Phyre2

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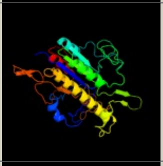
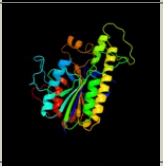
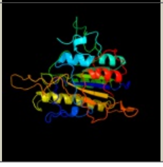
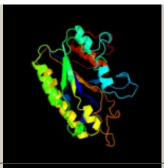
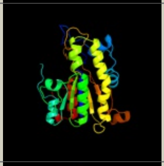
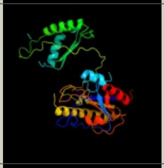
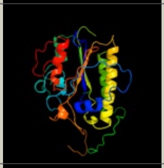
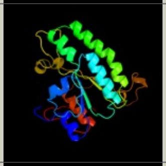
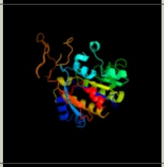
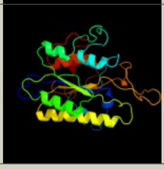
Description	P30845
Date	Thu Jan 5 11:46:29 GMT 2012
Unique Job ID	1728a83ca08272db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w8dB_	Alignment		100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid synthase 2; **PDBTitle:** distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
2	c2w5tA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
3	c3lxqB_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp1736; **PDBTitle:** the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
4	c2qzuA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
5	c3ed4A_	Alignment		100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
6	d1fsua_	Alignment		100.0	10	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
7	d1auka_	Alignment		100.0	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
8	c3b5qB_	Alignment		100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
9	d1hdha_	Alignment		100.0	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
10	c2vqrA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase; **PDBTitle:** crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily
11	d1p49a_	Alignment		100.0	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase

12	d1o98a2	Alignment		100.0	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
13	d2i09a1	Alignment		99.9	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
14	c2zktB_	Alignment		99.9	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
15	c3m8yC_	Alignment		99.9	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
16	c2gsoB_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
17	c3q3qA_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
18	c2i09A_	Alignment		99.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
19	c3szzA_	Alignment		99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
20	c2xr9A_	Alignment		99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
21	c2xrgA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
22	d1ei6a_	Alignment	not modelled	99.8	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
23	c1o98A_	Alignment	not modelled	99.7	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
24	c3igzB_	Alignment	not modelled	99.6	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
25	c2d1gB_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
26	c2iucB_	Alignment	not modelled	99.2	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
27	d1y6va1	Alignment	not modelled	99.1	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
28	c1ew2A_	Alignment	not modelled	99.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase

29	d1zeda1	Alignment	not modelled	99.0	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
30	d1k7ha_	Alignment	not modelled	98.8	15	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
31	c3a52A_	Alignment	not modelled	98.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
32	c2w0yB_	Alignment	not modelled	98.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
33	c2x98A_	Alignment	not modelled	98.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
34	c3e2dB_	Alignment	not modelled	98.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
35	c3iddA_	Alignment	not modelled	95.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
36	d1b4ub_	Alignment	not modelled	68.2	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
37	d1s1qa_	Alignment	not modelled	67.1	21	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
38	d1s95a_	Alignment	not modelled	41.2	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
39	c2xmoB_	Alignment	not modelled	41.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
40	d1uzdc1	Alignment	not modelled	33.2	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
41	d1l5oa_	Alignment	not modelled	31.7	40	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
42	d1j33a_	Alignment	not modelled	31.2	27	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
43	d1ej7s_	Alignment	not modelled	27.9	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
44	d8ruci_	Alignment	not modelled	23.4	17	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
45	c3uoaB_	Alignment	not modelled	20.7	24	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** crystal structure of the malt1 paracaspase (p21 form)
46	c3bijC_	Alignment	not modelled	19.4	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein gsu0716; **PDBTitle:** crystal structure of protein gsu0716 from geobacter2 sulfurreducens. northeast structural genomics target gsr13
47	d2b8ea1	Alignment	not modelled	18.6	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
48	c2xokG_	Alignment	not modelled	17.0	15	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** refined structure of yeast f1c10 atpase complex to 3 a2 resolution
49	d1xo1a2	Alignment	not modelled	16.9	12	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
50	d1fs0g_	Alignment	not modelled	16.8	21	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
51	d1tfra2	Alignment	not modelled	16.6	16	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
52	d2nvpa1	Alignment	not modelled	16.3	23	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
53	d2hkja2	Alignment	not modelled	14.8	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
54	d1uf3a_	Alignment	not modelled	14.6	9	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases

						Family:TT1561-like
55	c1jaeA_	Alignment	not modelled	14.4	16	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
56	c3oaaO_	Alignment	not modelled	14.3	17	**PDB header:**hydrolase/transport protein **Chain:** O: **PDB Molecule:**atp synthase gamma chain; **PDBTitle:** structure of the e.coli f1-atp synthase inhibited by subunit epsilon
57	c2ihnA_	Alignment	not modelled	13.9	12	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
58	d1yj5a1	Alignment	not modelled	12.8	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
59	d2bdua1	Alignment	not modelled	12.5	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
60	d1usha2	Alignment	not modelled	11.7	26	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
61	d1wdds_	Alignment	not modelled	11.6	19	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
62	d1cmwa2	Alignment	not modelled	11.5	8	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
63	c2w6jG_	Alignment	not modelled	11.0	22	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
64	d1qopb_	Alignment	not modelled	10.1	24	**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
65	d1a3xa3	Alignment	not modelled	10.1	19	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
66	c3kccA_	Alignment	not modelled	9.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**catabolite gene activator; **PDBTitle:** crystal structure of d138l mutant of catabolite gene activator protein
67	d2hy1a1	Alignment	not modelled	9.9	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
68	c2hy1A_	Alignment	not modelled	9.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
69	c2qe7G_	Alignment	not modelled	9.7	37	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
70	c3ib7A_	Alignment	not modelled	9.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
71	d2fiqa1	Alignment	not modelled	9.0	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
72	d2f9zc1	Alignment	not modelled	8.9	23	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**CheD-like
73	d1fyea_	Alignment	not modelled	8.7	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
74	c3qfnA_	Alignment	not modelled	8.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
75	c3e20C_	Alignment	not modelled	8.7	11	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
76	c2pr7A_	Alignment	not modelled	8.6	20	**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
77	c1zreB_	Alignment	not modelled	8.3	15	**PDB header:**gene regulation/dna **Chain:** B: **PDB Molecule:**catabolite gene activator; **PDBTitle:** 4 crystal structures of cap-dna with all base-pair2 substitutions at position 6, cap-[6g;17c]icap38 dna
78	d1jaea2	Alignment	not modelled	8.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
79	c3qg5D_	Alignment	not modelled	8.2	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair

80	c3e37B_	Alignment	not modelled	8.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein farnesyltransferase subunit beta; **PDBTitle:** protein farnesyltransferase complexed with bisubstrate2 ethylenediamine scaffold inhibitor 5
81	d1wpga2	Alignment	not modelled	8.1	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
82	c2zqeA_	Alignment	not modelled	8.1	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
83	c2agaA_	Alignment	not modelled	8.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**machado-joseph disease protein 1; **PDBTitle:** de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain
84	c3t1iC_	Alignment	not modelled	8.0	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
85	d2h6fb1	Alignment	not modelled	7.9	14	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Protein prenyltransferases
86	d1okga1	Alignment	not modelled	7.8	8	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
87	c1zgxB_	Alignment	not modelled	7.7	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**guanyl-specific ribonuclease sa; **PDBTitle:** crystal structure of ribonuclease mutant
88	d1jl3a_	Alignment	not modelled	7.7	11	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
89	d1i5za2	Alignment	not modelled	7.7	15	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
90	d1d2na_	Alignment	not modelled	7.6	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
91	d2nxfa1	Alignment	not modelled	7.5	9	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
92	c2vzaD_	Alignment	not modelled	7.5	14	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**cell filamentation protein; **PDBTitle:** type iv secretion system effector protein bepa
93	d2jdig1	Alignment	not modelled	7.4	33	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
94	c2zbkB_	Alignment	not modelled	7.4	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
95	c3j08A_	Alignment	not modelled	7.4	18	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
96	c2k23A_	Alignment	not modelled	7.3	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 2; **PDBTitle:** solution structure analysis of the rlcn2
97	c3gd5D_	Alignment	not modelled	7.3	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
98	d1yp2a2	Alignment	not modelled	7.3	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**glucose-1-phosphate thymidylyltransferase
99	c2l3nA_	Alignment	not modelled	7.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein rap1, telomere length regulator taz1; **PDBTitle:** solution structure of rap1-taz1 fusion protein