Phyre2

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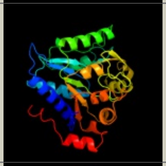
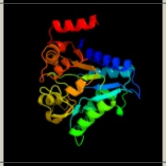
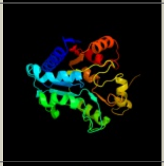
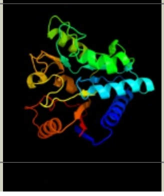
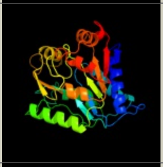
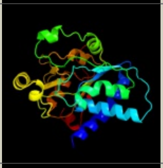
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fsfa_	Alignment		100.0	100	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
2	d1ne7a_	Alignment		100.0	58	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
3	c3hn6D_	Alignment		100.0	61	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
4	c2j0eA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
5	c3icoA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from2 mycobacterium tuberculosis
6	c3oc6A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
7	c1y89B_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**devb protein; **PDBTitle:** crystal structure of devb protein
8	c3e15D_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** 6-phosphogluconolactonase from plasmodium vivax
9	c1pbtA_	Alignment		100.0	20	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
10	c3cssA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
11	d1vl1a_	Alignment		100.0	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like

12	c3lwdA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
13	c3lhiA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
14	c2bkxB_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
15	c3nwpA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
16	c2ri0B_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
17	d2gnpa1	Alignment		99.7	11	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
18	c2w48D_	Alignment		99.6	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
19	c3nzeB_	Alignment		99.5	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator, sugar-binding family; **PDBTitle:** the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
20	c2o0mA_	Alignment		99.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, sorc family; **PDBTitle:** the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
21	d2o0ma1	Alignment	not modelled	99.5	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
22	d3efba1	Alignment	not modelled	99.5	11	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
23	d2okga1	Alignment	not modelled	98.9	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
24	c3kv1A_	Alignment	not modelled	98.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
25	d2r5fa1	Alignment	not modelled	98.3	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
26	c2e21A_	Alignment	not modelled	83.8	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
27	c3a2kB_	Alignment	not modelled	81.9	12	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
28	d1ni5a1	Alignment	not modelled	67.8	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
29	c2goyC_	Alignment	not modelled	64.7	8	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps

30	d1wxia1	Alignment	not modelled	51.1	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
31	d1xnga1	Alignment	not modelled	44.4	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
32	d1kqpa_	Alignment	not modelled	43.9	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
33	c1ni5A_	Alignment	not modelled	39.2	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
34	c2i2aA_	Alignment	not modelled	38.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase 1; **PDBTitle:** crystal structure of lmnadk1 from listeria monocytogenes
35	d1sura_	Alignment	not modelled	38.0	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
36	c1mwmA_	Alignment	not modelled	35.6	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
37	d1pjqa3	Alignment	not modelled	32.7	19	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
38	d1wy5a1	Alignment	not modelled	32.3	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
39	c3u7jA_	Alignment	not modelled	31.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
40	c2o8vA_	Alignment	not modelled	30.2	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
41	d2zgya2	Alignment	not modelled	26.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
42	c3dpiA_	Alignment	not modelled	26.2	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
43	c3q4gA_	Alignment	not modelled	26.2	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
44	d3clsc1	Alignment	not modelled	25.4	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
45	c3p52B_	Alignment	not modelled	25.2	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
46	c1zunA_	Alignment	not modelled	24.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
47	c2pjmA_	Alignment	not modelled	23.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
48	c3fiuD_	Alignment	not modelled	23.7	8	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
49	d1a7ja_	Alignment	not modelled	23.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
50	c1xhoB_	Alignment	not modelled	22.3	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**chorismate mutase; **PDBTitle:** chorismate mutase from clostridium thermocellum cth-682
51	d1xhoa_	Alignment	not modelled	22.3	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
52	c3sftA_	Alignment	not modelled	21.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate methylesterase **PDBTitle:** crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
53	c3hheA_	Alignment	not modelled	18.4	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
54	c3l7oB_	Alignment	not modelled	18.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
55	d1wd5a_	Alignment	not modelled	17.1	28	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
						Fold:FAD/NAD(P)-binding domain

56	d1rp0a1	Alignment	not modelled	15.9	16	**Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
57	c1lk5C_	Alignment	not modelled	15.8	35	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-ribose-5-phosphate isomerase; **PDBTitle:** structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
58	c1gpmD_	Alignment	not modelled	15.8	21	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
59	d1zuna1	Alignment	not modelled	15.0	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
60	c3uowB_	Alignment	not modelled	14.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
61	c2z5eA_	Alignment	not modelled	13.3	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**proteasome assembling chaperone 3; **PDBTitle:** crystal structure of proteasome assembling chaperone 3
62	d2fvta1	Alignment	not modelled	13.1	22	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
63	c1xtzA_	Alignment	not modelled	12.7	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
64	c3tqiB_	Alignment	not modelled	12.5	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
65	d1odfa_	Alignment	not modelled	12.3	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
66	d1dbfa_	Alignment	not modelled	11.9	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
67	c2vawA_	Alignment	not modelled	11.8	27	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
68	d1ydha_	Alignment	not modelled	11.7	23	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
69	c3kwmC_	Alignment	not modelled	11.6	27	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
70	c1dd9A_	Alignment	not modelled	11.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** structure of the dnag catalytic core
71	d1dd9a_	Alignment	not modelled	11.4	18	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**DNA primase DnaG catalytic core
72	c2q4dB_	Alignment	not modelled	11.3	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
73	c2r5kE_	Alignment	not modelled	11.2	25	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 11
74	c1x1qA_	Alignment	not modelled	11.1	2	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
75	d2vapa1	Alignment	not modelled	11.0	24	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
76	c2pv0A_	Alignment	not modelled	10.9	19	**PDB header:**transferase regulator **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3-like; **PDBTitle:** dna methyltransferase 3 like protein (dnmt3l)
77	c2dplA_	Alignment	not modelled	10.8	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3
78	c3maxB_	Alignment	not modelled	10.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histone deacetylase 2; **PDBTitle:** crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
79	d1rq2a1	Alignment	not modelled	10.6	24	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
80	d1h9aa1	Alignment	not modelled	10.2	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	c2q1yB_	Alignment	not modelled	10.0	24	**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

82	d1k92a1	Alignment	not modelled	10.0	6	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
83	d1r6ea_	Alignment	not modelled	9.9	12	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
84	c1dzlA_	Alignment	not modelled	9.7	50	**PDB header:**virus **Chain: A: PDB Molecule:**late major capsid protein l1; **PDBTitle:** l1 protein of human papillomavirus 16
85	d1dzla_	Alignment	not modelled	9.7	50	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group I dsDNA viruses **Family:**Papovaviridae-like VP
86	d1ofua1	Alignment	not modelled	9.7	29	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
87	c2r5iL_	Alignment	not modelled	9.4	25	**PDB header:**viral protein **Chain: L: PDB Molecule:**l1 protein; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 18
88	c1ofuB_	Alignment	not modelled	9.4	27	**PDB header:**bacterial cell division inhibitor **Chain: B: PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of sula:ftsz from pseudomonas aeruginosa
89	c1a2oB_	Alignment	not modelled	9.3	50	**PDB header:**bacterial chemotaxis **Chain: B: PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
90	d2uz9a1	Alignment	not modelled	9.3	47	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**SAH/MTA deaminase-like
91	c3c8uA_	Alignment	not modelled	9.3	15	**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
92	d1ufya_	Alignment	not modelled	9.2	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
93	c3ewbX_	Alignment	not modelled	9.2	13	**PDB header:**transferase **Chain: X: PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
94	c2gfqC_	Alignment	not modelled	8.9	21	**PDB header:**structural genomics, unknown function **Chain: C: PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
95	c1uj6A_	Alignment	not modelled	8.8	27	**PDB header:**isomerase **Chain: A: PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
96	d3bzka5	Alignment	not modelled	8.8	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
97	d1chda_	Alignment	not modelled	8.7	50	**Fold:**Methylesterase CheB, C-terminal domain **Superfamily:**Methylesterase CheB, C-terminal domain **Family:**Methylesterase CheB, C-terminal domain
98	c2oq2B_	Alignment	not modelled	8.7	11	**PDB header:**oxidoreductase **Chain: B: PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
99	d2ftwa1	Alignment	not modelled	8.6	38	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)