Phyre^2

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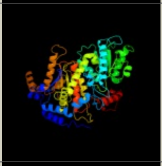
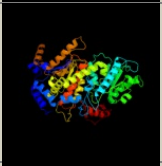
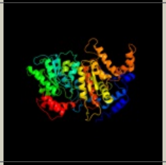
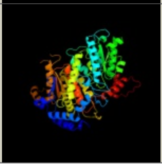
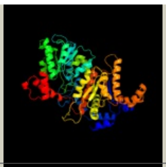
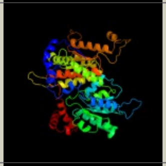
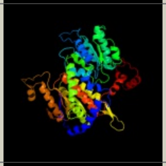
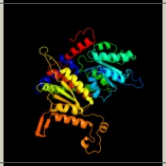
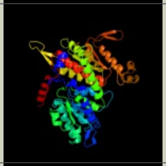
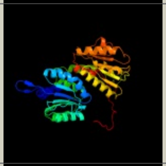
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nbuC_	Alignment		100.0	100	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of pgi glucosephosphate isomerase
2	c3hjbA_	Alignment		100.0	77	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
3	d1iata_	Alignment		100.0	66	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
4	d1q50a_	Alignment		100.0	59	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
5	d1u0fa_	Alignment		100.0	64	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
6	d1gzda_	Alignment		100.0	66	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
7	d1hm5a_	Alignment		100.0	66	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
8	c1t10A_	Alignment		100.0	59	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
9	c2o2cB_	Alignment		100.0	58	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
10	c2wu8A_	Alignment		100.0	53	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
11	c3pr3B_	Alignment		100.0	42	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate

12	c3ljkA_	Alignment		100.0	49	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
13	c3ujhB_	Alignment		100.0	45	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
14	d1c7qa_	Alignment		100.0	25	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
15	c3ff1B_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
16	c2q8nB_	Alignment		100.0	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
17	c1zzgB_	Alignment		100.0	25	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
18	d1x9ia_	Alignment		99.1	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
19	c3c3jA_	Alignment		99.0	12	**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
20	c3euaD_	Alignment		99.0	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
21	c2a3nA_	Alignment	not modelled	98.9	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative glucosamine-fructose-6-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
22	c3hbaA_	Alignment	not modelled	98.8	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (sden_2705)2 from shewanella denitrificans os217 at 2.00 a resolution
23	c3fkjA_	Alignment	not modelled	98.8	16	**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
24	c2zj3A_	Alignment	not modelled	98.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate **PDBTitle:** isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
25	c3g68A_	Alignment	not modelled	98.7	15	**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
26	d1j5xa_	Alignment	not modelled	98.7	11	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
27	c3knzA_	Alignment	not modelled	98.6	13	**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
						PDB header:isomerase

28	c3i0zB_	Alignment	not modelled	98.6	10	**Chain:** B: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of putative putative tagatose-6-phosphate2 ketose/aldose isomerase (np_344614.1) from streptococcus pneumoniae3 tigr4 at 1.70 a resolution
29	c3fj1A_	Alignment	not modelled	98.5	11	**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
30	c2puwA_	Alignment	not modelled	98.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isomerase domain of glutamine-fructose-6-phosphate **PDBTitle:** the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
31	c3odpA_	Alignment	not modelled	98.5	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of a putative tagatose-6-phosphate ketose/aldose2 isomerase (nt01cx_0292) from clostridium novyi nt at 2.35 a3 resolution
32	c2decA_	Alignment	not modelled	98.4	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**325aa long hypothetical protein; **PDBTitle:** crystal structure of the ph0510 protein from pyrococcus horikoshii ot3
33	d1moqa_	Alignment	not modelled	98.4	12	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**double-SIS domain
34	c2amlB_	Alignment	not modelled	98.1	12	**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
35	c1jxaA_	Alignment	not modelled	98.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine 6-phosphate synthase; **PDBTitle:** glucosamine 6-phosphate synthase with glucose 6-phosphate
36	c3tbfA_	Alignment	not modelled	98.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucosamine--fructose-6-phosphate aminotransferase **PDBTitle:** c-terminal domain of glucosamine-fructose-6-phosphate aminotransferase2 from francisella tularensis.
37	d1x92a_	Alignment	not modelled	97.9	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
38	c3shoA_	Alignment	not modelled	97.5	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
39	d1tk9a_	Alignment	not modelled	97.4	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
40	c2yvaB_	Alignment	not modelled	97.3	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
41	d1x94a_	Alignment	not modelled	97.3	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
42	d1vima_	Alignment	not modelled	97.3	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
43	c1nriA_	Alignment	not modelled	97.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
44	d1nria_	Alignment	not modelled	97.2	19	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
45	d1m3sa_	Alignment	not modelled	97.1	22	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
46	c2x3yA_	Alignment	not modelled	97.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
47	c3fxaA_	Alignment	not modelled	97.0	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
48	c3etnD_	Alignment	not modelled	96.9	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative phosphosugar isomerase involved in capsule **PDBTitle:** crystal structure of putative phosphosugar isomerase involved in2 capsule formation (yp_209877.1) from bacteroides fragilis nctc 93433 at 1.70 a resolution
49	d1jeoa_	Alignment	not modelled	96.8	21	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
50	c3cvjB_	Alignment	not modelled	96.8	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
51	c2xhzC_	Alignment	not modelled	96.5	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography

52	c3trjC_	Alignment	not modelled	96.5	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
53	d1p3da1	Alignment	not modelled	86.6	20	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
54	d1chda_	Alignment	not modelled	84.3	13	**Fold:**Methylesterase CheB, C-terminal domain **Superfamily:**Methylesterase CheB, C-terminal domain **Family:**Methylesterase CheB, C-terminal domain
55	c3sftA_	Alignment	not modelled	77.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
56	d1p17b_	Alignment	not modelled	68.3	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
57	d1w5fa1	Alignment	not modelled	65.8	28	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
58	d1q2la3	Alignment	not modelled	64.5	16	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
59	d1zbsa2	Alignment	not modelled	61.1	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
60	c3ezxA_	Alignment	not modelled	58.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**monomethylamine corrinoid protein 1; **PDBTitle:** structure of methanosarcina barkeri monomethylamine2 corrinoid protein
61	c3ca8B_	Alignment	not modelled	51.5	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
62	c2eklA_	Alignment	not modelled	51.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
63	c2r6r1_	Alignment	not modelled	49.7	29	**PDB header:**cell cycle **Chain:** 1: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** aquifex aeolicus ftsz
64	d1liua3	Alignment	not modelled	48.5	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
65	d1j99a_	Alignment	not modelled	38.5	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
66	d1q20a_	Alignment	not modelled	37.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
67	c1w59B_	Alignment	not modelled	37.1	16	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
68	d1k75a_	Alignment	not modelled	36.9	22	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
69	c2rhoB_	Alignment	not modelled	36.4	20	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
70	c1zd1B_	Alignment	not modelled	36.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1
71	c1a2oB_	Alignment	not modelled	35.5	13	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
72	d1e0ta3	Alignment	not modelled	35.2	15	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
73	c3d3qB_	Alignment	not modelled	31.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
74	c2h8kA_	Alignment	not modelled	30.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap
75	c2y0fD_	Alignment	not modelled	30.1	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
76	d1rq2a1	Alignment	not modelled	30.1	24	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
77	d1a3xa3	Alignment	not modelled	29.6	14	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
						PDB header:cell division

78	c1w5fA_	Alignment	not modelled	28.6	28	**Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz, t7 mutated, domain swapped (t. maritima)
79	d1hgxa_	Alignment	not modelled	28.5	8	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
80	d1aqua_	Alignment	not modelled	28.2	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
81	d2vapa1	Alignment	not modelled	27.7	17	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
82	d1o82a_	Alignment	not modelled	27.3	41	**Fold:**Saposin-like **Superfamily:**Bacteriocin AS-48 **Family:**Bacteriocin AS-48
83	c2vxyA_	Alignment	not modelled	26.8	26	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution
84	d1yqea1	Alignment	not modelled	26.2	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
85	d2g50a3	Alignment	not modelled	26.0	9	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
86	c3eplA_	Alignment	not modelled	23.5	19	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
87	d1tc1a_	Alignment	not modelled	22.8	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
88	c2jkzB_	Alignment	not modelled	22.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
89	c2f00A_	Alignment	not modelled	22.3	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
90	d1q44a_	Alignment	not modelled	20.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
91	d1j6ua1	Alignment	not modelled	20.3	17	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
92	c3louB_	Alignment	not modelled	20.0	9	**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
93	c3nrbD_	Alignment	not modelled	19.9	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
94	c3l76B_	Alignment	not modelled	19.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
95	d1xrsb1	Alignment	not modelled	19.6	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
96	d1t57a_	Alignment	not modelled	19.3	18	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
97	d2gv8a2	Alignment	not modelled	18.6	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
98	d2ahua2	Alignment	not modelled	18.6	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
99	c3n0vD_	Alignment	not modelled	18.4	12	**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