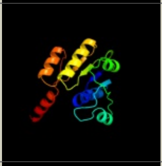
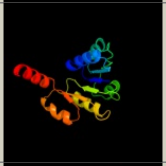
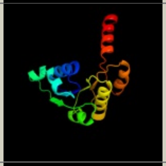
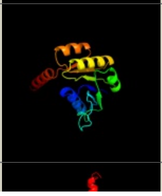
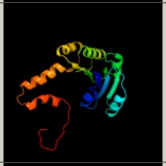
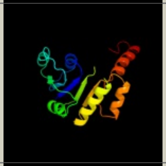
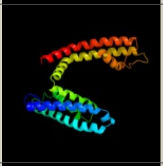
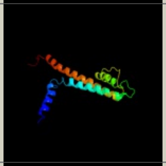
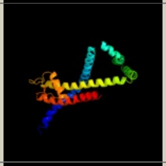
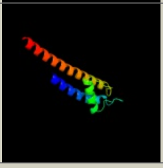
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P31069
Date	Wed Jan 25 15:20:48 GMT 2012
Unique Job ID	56be85d3f8a1469f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1lnqC_	Alignment		100.0	25	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**potassium channel related protein; **PDBTitle:** crystal structure of mthk at 3.3 a
2	d1id1a_	Alignment		100.0	100	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
3	c3fwzA_	Alignment		99.9	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
4	c3eywA_	Alignment		99.9	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
5	d2fy8a1	Alignment		99.9	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
6	d1lssa_	Alignment		99.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
7	c2g1uA_	Alignment		99.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
8	c2fy8A_	Alignment		99.9	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**calcium-gated potassium channel mthk; **PDBTitle:** crystal structure of mthk rck domain in its ligand-free gating-ring2 form
9	c3llvA_	Alignment		99.8	16	**PDB header:**nad(p) binding protein **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
10	c3c85A_	Alignment		99.8	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative glutathione-regulated potassium-efflux system **PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
11	d2hmva1	Alignment		99.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain

12	c3l4bG_	Alignment		99.8	19	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**trka k+ channel protien tm1088b; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
13	c3u6nC_	Alignment		99.8	18	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**high-conductance ca2+-activated k+ channel protein; **PDBTitle:** open structure of the bk channel gating ring
14	c3mt5A_	Alignment		99.7	20	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**potassium large conductance calcium-activated channel, **PDBTitle:** crystal structure of the human bk gating apparatus
15	c3nafA_	Alignment		99.7	18	**PDB header:**ion transport **Chain:** A: **PDB Molecule:**calcium-activated potassium channel subunit alpha-1; **PDBTitle:** structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel)
16	c2r9rH_	Alignment		99.6	13	**PDB header:**membrane protein, transport protein **Chain:** H: **PDB Molecule:**paddle chimera voltage gated potassium channel kv1.2-kv2.1; **PDBTitle:** shaker family voltage dependent potassium channel (kv1.2-kv2.1 paddle2 chimera channel) in association with beta subunit
17	c3behA_	Alignment		99.5	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mll3241 protein; **PDBTitle:** structure of a bacterial cyclic nucleotide regulated ion channel
18	d1f6ga_	Alignment		99.4	24	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
19	d1orqc_	Alignment		99.3	14	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
20	d1r3jc_	Alignment		99.2	24	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
21	c2kb1A_	Alignment	not modelled	99.2	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**wsk3; **PDBTitle:** nmr studies of a channel protein without membrane:2 structure and dynamics of water-solubilized kcsa
22	d2a9ha1	Alignment	not modelled	99.1	24	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
23	c3e8gB_	Alignment	not modelled	99.1	20	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**potassium channel protein; **PDBTitle:** crystal structure of the the open nak channel-na+/ca2+ complex
24	c3ifxB_	Alignment	not modelled	99.0	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**voltage-gated potassium channel; **PDBTitle:** crystal structure of the spin-labeled kcsa mutant v48r1
25	c2qksA_	Alignment	not modelled	99.0	22	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**kir3.1-prokaryotic kir channel chimera; **PDBTitle:** crystal structure of a kir3.1-prokaryotic kir channel chimera
26	c1xl6B_	Alignment	not modelled	99.0	23	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**inward rectifier potassium channel; **PDBTitle:** intermediate gating structure 2 of the inwardly rectifying k+ channel2 kirbac3.1
27	d1xl4a2	Alignment	not modelled	99.0	23	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
28	d1p7ba2	Alignment	not modelled	98.8	24	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
29	c1p7bB_	Alignment	not modelled	98.6	23	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**integral membrane channel and cytosolic domains;

						PDBTitle: crystal structure of an inward rectifier potassium channel
30	c3jycA_	Alignment	not modelled	98.4	20	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**inward-rectifier k+ channel kir2.2; **PDBTitle:** crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
31	d1e5qa1	Alignment	not modelled	98.3	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
32	d1pjqa1	Alignment	not modelled	98.3	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
33	d1lnqa2	Alignment	not modelled	98.3	33	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
34	c2qx7A_	Alignment	not modelled	97.9	10	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
35	d2h8pc1	Alignment	not modelled	97.7	22	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
36	d1xgka_	Alignment	not modelled	97.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
37	c3ic5A_	Alignment	not modelled	97.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
38	c2we7A_	Alignment	not modelled	97.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
39	d2pgda2	Alignment	not modelled	97.1	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
40	d1kyqa1	Alignment	not modelled	97.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
41	c3ktdC_	Alignment	not modelled	97.0	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
42	d1qyca_	Alignment	not modelled	97.0	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	c1e5lA_	Alignment	not modelled	97.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
44	d2jfga1	Alignment	not modelled	96.9	13	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
45	c2axqA_	Alignment	not modelled	96.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
46	c3orqA_	Alignment	not modelled	96.9	16	**PDB header:**ligase,biosynthetic protein **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide synthetase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
47	d1qyda_	Alignment	not modelled	96.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
48	c1kyqC_	Alignment	not modelled	96.8	13	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
49	d1n7ha_	Alignment	not modelled	96.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
50	c2c20D_	Alignment	not modelled	96.7	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of udp-glucose 4-epimerase
51	d1pjca1	Alignment	not modelled	96.7	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
52	c2iz1C_	Alignment	not modelled	96.7	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data
53	c3dhyC_	Alignment	not modelled	96.7	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
54	c1kjjA_	Alignment	not modelled	96.7	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
						PDB header:transferase/oxidoreductase/lyase

55	c1pjtB_	Alignment	not modelled	96.6	20	**Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
56	c2zcuA_	Alignment	not modelled	96.6	18	**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
57	c3q2oB_	Alignment	not modelled	96.6	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
58	c3on5B_	Alignment	not modelled	96.6	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bh1974 protein; **PDBTitle:** crystal structure of a xanthine dehydrogenase (bh1974) from bacillus2 halodurans at 2.80 a resolution
59	c2pv7B_	Alignment	not modelled	96.6	7	**PDB header:**isomerase, oxidoreductase **Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) **PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
60	c3c1oA_	Alignment	not modelled	96.6	8	**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
61	c3i5mA_	Alignment	not modelled	96.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative leucoanthocyanidin reductase 1; **PDBTitle:** structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
62	c2x4gA_	Alignment	not modelled	96.5	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
63	c2vrcD_	Alignment	not modelled	96.5	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**triphenylmethane reductase; **PDBTitle:** crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
64	c3dfzB_	Alignment	not modelled	96.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
65	d1ek6a_	Alignment	not modelled	96.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
66	c1pgjA_	Alignment	not modelled	96.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
67	c3oneA_	Alignment	not modelled	96.4	15	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
68	c2gn9B_	Alignment	not modelled	96.4	10	**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
69	c3n58D_	Alignment	not modelled	96.4	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
70	c3uvzB_	Alignment	not modelled	96.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
71	d1bg6a2	Alignment	not modelled	96.3	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
72	d1t2aa_	Alignment	not modelled	96.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
73	c1t2aC_	Alignment	not modelled	96.3	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
74	d1i24a_	Alignment	not modelled	96.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
75	c2q1uA_	Alignment	not modelled	96.3	16	**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
76	c2rirA_	Alignment	not modelled	96.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
77	c2hg5D_	Alignment	not modelled	96.2	23	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**kcsa channel; **PDBTitle:** cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
78	d1orra_	Alignment	not modelled	96.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases

79	c3e48B_	Alignment	not modelled	96.1	12	**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
80	c2q1wC_	Alignment	not modelled	96.1	16	**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+
81	c3ggpA_	Alignment	not modelled	96.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
82	c1z7eC_	Alignment	not modelled	96.1	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
83	c3k5iB_	Alignment	not modelled	96.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole carboxylase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimadazole ribonucleotide
84	c2f1kD_	Alignment	not modelled	96.1	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
85	d2f1ka2	Alignment	not modelled	96.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
86	d1kjqa2	Alignment	not modelled	96.0	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
87	d1rpna_	Alignment	not modelled	96.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	c3gpiA_	Alignment	not modelled	96.0	13	**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
89	d1ks9a2	Alignment	not modelled	96.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
90	c2exxB_	Alignment	not modelled	96.0	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hscarg protein; **PDBTitle:** crystal structure of hscarg from homo sapiens in complex with nadp
91	c3fwnB_	Alignment	not modelled	96.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
92	c3gvpB_	Alignment	not modelled	96.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
93	c3enkB_	Alignment	not modelled	95.9	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
94	d1np3a2	Alignment	not modelled	95.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
95	d1wvga1	Alignment	not modelled	95.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
96	d1pgja2	Alignment	not modelled	95.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
97	d1z45a2	Alignment	not modelled	95.8	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	c2pzlB_	Alignment	not modelled	95.8	22	**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
99	c3slgB_	Alignment	not modelled	95.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pbgp3 protein; **PDBTitle:** crystal structure of pbgp3 protein from burkholderia pseudomallei
100	c1np3B_	Alignment	not modelled	95.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
101	d1bxka_	Alignment	not modelled	95.8	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
102	c1v8bA_	Alignment	not modelled	95.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
						PDB header:lyase

103	c1n7gB_	Alignment	not modelled	95.8	12	**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.
104	c1luaA_	Alignment	not modelled	95.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methylene tetrahydromethanopterin dehydrogenase; **PDBTitle:** structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
105	c3triB_	Alignment	not modelled	95.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
106	c2dwcB_	Alignment	not modelled	95.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
107	c3d64A_	Alignment	not modelled	95.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
108	c2g5cD_	Alignment	not modelled	95.8	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
109	d1udca_	Alignment	not modelled	95.7	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
110	d2pv7a2	Alignment	not modelled	95.7	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
111	c2pk3B_	Alignment	not modelled	95.7	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
112	c1z45A_	Alignment	not modelled	95.7	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
113	c3dqpA_	Alignment	not modelled	95.7	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.
114	d1kewa_	Alignment	not modelled	95.6	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
115	c3d4oA_	Alignment	not modelled	95.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
116	c2ph5A_	Alignment	not modelled	95.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
117	d1a9xa4	Alignment	not modelled	95.6	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
118	c2p5uC_	Alignment	not modelled	95.6	17	**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
119	d1oc2a_	Alignment	not modelled	95.6	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
120	c1gpjA_	Alignment	not modelled	95.6	17	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri