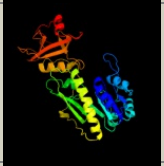
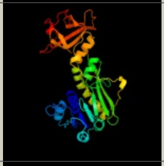
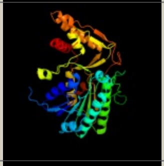
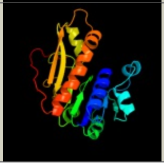
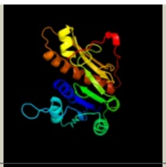
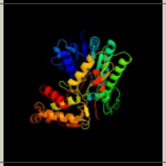
Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	P77398
Date	Thu Jan 5 12:28:36 GMT 2012
Unique Job ID	02c11fb33aedbb0d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z7eC_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
2	c1yrwA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
3	c1fmtA_	Alignment		100.0	29	**PDB header:**formyltransferase **Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli
4	c3rfoA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** crystal structure of methyionyl-trna formyltransferase from bacillus2 anthracis
5	c3tqqA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
6	c3q0iA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae
7	c1s3iA_	Alignment		100.0	28	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** crystal structure of the n terminal hydrolase domain of 10-2 formyltetrahydrofolate dehydrogenase
8	c1z45A_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**gal10 bifunctional protein; **PDBTitle:** crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces3 cerevisiae complexed with nad, udp-glucose, and galactose
9	d1i24a_	Alignment		100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
10	d2blna2	Alignment		100.0	99	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
11	d2bw0a2	Alignment		100.0	27	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase

12	d1fmta2	Alignment		100.0	30	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
13	d1s3ia2	Alignment		100.0	26	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
14	d2blla1	Alignment		100.0	100	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
15	c1zghA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from clostridium thermocellum
16	d2b69a1	Alignment		100.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
17	c2b69A_	Alignment		100.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**udp-glucuronate decarboxylase 1; **PDBTitle:** crystal structure of human udp-glucoronic acid decarboxylase
18	c3slgB_	Alignment		100.0	51	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pbgp3 protein; **PDBTitle:** crystal structure of pbgp3 protein from burkholderia pseudomallei
19	c3kcqA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
20	d1e6ua_	Alignment		100.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
21	d1rkxa_	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
22	d1oc2a_	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
23	d2c5aa1	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
24	c2z1mC_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**gdp-d-mannose dehydratase; **PDBTitle:** crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
25	d1jkxa_	Alignment	not modelled	100.0	23	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
26	d1kewa_	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
27	d1gy8a_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
28	d1orra_	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
29	c1n7gB	Alignment	not modelled	100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**gdp-d-mannose-4,6-dehydratase;

29	c1n7gB_	Alignment	not modelled	100.0	19	**PDBTitle:** crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
30	c3enkB_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
31	d1wvga1	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
32	c3lu1C_	Alignment	not modelled	100.0	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**wbgu; **PDBTitle:** crystal structure analysis of wbgu: a udp-galnac 4-epimerase
33	c2hunB_	Alignment	not modelled	100.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**336aa long hypothetical dtdp-glucose 4,6-dehydratase; **PDBTitle:** crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
34	d1db3a_	Alignment	not modelled	100.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
35	c2v6gA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**progesterone 5-beta-reductase; **PDBTitle:** structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
36	d1n7ha_	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
37	d1t2aa_	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
38	c1t2aC_	Alignment	not modelled	100.0	19	**PDB header:**structural genomics,lyase **Chain:** C: **PDB Molecule:**gdp-mannose 4,6 dehydratase; **PDBTitle:** crystal structure of human gdp-d-mannose 4,6-dehydratase
39	c2ywrA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
40	d1ek6a_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
41	c2c20D_	Alignment	not modelled	100.0	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of udp-glucose 4-epimerase
42	d1sb8a_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	d1r6da_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
44	c3dcjA_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
45	d1rpna_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	c3tqrA_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
47	d1z45a2	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
48	c2hrzA_	Alignment	not modelled	100.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** the crystal structure of the nucleoside-diphosphate-sugar epimerase2 from agrobacterium tumefaciens
49	c2pk3B_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gdp-6-deoxy-d-lyxo-4-hexulose reductase; **PDBTitle:** crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
50	c2q1uA_	Alignment	not modelled	100.0	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
51	c2iodD_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydroflavonol 4-reductase; **PDBTitle:** binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
52	d1bxka_	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
53	c2p5uC_	Alignment	not modelled	100.0	26	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of thermus thermophilus hb8 udp-

						glucose 4-2 epimerase complex with nad
54	c3p9xB_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
55	d1meoa_	Alignment	not modelled	100.0	21	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
56	d1y1pa1	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
57	c3a1nB_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ndp-sugar epimerase; **PDBTitle:** crystal structure of l-threonine dehydrogenase from2 hyperthermophilic archaeon thermoplasma volcanium
58	c3oh8A_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate sugar epimerase (sula family); **PDBTitle:** crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
59	c2yy7B_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-threonine dehydrogenase; **PDBTitle:** crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
60	d1udca_	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
61	c2pzlB_	Alignment	not modelled	100.0	20	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme2 wbmg in complex with nad and udp
62	c2p4hX_	Alignment	not modelled	100.0	19	**PDB header:**plant protein **Chain:** X: **PDB Molecule:**vestitone reductase; **PDBTitle:** crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
63	c3eheB_	Alignment	not modelled	100.0	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase (gale-1); **PDBTitle:** crystal structure of udp-glucose 4 epimerase (gale-1) from2 archaeoglobus fulgidus
64	c2q1wC_	Alignment	not modelled	100.0	21	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
65	c3icpA_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of udp-galactose 4-epimerase
66	c3m2pD_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 4-epimerase; **PDBTitle:** the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
67	c2x4gA_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
68	d1n2sa_	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
69	d1vl0a_	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
70	c2rh8A_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anthocyanidin reductase; **PDBTitle:** structure of apo anthocyanidin reductase from vitis vinifera
71	c2gn9B_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**udp-glcnac c6 dehydratase; **PDBTitle:** crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
72	c3n0vD_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
73	c2x86K_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** K: **PDB Molecule:**adp-l-glycero-d-manno-heptose-6-epimerase; **PDBTitle:** agme bound to adp-b-mannose
74	c3o1lB_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
75	c2ydyA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine adenosyltransferase 2 subunit beta; **PDBTitle:** crystal structure of human s-adenosylmethionine synthetase2 2, beta subunit in orthorhombic crystal form
76	c3louB_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
77	c3sc6F_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** 2.65 angstrom resolution crystal structure of dtdp-4-

						dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
78	c2zklA_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
79	c3nrbD_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
80	d1eq2a_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
81	c3obiC_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
82	c3nzoB_	Alignment	not modelled	100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**udp-n-acetylglucosamine 4,6-dehydratase; **PDBTitle:** udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
83	c3iusB_	Alignment	not modelled	100.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss
84	c2ggsB_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**273aa long hypothetical dtdp-4-dehydrorhamnose **PDBTitle:** crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
85	d1zgha2	Alignment	not modelled	100.0	15	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
86	c3gpiA_	Alignment	not modelled	100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
87	d1xgka_	Alignment	not modelled	100.0	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	c2qx7A_	Alignment	not modelled	100.0	19	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
89	d1qyda_	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
90	c3e48B_	Alignment	not modelled	100.0	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
91	d1qyca_	Alignment	not modelled	100.0	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
92	c3c1oA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol synthase; **PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
93	c3rfxB_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
94	c3ay3C_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
95	c3i5mA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative leucoanthocyanidin reductase 1; **PDBTitle:** structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
96	c2gasA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isoflavone reductase; **PDBTitle:** crystal structure of isoflavone reductase
97	c2exxB_	Alignment	not modelled	99.9	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hscarg protein; **PDBTitle:** crystal structure of hscarg from homo sapiens in complex with nadp
98	c2zcuA_	Alignment	not modelled	99.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized oxidoreductase ytfg; **PDBTitle:** crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
99	c3e8xA_	Alignment	not modelled	99.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad-dependent epimerase/dehydratase; **PDBTitle:** putative nad-dependent epimerase/dehydratase from bacillus halodurans.
100	c2vrcD_	Alignment	not modelled	99.9	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**triphenylmethane reductase; **PDBTitle:** crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
101	d2blna1	Alignment	not modelled	99.9	100	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain

102	c3dqpA_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase ylbe; **PDBTitle:** crystal structure of the oxidoreductase ylbe from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
103	d2q46a1	Alignment	not modelled	99.9	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
104	c3dhnA_	Alignment	not modelled	99.9	17	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
105	c3h2sA_	Alignment	not modelled	99.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nadh-flavin reductase; **PDBTitle:** crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
106	d1fmta1	Alignment	not modelled	99.9	27	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
107	c3qvoA_	Alignment	not modelled	99.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nmra family protein; **PDBTitle:** structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
108	d1hdoa_	Alignment	not modelled	99.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
109	d1s3ia1	Alignment	not modelled	99.9	29	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
110	d2a35a1	Alignment	not modelled	99.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
111	d2bw0a1	Alignment	not modelled	99.9	26	**Fold:**FMT C-terminal domain-like **Superfamily:**FMT C-terminal domain-like **Family:**Post formyltransferase domain
112	d2bkaa1	Alignment	not modelled	99.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
113	d2fmua1	Alignment	not modelled	99.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
114	c3ew7A_	Alignment	not modelled	99.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo0794 protein; **PDBTitle:** crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
115	c3r6dA_	Alignment	not modelled	99.7	16	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of nad-dependent epimerase/dehydratase from2 veillonella parvula dsm 2008 with cz-methylated lysine
116	c2jahB_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**clavulanic acid dehydrogenase; **PDBTitle:** biochemical and structural analysis of the clavulanic acid2 dehydeogenase (cad) from streptomyces clavuligerus
117	d1mlda1	Alignment	not modelled	99.5	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
118	c3grkE_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
119	c3lylB_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
120	d1hyea1	Alignment	not modelled	99.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like