Phyre^2

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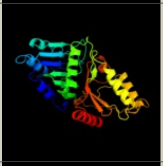
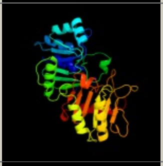
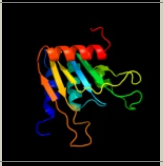
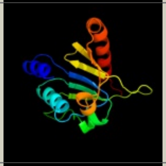
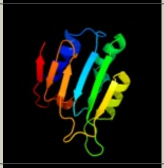
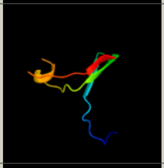
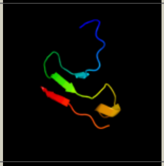
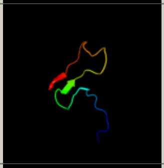
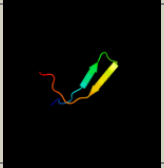
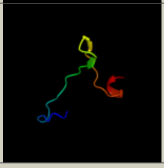
Description	P23830
Date	Wed Jan 25 15:20:43 GMT 2012
Unique Job ID	b8a9660c6f91851a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hsiC_	Alignment		100.0	46	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphatidylserine synthase; **PDBTitle:** crystal structure of phosphatidylserine synthase haemophilus2 influenzae rd kw20
2	c1v0sA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase d; **PDBTitle:** uninhibited form of phospholipase d from streptomyces sp.2 strain pmf
3	d1v0wa1	Alignment		99.9	14	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Phospholipase D
4	c1xdoB_	Alignment		99.9	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
5	d1xdpa3	Alignment		99.9	18	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
6	d1byra_	Alignment		99.9	15	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Nuclease
7	d1v0wa2	Alignment		99.9	19	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Phospholipase D
8	c2o8rA_	Alignment		99.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
9	d2o8ra3	Alignment		98.5	14	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
10	d1xdpa4	Alignment		98.1	15	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
11	c1q32C_	Alignment		97.9	14	**PDB header:**replication,transcription,hydrolase **Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase; **PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna2 phosphodiesterase

12	c3sq3C_	Alignment		97.7	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna phosphodiesterase2 h182a mutant
13	d2o8ra4	Alignment		97.4	13	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
14	c2c1lA_	Alignment		97.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease; **PDBTitle:** structure of the bfii restriction endonuclease
15	d1jy1a2	Alignment		95.8	30	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
16	c1nopB_	Alignment		95.6	35	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure of human tyrosyl-dna phosphodiesterase2 (tdp1) in complex with vanadate, dna and a human3 topoisomerase i-derived peptide
17	d1q32a2	Alignment		94.1	30	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
18	d2f5tx2	Alignment		62.9	16	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**TrmB middle domain-like
19	d1qzqa1	Alignment		62.8	29	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
20	d1q32a1	Alignment		51.7	11	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
21	c2f5tX_	Alignment	not modelled	51.3	16	**PDB header:**transcription **Chain:** X: **PDB Molecule:**archaeal transcriptional regulator trmb; **PDBTitle:** crystal structure of the sugar binding domain of the archaeal2 transcriptional regulator trmb
22	d1jy1a1	Alignment	not modelled	38.2	14	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
23	c2a5hC_	Alignment	not modelled	37.2	11	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase; **PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
24	d1vdda_	Alignment	not modelled	22.7	22	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
25	c1vddC_	Alignment	not modelled	20.0	22	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
26	d1f0ya2	Alignment	not modelled	18.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
27	d1gz0a2	Alignment	not modelled	17.3	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
28	c2x7mA_	Alignment	not modelled	17.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from

						methanopyrus2 kandleri at 1.5 a resolution
29	d1f8ya_	Alignment	not modelled	16.8	6	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
30	c1t3gB_	Alignment	not modelled	16.7	8	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**x-linked interleukin-1 receptor accessory **PDBTitle:** crystal structure of the toll/interleukin-1 receptor (tir)2 domain of human il-1rapl
31	c3hu5B_	Alignment	not modelled	16.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
32	d2bdea1	Alignment	not modelled	16.0	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**5' nucleotidase-like
33	d1s2da_	Alignment	not modelled	16.0	14	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
34	d1e8ob_	Alignment	not modelled	15.8	11	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
35	c1b9xC_	Alignment	not modelled	15.5	21	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**protein (phosducin); **PDBTitle:** structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
36	c2l82A_	Alignment	not modelled	15.5	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein or32; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
37	d1x9ga_	Alignment	not modelled	13.9	14	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
38	d1gz0f2	Alignment	not modelled	13.0	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
39	d1914a2	Alignment	not modelled	11.5	12	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
40	d1j5pa4	Alignment	not modelled	11.4	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	c1zrwA_	Alignment	not modelled	10.9	46	**PDB header:**antimicrobial protein, antibiotic **Chain:** A: **PDB Molecule:**spinigerin; **PDBTitle:** solution structure of spinigerin in h20/tfe 10%
42	c1zrvA_	Alignment	not modelled	10.9	46	**PDB header:**antimicrobial protein, antibiotic **Chain:** A: **PDB Molecule:**spinigerin; **PDBTitle:** solution structure of spinigerin in h20/tfe 50%
43	c2b34C_	Alignment	not modelled	10.4	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
44	c2jcmA_	Alignment	not modelled	10.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic purine 5'-nucleotidase; **PDBTitle:** crystal structure of human cytosolic 5'-nucleotidase ii in2 complex with beryllium trifluoride
45	c3gbcA_	Alignment	not modelled	9.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrazinamidase/nicotinamidas pnca; **PDBTitle:** determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
46	c2r60A_	Alignment	not modelled	9.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
47	c2jz2A_	Alignment	not modelled	9.4	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
48	d1ldna1	Alignment	not modelled	9.3	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
49	c3l2iB_	Alignment	not modelled	9.3	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
50	c2kxeA_	Alignment	not modelled	9.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii small subunit; **PDBTitle:** n-terminal domain of the dp1 subunit of an archaeal d-family dna2 polymerase
51	c1g4wR_	Alignment	not modelled	8.9	11	**PDB header:**signaling protein **Chain:** R: **PDB Molecule:**protein tyrosine phosphatase sptp; **PDBTitle:** crystal structure of the salmonella tyrosine phosphatase2 and gtpase activating protein sptp
52	d1m6ia2	Alignment	not modelled	8.8	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
						Fold:NAD(P)-binding Rossmann-fold domains

53	d1guza1	Alignment	not modelled	8.5	13	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
54	c3ua4A_	Alignment	not modelled	8.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arginine n-methyltransferase 5; **PDBTitle:** crystal structure of protein arginine methyltransferase prmt5
55	c3dy0B_	Alignment	not modelled	7.9	20	**PDB header:**blood clotting, hydrolase inhibitor **Chain:** B: **PDB Molecule:**c-terminus plasma serine protease inhibitor; **PDBTitle:** crystal structure of cleaved pci bound to heparin
56	c1xeaD_	Alignment	not modelled	7.8	8	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
57	d1ojua1	Alignment	not modelled	7.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
58	d1im5a_	Alignment	not modelled	7.5	11	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
59	c3gt0A_	Alignment	not modelled	7.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
60	c1lq8H_	Alignment	not modelled	7.4	20	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**plasma serine protease inhibitor; **PDBTitle:** crystal structure of cleaved protein c inhibitor
61	d2g8la1	Alignment	not modelled	7.2	24	**Fold:**AF1104-like **Superfamily:**AF1104-like **Family:**AF1104-like
62	c3oqhB_	Alignment	not modelled	7.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein yvmc; **PDBTitle:** crystal structure of b. licheniformis cdps yvmc-blic
63	d1czan3	Alignment	not modelled	6.9	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
64	d5ldha1	Alignment	not modelled	6.7	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
65	d1x94a_	Alignment	not modelled	6.4	10	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
66	d1sjpa3	Alignment	not modelled	6.3	6	**Fold:**GroEL-intermediate domain like **Superfamily:**GroEL-intermediate domain like **Family:**GroEL-like chaperone, intermediate domain
67	d1obba1	Alignment	not modelled	6.3	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
68	d1llda1	Alignment	not modelled	6.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
69	d1gqna_	Alignment	not modelled	6.3	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
70	c3qufB_	Alignment	not modelled	6.3	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**extracellular solute-binding protein, family 1; **PDBTitle:** the structure of a family 1 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
71	d1ez4a1	Alignment	not modelled	6.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
72	d1u8xx1	Alignment	not modelled	6.2	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
73	d1up7a1	Alignment	not modelled	6.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
74	d2zdra2	Alignment	not modelled	6.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
75	c1llcA_	Alignment	not modelled	6.1	14	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** structure determination of the allosteric l-lactate dehydrogenase from2 lactobacillus casei at 3.0 angstroms resolution
76	c2x0dA_	Alignment	not modelled	6.1	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
77	d1jjcb4	Alignment	not modelled	6.1	13	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
78	d1a0rp_	Alignment	not modelled	6.1	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Phosducin
79	c2v6bB_	Alignment	not modelled	5.7	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of lactate dehydrogenase from

						deinococcus2 radiodurans (apo form)
80	c2yvaB_	Alignment	not modelled	5.7	7	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
81	c2qupA_	Alignment	not modelled	5.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh1478 protein; **PDBTitle:** crystal structure of uncharacterized protein bh1478 from bacillus2 halodurans
82	c2krcA_	Alignment	not modelled	5.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta; **PDBTitle:** solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
83	d4pgaa_	Alignment	not modelled	5.6	12	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
84	c1a5zA_	Alignment	not modelled	5.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** lactate dehydrogenase from thermotoga maritima (tmldh)
85	d1llca1	Alignment	not modelled	5.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
86	d1ldma1	Alignment	not modelled	5.5	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
87	c3js3C_	Alignment	not modelled	5.5	8	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
88	d2dx5a1	Alignment	not modelled	5.5	19	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**VPS36 N-terminal domain-like
89	c3bsmD_	Alignment	not modelled	5.5	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of d-mannonate dehydratase from2 chromohalobacter salexigens
90	d1x92a_	Alignment	not modelled	5.4	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
91	d2bisa1	Alignment	not modelled	5.4	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
92	c1914A_	Alignment	not modelled	5.3	12	**PDB header:**alu domain **Chain:** A: **PDB Molecule:**signal recognition particle 9/14 fusion protein; **PDBTitle:** signal recognition particle alu rna binding heterodimer, srp9/14
93	d2p61a1	Alignment	not modelled	5.3	7	**Fold:**Four-helical up-and-down bundle **Superfamily:**TM1646-like **Family:**TM1646-like
94	c2pr7A_	Alignment	not modelled	5.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family; **PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
95	d2bf5a1	Alignment	not modelled	5.2	14	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
96	c2x3yA_	Alignment	not modelled	5.2	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
97	c2aj6A_	Alignment	not modelled	5.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein mw0638; **PDBTitle:** crystal structure of a putative gnat family acetyltransferase (mw0638)2 from staphylococcus aureus subsp. aureus at 1.63 a resolution
98	c2p61A_	Alignment	not modelled	5.1	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein tm_1646; **PDBTitle:** crystal structure of protein tm1646 from thermotoga2 maritima, pfam duf327