










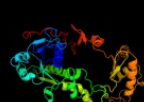














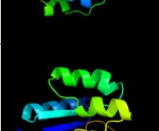
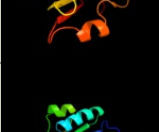
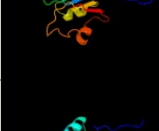




# Phyre2

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Description	P76518
Date	Thu Jan 5 12:23:58 GMT 2012
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2vjma1</a>	 Alignment		100.0	32	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
2	<a href="#">d1xk7a1</a>	 Alignment		100.0	23	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
3	<a href="#">d1q7ea_</a>	 Alignment		100.0	32	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
4	<a href="#">c1xa3B_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> crotonobetainyl-coa:carnitine coa-transferase; <b>PDBTitle:</b> crystal structure of caib, a type iii coa transferase in2 carnitine metabolism
5	<a href="#">d1x74a1</a>	 Alignment		100.0	27	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
6	<a href="#">c2g04B_</a>	 Alignment		100.0	28	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> probable fatty-acid-coa racemase far; <b>PDBTitle:</b> crystal structure of fatty acid-coa racemase from mycobacterium2 tuberculosis h37rv
7	<a href="#">c3p2yA_</a>	 Alignment		95.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine dehydrogenase/pyridine nucleotide transhydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
8	<a href="#">c2bruB_</a>	 Alignment		95.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
9	<a href="#">d1l7da1</a>	 Alignment		94.6	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
10	<a href="#">c3dhyC_</a>	 Alignment		94.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
11	<a href="#">c1wwkA_</a>	 Alignment		94.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3

12	<a href="#">c3kboB</a>	Alignment		94.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate/hydroxypyruvate reductase a; <b>PDBTitle:</b> 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from salmonella typhimurium in complex with nadp
13	<a href="#">c1pjca</a>	Alignment		93.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-alanine dehydrogenase); <b>PDBTitle:</b> l-alanine dehydrogenase complexed with nad
14	<a href="#">c1v8bA</a>	Alignment		93.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteine; <b>PDBTitle:</b> crystal structure of a hydrolase
15	<a href="#">c2omeA</a>	Alignment		93.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal-binding protein 2; <b>PDBTitle:</b> crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
16	<a href="#">c3oneA</a>	Alignment		93.6	18	<b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteine; <b>PDBTitle:</b> crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
17	<a href="#">d1gdha1</a>	Alignment		93.4	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
18	<a href="#">d2dlad1</a>	Alignment		93.2	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
19	<a href="#">c2rirA</a>	Alignment		93.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
20	<a href="#">c2q76A</a>	Alignment		93.1	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of human 3-phosphoglycerate dehydrogenase
21	<a href="#">c1l7eC</a>	Alignment	not modelled	92.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinamide nucleotide transhydrogenase, <b>PDBTitle:</b> crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
22	<a href="#">d1vgya1</a>	Alignment	not modelled	92.5	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
23	<a href="#">c3gvpB</a>	Alignment	not modelled	92.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylhomocysteine 3; <b>PDBTitle:</b> human sahh-like domain of human adenosylhomocysteine 3
24	<a href="#">d1pjca1</a>	Alignment	not modelled	92.4	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
25	<a href="#">c2gcqB</a>	Alignment	not modelled	92.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate reductase/hydroxypyruvate reductase; <b>PDBTitle:</b> ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
26	<a href="#">d1qp8a1</a>	Alignment	not modelled	92.3	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
27	<a href="#">d1mx3a1</a>	Alignment	not modelled	92.2	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
28	<a href="#">d2naca1</a>	Alignment	not modelled	92.2	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

29	<a href="#">d1dxya1</a>	Alignment	not modelled	92.0	19	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
30	<a href="#">c3d64A</a>	Alignment	not modelled	92.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
31	<a href="#">c1gdhA</a>	Alignment	not modelled	91.8	9	<b>PDB header:</b> oxidoreductase(choh (d)-nad(p)+ (a)) <b>Chain:</b> A: <b>PDB Molecule:</b> d-glycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
32	<a href="#">c3hg7A</a>	Alignment	not modelled	91.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase family <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
33	<a href="#">c2dbqA</a>	Alignment	not modelled	91.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxylate reductase; <b>PDBTitle:</b> crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
34	<a href="#">c3evtA</a>	Alignment	not modelled	91.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
35	<a href="#">c3gvxA</a>	Alignment	not modelled	91.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerate dehydrogenase related protein; <b>PDBTitle:</b> crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
36	<a href="#">d1j4aa1</a>	Alignment	not modelled	91.2	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
37	<a href="#">c2pi1C</a>	Alignment	not modelled	91.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
38	<a href="#">c2cukC</a>	Alignment	not modelled	90.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerate dehydrogenase/glyoxylate reductase; <b>PDBTitle:</b> crystal structure of tt0316 protein from thermus thermophilus hb8
39	<a href="#">c3d4oA</a>	Alignment	not modelled	90.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
40	<a href="#">c2eezG</a>	Alignment	not modelled	90.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from themus thermophilus
41	<a href="#">d1li4a1</a>	Alignment	not modelled	90.4	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
42	<a href="#">c1xdwA</a>	Alignment	not modelled	90.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad+-dependent (r)-2-hydroxyglutarate <b>PDBTitle:</b> nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
43	<a href="#">d1np3a2</a>	Alignment	not modelled	89.6	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
44	<a href="#">c3bazA</a>	Alignment	not modelled	89.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
45	<a href="#">c1luaA</a>	Alignment	not modelled	89.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methylene tetrahydromethanopterin dehydrogenase; <b>PDBTitle:</b> structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
46	<a href="#">c2eklA</a>	Alignment	not modelled	88.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> structure of st1218 protein from sulfolobus tokodaii
47	<a href="#">c1d4fD</a>	Alignment	not modelled	88.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylhomocysteine hydrolase; <b>PDBTitle:</b> crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
48	<a href="#">d1sc6a1</a>	Alignment	not modelled	88.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
49	<a href="#">c1qp8A</a>	Alignment	not modelled	87.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
50	<a href="#">c1j4aA</a>	Alignment	not modelled	87.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
51	<a href="#">c3n58D</a>	Alignment	not modelled	87.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
52	<a href="#">c2j6iC</a>	Alignment	not modelled	87.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
53	<a href="#">d1to3a</a>	Alignment	not modelled	86.8	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase

					<b>Family:</b> Class I aldolase
54	<a href="#">d1m1na_</a>	Alignment	not modelled	86.5	20 <b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
55	<a href="#">c2p2gD_</a>	Alignment	not modelled	85.9	17 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
56	<a href="#">d1pg5a2</a>	Alignment	not modelled	85.7	13 <b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
57	<a href="#">c2xdoC_</a>	Alignment	not modelled	85.2	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tebx2 protein; <b>PDBTitle:</b> structure of the tetracycline degrading monooxygenase tebx2 from2 bacteroides thetaiotaomicron
58	<a href="#">d1v8ba1</a>	Alignment	not modelled	84.5	18 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
59	<a href="#">c1np3B_</a>	Alignment	not modelled	84.1	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetoxyhydroxy acid isomeroreductase from2 pseudomonas aeruginosa
60	<a href="#">c3n7uD_</a>	Alignment	not modelled	83.6	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
61	<a href="#">d1ekxa2</a>	Alignment	not modelled	82.8	13 <b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
62	<a href="#">c2vhyB_</a>	Alignment	not modelled	81.5	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
63	<a href="#">c3gg9C_</a>	Alignment	not modelled	80.3	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase oxidoreductase protein; <b>PDBTitle:</b> crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
64	<a href="#">d1vlva2</a>	Alignment	not modelled	80.2	16 <b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
65	<a href="#">c1dxyA_</a>	Alignment	not modelled	80.0	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxysicaproate dehydrogenase; <b>PDBTitle:</b> structure of d-2-hydroxysicaproate dehydrogenase
66	<a href="#">c2d0iC_</a>	Alignment	not modelled	79.9	11 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure ph0520 protein from pyrococcus horikoshii ot3
67	<a href="#">d2jfga1</a>	Alignment	not modelled	79.8	17 <b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
68	<a href="#">d1c1da1</a>	Alignment	not modelled	79.5	21 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
69	<a href="#">c2nacA_</a>	Alignment	not modelled	77.7	13 <b>PDB header:</b> oxidoreductase(aldehyde(d),nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent formate dehydrogenase; <b>PDBTitle:</b> high resolution structures of holo and apo formate dehydrogenase
70	<a href="#">c2vouA_</a>	Alignment	not modelled	77.1	17 <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
71	<a href="#">c1a1saA_</a>	Alignment	not modelled	76.4	20 <b>PDB header:</b> transcarbamylase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> ornithine carbamoyltransferase from pyrococcus furiosus
72	<a href="#">c2w2kB_</a>	Alignment	not modelled	76.2	9 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mandelate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
73	<a href="#">d1u7za_</a>	Alignment	not modelled	75.2	17 <b>Fold:</b> Ribokinase-like <b>Superfamily:</b> CoaB-like <b>Family:</b> CoaB-like
74	<a href="#">c1qo8A_</a>	Alignment	not modelled	73.6	26 <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
75	<a href="#">c3a1IA_</a>	Alignment	not modelled	73.5	17 <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
76	<a href="#">c3nlcA_</a>	Alignment	not modelled	73.3	27 <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
77	<a href="#">d1dxha2</a>	Alignment	not modelled	72.3	14 <b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
78	<a href="#">d1seza1</a>	Alignment	not modelled	72.0	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
79	<a href="#">c2gibH_</a>	Alignment	not modelled	70.5	27 <b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> putative aldolase mj0400;

79	<a href="#">c2qjnn_</a>	Alignment	not modelled	70.3	27	<b>PDBTitle:</b> m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate <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 <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 <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 <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. <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
80	<a href="#">c1d4cB_</a>	Alignment	not modelled	69.6	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
81	<a href="#">c2v1dA_</a>	Alignment	not modelled	69.1	24	<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
82	<a href="#">c2xagA_</a>	Alignment	not modelled	69.1	24	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
83	<a href="#">c1f8sA_</a>	Alignment	not modelled	68.8	20	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> UDP-galactopyranose mutase, N-terminal domain
84	<a href="#">c3ka7A_</a>	Alignment	not modelled	68.4	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
85	<a href="#">d1b0aa1</a>	Alignment	not modelled	67.9	19	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nife; <b>PDBTitle:</b> precursor bound nifen <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0341 protein in rsp 3' region; <b>PDBTitle:</b> crystal structure of the sam-dependent methyltransferase2 ngo1261 from neisseria gonorrhoeae, northeast structural3 genomics consortium target ngr48
86	<a href="#">c1jrxA_</a>	Alignment	not modelled	67.8	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
87	<a href="#">d1pvva2</a>	Alignment	not modelled	67.5	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> S-adenosylhomocystein hydrolase
88	<a href="#">d1i8ta1</a>	Alignment	not modelled	67.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1 <b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> d-erythronate-4-phosphate dehydrogenase complexed with nad
89	<a href="#">d1a4ia1</a>	Alignment	not modelled	66.7	21	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
90	<a href="#">c3pdiG_</a>	Alignment	not modelled	66.6	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
91	<a href="#">c2r6za_</a>	Alignment	not modelled	66.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> the active form of phosphoglycerate dehydrogenase
92	<a href="#">d2dw4a2</a>	Alignment	not modelled	66.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
93	<a href="#">d1li4a2</a>	Alignment	not modelled	65.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
94	<a href="#">c3d8xB_</a>	Alignment	not modelled	65.5	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
95	<a href="#">c3oetF_</a>	Alignment	not modelled	65.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
96	<a href="#">d1qh8a_</a>	Alignment	not modelled	65.0	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Arginine methyltransferase
97	<a href="#">d1g6q1_</a>	Alignment	not modelled	64.6	27	<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
98	<a href="#">c1ybaC_</a>	Alignment	not modelled	64.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of the complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
99	<a href="#">c2ef0A_</a>	Alignment	not modelled	63.7	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases
100	<a href="#">c2gk4A_</a>	Alignment	not modelled	63.4	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
101	<a href="#">d2ivda1</a>	Alignment	not modelled	62.8	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
102	<a href="#">c3ihmB_</a>	Alignment	not modelled	62.7	10	<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
103	<a href="#">c1f6mF_</a>	Alignment	not modelled	62.1	3	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of the complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
104	<a href="#">d2pkwa1</a>	Alignment	not modelled	62.0	29	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases



						<b>Family:</b> YhiQ-like
105	<a href="#">c2jb1B_</a>	Alignment	not modelled	61.4	20	<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
106	<a href="#">c2e1mA_</a>	Alignment	not modelled	61.4	21	<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
107	<a href="#">c2vdcl_</a>	Alignment	not modelled	61.4	16	<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.
108	<a href="#">c1zx9A_</a>	Alignment	not modelled	61.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
109	<a href="#">c1a4iB_</a>	Alignment	not modelled	60.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase / <b>PDBTitle:</b> human tetrahydrofolate dehydrogenase / cyclohydrolase
110	<a href="#">c1bxgA_</a>	Alignment	not modelled	60.7	22	<b>PDB header:</b> amino acid dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine dehydrogenase; <b>PDBTitle:</b> phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate
111	<a href="#">c3grfA_</a>	Alignment	not modelled	60.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
112	<a href="#">c2yg4B_</a>	Alignment	not modelled	60.4	20	<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
113	<a href="#">d1ps9a3</a>	Alignment	not modelled	60.2	10	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
114	<a href="#">c1vdcA_</a>	Alignment	not modelled	60.1	3	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dependent thioredoxin reductase; <b>PDBTitle:</b> structure of nadph dependent thioredoxin reductase
115	<a href="#">c3bkWB_</a>	Alignment	not modelled	60.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> s-adenosylmethionine dependent methyltransferase; <b>PDBTitle:</b> crystal structure of s-adenosylmethionine dependent methyltransferase2 (np_104914.1) from mesorhizobium loti at 1.60 a resolution
116	<a href="#">c1sezA_</a>	Alignment	not modelled	59.9	20	<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
117	<a href="#">c2a87A_</a>	Alignment	not modelled	59.8	13	<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
118	<a href="#">c2i0zA_</a>	Alignment	not modelled	59.6	21	<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
119	<a href="#">c1yvvB_</a>	Alignment	not modelled	59.5	16	<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.
120	<a href="#">c3f8rD_</a>	Alignment	not modelled	58.6	7	<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