Phyre^2

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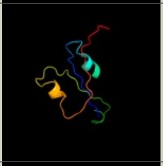
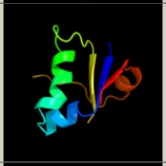
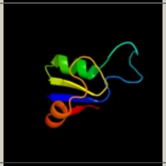
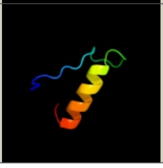
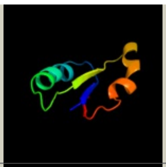
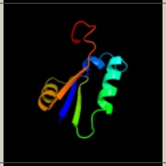
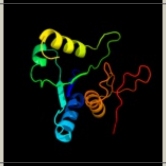
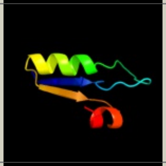
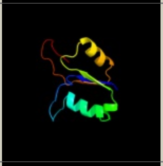
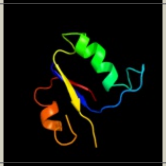
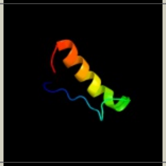
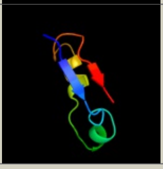
Description	P37182
Date	Thu Jan 5 11:54:57 GMT 2012
Unique Job ID	77ad7ae5b8910128

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cfza_	Alignment		100.0	99	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Hydrogenase maturating endopeptidase HybD
2	c2e85B_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrogenase 3 maturation protease; **PDBTitle:** crystal structure of the hydrogenase 3 maturation protease
3	c3pu6A_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of an uncharacterized protein from wolinella2 succinogenes
4	d1c8ba_	Alignment		96.2	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
5	d2ptha_	Alignment		94.8	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
6	d1t0ia_	Alignment		88.3	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
7	c1ks9A_	Alignment		86.3	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** ketopantoate reductase from escherichia coli
8	c2ofpB_	Alignment		85.5	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketopantoate reductase; **PDBTitle:** crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
9	c3ckyA_	Alignment		85.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-hydroxymethyl glutarate dehydrogenase; **PDBTitle:** structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
10	d1n1ea2	Alignment		84.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
11	c3v2iA_	Alignment		84.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis

12	d1txga2	Alignment		83.3	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
13	c3lcmB_	Alignment		82.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
14	d2c42a3	Alignment		82.8	9	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
15	d1mv8a2	Alignment		82.6	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
16	c2zklA_	Alignment		82.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**capsular polysaccharide synthesis enzyme cap5f; **PDBTitle:** crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
17	c1txgA_	Alignment		82.4	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
18	c3neaA_	Alignment		82.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
19	c3ic5A_	Alignment		82.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
20	c3g17H_	Alignment		81.4	23	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**similar to 2-dehydropantoate 2-reductase; **PDBTitle:** structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
21	c2f1kD_	Alignment	not modelled	79.8	37	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
22	c1ojuA_	Alignment	not modelled	79.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
23	c3l4bG_	Alignment	not modelled	78.0	20	**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
24	c3jviA_	Alignment	not modelled	77.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
25	d2vapa1	Alignment	not modelled	77.6	23	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
26	c3vh1A_	Alignment	not modelled	77.4	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of saccharomyces cerevisiae atg7 (1-595)
27	d2f1ka2	Alignment	not modelled	77.2	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
28	d1w5fa1	Alignment	not modelled	76.5	28	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like

						Family: Tubulin, GTPase domain
29	c3rh0A_	Alignment	not modelled	76.2	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
30	d1lssa_	Alignment	not modelled	76.1	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
31	c3l6dB_	Alignment	not modelled	76.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
32	d1ks9a2	Alignment	not modelled	75.9	36	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
33	c3vh3A_	Alignment	not modelled	75.6	29	**PDB header:**metal binding protein/protein transport **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of atg7ctd-atg8 complex
34	d1a5za1	Alignment	not modelled	75.4	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
35	c1w5fA_	Alignment	not modelled	75.2	28	**PDB header:**cell division **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz, t7 mutated, domain swapped (t. maritima)
36	c2y0dB_	Alignment	not modelled	74.5	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
37	c1u2pA_	Alignment	not modelled	72.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
38	c1a5zA_	Alignment	not modelled	72.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** lactate dehydrogenase from thermotoga maritima (tmldh)
39	c2gf2B_	Alignment	not modelled	72.6	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of human hydroxyisobutyrate dehydrogenase
40	d1guza1	Alignment	not modelled	72.4	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
41	c2cwdA_	Alignment	not modelled	71.6	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
42	c3gucB_	Alignment	not modelled	71.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ubiquitin-like modifier-activating enzyme 5; **PDBTitle:** human ubiquitin-activating enzyme 5 in complex with amppnp
43	c3qhaB_	Alignment	not modelled	71.3	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
44	c3eywA_	Alignment	not modelled	70.6	27	**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
45	d1rtta_	Alignment	not modelled	70.4	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
46	d1ojua1	Alignment	not modelled	70.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
47	c4a26B_	Alignment	not modelled	70.1	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
48	c3gg2B_	Alignment	not modelled	69.8	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sugar dehydrogenase, udp-glucose/gdp-mannose **PDBTitle:** crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
49	d1jf8a_	Alignment	not modelled	69.6	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
50	d2nqra3	Alignment	not modelled	69.4	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
51	c2z2vA_	Alignment	not modelled	68.9	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
52	c2z2jA_	Alignment	not modelled	68.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
53	c1y8qD_	Alignment	not modelled	67.9	29	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ubiquitin-like 2 activating enzyme e1b; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex

54	d2b0ja2	Alignment	not modelled	67.8	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
55	c2uyyD_	Alignment	not modelled	67.2	37	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
56	c3nepX_	Alignment	not modelled	66.8	28	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
57	c1mv8A_	Alignment	not modelled	66.6	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gdp-mannose 6-dehydrogenase; **PDBTitle:** 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
58	c1w59B_	Alignment	not modelled	66.1	23	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
59	d1gv0a1	Alignment	not modelled	66.0	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
60	c1zfnA_	Alignment	not modelled	65.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase thif; **PDBTitle:** structural analysis of escherichia coli thif
61	c3ghyA_	Alignment	not modelled	65.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
62	d2cmda1	Alignment	not modelled	65.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
63	c1vkzA_	Alignment	not modelled	65.3	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
64	c3dojA_	Alignment	not modelled	65.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
65	d1pgja2	Alignment	not modelled	64.7	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
66	d9ldta1	Alignment	not modelled	64.1	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
67	c2h1fB_	Alignment	not modelled	63.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
68	c3gznB_	Alignment	not modelled	61.6	24	**PDB header:**protein binding/ligase **Chain:** B: **PDB Molecule:**nedd8-activating enzyme e1 catalytic subunit; **PDBTitle:** structure of nedd8-activating enzyme in complex with nedd82 and mln4924
69	c2gi4A_	Alignment	not modelled	61.5	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
70	d2g2ca1	Alignment	not modelled	61.4	5	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
71	c3kydB_	Alignment	not modelled	61.2	29	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sumo-activating enzyme subunit 2; **PDBTitle:** human sumo e1~sumo1-amp tetrahedral intermediate mimic
72	d1ryba_	Alignment	not modelled	60.7	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
73	c2l18A_	Alignment	not modelled	60.0	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
74	c8ldhA_	Alignment	not modelled	59.0	34	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**m4 apo-lactate dehydrogenase; **PDBTitle:** refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
75	c2q1yB_	Alignment	not modelled	58.9	30	**PDB header:**cell cycle, signaling protein **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
76	c2v6bB_	Alignment	not modelled	58.7	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
77	d1j5pa4	Alignment	not modelled	58.6	50	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
78	c3g0oA_	Alignment	not modelled	58.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
79	c3egoB_	Alignment	not modelled	58.2	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis

80	c1nhqA_	Alignment	not modelled	54.9	26	**PDB header:**oxidoreductase (h2o2(a)) **Chain:** A: **PDB Molecule:**nadh peroxidase; **PDBTitle:** crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
81	d1yovb1	Alignment	not modelled	54.9	24	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Ubiquitin activating enzymes (UBA)
82	d5pnta_	Alignment	not modelled	54.1	20	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
83	c3prjB_	Alignment	not modelled	54.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
84	c2pjkA_	Alignment	not modelled	53.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
85	c3h9gA_	Alignment	not modelled	53.6	24	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**mccb protein; **PDBTitle:** crystal structure of e. coli mccb + mcca-n7isoasn
86	d1dg9a_	Alignment	not modelled	52.3	23	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
87	d1ydga_	Alignment	not modelled	51.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
88	c3rofA_	Alignment	not modelled	51.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine-phosphatase ptpa; **PDBTitle:** crystal structure of the s. aureus protein tyrosine phosphatase ptpa
89	d1nhpa1	Alignment	not modelled	51.7	34	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
90	d1jaya_	Alignment	not modelled	51.5	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
91	d1t2da1	Alignment	not modelled	50.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
92	d1sc6a2	Alignment	not modelled	50.6	16	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
93	c1zggA_	Alignment	not modelled	48.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative low molecular weight protein-tyrosine- **PDBTitle:** solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
94	c3m2pD_	Alignment	not modelled	47.9	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
95	c2hunB_	Alignment	not modelled	47.8	27	**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
96	d1i36a2	Alignment	not modelled	47.5	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
97	d1vl0a_	Alignment	not modelled	47.3	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	c3plnA_	Alignment	not modelled	47.3	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
99	c1i36A_	Alignment	not modelled	47.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein mth1747; **PDBTitle:** structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
100	d1a9xa3	Alignment	not modelled	46.3	22	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
101	d1pjca1	Alignment	not modelled	46.3	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
102	c2dc1A_	Alignment	not modelled	46.2	41	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
103	c1d4fD_	Alignment	not modelled	45.3	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
						PDB header:oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate

104	c2cukC_	Alignment	not modelled	45.2	16	reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
105	c3bioB_	Alignment	not modelled	45.2	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
106	d1leha1	Alignment	not modelled	44.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
107	c2p5uC_	Alignment	not modelled	44.4	55	**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
108	c1gv1D_	Alignment	not modelled	44.1	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
109	d1d1qa_	Alignment	not modelled	43.6	16	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
110	c3ju3A_	Alignment	not modelled	42.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; **PDBTitle:** crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
111	c3hn2A_	Alignment	not modelled	42.4	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
112	d1y1la_	Alignment	not modelled	41.9	18	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
113	c3f46A_	Alignment	not modelled	41.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydromethanopterin hydrogenase; **PDBTitle:** the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii
114	c2o3jC_	Alignment	not modelled	41.7	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of caenorhabditis elegans udp-glucose dehydrogenase
115	c2qytA_	Alignment	not modelled	41.6	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
116	d1iira_	Alignment	not modelled	41.3	21	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
117	c2vhyB_	Alignment	not modelled	41.1	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
118	c2ew2B_	Alignment	not modelled	41.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase, putative; **PDBTitle:** crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
119	c2q3eH_	Alignment	not modelled	40.7	21	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
120	d1jl3a_	Alignment	not modelled	40.4	24	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases