hyuA_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf
107	<a href="#">c1x31A_</a>	Alignment	not modelled	99.0	18	<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
108	<a href="#">c3nlcA_</a>	Alignment	not modelled	99.0	14	<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
109	<a href="#">c2a87A_</a>	Alignment	not modelled	99.0	10	<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
110	<a href="#">c2bs3A_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinol-fumarate reductase flavoprotein subunit a; <b>PDBTitle:</b> glu c180 -> gln variant quinol:fumarate reductase from2 wollinella succinogenes
111	<a href="#">c2uzzD_</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> n-methyl-l-tryptophan oxidase; <b>PDBTitle:</b> x-ray structure of n-methyl-l-tryptophan oxidase (mtox)
112	<a href="#">d1chua2</a>	Alignment	not modelled	98.9	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
113	<a href="#">c2gqfA_</a>	Alignment	not modelled	98.9	15	<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 influenzae2 rd
114	<a href="#">c1vqwB_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein with similarity to flavin-containing <b>PDBTitle:</b> crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
115	<a href="#">c2nvkX_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from drosophila2 melanogaster
116	<a href="#">c3rhaA_</a>	Alignment	not modelled	98.9	31	<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 aureus
117	<a href="#">c1ojtA_</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
118	<a href="#">c2yg4B_</a>	Alignment	not modelled	98.9	36	<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
119	<a href="#">c3urhB_</a>	Alignment	not modelled	98.9	17	<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
120	<a href="#">d2bcgg1</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain