Phyre^2

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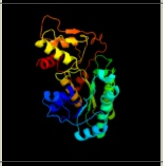
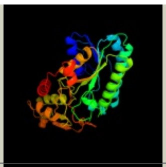
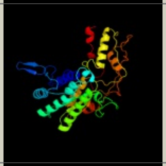
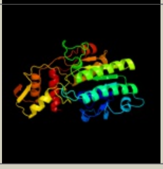
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x86K_	Alignment		100.0	100	**PDB header:**isomerase **Chain:** K: **PDB Molecule:**adp-l-glycero-d-manno-heptose-6-epimerase; **PDBTitle:** agme bound to adp-b-mannose
2	c1z7eC_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
3	c1z45A_	Alignment		100.0	20	**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
4	c2z1mC_	Alignment		100.0	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**gdp-d-mannose dehydratase; **PDBTitle:** crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
5	d1rpna_	Alignment		100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
6	d1i24a_	Alignment		100.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
7	c2b69A_	Alignment		100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**udp-glucuronate decarboxylase 1; **PDBTitle:** crystal structure of human udp-glucoronic acid decarboxylase
8	d2b69a1	Alignment		100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
9	d2c5aa1	Alignment		100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
10	c2pk3B_	Alignment		100.0	18	**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
11	d1n7ha_	Alignment		100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

12	c1n7gB_	Alignment		100.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**gdp-d-mannose-4,6-dehydratase; **PDBTitle:** crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
13	d1eq2a_	Alignment		100.0	97	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
14	d1db3a_	Alignment		100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
15	d1t2aa_	Alignment		100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
16	c1t2aC_	Alignment		100.0	18	**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
17	d1oc2a_	Alignment		100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
18	c3a1nB_	Alignment		100.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ndp-sugar epimerase; **PDBTitle:** crystal structure of l-threonine dehydrogenase from2 hyperthermophilic archaeon thermoplasma volcanium
19	c3enkB_	Alignment		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
20	c3eheB_	Alignment		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
21	c2hunB_	Alignment	not modelled	100.0	20	**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
22	d1sb8a_	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
23	c2c20D_	Alignment	not modelled	100.0	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of udp-glucose 4-epimerase
24	d1r6da_	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
25	c3lu1C_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**wbgu; **PDBTitle:** crystal structure analysis of wbgu: a udp-galnac 4-epimerase
26	c2rh8A_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anthocyanidin reductase; **PDBTitle:** structure of apo anthocyanidin reductase from vitis vinifera
27	d1kewa_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
28	c2iodD_	Alignment	not modelled	100.0	15	**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

29	d1bxka_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
30	d1e6ua_	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
31	d2blla1	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
32	c2v6gA_	Alignment	not modelled	100.0	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**progesterone 5-beta-reductase; **PDBTitle:** structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
33	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
34	c2p4hX_	Alignment	not modelled	100.0	17	**PDB header:**plant protein **Chain:** X: **PDB Molecule:**vestitone reductase; **PDBTitle:** crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
35	d1orra_	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
36	c2hrzA_	Alignment	not modelled	100.0	13	**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
37	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
38	d1z45a2	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
39	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
40	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
41	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
42	c2q1wC_	Alignment	not modelled	100.0	18	**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+
43	c2p5uC_	Alignment	not modelled	100.0	24	**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
44	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
45	d1udca_	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	c2yy7B_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-threonine dehydrogenase; **PDBTitle:** crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
47	c2x4gA_	Alignment	not modelled	100.0	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
48	c2q1uA_	Alignment	not modelled	100.0	21	**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
49	c3m2pD_	Alignment	not modelled	100.0	21	**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
50	c3slgB_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pbgp3 protein; **PDBTitle:** crystal structure of pbgp3 protein from burkholderia pseudomallei
51	d1y1pa1	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
52	d1vl0a_	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
53	c3iusB_	Alignment	not modelled	100.0	14	**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
						PDB header:isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate sugar epimerase

54	c3oh8A_	Alignment	not modelled	100.0	14	(sula family); **PDBTitle:** crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
55	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
56	c2ydyA_	Alignment	not modelled	100.0	20	**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
57	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
58	c3sc6F_	Alignment	not modelled	100.0	12	**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
59	c2ggsB_	Alignment	not modelled	100.0	13	**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
60	c2zklA_	Alignment	not modelled	99.9	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
61	c2gn9B_	Alignment	not modelled	99.9	15	**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
62	c3e48B_	Alignment	not modelled	99.9	13	**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
63	d1xgka_	Alignment	not modelled	99.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
64	c2qx7A_	Alignment	not modelled	99.9	12	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
65	c3i5mA_	Alignment	not modelled	99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative leucoanthocyanidin reductase 1; **PDBTitle:** structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
66	d1qyda_	Alignment	not modelled	99.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
67	c3c1oA_	Alignment	not modelled	99.9	12	**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
68	c2zcuA_	Alignment	not modelled	99.9	16	**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
69	c2gasA_	Alignment	not modelled	99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isoflavone reductase; **PDBTitle:** crystal structure of isoflavone reductase
70	d1qyca_	Alignment	not modelled	99.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
71	c2exxB_	Alignment	not modelled	99.8	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hscarg protein; **PDBTitle:** crystal structure of hscarg from homo sapiens in complex with nadp
72	d2q46a1	Alignment	not modelled	99.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
73	c2vrcD_	Alignment	not modelled	99.8	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**triphenylmethane reductase; **PDBTitle:** crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
74	c3rfxB_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
75	c3ay3C_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
76	c3e8xA_	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad-dependent epimerase/dehydratase; **PDBTitle:** putative nad-dependent epimerase/dehydratase from bacillus halodurans.
77	c3h2sA_	Alignment	not modelled	99.8	14	**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.
						PDB header:isomerase, lyase

78	c3dhnA_	Alignment	not modelled	99.8	15	**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.
79	c3nzoB_	Alignment	not modelled	99.8	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**udp-n-acetylglucosamine 4,6-dehydratase; **PDBTitle:** udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
80	c3dqpA_	Alignment	not modelled	99.7	13	**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.
81	d2bkaa1	Alignment	not modelled	99.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
82	d1hdoa_	Alignment	not modelled	99.6	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
83	d2a35a1	Alignment	not modelled	99.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
84	c3ew7A_	Alignment	not modelled	99.6	18	**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.
85	c3qvoA_	Alignment	not modelled	99.5	13	**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.
86	c3r6dA_	Alignment	not modelled	99.4	17	**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
87	d2fmua1	Alignment	not modelled	99.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	c2jahB_	Alignment	not modelled	99.1	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
89	c3p19A_	Alignment	not modelled	99.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative blue fluorescent protein; **PDBTitle:** improved nadph-dependent blue fluorescent protein
90	d1sbya1	Alignment	not modelled	98.9	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	d1mlda1	Alignment	not modelled	98.9	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
92	d2gdza1	Alignment	not modelled	98.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	d1jtva_	Alignment	not modelled	98.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
94	c3ppiA_	Alignment	not modelled	98.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase type-2; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
95	d1hyea1	Alignment	not modelled	98.8	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
96	c3l77A_	Alignment	not modelled	98.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain alcohol dehydrogenase; **PDBTitle:** x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
97	d1ooea_	Alignment	not modelled	98.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	d2ag5a1	Alignment	not modelled	98.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	c3lylB_	Alignment	not modelled	98.7	15	**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
100	d2a4ka1	Alignment	not modelled	98.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
101	c3un1D_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
102	d1dhra_	Alignment	not modelled	98.7	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						PDB header:oxidoreductase

103	c2p68A_	Alignment	not modelled	98.7	12	**Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
104	c3m1aF_	Alignment	not modelled	98.7	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** the crystal structure of a short-chain dehydrogenase from2 streptomyces avermitilis to 2a
105	d1ulsa_	Alignment	not modelled	98.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
106	d1uaya_	Alignment	not modelled	98.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
107	d1qsga_	Alignment	not modelled	98.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
108	c2hlpB_	Alignment	not modelled	98.6	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of the e267r mutant of a halophilic2 malate dehydrogenase in the apo form
109	c3f9iB_	Alignment	not modelled	98.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 rickettsia prowazekii
110	c3ezlA_	Alignment	not modelled	98.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
111	c3iccA_	Alignment	not modelled	98.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 3-oxoacyl-(acyl carrier protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
112	c3v2gA_	Alignment	not modelled	98.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
113	c3guyE_	Alignment	not modelled	98.6	11	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a short-chain dehydrogenase/reductase from vibrio2 parahaemolyticus
114	c3oidA_	Alignment	not modelled	98.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadph]; **PDBTitle:** crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
115	d1xu9a_	Alignment	not modelled	98.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
116	c2dteB_	Alignment	not modelled	98.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glucose 1-dehydrogenase related protein; **PDBTitle:** structure of thermoplasma acidophilum aldohexose dehydrogenase (aldt)2 in complex with nadh
117	d1edoa_	Alignment	not modelled	98.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
118	d1gega_	Alignment	not modelled	98.6	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	c3ijrF_	Alignment	not modelled	98.6	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
120	c3sjuA_	Alignment	not modelled	98.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**keto reductase; **PDBTitle:** hedamycin polyketide ketoreductase bound to nadph