Phyre^2

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Description	P0AG03
Date	Thu Jan 5 11:27:43 GMT 2012
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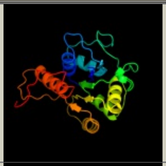
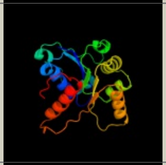
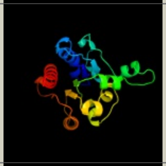
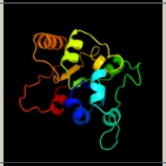
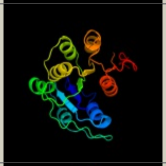
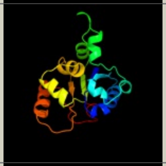
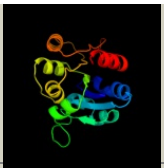
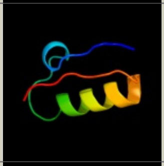
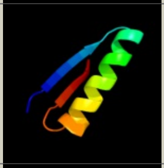
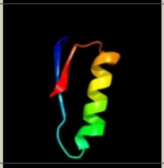
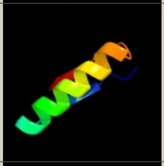
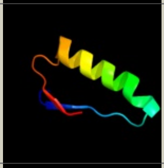
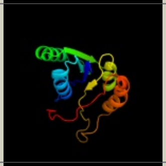
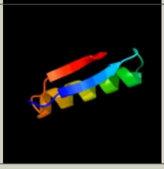
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3zquA_	Alignment		100.0	42	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
2	d1sbza_	Alignment		100.0	54	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
3	c2ejbA_	Alignment		100.0	43	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
4	c1mvlA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ppc decarboxylase athal3a; **PDBTitle:** ppc decarboxylase mutant c175s
5	d1mvla_	Alignment		100.0	18	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
6	d1g5qa_	Alignment		100.0	14	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
7	c3lqkA_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
8	c3qjgD_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**epidermin biosynthesis protein epid; **PDBTitle:** epidermin biosynthesis protein epid from staphylococcus aureus
9	c3mcuF_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dipicolinate synthase, b chain; **PDBTitle:** crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
10	d1qzua_	Alignment		100.0	19	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
11	c1qzuB_	Alignment		100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein mds018; **PDBTitle:** crystal structure of human phosphopantothenoylcysteine decarboxylase

12	d1p3y1_	Alignment		100.0	16	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
13	c2q1wC_	Alignment		93.5	22	**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+
14	d1bxka_	Alignment		93.1	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
15	c3dhnA_	Alignment		92.7	35	**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.
16	c3gpiA_	Alignment		92.4	23	**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
17	c3ia7A_	Alignment		92.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
18	d1oc2a_	Alignment		91.8	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
19	c3mt0A_	Alignment		90.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1789; **PDBTitle:** the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
20	d2z3va1	Alignment		90.7	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
21	d2p1ra1	Alignment	not modelled	90.6	12	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
22	d1f0ka_	Alignment	not modelled	90.6	22	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
23	c3c1oA_	Alignment	not modelled	90.4	22	**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
24	d1hdoa_	Alignment	not modelled	89.7	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
25	d1mjha_	Alignment	not modelled	88.6	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
26	c3s3tD_	Alignment	not modelled	88.5	10	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
27	c2qx7A_	Alignment	not modelled	87.7	22	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
28	c3hgmD_	Alignment	not modelled	86.6	23	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**universal stress protein tead; **PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata

29	d1tq8a_	Alignment	not modelled	86.5	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
30	c2ehdB_	Alignment	not modelled	86.1	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, short-chain dehydrogenase/reductase family; **PDBTitle:** crystal structure analysis of oxidoreductase
31	d1udca_	Alignment	not modelled	85.3	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
32	c3rfxB_	Alignment	not modelled	85.2	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
33	c3loqA_	Alignment	not modelled	85.1	12	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304
34	c3ouzA_	Alignment	not modelled	84.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
35	d1pn3a_	Alignment	not modelled	84.2	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
36	d1gy8a_	Alignment	not modelled	84.0	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
37	d1q0qa2	Alignment	not modelled	83.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
38	d2q49a1	Alignment	not modelled	83.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
39	c3icpA_	Alignment	not modelled	83.5	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of udp-galactose 4-epimerase
40	c3dzcA_	Alignment	not modelled	83.5	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
41	c1drwA_	Alignment	not modelled	83.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
42	d1v4va_	Alignment	not modelled	82.8	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
43	d1o6ca_	Alignment	not modelled	82.1	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
44	d1rpna_	Alignment	not modelled	81.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
45	c2p5uC_	Alignment	not modelled	81.7	27	**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
46	d1rrva_	Alignment	not modelled	80.8	25	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
47	d1iira_	Alignment	not modelled	80.6	19	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
48	c2pzlB_	Alignment	not modelled	80.4	27	**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
49	c2pk3B_	Alignment	not modelled	80.3	30	**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	d1e5qa1	Alignment	not modelled	80.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
51	c1k5hB_	Alignment	not modelled	79.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase
52	d1q77a_	Alignment	not modelled	79.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
53	c3m2pD_	Alignment	not modelled	79.7	13	**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
54	c3idfA_	Alignment	not modelled	79.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usp-like protein; **PDBTitle:** the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a
						Fold:NAD(P)-binding Rossmann-fold domains

55	d1kewa_	Alignment	not modelled	79.3	23	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
56	d1n7ha_	Alignment	not modelled	77.7	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
57	c3hskB_	Alignment	not modelled	77.3	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
58	d1ex9a_	Alignment	not modelled	77.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
59	c3fg9B_	Alignment	not modelled	76.9	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein of universal stress protein uspa family; **PDBTitle:** the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
60	d2c5aa1	Alignment	not modelled	76.7	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
61	d2cvoa1	Alignment	not modelled	76.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
62	d1ek6a_	Alignment	not modelled	75.1	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
63	c2ydyA_	Alignment	not modelled	75.0	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
64	c3ab8B_	Alignment	not modelled	74.9	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein ttha0350; **PDBTitle:** crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
65	d2q46a1	Alignment	not modelled	74.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
66	c1n7gB_	Alignment	not modelled	74.7	29	**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.
67	c2iyaB_	Alignment	not modelled	74.5	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
68	d1rz3a_	Alignment	not modelled	74.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
69	c2hunB_	Alignment	not modelled	74.3	12	**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
70	c3ew7A_	Alignment	not modelled	74.0	16	**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.
71	c2x4gA_	Alignment	not modelled	73.9	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
72	d1jmva_	Alignment	not modelled	73.8	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
73	c3slgB_	Alignment	not modelled	73.7	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pbgp3 protein; **PDBTitle:** crystal structure of pbgp3 protein from burkholderia pseudomallei
74	c3a2kB_	Alignment	not modelled	73.6	24	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
75	c2ggsB_	Alignment	not modelled	70.8	33	**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
76	d2blla1	Alignment	not modelled	70.8	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
77	c3sc6F_	Alignment	not modelled	70.6	29	**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	c2dumD_	Alignment	not modelled	70.4	15	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
79	c2pfsA_	Alignment	not modelled	69.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from

						nitrosomonas2 europaea
80	d1f6da_	Alignment	not modelled	69.8	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
81	c2iodD_	Alignment	not modelled	69.4	26	**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
82	c3tovB_	Alignment	not modelled	68.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
83	c2jzcA_	Alignment	not modelled	68.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine transferase subunit **PDBTitle:** nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
84	d1t1ra2	Alignment	not modelled	67.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
85	c3a14B_	Alignment	not modelled	67.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
86	c2f1rA_	Alignment	not modelled	67.0	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
87	c3p19A_	Alignment	not modelled	66.9	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative blue fluorescent protein; **PDBTitle:** improved nadph-dependent blue fluorescent protein
88	c3c8uA_	Alignment	not modelled	66.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
89	c3asyB_	Alignment	not modelled	66.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine kinase; **PDBTitle:** ligand-free structure of uridine kinase from thermus thermophilus hb8
90	d1ru8a_	Alignment	not modelled	65.8	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
91	d1n2sa_	Alignment	not modelled	65.6	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
92	d1odfa_	Alignment	not modelled	65.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
93	c2p6pB_	Alignment	not modelled	64.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
94	c3ay3C_	Alignment	not modelled	64.6	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
95	d1sb8a_	Alignment	not modelled	64.4	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
96	c3enkB_	Alignment	not modelled	64.3	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
97	d1orra_	Alignment	not modelled	64.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	d1q3ta_	Alignment	not modelled	63.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
99	d1a9xa4	Alignment	not modelled	63.6	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
100	c3s40C_	Alignment	not modelled	63.3	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
101	d1fjha_	Alignment	not modelled	62.9	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
102	c2x86K_	Alignment	not modelled	62.8	27	**PDB header:**isomerase **Chain:** K: **PDB Molecule:**adp-l-glycero-d-manno-heptose-6-epimerase; **PDBTitle:** agme bound to adp-b-mannose
103	c2b69A_	Alignment	not modelled	62.2	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**udp-glucuronate decarboxylase 1; **PDBTitle:** crystal structure of human udp-glucoronic acid decarboxylase
104	d2b69a1	Alignment	not modelled	62.2	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Tyrosine-dependent oxidoreductases
105	c1kh2D_	Alignment	not modelled	62.2	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
106	c2c20D_	Alignment	not modelled	61.8	24	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of udp-glucose 4-epimerase
107	d2fmua1	Alignment	not modelled	61.4	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
108	c3ghyA_	Alignment	not modelled	61.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
109	c3iusB_	Alignment	not modelled	61.1	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
110	c1ulzA_	Alignment	not modelled	61.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
111	c2rh8A_	Alignment	not modelled	60.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anthocyanidin reductase; **PDBTitle:** structure of apo anthocyanidin reductase from vitis vinifera
112	c2h1fB_	Alignment	not modelled	60.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
113	c2q49B_	Alignment	not modelled	58.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g19940
114	d1ni5a1	Alignment	not modelled	58.4	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
115	d1rkxa_	Alignment	not modelled	58.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
116	d1sq5a_	Alignment	not modelled	58.0	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
117	c3h2sA_	Alignment	not modelled	57.9	21	**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.
118	d1e6ua_	Alignment	not modelled	57.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	c2eghA_	Alignment	not modelled	57.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
120	d1wvga1	Alignment	not modelled	57.8	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases