Phyre2

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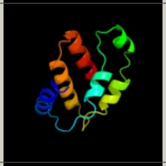
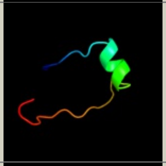
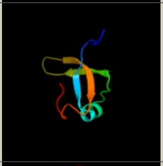
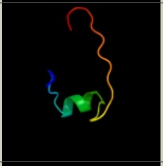
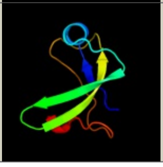
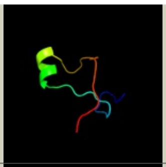
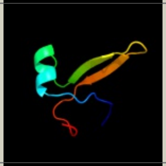
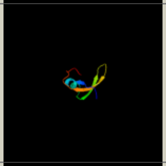
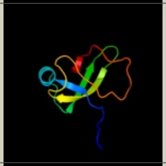
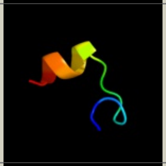
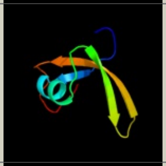
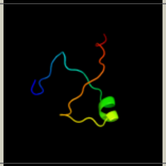
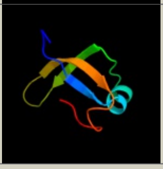
Description	P0ADC3
Date	Thu Jan 5 11:20:34 GMT 2012
Unique Job ID	abb7feef5cac83bc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ftjA_	Alignment		98.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrolide export atp-binding/permease protein **PDBTitle:** crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
2	c3is6A_	Alignment		97.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative permease protein, abc transporter; **PDBTitle:** the crystal structure of a domain of a putative permease protein from2 porphyromonas gingivalis to 2a
3	c1ciiA_	Alignment		83.2	14	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
4	d1h0ha1	Alignment		38.5	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
5	d1vlfm1	Alignment		34.8	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
6	d1tmoa1	Alignment		33.0	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
7	d1mvfd_	Alignment		32.7	16	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
8	d1kqfa1	Alignment		30.8	23	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
9	c2iv2X_	Alignment		29.8	12	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**formate dehydrogenase h; **PDBTitle:** reinterpretation of reduced form of formate dehydrogenase h2 from e. coli
10	d1ub4c_	Alignment		29.1	16	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
11	d1g8ka1	Alignment		28.9	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain

12	c2a8vA_	Alignment		27.3	11	**PDB header:**protein/rna **Chain:** A: **PDB Molecule:**rna binding domain of rho transcription **PDBTitle:** rho transcription termination factor/rna complex
13	d1ogya1	Alignment		25.9	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
14	d2jioa1	Alignment		25.8	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
15	c1eu1A_	Alignment		25.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dimethyl sulfoxide reductase; **PDBTitle:** the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
16	d2iv2x1	Alignment		24.2	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
17	c3ltiA_	Alignment		24.2	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains
18	d1y5ia1	Alignment		24.0	20	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
19	d1a62a2	Alignment		22.9	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
20	c2v45A_	Alignment		22.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
21	d3dhwa1	Alignment	not modelled	21.4	15	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
22	d1eu1a1	Alignment	not modelled	21.0	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
23	d1dmra1	Alignment	not modelled	20.4	11	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
24	c1h5nC_	Alignment	not modelled	17.6	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dmso reductase; **PDBTitle:** dmso reductase modified by the presence of dms and air
25	c2ivfA_	Alignment	not modelled	17.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
26	c1h0hA_	Alignment	not modelled	16.8	15	**PDB header:**dehydrogenase **Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit); **PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas
27	c1tmoA_	Alignment	not modelled	15.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase; **PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia
28	d1e32a1	Alignment	not modelled	14.3	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like

29	c2e7zA_	Alignment	not modelled	13.4	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetylene hydratase ahy; **PDBTitle:** acetylene hydratase from pelobacter acetylenicus
30	c1vlfQ_	Alignment	not modelled	12.8	18	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**pyrogallol hydroxytransferase large subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene
31	c1kqgA_	Alignment	not modelled	12.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit; **PDBTitle:** formate dehydrogenase n from e. coli
32	d1cola_	Alignment	not modelled	12.4	14	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
33	c2yujA_	Alignment	not modelled	11.9	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
34	c2pjhB_	Alignment	not modelled	11.6	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
35	c2ht2B_	Alignment	not modelled	11.6	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
36	c1g8jC_	Alignment	not modelled	11.5	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
37	c2glwA_	Alignment	not modelled	10.8	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii
38	c1zc1A_	Alignment	not modelled	10.7	14	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
39	c1y5iA_	Alignment	not modelled	10.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**respiratory nitrate reductase 1 alpha chain; **PDBTitle:** the crystal structure of the narghi mutant nari-k86a
40	c1ogyA_	Alignment	not modelled	10.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
41	d1cz5a1	Alignment	not modelled	10.4	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
42	c3fewX_	Alignment	not modelled	10.3	17	**PDB header:**immune system **Chain:** X: **PDB Molecule:**colicin s4; **PDBTitle:** structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
43	c2l66B_	Alignment	not modelled	10.3	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
44	d1otsa_	Alignment	not modelled	10.1	12	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
45	c2cwbA_	Alignment	not modelled	10.1	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g **PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
46	d2vbua1	Alignment	not modelled	9.9	23	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
47	c1wr1B_	Alignment	not modelled	9.9	8	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
48	d1ylea1	Alignment	not modelled	9.8	31	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
49	d2dnaa1	Alignment	not modelled	9.6	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
50	d2bwba1	Alignment	not modelled	9.5	8	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
51	c2nyaF_	Alignment	not modelled	9.5	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**periplasmic nitrate reductase; **PDBTitle:** crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
52	c2ki8A_	Alignment	not modelled	9.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase, **PDBTitle:** solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
53	c2dahA_	Alignment	not modelled	9.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-3; **PDBTitle:** solution structure of the c-terminal uba domain in the2 human ubiquilin 3
						PDB header:structural genomics, unknown function

54	c2dnaA_	Alignment	not modelled	8.8	16	**Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
55	d1veja1	Alignment	not modelled	8.8	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
56	d2daha1	Alignment	not modelled	8.7	16	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
57	c2w1tB_	Alignment	not modelled	8.7	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
58	d1dzfa2	Alignment	not modelled	8.6	22	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
59	c2vpyE_	Alignment	not modelled	8.3	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**thiosulfate reductase; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
60	d2yvxa3	Alignment	not modelled	8.3	18	**Fold:**MgtE membrane domain-like **Superfamily:**MgtE membrane domain-like **Family:**MgtE membrane domain-like
61	c2fugC_	Alignment	not modelled	8.3	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
62	c2jy5A_	Alignment	not modelled	7.6	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
63	d1rqpa1	Alignment	not modelled	7.4	22	**Fold:**Bacterial fluorinating enzyme, C-terminal domain **Superfamily:**Bacterial fluorinating enzyme, C-terminal domain **Family:**Bacterial fluorinating enzyme, C-terminal domain
64	d1scjb_	Alignment	not modelled	7.3	16	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
65	c1cz5A_	Alignment	not modelled	7.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vcp-like atpase; **PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
66	d1hmja_	Alignment	not modelled	7.2	18	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
67	c2fhdA_	Alignment	not modelled	7.1	5	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
68	d2fy9a1	Alignment	not modelled	7.1	16	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
69	d1yfba1	Alignment	not modelled	7.0	19	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
70	c1wlfA_	Alignment	not modelled	6.8	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisome biogenesis factor 1; **PDBTitle:** structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
71	c2k21A_	Alignment	not modelled	6.8	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
72	c2k29A_	Alignment	not modelled	6.7	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
73	d1dv0a_	Alignment	not modelled	6.7	8	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
74	c2yvxD_	Alignment	not modelled	6.6	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
75	c3nd0A_	Alignment	not modelled	6.4	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
76	c2w2mP_	Alignment	not modelled	6.3	30	**PDB header:**hydrolase/receptor **Chain:** P: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** wt pcsk9-deltac bound to wt egf-a of ldlr
77	c2pmwA_	Alignment	not modelled	6.3	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** the crystal structure of proprotein convertase subtilisin2 kexin type 9 (pcsk9)
78	c2p4eP_	Alignment	not modelled	6.3	30	**PDB header:**hydrolase **Chain:** P: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** crystal structure of pcsk9
79	d2cu3a1	Alignment	not modelled	6.1	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
80	c2e75E_	Alignment	not modelled	6.1	20	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-

						nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
81	c2e76E_	Alignment	not modelled	6.1	20	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
82	c1vf5R_	Alignment	not modelled	6.1	20	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
83	d2e74e1	Alignment	not modelled	6.1	20	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
84	c1vf5E_	Alignment	not modelled	6.1	20	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**protein pet l; **PDBTitle:** crystal structure of cytochrome b6f complex from m.laminosus
85	c2e74E_	Alignment	not modelled	6.1	20	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from m.laminosus
86	c2kncB_	Alignment	not modelled	6.0	12	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
87	d1spbp_	Alignment	not modelled	6.0	15	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
88	c2kncA_	Alignment	not modelled	5.9	22	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
89	d1yloa1	Alignment	not modelled	5.7	24	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
90	d1zq1a1	Alignment	not modelled	5.7	11	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
91	d1q08a_	Alignment	not modelled	5.7	8	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
92	c2kl0A_	Alignment	not modelled	5.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
93	c2cw5B_	Alignment	not modelled	5.6	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**bacterial fluorinating enzyme homolog; **PDBTitle:** crystal structure of a conserved hypothetical protein from2 thermus thermophilus hb8
94	c2jpcA_	Alignment	not modelled	5.6	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
95	d1dgsa2	Alignment	not modelled	5.6	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
96	d2d6fa1	Alignment	not modelled	5.5	14	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
97	d3d31c1	Alignment	not modelled	5.5	15	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
98	c3d31D_	Alignment	not modelled	5.5	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**sulfate/molybdate abc transporter, permease **PDBTitle:** modbc from methanosarcina acetivorans
99	c2f4nA_	Alignment	not modelled	5.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein mj1651; **PDBTitle:** crystal structure of protein mj1651 from methanococcus2 jannaschii dsm 2661, pfam duf62