Phyre^2

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Description	P12281
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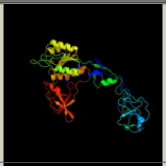
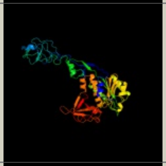
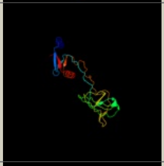
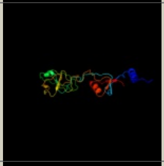
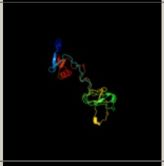
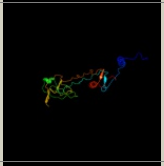
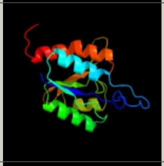
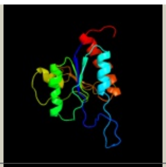
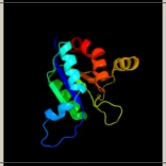
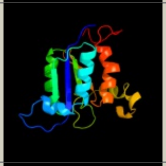
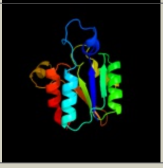
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nqqA_	Alignment		100.0	100	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
2	c1uz5A_	Alignment		100.0	35	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
3	c2fu3A_	Alignment		100.0	36	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
4	c1wu2B_	Alignment		100.0	30	**PDB header:**structural genomics,biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis moea protein; **PDBTitle:** crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
5	d2nqra2	Alignment		100.0	99	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
6	d1uz5a2	Alignment		100.0	32	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
7	d1wu2a2	Alignment		100.0	35	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
8	d2ftsa2	Alignment		100.0	37	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
9	d2nqra3	Alignment		100.0	100	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
10	d2ftsa3	Alignment		100.0	43	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
11	d1uz5a3	Alignment		100.0	43	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like

12	d1wu2a3	Alignment		100.0	28	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
13	c2pjkA_	Alignment		100.0	21	**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
14	d1y5ea1	Alignment		100.0	22	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
15	d1xi8a3	Alignment		100.0	30	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
16	c2is8A_	Alignment		100.0	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
17	d1jlja_	Alignment		100.0	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
18	d1mkza_	Alignment		100.0	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
19	d2g2ca1	Alignment		100.0	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
20	c3kbqA_	Alignment		100.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
21	c3rfqC_	Alignment	not modelled	100.0	24	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
22	c2g4rB_	Alignment	not modelled	100.0	18	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
23	d1uuya_	Alignment	not modelled	100.0	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
24	d2f7wa1	Alignment	not modelled	99.9	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
25	d1di6a_	Alignment	not modelled	99.9	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
26	d1xi8a2	Alignment	not modelled	99.7	27	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
27	d2nqra1	Alignment	not modelled	99.7	100	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
28	d2ftsa1	Alignment	not modelled	99.4	24	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
						Fold:beta-clip

29	d1wu2a1	Alignment	not modelled	99.4	18	**Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
30	d1xi8a1	Alignment	not modelled	99.3	26	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
31	d1uz5a1	Alignment	not modelled	99.2	21	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
32	c2rirA_	Alignment	not modelled	94.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
33	d1l7da1	Alignment	not modelled	94.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
34	c3d4oA_	Alignment	not modelled	93.6	21	**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
35	c3c7cB_	Alignment	not modelled	92.6	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**octopine dehydrogenase; **PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
36	c2yxbA_	Alignment	not modelled	92.3	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
37	d1gpma2	Alignment	not modelled	91.8	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
38	c1l9xA_	Alignment	not modelled	91.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
39	d1l9xa_	Alignment	not modelled	91.4	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
40	d1yq9a1	Alignment	not modelled	91.2	17	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
41	d7reqa2	Alignment	not modelled	90.9	25	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
42	d1pjca1	Alignment	not modelled	90.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
43	d1i7qb_	Alignment	not modelled	90.6	13	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
44	c3d54D_	Alignment	not modelled	90.3	24	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
45	c3louB_	Alignment	not modelled	90.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
46	d1ccwa_	Alignment	not modelled	90.2	25	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
47	c3myrE_	Alignment	not modelled	89.6	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
48	c3n0vD_	Alignment	not modelled	89.4	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
49	c3en0A_	Alignment	not modelled	89.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
50	d1fmfa_	Alignment	not modelled	89.2	19	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
51	c3o1lB_	Alignment	not modelled	89.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
52	d1t3ta2	Alignment	not modelled	88.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
53	c3l4eA_	Alignment	not modelled	88.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
54	c3rgwS_	Alignment	not modelled	87.7	10	**PDB header:**oxidoreductase/oxidoreductase **Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk; **PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
						PDB header:oxidoreductase

55	c1np3B_	Alignment	not modelled	86.9	33	**Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
56	d1i1qb_	Alignment	not modelled	86.9	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
57	c3p2yA_	Alignment	not modelled	86.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
58	d1wl8a1	Alignment	not modelled	86.1	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
59	d1qdlb_	Alignment	not modelled	86.1	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
60	d1q7ra_	Alignment	not modelled	85.9	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
61	d1ka9h_	Alignment	not modelled	85.5	38	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
62	d2a9va1	Alignment	not modelled	85.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
63	d1bg6a2	Alignment	not modelled	85.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
64	c3fijD_	Alignment	not modelled	84.3	32	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
65	c2wpnA_	Alignment	not modelled	83.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [nifese] hydrogenase, small subunit; **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
66	d1frfs_	Alignment	not modelled	83.7	13	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
67	c2issF_	Alignment	not modelled	83.7	28	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
68	c1pjcA_	Alignment	not modelled	83.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (l-alanine dehydrogenase); **PDBTitle:** l-alanine dehydrogenase complexed with nad
69	d1uxja1	Alignment	not modelled	83.1	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
70	d1wuis1	Alignment	not modelled	82.0	17	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
71	d1y6ja1	Alignment	not modelled	82.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
72	d2nv0a1	Alignment	not modelled	81.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
73	d1jvna2	Alignment	not modelled	81.7	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
74	d1agxa_	Alignment	not modelled	80.8	14	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
75	c2d6fA_	Alignment	not modelled	80.4	16	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
76	c3melC_	Alignment	not modelled	80.3	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase family protein; **PDBTitle:** crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150
77	c3cumA_	Alignment	not modelled	80.2	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
78	c2y0dB_	Alignment	not modelled	79.6	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
79	c3r74B_	Alignment	not modelled	79.2	21	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
						Fold: Glutaminase/Asparaginase

80	d1zq1a2	Alignment	not modelled	78.7	14	**Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
81	c3dfuB_	Alignment	not modelled	78.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein from 6-phosphogluconate **PDBTitle:** crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution
82	c2eezG_	Alignment	not modelled	78.0	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase from themus thermophilus
83	d1cc1s_	Alignment	not modelled	77.8	14	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
84	c1wwkA_	Alignment	not modelled	77.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
85	d4pgaa_	Alignment	not modelled	77.1	22	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
86	d9ldta1	Alignment	not modelled	77.0	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
87	d2naca2	Alignment	not modelled	77.0	23	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
88	c1vpdA_	Alignment	not modelled	76.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
89	d1i36a2	Alignment	not modelled	75.5	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
90	d1dlja3	Alignment	not modelled	75.4	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain **Family:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
91	c3ihkC_	Alignment	not modelled	75.2	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83
92	c3cq9C_	Alignment	not modelled	75.1	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uncharacterized protein lp_1622; **PDBTitle:** crystal structure of the lp_1622 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr114
93	c1u4sA_	Alignment	not modelled	75.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
94	c2i99A_	Alignment	not modelled	74.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mu-crystallin homolog; **PDBTitle:** crystal structure of human mu_crystallin at 2.6 angstrom
95	d1ldna1	Alignment	not modelled	74.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
96	c2vhyB_	Alignment	not modelled	73.9	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
97	c3n7uD_	Alignment	not modelled	73.5	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
98	c3k13A_	Alignment	not modelled	73.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
99	c3nxkE_	Alignment	not modelled	73.4	21	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
100	c3rggD_	Alignment	not modelled	73.4	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
101	d1s1ma1	Alignment	not modelled	73.2	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
102	d1vmka_	Alignment	not modelled	72.7	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
103	d3bgsa1	Alignment	not modelled	72.7	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
104	c3lm8D_	Alignment	not modelled	72.6	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine pyrophosphokinase; **PDBTitle:** crystal structure of thiamine pyrophosphokinase from2

						bacillus subtilis, northeast structural genomics consortium3 target sr677
105	c2j6iC_	Alignment	not modelled	72.5	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
106	c3lp6D_	Alignment	not modelled	72.5	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
107	c2ppwA_	Alignment	not modelled	72.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
108	d1gdha1	Alignment	not modelled	72.3	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
109	c2xecD_	Alignment	not modelled	72.2	23	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
110	d2naca1	Alignment	not modelled	72.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
111	d3bula2	Alignment	not modelled	71.9	20	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
112	c2g76A_	Alignment	not modelled	71.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
113	c3e7hA_	Alignment	not modelled	71.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** the crystal structure of the beta subunit of the dna-2 directed rna polymerase from vibrio cholerae o1 biovar3 eltor
114	d1k9vf_	Alignment	not modelled	71.4	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
115	d1j4aa1	Alignment	not modelled	71.4	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
116	c1y80A_	Alignment	not modelled	71.1	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
117	c3onoA_	Alignment	not modelled	70.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
118	c3he8A_	Alignment	not modelled	70.7	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
119	d1o7ja_	Alignment	not modelled	70.3	17	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
120	c2vq3B_	Alignment	not modelled	70.3	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**metalloreductase steap3; **PDBTitle:** crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle