Phyre2

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Description	P30126
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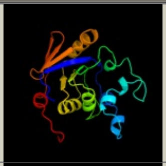
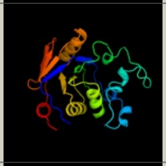
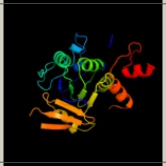
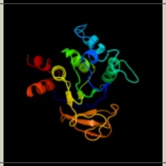
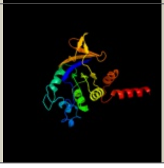
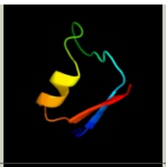
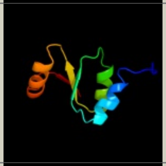
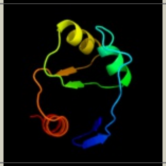
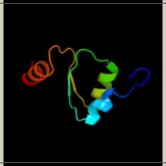
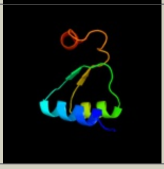
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3q3wB_	Alignment		100.0	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
2	c2hcuA_	Alignment		100.0	47	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
3	c3h5jA_	Alignment		100.0	45	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
4	d1v7la_	Alignment		100.0	30	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
5	c2pkpA_	Alignment		100.0	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
6	d1acoa1	Alignment		100.0	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
7	d2b3ya1	Alignment		100.0	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
8	d1l5ja2	Alignment		100.0	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
9	c2b3yB_	Alignment		100.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**iron-responsive element binding protein 1; **PDBTitle:** structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
10	c5acnA_	Alignment		100.0	21	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
11	c1l5jB_	Alignment		99.7	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aconitate hydratase 2; **PDBTitle:** crystal structure of e. coli aconitase b.

12	c1t6zB_	Alignment		65.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
13	d1eo1a_	Alignment		56.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
14	c2yx6C_	Alignment		56.2	9	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein ph0822; **PDBTitle:** crystal structure of ph0822
15	c3op1A_	Alignment		55.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
16	d1o13a_	Alignment		51.8	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
17	d1rdua_	Alignment		49.3	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
18	c2qtdA_	Alignment		46.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein mj0327; **PDBTitle:** crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution
19	d1t3va_	Alignment		41.1	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
20	c2wfbA_	Alignment		36.7	8	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein orp; **PDBTitle:** high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
21	c2dlnA_	Alignment	not modelled	33.9	22	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
22	c1vkzA_	Alignment	not modelled	32.1	34	**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
23	c3la8A_	Alignment	not modelled	29.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative purine nucleoside phosphorylase; **PDBTitle:** the crystal structure of smu.1229 from streptococcus mutans ua159
24	d1cmia_	Alignment	not modelled	29.5	24	**Fold:**DLC **Superfamily:**DLC **Family:**DLC
25	c3c3jA_	Alignment	not modelled	29.3	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
26	d1vkza2	Alignment	not modelled	29.3	45	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
27	d3e2ba1	Alignment	not modelled	29.0	24	**Fold:**DLC **Superfamily:**DLC **Family:**DLC
28	d1a9xa3	Alignment	not modelled	28.9	36	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like

29	c3t07D_	Alignment	not modelled	28.2	14	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
30	d1xjha_	Alignment	not modelled	28.1	37	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
31	c3uvzB_	Alignment	not modelled	27.1	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
32	c1z34A_	Alignment	not modelled	26.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
33	d1okkd2	Alignment	not modelled	25.3	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
34	d1nyta1	Alignment	not modelled	23.9	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
35	c3fj1A_	Alignment	not modelled	23.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
36	c2zj3A_	Alignment	not modelled	23.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
37	c1m6vE_	Alignment	not modelled	23.0	26	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
38	d1t0tv_	Alignment	not modelled	22.3	23	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
39	d2gp4a1	Alignment	not modelled	21.8	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
40	d1zyma2	Alignment	not modelled	21.6	9	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
41	c2re2A_	Alignment	not modelled	21.1	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized protein ta1041; **PDBTitle:** crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
42	d1vdha_	Alignment	not modelled	20.6	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
43	c3bgdB_	Alignment	not modelled	20.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiopurine s-methyltransferase; **PDBTitle:** thiopurine s-methyltransferase
44	c3pg8B_	Alignment	not modelled	19.6	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
45	d2hi6a1	Alignment	not modelled	19.5	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
46	d1a9xa4	Alignment	not modelled	19.3	24	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
47	c2xd4A_	Alignment	not modelled	19.1	34	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
48	c3idwA_	Alignment	not modelled	18.9	14	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
49	c1tcvB_	Alignment	not modelled	18.9	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine-nucleoside phosphorylase; **PDBTitle:** crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
50	c2amlB_	Alignment	not modelled	17.9	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
51	c2jgqB_	Alignment	not modelled	17.8	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
52	c3m4qA_	Alignment	not modelled	17.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
53	d1oqya1	Alignment	not modelled	17.4	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like

						Family:UBA domain
54	c3knzA_	Alignment	not modelled	17.3	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative sugar binding protein; **PDBTitle:** crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
55	c2ip4A_	Alignment	not modelled	17.0	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
56	c3ijrF_	Alignment	not modelled	16.9	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
57	c2cunA_	Alignment	not modelled	16.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
58	d1f8fa1	Alignment	not modelled	16.7	9	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
59	c3cxtA_	Alignment	not modelled	16.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
60	d2btma_	Alignment	not modelled	16.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
61	d1d3va_	Alignment	not modelled	15.6	35	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
62	d1c55a_	Alignment	not modelled	15.5	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
63	d1uadc_	Alignment	not modelled	15.1	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Other IPT/TIG domains
64	c2qk4A_	Alignment	not modelled	14.9	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trifunctional purine biosynthetic protein adenosine-3; **PDBTitle:** human glycinamide ribonucleotide synthetase
65	d1n55a_	Alignment	not modelled	14.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
66	d1vhwa_	Alignment	not modelled	14.6	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
67	d1fe0a_	Alignment	not modelled	14.6	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
68	d1neya_	Alignment	not modelled	14.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
69	d2z06a1	Alignment	not modelled	14.2	29	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TTHA0625-like
70	d1jx4a1	Alignment	not modelled	14.2	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
71	d2ceva_	Alignment	not modelled	14.1	27	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
72	c3g68A_	Alignment	not modelled	13.9	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
73	d2bzga1	Alignment	not modelled	13.9	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
74	c1ezaA_	Alignment	not modelled	13.6	9	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
75	d1li4a2	Alignment	not modelled	13.5	31	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**S-adenosylhomocystein hydrolase
76	c1wydB_	Alignment	not modelled	13.2	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
77	d1mvfd_	Alignment	not modelled	12.9	19	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
78	d2ac7a1	Alignment	not modelled	12.7	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases

79	c3rd5A_	Alignment	not modelled	12.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mypaa.01249.c; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
80	d1xg5a_	Alignment	not modelled	12.6	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
81	c3kvoB_	Alignment	not modelled	12.5	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hydroxysteroid dehydrogenase-like protein 2; **PDBTitle:** crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsdl2)
82	c3bk7A_	Alignment	not modelled	12.4	18	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
83	c3nn4C_	Alignment	not modelled	12.3	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**chlorite dismutase; **PDBTitle:** structure of chlorite dismutase from candidatus nitrospira defluvii2 r173k mutant
84	d3c8ya1	Alignment	not modelled	12.2	25	**Fold:**Fe-only hydrogenase **Superfamily:**Fe-only hydrogenase **Family:**Fe-only hydrogenase
85	c2d2aA_	Alignment	not modelled	12.0	25	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sufa protein; **PDBTitle:** crystal structure of escherichia coli sufa involved in2 biosynthesis of iron-sulfur clusters
86	d1mo0a_	Alignment	not modelled	12.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
87	d1cb0a_	Alignment	not modelled	11.8	38	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
88	d1o5xa_	Alignment	not modelled	11.8	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
89	c3fkjA_	Alignment	not modelled	11.7	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
90	d2bela_	Alignment	not modelled	11.6	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	c1wj9A_	Alignment	not modelled	11.6	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**crispr-associated protein; **PDBTitle:** crystal structure of a crispr-associated protein from2 thermus thermophilus
92	c2vxhF_	Alignment	not modelled	11.6	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**chlorite dismutase; **PDBTitle:** the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
93	d1assa_	Alignment	not modelled	11.4	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
94	c3khsB_	Alignment	not modelled	11.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
95	c3fa4D_	Alignment	not modelled	11.3	11	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2,3-dimethylmalate lyase; **PDBTitle:** crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
96	d1dcfa_	Alignment	not modelled	11.3	25	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
97	d1reoa1	Alignment	not modelled	11.3	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
98	d1cyga1	Alignment	not modelled	11.2	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
99	c3tl6B_	Alignment	not modelled	11.1	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica