

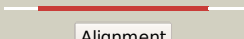

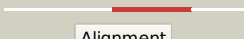












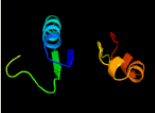






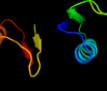

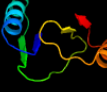


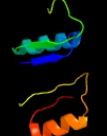



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0372c_(-)_448631_449386
Date	Tue Jul 23 14:50:44 BST 2019
Unique Job ID	ab6a088e565185bd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2we7A_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xanthine dehydrogenase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
2	<a href="#">c3on5B_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bh1974 protein; <b>PDBTitle:</b> crystal structure of a xanthine dehydrogenase (bh1974) from bacillus2 halodurans at 2.80 a resolution
3	<a href="#">c3llvA_</a>	 Alignment		97.5	14	<b>PDB header:</b> nad(p) binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase-related protein; <b>PDBTitle:</b> the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
4	<a href="#">c2g1uA_</a>	 Alignment		97.3	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm1088a; <b>PDBTitle:</b> crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
5	<a href="#">c5nc8B_</a>	 Alignment		96.8	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> potassium efflux system protein; <b>PDBTitle:</b> shewanella denitrificans kef ctd in amp bound form
6	<a href="#">d1lssa_</a>	 Alignment		96.5	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
7	<a href="#">c4g65A_</a>	 Alignment		96.5	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> trk system potassium uptake protein trka; <b>PDBTitle:</b> potassium transporter peripheral membrane component (trka) from vibrio2 vulnificus
8	<a href="#">c3ic5A_</a>	 Alignment		96.4	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
9	<a href="#">c1dxyA_</a>	 Alignment		96.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> structure of d-2-hydroxyisocaproate dehydrogenase
10	<a href="#">c4gx5D_</a>	 Alignment		96.3	11	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> trka domain protein; <b>PDBTitle:</b> gsuk channel
11	<a href="#">c3fwzA_</a>	 Alignment		96.3	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein ybal; <b>PDBTitle:</b> crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli

12	<a href="#">d1kjq2</a>	Alignment		96.3	17	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
13	<a href="#">d2hmva1</a>	Alignment		96.1	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
14	<a href="#">c2cukC</a>	Alignment		96.1	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
15	<a href="#">c3q2oB</a>	Alignment		96.1	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
16	<a href="#">c2dbqA</a>	Alignment		96.1	18	<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)
17	<a href="#">c3l4bG</a>	Alignment		96.1	18	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> trka k+ channel protien tm1088b; <b>PDBTitle:</b> crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
18	<a href="#">c3evtA</a>	Alignment		96.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
19	<a href="#">c1j4aA</a>	Alignment		95.9	15	<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
20	<a href="#">c6ih2B</a>	Alignment		95.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphite dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
21	<a href="#">c5j23D</a>	Alignment	not modelled	95.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc04462 (smghrb) from sinorhizobium meliloti in complex3 with 2'-phospho- adp-ribose
22	<a href="#">d2jfga1</a>	Alignment	not modelled	95.9	20	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
23	<a href="#">c5tulA</a>	Alignment	not modelled	95.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline destructase tet(55); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(55)
24	<a href="#">c4zqbB</a>	Alignment	not modelled	95.9	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent dehydrogenase from2 rhodobactersphaeroides in complex with nadp and sulfate
25	<a href="#">c4g2nA</a>	Alignment	not modelled	95.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; <b>PDBTitle:</b> crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
26	<a href="#">c5tx7A</a>	Alignment	not modelled	95.8	28	<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 from desulfovibrio vulgaris
27	<a href="#">d1dxya1</a>	Alignment	not modelled	95.8	22	<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>PDB header:</b> oxidoreductase

28	<a href="#">c3wwyA_</a>	Alignment	not modelled	95.8	27	<b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
29	<a href="#">c3eywA_</a>	Alignment	not modelled	95.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
30	<a href="#">d3c96a1</a>	Alignment	not modelled	95.7	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
31	<a href="#">c3k5pA_</a>	Alignment	not modelled	95.7	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
32	<a href="#">c3uvzB_</a>	Alignment	not modelled	95.7	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
33	<a href="#">c3bazA_</a>	Alignment	not modelled	95.7	19	<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+
34	<a href="#">c2d0iC_</a>	Alignment	not modelled	95.7	18	<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
35	<a href="#">c3kboB_</a>	Alignment	not modelled	95.7	24	<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) from2 salmonella typhimurium in complex with nadp
36	<a href="#">c1wwkA_</a>	Alignment	not modelled	95.7	21	<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
37	<a href="#">c1ybaC_</a>	Alignment	not modelled	95.6	30	<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
38	<a href="#">c3gmbB_</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <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
39	<a href="#">c2eklA_</a>	Alignment	not modelled	95.6	18	<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
40	<a href="#">d1id1a_</a>	Alignment	not modelled	95.6	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
41	<a href="#">c4weqA_</a>	Alignment	not modelled	95.5	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc02828 (smghra) from sinorhizobium meliloti in complex3 with nadp and sulfate
42	<a href="#">c3allA_</a>	Alignment	not modelled	95.5	13	<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
43	<a href="#">c4prkB_</a>	Alignment	not modelled	95.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-phosphoerythronate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
44	<a href="#">c3orqA_</a>	Alignment	not modelled	95.5	10	<b>PDB header:</b> ligase,biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
45	<a href="#">c4lswA_</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyacid dehydrogenase protein; <b>PDBTitle:</b> crystallization and structural analysis of 2-hydroxyacid dehydrogenase2 from ketogulonigenium vulgare y25
46	<a href="#">c2gcbB_</a>	Alignment	not modelled	95.4	21	<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
47	<a href="#">c5mh5A_</a>	Alignment	not modelled	95.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> d-2-hydroxyacid dehydrogenases (d2-hdh) from haloferax mediterranei in2 complex with 2-keto-hexanoic acid and nadp+ (1.4 a resolution)
48	<a href="#">c3wwzB_</a>	Alignment	not modelled	95.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-lactate dehydrogenase (fermentative); <b>PDBTitle:</b> the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
49	<a href="#">d1mx3a1</a>	Alignment	not modelled	95.4	27	<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
50	<a href="#">c4txkA_</a>	Alignment	not modelled	95.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-methionine sulfoxide oxidase mical1; <b>PDBTitle:</b> construct of mical-1 containing the monooxygenase and calponin2 homology domains
51	<a href="#">d1vgya1</a>	Alignment	not modelled	95.3	30	<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
52	<a href="#">c5fn0C</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> kynurenine 3-monoxygenase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens kynurenine-3-2 monoxygenase (kmo) in complex with gsk180
53	<a href="#">d1j4aa1</a>	Alignment	not modelled	95.3	22	<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
54	<a href="#">c4n18A</a>	Alignment	not modelled	95.3	36	<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 klebsiella pneumoniae 342
55	<a href="#">c2omeA</a>	Alignment	not modelled	95.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ic-terminal-binding protein 2; <b>PDBTitle:</b> crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
56	<a href="#">d2ldda1</a>	Alignment	not modelled	95.3	22	<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
57	<a href="#">c2g76A</a>	Alignment	not modelled	95.3	25	<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
58	<a href="#">c4cukA</a>	Alignment	not modelled	95.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> structure of salmonella d-lactate dehydrogenase in complex2 with nadh
59	<a href="#">d1sc6a1</a>	Alignment	not modelled	95.3	27	<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
60	<a href="#">c2pi1C</a>	Alignment	not modelled	95.2	15	<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
61	<a href="#">c4gvlB</a>	Alignment	not modelled	95.2	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trka domain protein; <b>PDBTitle:</b> crystal structure of the gsk rck domain
62	<a href="#">c4njmA</a>	Alignment	not modelled	95.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase, putative; <b>PDBTitle:</b> crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
63	<a href="#">c4gx2B</a>	Alignment	not modelled	95.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> trka domain protein; <b>PDBTitle:</b> gsuk channel bound to nad
64	<a href="#">c3n7uD</a>	Alignment	not modelled	95.2	22	<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
65	<a href="#">c2yq4C</a>	Alignment	not modelled	95.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from lactobacillus delbrueckii ssp. bulgaricus
66	<a href="#">c3gvxA</a>	Alignment	not modelled	95.1	18	<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
67	<a href="#">c2qa2A</a>	Alignment	not modelled	95.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide oxygenase cabc; <b>PDBTitle:</b> crystal structure of cabc, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution
68	<a href="#">c2xdoC</a>	Alignment	not modelled	95.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetx2 protein; <b>PDBTitle:</b> structure of the tetracycline degrading monoxygenase tetx2 from2 bacteroides thetaiotaomicron
69	<a href="#">c1gdhA</a>	Alignment	not modelled	95.0	25	<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
70	<a href="#">c4bk2A</a>	Alignment	not modelled	95.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable salicylate monoxygenase; <b>PDBTitle:</b> crystal structure of 3-hydroxybenzoate 6-hydroxylase2 uncovers lipid-assisted flavoprotein strategy for3 regioselective aromatic hydroxylation: q301e mutant
71	<a href="#">c5eowA</a>	Alignment	not modelled	95.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-hydroxynicotinate 3-monoxygenase; <b>PDBTitle:</b> crystal structure of 6-hydroxynicotinic acid 3-monoxygenase from2 pseudomonas putida kt2440
72	<a href="#">c5tukC</a>	Alignment	not modelled	94.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetracycline destructase tet(51); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(51)
73	<a href="#">c4xkjA</a>	Alignment	not modelled	94.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> a novel d-lactate dehydrogenase from sporolactobacillus sp
74	<a href="#">c5xgvB</a>	Alignment	not modelled	94.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyre3; <b>PDBTitle:</b> the structure of diels-alderase pyre3 in the biosynthetic pathway of2 pyrroindomycins
75	<a href="#">d1qp8a1</a>	Alignment	not modelled	94.9	12	<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
76	<a href="#">c4xcvA</a>	Alignment	not modelled	94.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> probable 2-hydroxyacid dehydrogenase from rhizobium

						etli cfn 42 in2 complex with nadph <b>PDB header:</b> oxidoreductase
77	<a href="#">c2vouA_</a>	Alignment	not modelled	94.9	11	<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
78	<a href="#">c4cy8A_</a>	Alignment	not modelled	94.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxybiphenyl 3-monooxygenase; <b>PDBTitle:</b> 2-hydroxybiphenyl 3-monooxygenase (hbpa) in complex with fad
79	<a href="#">c4hy3D_</a>	Alignment	not modelled	94.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoglycerate oxidoreductase; <b>PDBTitle:</b> crystal structure of a phosphoglycerate oxidoreductase from rhizobium2 etli
80	<a href="#">c2qa1A_</a>	Alignment	not modelled	94.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide oxygenase pgae; <b>PDBTitle:</b> crystal structure of pgae, an aromatic hydroxylase involved in2 angucycline biosynthesis
81	<a href="#">c1qp8A_</a>	Alignment	not modelled	94.7	12	<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
82	<a href="#">c1xdwA_</a>	Alignment	not modelled	94.7	15	<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
83	<a href="#">c5butG_</a>	Alignment	not modelled	94.7	9	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> ktr system potassium uptake protein a,ktr system potassium <b>PDBTitle:</b> crystal structure of inactive conformation of ktrab k+ transporter
84	<a href="#">c1ygyA_</a>	Alignment	not modelled	94.7	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
85	<a href="#">d1e5qa1</a>	Alignment	not modelled	94.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
86	<a href="#">d2voua1</a>	Alignment	not modelled	94.7	11	<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="#">c3hg7A_</a>	Alignment	not modelled	94.6	21	<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
88	<a href="#">c4j7cA_</a>	Alignment	not modelled	94.6	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ktr system potassium uptake protein a; <b>PDBTitle:</b> ktrab potassium transporter from bacillus subtilis
89	<a href="#">c5tueB_</a>	Alignment	not modelled	94.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> tetracycline destructase tet(50); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(50)
90	<a href="#">c4j33B_</a>	Alignment	not modelled	94.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine 3-monooxygenase; <b>PDBTitle:</b> crystal structure of kynurenine 3-monooxygenase (kmo-394)
91	<a href="#">c3rp7A_</a>	Alignment	not modelled	94.6	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoprotein monooxygenase; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae hpox complexed with fad and2 uric acid
92	<a href="#">c4e5kC_</a>	Alignment	not modelled	94.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphite dehydrogenase (thermostable variant); <b>PDBTitle:</b> thermostable phosphite dehydrogenase in complex with nad and sulfite
93	<a href="#">c2rgjA_</a>	Alignment	not modelled	94.6	16	<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
94	<a href="#">c4xa8A_</a>	Alignment	not modelled	94.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase nad-binding; <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from xanthobacter autotrophicus py2
95	<a href="#">c5kowA_</a>	Alignment	not modelled	94.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pentachlorophenol 4-monooxygenase; <b>PDBTitle:</b> structure of rifampicin monooxygenase
96	<a href="#">c2w2kB_</a>	Alignment	not modelled	94.5	22	<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 rhodoturla graminis2 d-mandelate dehydrogenase at 1.8a.
97	<a href="#">c2j6iC_</a>	Alignment	not modelled	94.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> candida boidinii formate dehydrogenase (fdh) c-terminal mutant
98	<a href="#">c3k5iB_</a>	Alignment	not modelled	94.5	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyl-aminoimidazole carboxylase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-aminoimidazole3 ribonucleotide
99	<a href="#">c4egjD_</a>	Alignment	not modelled	94.4	24	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> d-alanine--d-alanine ligase; <b>PDBTitle:</b> crystal structure of d-alanine-d-alanine ligase from burkholderia2 xenovorans
100	<a href="#">c2bryA_</a>	Alignment	not modelled	94.4	13	<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
101	<a href="#">d2naca1</a>	Alignment	not modelled	94.4	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
102	<a href="#">c2r0gB</a>	Alignment	not modelled	94.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rebc; <b>PDBTitle:</b> chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
103	<a href="#">c4hb9A</a>	Alignment	not modelled	94.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> similarities with probable monooxygenase; <b>PDBTitle:</b> crystal structure of a putative fad containing monooxygenase from2 photorhabdus luminescens subsp. laumondii tto1 (target psi-012791)
104	<a href="#">c3c4aA</a>	Alignment	not modelled	94.2	10	<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 fad from2 chromobacterium violaceum. northeast structural genomics consortium3 target cvr158
105	<a href="#">d1gdha1</a>	Alignment	not modelled	94.2	31	<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
106	<a href="#">d1reoa1</a>	Alignment	not modelled	94.2	5	<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
107	<a href="#">c2dc1A</a>	Alignment	not modelled	94.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
108	<a href="#">c2nacA</a>	Alignment	not modelled	94.2	21	<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
109	<a href="#">c5x68B</a>	Alignment	not modelled	94.2	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine 3-monoxygenase; <b>PDBTitle:</b> crystal structure of human kmo
110	<a href="#">c3fn4A</a>	Alignment	not modelled	94.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent formate dehydrogenase; <b>PDBTitle:</b> apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
111	<a href="#">c3wnvA</a>	Alignment	not modelled	93.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxylate reductase; <b>PDBTitle:</b> crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
112	<a href="#">c2e1mA</a>	Alignment	not modelled	93.9	22	<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
113	<a href="#">c1kijA</a>	Alignment	not modelled	93.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase 2; <b>PDBTitle:</b> crystal structure of glycinamide ribonucleotide transformylase in2 complex with mg-atp-gamma-s
114	<a href="#">c3fmwC</a>	Alignment	not modelled	93.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxygenase; <b>PDBTitle:</b> the crystal structure of mtmoiv, a baeyer-villiger monooxygenase from2 the mithramycin biosynthetic pathway in streptomyces argillaceus.
115	<a href="#">d1ps9a3</a>	Alignment	not modelled	93.9	11	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
116	<a href="#">c3ax6C</a>	Alignment	not modelled	93.9	15	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
117	<a href="#">c4k2xB</a>	Alignment	not modelled	93.9	19	<b>PDB header:</b> oxidoreductase, flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> polyketide oxygenase/hydroxylase; <b>PDBTitle:</b> oxs anhydrotetracycline hydroxylase from streptomyces rimosus
118	<a href="#">d1l7da1</a>	Alignment	not modelled	93.8	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
119	<a href="#">c6j0zC</a>	Alignment	not modelled	93.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative angucycline-like polyketide oxygenase; <b>PDBTitle:</b> crystal structure of alpK
120	<a href="#">c4mamB</a>	Alignment	not modelled	93.7	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> the crystal structure of phosphoribosylaminoimidazole carboxylase2 atpase subunit of francisella tularensis subsp. tularensis schu s4 in3 complex with an adp analog, amp-cp