Phyre2

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Description	P00452
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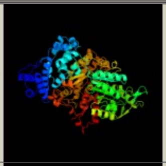
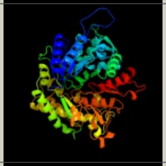
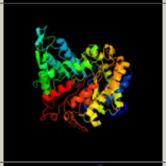
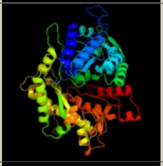
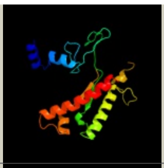
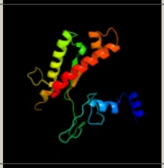
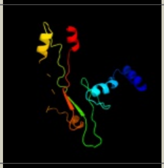
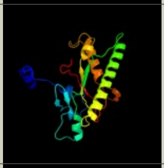
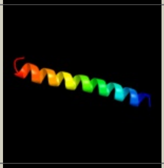
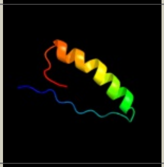
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r1rB_	Alignment		100.0	100	**PDB header:**complex (oxidoreductase/peptide) **Chain:** B: **PDB Molecule:**ribonucleotide reductase r1 protein; **PDBTitle:** ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
2	c3hnfA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large subunit; **PDBTitle:** crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
3	c2whgA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large **PDBTitle:** human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
4	c1pemA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase 2 alpha **PDBTitle:** ribonucleotide reductase protein r1e from salmonella2 typhimurium
5	c2cvuA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large chain **PDBTitle:** structures of yeast ribonucleotide reductase i
6	d1rlra2	Alignment		100.0	99	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain
7	c1xjeA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleotide reductase, b12-dependent; **PDBTitle:** structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dttp-gdp complex
8	d1peqa2	Alignment		100.0	25	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain
9	d1l1la_	Alignment		100.0	15	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**B12-dependent (class II) ribonucleotide reductase
10	d1rlra1	Alignment		100.0	100	**Fold:**R1 subunit of ribonucleotide reductase, N-terminal domain **Superfamily:**R1 subunit of ribonucleotide reductase, N-terminal domain **Family:**R1 subunit of ribonucleotide reductase, N-terminal domain
11	d1peqa1	Alignment		100.0	14	**Fold:**R1 subunit of ribonucleotide reductase, N-terminal domain **Superfamily:**R1 subunit of ribonucleotide reductase, N-terminal domain **Family:**R1 subunit of ribonucleotide reductase, N-terminal domain

12	d1hk8a_	Alignment		95.3	13	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
13	c1hk8A_	Alignment		95.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
14	d1h16a_	Alignment		86.4	19	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
15	d1qhma_	Alignment		43.8	17	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
16	c2f3oB_	Alignment		43.3	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
17	d1r9da_	Alignment		42.8	16	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
18	d1h3ob_	Alignment		34.1	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
19	d2okqa1	Alignment		33.0	8	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YbaA-like
20	d1vjfa_	Alignment		31.5	18	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
21	c2okqB_	Alignment	not modelled	22.8	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ybaa; **PDBTitle:** crystal structure of unknown conserved ybaa protein from2 shigella flexneri
22	c2bjgB_	Alignment	not modelled	22.6	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**choloylglycine hydrolase; **PDBTitle:** crystal structure of conjugated bile acid hydrolase from2 clostridium perfringens in complex with reaction products3 taurine and deoxycholate
23	c2hezB_	Alignment	not modelled	20.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bile salt hydrolase; **PDBTitle:** bifidobacterium longum bile salt hydrolase
24	d2pvaa_	Alignment	not modelled	19.7	12	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Penicillin V acylase
25	d1j09a2	Alignment	not modelled	19.2	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
26	d2ccqa1	Alignment	not modelled	18.5	16	**Fold:**PUG domain-like **Superfamily:**PUG domain-like **Family:**PUG domain
27	c1pgjA_	Alignment	not modelled	14.7	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
28	c3pg6D_	Alignment	not modelled	14.5	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**e3 ubiquitin-protein ligase dtx3l; **PDBTitle:** the carboxyl terminal domain of human deltex 3-like

29	d2b4va2	Alignment	not modelled	13.7	44	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**RNA editing terminal uridyl transferase 2, RET2, catalytic domain
30	c2iz1C_	Alignment	not modelled	13.7	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data
31	d1vmha_	Alignment	not modelled	12.1	13	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
32	d1vmfa_	Alignment	not modelled	12.1	16	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
33	d1ywsa1	Alignment	not modelled	12.1	21	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
34	d1mska_	Alignment	not modelled	12.1	20	**Fold:**Methionine synthase activation domain-like **Superfamily:**Methionine synthase activation domain-like **Family:**Methionine synthase SAM-binding domain
35	c2p4qA_	Alignment	not modelled	12.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating 1; **PDBTitle:** crystal structure analysis of gnd1 in saccharomyces cerevisiae
36	c2jr7A_	Alignment	not modelled	11.6	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**dph3 homolog; **PDBTitle:** solution structure of human desr1
37	d1vmja_	Alignment	not modelled	11.5	26	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
38	d1wgea1	Alignment	not modelled	11.2	21	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
39	d1avca2	Alignment	not modelled	10.9	14	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
40	d1vkia_	Alignment	not modelled	10.5	13	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
41	c2p6hB_	Alignment	not modelled	10.3	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
42	c2xrgA_	Alignment	not modelled	10.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
43	c2oqcB_	Alignment	not modelled	10.3	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**penicillin v acylase; **PDBTitle:** crystal structure of penicillin v acylase from bacillus subtilis
44	d1xn7a_	Alignment	not modelled	10.3	64	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein YhgG
45	d2d0ob1	Alignment	not modelled	9.6	10	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Dehydratase-reactivating factor beta subunit
46	c3rcqA_	Alignment	not modelled	9.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartyl/asparaginyl beta-hydroxylase; **PDBTitle:** crystal structure of human aspartate beta-hydroxylase isoform a
47	c2qlwA_	Alignment	not modelled	8.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rhau; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
48	c2qlxA_	Alignment	not modelled	8.9	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**l-rhamnose mutarotase; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
49	d1vpha_	Alignment	not modelled	8.7	14	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
50	c2p6cB_	Alignment	not modelled	8.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**aq_2013 protein; **PDBTitle:** crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
51	d1wiga2	Alignment	not modelled	8.3	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
52	d2g5ca2	Alignment	not modelled	8.3	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
53	c3dzbA_	Alignment	not modelled	8.2	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
54	c2xr9A_	Alignment	not modelled	7.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
						Fold:UDP-Glycosyltransferase/glycogen phosphorylase

55	d1f6da_	Alignment	not modelled	7.7	18	**Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
56	d1x8da1	Alignment	not modelled	7.5	40	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YiiL-like
57	c1vraA_	Alignment	not modelled	7.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginine biosynthesis bifunctional protein argj; **PDBTitle:** crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
58	c2g5cD_	Alignment	not modelled	7.4	32	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
59	d1gv2a2	Alignment	not modelled	7.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
60	d1f0ya2	Alignment	not modelled	7.3	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
61	c2pv7B_	Alignment	not modelled	7.2	39	**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
62	c3sggA_	Alignment	not modelled	7.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical hydrolase; **PDBTitle:** crystal structure of a hypothetical hydrolase (bt_2193) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
63	c1idzA_	Alignment	not modelled	7.0	24	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**mouse c-myb dna-binding domain repeat 3; **PDBTitle:** structure of myb transforming protein, nmr, 20 structures
64	c3kowH_	Alignment	not modelled	6.9	20	**PDB header:**metal binding protein **Chain:** H: **PDB Molecule:**d-ornithine aminomutase s component; **PDBTitle:** crystal structure of ornithine 4,5 aminomutase backsoaked complex
65	c3ggpA_	Alignment	not modelled	6.8	32	**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+
66	d1dm5a_	Alignment	not modelled	6.8	19	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
67	d1at3a_	Alignment	not modelled	6.7	30	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
68	d2csba2	Alignment	not modelled	6.7	21	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
69	c2wasA_	Alignment	not modelled	6.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase; **PDBTitle:** structure of the fungal type i fas ppt domain
70	d1wdka3	Alignment	not modelled	6.6	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
71	d2pgda2	Alignment	not modelled	6.6	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
72	d1hm6a_	Alignment	not modelled	6.5	18	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
73	d1nbwb_	Alignment	not modelled	6.4	25	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Dehydratase-reactivating factor beta subunit
74	c2ep9A_	Alignment	not modelled	6.3	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-gulonate 3-dehydrogenase; **PDBTitle:** crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
75	d1chua3	Alignment	not modelled	6.2	15	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
76	c3crw1_	Alignment	not modelled	6.2	16	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**xpd/rad3 related dna helicase; **PDBTitle:** "xpd_apo"
77	d1eexb_	Alignment	not modelled	6.1	22	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Diol dehydratase, beta subunit
78	d1vzva_	Alignment	not modelled	5.9	30	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
79	c2c1fA_	Alignment	not modelled	5.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bifunctional endo-1,4-beta-xylanase a; **PDBTitle:** the structure of the family 11 xylanase from neocallimastix2 patriciarum
						Fold:NAD(P)-binding Rossmann-fold domains

80	d1i36a2	Alignment	not modelled	5.9	28	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
81	c2h1zA_	Alignment	not modelled	5.9	50	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hybrid atracotoxin; **PDBTitle:** structure of a dual-target spider toxin
82	d1wo8a1	Alignment	not modelled	5.8	13	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
83	d1hrti_	Alignment	not modelled	5.8	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
84	c2v4iA_	Alignment	not modelled	5.8	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate n-acetyltransferase 2 alpha chain; **PDBTitle:** structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (ntn) hydrolase, oat2
85	d1zeta1	Alignment	not modelled	5.8	20	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
86	d3cuma2	Alignment	not modelled	5.8	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
87	c2dwuA_	Alignment	not modelled	5.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
88	d1mbja_	Alignment	not modelled	5.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
89	c1mbjA_	Alignment	not modelled	5.8	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**myb proto-oncogene protein; **PDBTitle:** mouse c-myb dna-binding domain repeat 3
90	c2rpaA_	Alignment	not modelled	5.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**katanin p60 atpase-containing subunit a1; **PDBTitle:** the solution structure of n-terminal domain of microtubule severing2 enzyme
91	d1sfkb_	Alignment	not modelled	5.7	20	**Fold:**Flavivirus capsid protein C **Superfamily:**Flavivirus capsid protein C **Family:**Flavivirus capsid protein C
92	d1uoua1	Alignment	not modelled	5.7	18	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
93	c3njqB_	Alignment	not modelled	5.7	30	**PDB header:**viral protein/inhibitor **Chain:** B: **PDB Molecule:**orf 17; **PDBTitle:** crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
94	d1m9ia2	Alignment	not modelled	5.7	22	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
95	c2p6uA_	Alignment	not modelled	5.7	36	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
96	c2rafC_	Alignment	not modelled	5.7	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dinucleotide-binding oxidoreductase; **PDBTitle:** crystal structure of putative dinucleotide-binding2 oxidoreductase (np_786167.1) from lactobacillus plantarum3 at 1.60 a resolution
97	d1h4ga_	Alignment	not modelled	5.6	17	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
98	d2pv7a2	Alignment	not modelled	5.6	44	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
99	c2ysrA_	Alignment	not modelled	5.6	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dep domain-containing protein 1; **PDBTitle:** solution structure of the dep domain from human dep domain-2 containing protein 1