Phyre^2

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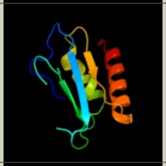
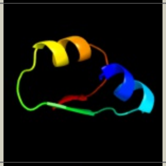
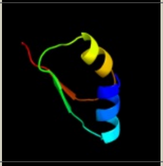
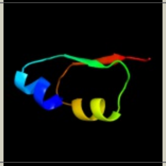
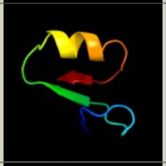
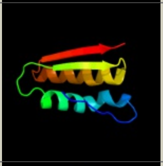
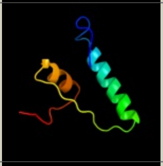
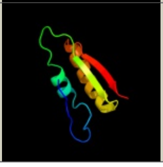
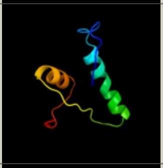
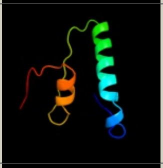
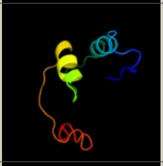
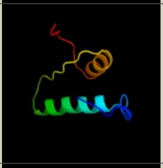
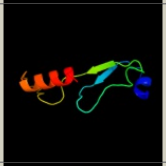
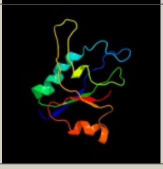
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bz1a1	Alignment		100.0	98	**Fold:**RibA-like **Superfamily:**RibA-like **Family:**RibA-like
2	d1oi2a_	Alignment		88.6	27	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
3	d1ghsa_	Alignment		86.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
4	c1un9B_	Alignment		86.1	27	**PDB header:**kinase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
5	d2cyga1	Alignment		86.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
6	d1aq0a_	Alignment		85.9	32	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
7	c3f55A_	Alignment		84.4	18	**PDB header:**hydrolase, allergen **Chain:** A: **PDB Molecule:**beta-1,3-glucanase; **PDBTitle:** crystal structure of the native endo beta-1,3-glucanase (hev b 2), a2 major allergen from hevea brasiliensis (space group p41)
8	c3ct4B_	Alignment		80.8	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts-dependent dihydroxyacetone kinase, **PDBTitle:** structure of dha-kinase subunit dhak from l. lactis
9	d1un8a4	Alignment		71.4	28	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
10	d1n71a_	Alignment		70.9	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
11	c2iu6B_	Alignment		70.3	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** regulation of the dha operon of lactococcus lactis

12	d1v96a1	Alignment		70.1	19	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
13	d2g3aa1	Alignment		62.4	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
14	d1u6ma_	Alignment		60.8	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
15	d1y9wa1	Alignment		54.3	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
16	c2reeB_	Alignment		47.2	18	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** crystal structure of the loading gnatl domain of cura from lyngbya2 majuscula
17	d1y82a1	Alignment		45.4	21	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**PIN domain
18	d1y9ka1	Alignment		43.4	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
19	c2w62A_	Alignment		42.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycolipid-anchored surface protein 2; **PDBTitle:** saccharomyces cerevisiae gas2p in complex with2 laminaripentaose
20	d16pka_	Alignment		41.9	28	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
21	c3dr8B_	Alignment	not modelled	41.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ynca; **PDBTitle:** structure of ynca, a putative acetyltransferase from salmonella2 typhimurium with its cofactor acetyl-coa
22	d1lssa_	Alignment	not modelled	38.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
23	d1qh5a_	Alignment	not modelled	38.6	21	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
24	c3kc2A_	Alignment	not modelled	36.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
25	c2g1uA_	Alignment	not modelled	33.6	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
26	d1o8ca2	Alignment	not modelled	32.5	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
27	d2cy2a1	Alignment	not modelled	30.8	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
28	d2je8a5	Alignment	not modelled	30.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
						Fold:7-stranded beta/alpha barrel

29	d1m65a_	Alignment	not modelled	30.2	20	**Superfamily:**PHP domain-like **Family:**PHP domain
30	d1k7ka_	Alignment	not modelled	29.5	32	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
31	d1i12a_	Alignment	not modelled	29.0	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
32	d2fiwa1	Alignment	not modelled	26.8	10	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
33	d1ltka_	Alignment	not modelled	25.7	21	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
34	c3iupB_	Alignment	not modelled	25.2	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadph:quinone oxidoreductase; **PDBTitle:** crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
35	c3f8kA_	Alignment	not modelled	24.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein acetyltransferase; **PDBTitle:** crystal structure of protein acetyltransferase (pat) from2 sulfolobus solfataricus
36	c3lodA_	Alignment	not modelled	23.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyl-coa n-acyltransferase; **PDBTitle:** the crystal structure of the putative acyl-coa n-acyltransferase from2 klebsiella pneumoniae subsp.pneumoniae mgh 78578
37	d1vhsa_	Alignment	not modelled	22.9	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
38	c3exnA_	Alignment	not modelled	22.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable acetyltransferase; **PDBTitle:** crystal structure of acetyltransferase from thermus thermophilus hb8
39	c3d8pB_	Alignment	not modelled	22.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyltransferase of gnat family; **PDBTitle:** crystal structure of acetyltransferase of gnat family (np_373092.1)2 from staphylococcus aureus mu50 at 2.20 a resolution
40	d2fiaa1	Alignment	not modelled	21.5	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
41	c3ecjC_	Alignment	not modelled	21.3	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**protein (homoprotocatechuate 2,3-dioxygenase); **PDBTitle:** structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
42	c2oh1A_	Alignment	not modelled	21.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase gnat family (yp_013287.1) from2 listeria monocytogenes 4b f2365 at 1.46 a resolution
43	d1s3za_	Alignment	not modelled	21.2	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
44	d1tiqa_	Alignment	not modelled	20.9	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
45	c2q0yA_	Alignment	not modelled	20.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of gcn5-related n-acetyltransferase (yp_295895.1)2 from ralstonia eutropha jmp134 at 1.80 a resolution
46	c2k5tA_	Alignment	not modelled	20.8	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein yhhk; **PDBTitle:** solution nmr structure of putative n-acetyl transferase2 yhhk from e. coli bound to coenzyme a: northeast3 structural genomics consortium target et106
47	d1qpga_	Alignment	not modelled	20.1	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
48	d1c1da1	Alignment	not modelled	20.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
49	c3e48B_	Alignment	not modelled	20.0	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
50	d1yvoa1	Alignment	not modelled	19.9	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
51	d1ghea_	Alignment	not modelled	19.4	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
52	d1yvka1	Alignment	not modelled	19.3	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
53	c3i9sA_	Alignment	not modelled	18.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v.cholerae. integron2 cassette protein vch_cass6
						PDB header:isomerase

54	c2xecD_	Alignment	not modelled	18.1	20	**Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
55	c2jlmE_	Alignment	not modelled	17.9	12	**PDB header:**transferase **Chain:** E: **PDB Molecule:**putative phosphinothricin n-acetyltransferase; **PDBTitle:** structure of a putative acetyltransferase (aciad1637) from2 acinetobacter baylyi adp1
56	d1k3ra1	Alignment	not modelled	17.8	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
57	d1kola2	Alignment	not modelled	17.4	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
58	d1vpea_	Alignment	not modelled	17.3	19	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
59	c2r1iB_	Alignment	not modelled	17.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (yp_831484.1) from2 arthrobacter sp. fb24 at 1.65 a resolution
60	d1bhga3	Alignment	not modelled	16.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
61	d2hmva1	Alignment	not modelled	16.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
62	c3mjdA_	Alignment	not modelled	16.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
63	d2b5ga1	Alignment	not modelled	16.0	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
64	c1ib1E_	Alignment	not modelled	15.7	16	**PDB header:**signaling protein/transferase **Chain:** E: **PDB Molecule:**serotonin n-acetyltransferase; **PDBTitle:** crystal structure of the 14-3-3 zeta:serotonin n-2 acetyltransferase complex
65	c2pc1A_	Alignment	not modelled	15.3	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase gnat family (np_688560.1) from2 streptococcus agalactiae 2603 at 1.28 a resolution
66	c2pswA_	Alignment	not modelled	15.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase 13; **PDBTitle:** human mak3 homolog in complex with coa
67	d1a9xa3	Alignment	not modelled	15.1	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
68	d1hjsa_	Alignment	not modelled	13.8	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
69	d1urha1	Alignment	not modelled	13.6	13	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
70	d1yx0a1	Alignment	not modelled	13.3	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
71	c3fncA_	Alignment	not modelled	12.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of a putative acetyltransferase from listeria2 innocua
72	c3q3vA_	Alignment	not modelled	11.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
73	d2f06a2	Alignment	not modelled	11.5	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
74	c3eywA_	Alignment	not modelled	11.5	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
75	d2ef7a1	Alignment	not modelled	11.2	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
76	d1v6sa_	Alignment	not modelled	11.1	21	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
77	d2aeea1	Alignment	not modelled	11.1	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
78	c3k9uA_	Alignment	not modelled	10.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**paia acetyltransferase; **PDBTitle:** crystal structure of paia acetyltransferase (ta0374) from thermoplasma2 acidophilum
79	c3pp9B_	Alignment	not modelled	10.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative streptothricin acetyltransferase; **PDBTitle:** 1.6 angstrom resolution crystal structure of putative streptothricin2 acetyltransferase from bacillus anthracis str. ames in complex with3 acetyl coenzyme a

80	d2v8qe1	Alignment	not modelled	10.1	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
81	d1m6ia3	Alignment	not modelled	9.9	40	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
82	d1mk4a_	Alignment	not modelled	9.8	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
83	c2zcuA_	Alignment	not modelled	9.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized oxidoreductase ytfg; **PDBTitle:** crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
84	d1v7ca_	Alignment	not modelled	9.3	26	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
85	d2jdca1	Alignment	not modelled	9.2	8	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
86	d1yr0a1	Alignment	not modelled	9.0	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
87	d2euia1	Alignment	not modelled	8.9	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
88	d1xrsb2	Alignment	not modelled	8.8	18	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
89	c2pdoG_	Alignment	not modelled	8.4	17	**PDB header:**transferase **Chain:** G: **PDB Molecule:**acetyltransferase ypea; **PDBTitle:** crystal structure of the putative acetyltransferase of gnat family2 from shigella flexneri
90	d3bzka2	Alignment	not modelled	8.3	10	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
91	c2jtqA_	Alignment	not modelled	8.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phage shock protein e; **PDBTitle:** rhodanese from e.coli
92	d1o8ba2	Alignment	not modelled	8.3	24	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
93	d1xp3a1	Alignment	not modelled	8.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
94	d1iyca_	Alignment	not modelled	8.2	29	**Fold:**Invertebrate chitin-binding proteins **Superfamily:**Invertebrate chitin-binding proteins **Family:**Antifungal peptide scarabaecin
95	d1ryla_	Alignment	not modelled	7.9	17	**Fold:**Hypothetical protein yfbM **Superfamily:**Hypothetical protein yfbM **Family:**Hypothetical protein yfbM
96	d1tt7a2	Alignment	not modelled	7.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
97	d1tafa_	Alignment	not modelled	7.8	29	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
98	c3efhB_	Alignment	not modelled	7.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
99	c2yzqA_	Alignment	not modelled	7.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1780; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii