



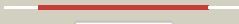









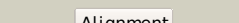

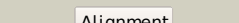



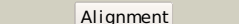


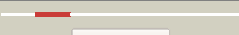
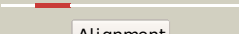
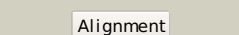

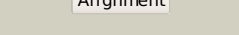
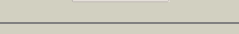

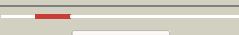
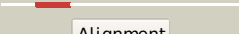
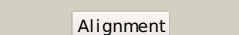

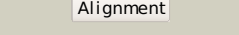
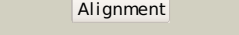

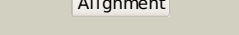
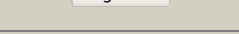
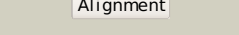

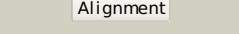
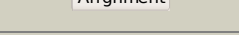
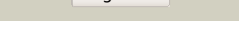



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1i8tB_</a>	 Alignment		100.0	100	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> strcuture of udp-galactopyranose mutase from e.coli
2	<a href="#">c1v0jB_</a>	 Alignment		100.0	43	<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
3	<a href="#">c2bi8A_</a>	 Alignment		100.0	37	<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 with2 reduced fad
4	<a href="#">c3hdql_</a>	 Alignment		100.0	37	<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
5	<a href="#">d1i8ta1</a>	 Alignment		100.0	100	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
6	<a href="#">d2bi7a1</a>	 Alignment		100.0	36	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
7	<a href="#">c2ivdA_</a>	 Alignment		100.0	12	<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
8	<a href="#">c1s3bB_</a>	 Alignment		100.0	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
9	<a href="#">c3lovA_</a>	 Alignment		100.0	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
10	<a href="#">c3nksA_</a>	 Alignment		100.0	12	<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
11	<a href="#">c1sezA_</a>	 Alignment		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

12	<a href="#">c3k7tB_</a>	Alignment		100.0	15	<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
13	<a href="#">c3i6dA_</a>	Alignment		100.0	18	<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
14	<a href="#">c2hkoA_</a>	Alignment		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
15	<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.
16	<a href="#">c2v1dA_</a>	Alignment		100.0	18	<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
17	<a href="#">c2xagA_</a>	Alignment		100.0	18	<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
18	<a href="#">c1f8sA_</a>	Alignment		100.0	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.
19	<a href="#">c3rhaA_</a>	Alignment		100.0	13	<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
20	<a href="#">c2yg4B_</a>	Alignment		100.0	14	<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="#">c2yr6A_</a>	Alignment	not modelled	100.0	13	<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
22	<a href="#">c3bnuA_</a>	Alignment	not modelled	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
23	<a href="#">d1o5wa1</a>	Alignment	not modelled	100.0	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
24	<a href="#">c2b9yA_</a>	Alignment	not modelled	100.0	12	<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
25	<a href="#">c2jb1B_</a>	Alignment	not modelled	100.0	18	<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
26	<a href="#">c1h83A_</a>	Alignment	not modelled	100.0	13	<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
27	<a href="#">d2v5za1</a>	Alignment	not modelled	100.0	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
28	<a href="#">c3ka7A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium

					target id3 mar208
29	<a href="#">d2dw4a2</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
30	<a href="#">c1ltxR</a>	Alignment	not modelled	100.0	15 <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
31	<a href="#">d2ivda1</a>	Alignment	not modelled	99.9	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
32	<a href="#">c3cpiH</a>	Alignment	not modelled	99.9	13 <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
33	<a href="#">d1b5qa1</a>	Alignment	not modelled	99.9	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
34	<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
35	<a href="#">d2iida1</a>	Alignment	not modelled	99.9	18 <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
36	<a href="#">d1reoa1</a>	Alignment	not modelled	99.9	18 <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
37	<a href="#">d1seza1</a>	Alignment	not modelled	99.9	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
38	<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
39	<a href="#">c3p1wA</a>	Alignment	not modelled	99.9	14 <b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> rabgdi protein; <b>PDBTitle:</b> crystal structure of rab gdi from plasmodium falciparum, pfl2060c
40	<a href="#">d1d5ta1</a>	Alignment	not modelled	99.9	12 <b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
41	<a href="#">c2elmA</a>	Alignment	not modelled	99.9	17 <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
42	<a href="#">d2bcggl</a>	Alignment	not modelled	99.9	17 <b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
43	<a href="#">d1vg0a1</a>	Alignment	not modelled	99.9	16 <b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GDI-like N domain
44	<a href="#">c3qj4A</a>	Alignment	not modelled	99.9	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> renalase; <b>PDBTitle:</b> crystal structure of human renalase (isoform 1)
45	<a href="#">c1yvvB</a>	Alignment	not modelled	99.8	15 <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.
46	<a href="#">c2eq7B</a>	Alignment	not modelled	99.5	40 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e3 component; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
47	<a href="#">c2q0lA</a>	Alignment	not modelled	99.4	25 <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+
48	<a href="#">c3ab1B</a>	Alignment	not modelled	99.4	30 <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
49	<a href="#">c1ndaD</a>	Alignment	not modelled	99.3	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> trypanothione oxidoreductase; <b>PDBTitle:</b> the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
50	<a href="#">c3urhB</a>	Alignment	not modelled	99.3	49 <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
51	<a href="#">c1ojtA</a>	Alignment	not modelled	99.3	28 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
52	<a href="#">c2gqfA</a>	Alignment	not modelled	99.3	38 <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
53	<a href="#">c2qaeA</a>	Alignment	not modelled	99.3	33 <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
54	<a href="#">c2i0za</a>	Alignment	not modelled	99.3	31 <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

55	<a href="#">c2c3dB</a>	 Alignment	not modelled	99.3	26	<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
56	<a href="#">c1ps9A</a>	 Alignment	not modelled	99.3	23	<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 2,4-2 dienoyl coa reductase
57	<a href="#">c3l8kB</a>	 Alignment	not modelled	99.3	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus
58	<a href="#">c2a87A</a>	 Alignment	not modelled	99.3	28	<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
59	<a href="#">c1dxC</a>	 Alignment	not modelled	99.3	38	<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
60	<a href="#">c3lzxB</a>	 Alignment	not modelled	99.3	32	<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)
61	<a href="#">c1v59B</a>	 Alignment	not modelled	99.3	33	<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+
62	<a href="#">c1zmcG</a>	 Alignment	not modelled	99.3	36	<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+
63	<a href="#">d2i0za1</a>	 Alignment	not modelled	99.3	32	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
64	<a href="#">c2gmhA</a>	 Alignment	not modelled	99.2	37	<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
65	<a href="#">c2nvkX</a>	 Alignment	not modelled	99.2	24	<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
66	<a href="#">c1zkqA</a>	 Alignment	not modelled	99.2	30	<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
67	<a href="#">c3dgzA</a>	 Alignment	not modelled	99.2	30	<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
68	<a href="#">c3o0hA</a>	 Alignment	not modelled	99.2	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase from bartonella henselae
69	<a href="#">c3fbsB</a>	 Alignment	not modelled	99.2	26	<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
70	<a href="#">c2w0hA</a>	 Alignment	not modelled	99.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase; <b>PDBTitle:</b> x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
71	<a href="#">c3nlcA</a>	 Alignment	not modelled	99.2	16	<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
72	<a href="#">d1v59a1</a>	 Alignment	not modelled	99.2	33	<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
73	<a href="#">d1onfa1</a>	 Alignment	not modelled	99.2	33	<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
74	<a href="#">c3r9uA</a>	 Alignment	not modelled	99.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> thioredoxin-disulfide reductase from campylobacter jejuni.
75	<a href="#">c3cgvA</a>	 Alignment	not modelled	99.2	41	<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
76	<a href="#">d1dxla1</a>	 Alignment	not modelled	99.2	38	<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
77	<a href="#">c1onfA</a>	 Alignment	not modelled	99.2	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glutathione reductase
78	<a href="#">c1zx9A</a>	 Alignment	not modelled	99.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
79	<a href="#">c1djnB</a>	 Alignment	not modelled	99.2	29	<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)
80	<a href="#">c1lpfB</a>	Alignment	not modelled	99.2	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
81	<a href="#">d1ojta1</a>	Alignment	not modelled	99.2	28	<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
82	<a href="#">c1geuA</a>	Alignment	not modelled	99.2	32	<b>PDB header:</b> oxidoreductase(flavoenzyme) <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> anatomy of an engineered nad-binding site
83	<a href="#">c2x3nA</a>	Alignment	not modelled	99.2	32	<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
84	<a href="#">d1neka2</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> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
85	<a href="#">c3k30B</a>	Alignment	not modelled	99.2	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from nocardioles simplex
86	<a href="#">c2hqmB</a>	Alignment	not modelled	99.2	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
87	<a href="#">d2gf3a1</a>	Alignment	not modelled	99.2	29	<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
88	<a href="#">c1xdiA</a>	Alignment	not modelled	99.2	23	<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
89	<a href="#">d1w4xa1</a>	Alignment	not modelled	99.2	35	<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
90	<a href="#">c3dmeB</a>	Alignment	not modelled	99.2	35	<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
91	<a href="#">c2olnA</a>	Alignment	not modelled	99.2	30	<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
92	<a href="#">c3jskN</a>	Alignment	not modelled	99.2	29	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> N: <b>PDB Molecule:</b> cypbp37 protein; <b>PDBTitle:</b> thiazole synthase from neurospora crassa
93	<a href="#">d1ryia1</a>	Alignment	not modelled	99.2	29	<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
94	<a href="#">c1ebdB</a>	Alignment	not modelled	99.2	34	<b>PDB header:</b> complex (oxidoreductase/transferase) <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
95	<a href="#">c2zbwA</a>	Alignment	not modelled	99.2	22	<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
96	<a href="#">d1qo8a2</a>	Alignment	not modelled	99.2	27	<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
97	<a href="#">d3lada1</a>	Alignment	not modelled	99.2	33	<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
98	<a href="#">c1tytA</a>	Alignment	not modelled	99.2	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase, oxidized form; <b>PDBTitle:</b> crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
99	<a href="#">c3bhkA</a>	Alignment	not modelled	99.1	27	<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
100	<a href="#">c3ctyA</a>	Alignment	not modelled	99.1	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of t. acidophilum thioredoxin reductase
101	<a href="#">c2a8xA</a>	Alignment	not modelled	99.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
102	<a href="#">c2eq8E</a>	Alignment	not modelled	99.1	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
103	<a href="#">d1y0pa2</a>	Alignment	not modelled	99.1	41	<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
104	<a href="#">d1djqa3</a>	Alignment	not modelled	99.1	29	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
105	<a href="#">c1x31A</a>	Alignment	not modelled	99.1	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcosine oxidase alpha subunit;



105	<a href="#">c1x31A_</a>	Alignment	not modelled	99.1	28	<b>PDBTitle:</b> crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
106	<a href="#">c2r9zB_</a>	Alignment	not modelled	99.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione amide reductase; <b>PDBTitle:</b> glutathione amide reductase from chromatium gracile
107	<a href="#">c1f6mF_</a>	Alignment	not modelled	99.1	24	<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+
108	<a href="#">c2cfyB_</a>	Alignment	not modelled	99.1	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of human thioredoxin reductase 1
109	<a href="#">c3e1tA_</a>	Alignment	not modelled	99.1	23	<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
110	<a href="#">c2vdcl_</a>	Alignment	not modelled	99.1	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
111	<a href="#">d1lpfa1</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> FAD/NAD-linked reductases, N-terminal and central domains
112	<a href="#">d2bs2a2</a>	Alignment	not modelled	99.1	19	<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="#">c3d1cA_</a>	Alignment	not modelled	99.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing putative monooxygenase; <b>PDBTitle:</b> crystal structure of flavin-containing putative monooxygenase2 (np_373108.1) from staphylococcus aureus mu50 at 2.40 a resolution
114	<a href="#">c3ic9D_</a>	Alignment	not modelled	99.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
115	<a href="#">c2xdoC_</a>	Alignment	not modelled	99.1	26	<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
116	<a href="#">c1w4xA_</a>	Alignment	not modelled	99.1	35	<b>PDB header:</b> oxygenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetone monooxygenase; <b>PDBTitle:</b> phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
117	<a href="#">c2ywlA_</a>	Alignment	not modelled	99.1	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase related protein; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-related protein ttha03702 from thermus thermophilus hb8
118	<a href="#">c2q7vA_</a>	Alignment	not modelled	99.1	30	<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
119	<a href="#">c1bwcA_</a>	Alignment	not modelled	99.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione reductase); <b>PDBTitle:</b> structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
120	<a href="#">d1d4ca2</a>	Alignment	not modelled	99.1	35	<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