Phyre2

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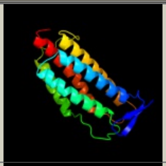
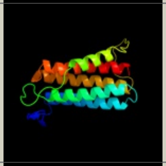
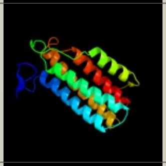
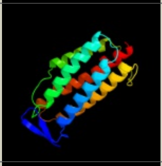
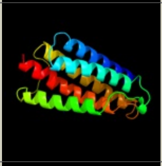
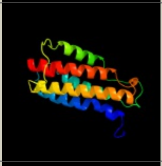
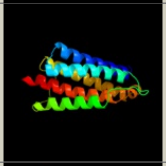
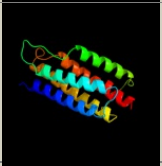
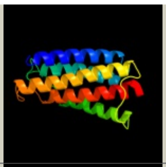
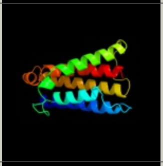
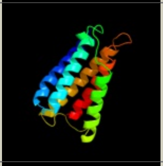
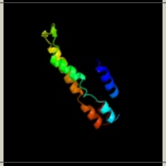
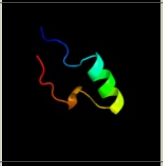
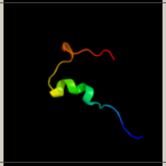
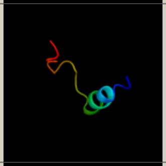
Description	P65643
Date	Thu Jan 5 12:10:17 GMT 2012
Unique Job ID	b73cc2aa2a814c69

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ke4B_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical cytosolic protein; **PDBTitle:** crystal structure of a pduo-type atp:cob(i)alamin adenosyltransferase2 from bacillus cereus
2	c2nt8A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase; **PDBTitle:** atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri
3	c3ci1A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase pduo-like protein; **PDBTitle:** structure of the pduo-type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri complexed3 with four-coordinate cob(ii)alamin and atp
4	c2zhzC_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase, putative; **PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
5	d1rtyb_	Alignment		100.0	18	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
6	c2ah6B_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bh1595, unknown conserved protein; **PDBTitle:** crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution
7	c2g2dA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:cobalamin adenosyltransferase; **PDBTitle:** crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis
8	c1wozA_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**177aa long conserved hypothetical protein (st1454); **PDBTitle:** crystal structure of uncharacterized protein st1454 from sulfolobus2 tokodaii
9	c1wvtA_	Alignment		100.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st2180; **PDBTitle:** crystal structure of uncharacterized protein st2180 from sulfolobus2 tokodaii
10	d1rtya_	Alignment		100.0	19	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
11	c1nogA_	Alignment		100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein ta0546; **PDBTitle:** crystal structure of conserved protein 0546 from thermoplasma2 acidophilum

12	d1noga_	Alignment		100.0	13	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
13	c2idxA_	Alignment		100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cob(i)yrinic acid a,c-diamide **PDBTitle:** structure of human atp:cobalamin adenosyltransferase bound2 to atp.
14	c1wy1B_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein ph0671; **PDBTitle:** crystal structure of the ph0671 protein from pyrococcus horikoshii ot3
15	c3t6gB_	Alignment		71.9	18	**PDB header:**signaling protein, cell adhesion **Chain:** B: **PDB Molecule:**breast cancer anti-estrogen resistance protein 1; **PDBTitle:** structure of the complex between nsp3 (shep1) and p130cas
16	d1niga_	Alignment		62.4	13	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Hypothetical protein Ta1238
17	d1w4ha1	Alignment		53.1	28	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
18	d1bala_	Alignment		48.2	29	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
19	d2cyua1	Alignment		46.8	33	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
20	d1r61a_	Alignment		41.0	25	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
21	c2eq9C_	Alignment	not modelled	38.6	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
22	c2eq7C_	Alignment	not modelled	37.2	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
23	c1w3dA_	Alignment	not modelled	35.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
24	c2p8tA_	Alignment	not modelled	33.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph0730; **PDBTitle:** hypothetical protein ph0730 from pyrococcus horikoshii ot3
25	c1zwvA_	Alignment	not modelled	32.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
26	c1w4kA_	Alignment	not modelled	30.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase e2; **PDBTitle:** peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
27	c1v9lA	Alignment	not modelled	27.4	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase;

27	c1v9lA_	Alignment	not modelled	27.4	29	**PDBTitle:** l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
28	c3dv0I_	Alignment	not modelled	26.7	20	**PDB header:**oxidoreductase/transferase **Chain:** I: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
29	c2eq8C_	Alignment	not modelled	26.6	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
30	d1b26a1	Alignment	not modelled	26.2	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
31	c3godA_	Alignment	not modelled	26.1	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cas1; **PDBTitle:** structural basis for dnase activity of a conserved protein2 implicated in crispr-mediated antiviral defense
32	d1eija_	Alignment	not modelled	26.1	50	**Fold:**RuvA C-terminal domain-like **Superfamily:**Double-stranded DNA-binding domain **Family:**Double-stranded DNA-binding domain
33	c2fh0A_	Alignment	not modelled	25.9	42	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical 16.0 kda protein in abf2-chl12 **PDBTitle:** nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
34	c2cooA_	Alignment	not modelled	25.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
35	d1w85i_	Alignment	not modelled	25.0	20	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
36	c2ek0B_	Alignment	not modelled	23.8	18	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**stage v sporulation protein s (spovs) related protein; **PDBTitle:** stage v sporolation protein s (spovs) from thermus thermophilus zinc2 form
37	d1gtma1	Alignment	not modelled	23.4	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
38	d1v9la1	Alignment	not modelled	23.1	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
39	c2jxnA_	Alignment	not modelled	22.7	42	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ymr074c; **PDBTitle:** solution structure of s. cerevisiae pdcd5-like protein ymr074cp
40	d1bvua1	Alignment	not modelled	22.2	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
41	c2hfqA_	Alignment	not modelled	21.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** nmr structure of protein ne1680 from nitrosomonas europaea:2 northeast structural genomics consortium target net5
42	d2hfqa1	Alignment	not modelled	21.9	27	**Fold:**NE1680-like **Superfamily:**NE1680-like **Family:**NE1680-like
43	c2tmgD_	Alignment	not modelled	21.6	35	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
44	d2q4qa1	Alignment	not modelled	21.3	9	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
45	c3k8zD_	Alignment	not modelled	21.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
46	c3nkdB_	Alignment	not modelled	20.2	22	**PDB header:**immune system **Chain:** B: **PDB Molecule:**crispr-associated protein cas1; **PDBTitle:** structure of crisp-associated protein cas1 from escherichia coli str.2 k-12
47	d2crua1	Alignment	not modelled	20.2	45	**Fold:**RuvA C-terminal domain-like **Superfamily:**Double-stranded DNA-binding domain **Family:**Double-stranded DNA-binding domain
48	d1h75a_	Alignment	not modelled	20.2	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
49	c3aogA_	Alignment	not modelled	19.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
50	c1nr1A_	Alignment	not modelled	19.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase 1; **PDBTitle:** crystal structure of the r463a mutant of human glutamate2 dehydrogenase
51	c2bmaA_	Alignment	not modelled	19.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase (nadp+); **PDBTitle:** the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs

52	d1euza1	Alignment	not modelled	19.4	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
53	d2bl7a1	Alignment	not modelled	18.8	21	**Fold:**Bromodomain-like **Superfamily:**Bacteriocin immunity protein-like **Family:**EntA-Im
54	d1g7oa1	Alignment	not modelled	18.5	33	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
55	d1st6a5	Alignment	not modelled	18.4	8	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
56	d2ge7a1	Alignment	not modelled	18.4	24	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
57	d1hwxa1	Alignment	not modelled	18.1	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
58	c3aoeC_	Alignment	not modelled	17.9	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
59	d1ryaa_	Alignment	not modelled	17.3	10	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
60	c2lafA_	Alignment	not modelled	17.2	22	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lipoprotein 34; **PDBTitle:** nmr solution structure of the n-terminal domain of the e. coli2 lipoprotein bamc
61	c1bvuF_	Alignment	not modelled	16.1	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** glutamate dehydrogenase from thermococcus litoralis
62	d1v43a1	Alignment	not modelled	15.8	33	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
63	d2giba1	Alignment	not modelled	15.5	17	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
64	d1rw1a_	Alignment	not modelled	15.2	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
65	c2q4dB_	Alignment	not modelled	14.9	5	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
66	c2yfqA_	Alignment	not modelled	14.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
67	c2qgoA_	Alignment	not modelled	14.8	33	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative fe-s biosynthesis protein; **PDBTitle:** crystal structure of a putative fe-s biosynthesis protein from2 lactobacillus acidophilus
68	c1zunA_	Alignment	not modelled	14.6	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
69	d2fvta1	Alignment	not modelled	13.6	11	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
70	d1ydha_	Alignment	not modelled	12.3	5	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
71	c3ebqA_	Alignment	not modelled	11.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**molecule: pppde1 (permuted papain fold **PDBTitle:** crystal structure of human pppde1
72	d2p2ea1	Alignment	not modelled	11.6	25	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
73	d1abaa_	Alignment	not modelled	11.3	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
74	c2wmyH_	Alignment	not modelled	11.2	21	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**putative acid phosphatase wzb; **PDBTitle:** crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
75	c3lfxE_	Alignment	not modelled	10.6	18	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of tm1797, a cas1 protein from thermotoga maritima
76	d1aw9a1	Alignment	not modelled	10.5	13	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
77	d2cjra1	Alignment	not modelled	10.3	14	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
78	d2dlka1	Alignment	not modelled	10.1	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers

						Family: Classic zinc finger, C2H2
79	d1c4ka3	Alignment	not modelled	10.0	4	**Fold:**Ornithine decarboxylase C-terminal domain **Superfamily:**Ornithine decarboxylase C-terminal domain **Family:**Ornithine decarboxylase C-terminal domain
80	d1oywa1	Alignment	not modelled	10.0	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like
81	d1r7ha_	Alignment	not modelled	9.9	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
82	c1iq8B_	Alignment	not modelled	9.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**archaeosine trna-guanine transglycosylase; **PDBTitle:** crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
83	c1y88A_	Alignment	not modelled	9.4	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1548; **PDBTitle:** crystal structure of protein of unknown function af1548
84	d1igna2	Alignment	not modelled	9.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of rap1
85	d16vpa_	Alignment	not modelled	9.3	22	**Fold:**Conserved core of transcriptional regulatory protein vp16 **Superfamily:**Conserved core of transcriptional regulatory protein vp16 **Family:**Conserved core of transcriptional regulatory protein vp16
86	c3gkxB_	Alignment	not modelled	9.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
87	d1in4a1	Alignment	not modelled	9.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
88	d1ixsb1	Alignment	not modelled	8.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
89	d1zuna1	Alignment	not modelled	8.7	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
90	c3e0sA_	Alignment	not modelled	8.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 chlorobium tepidum
91	c3f0iA_	Alignment	not modelled	8.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** arsenate reductase from vibrio cholerae.
92	c2yzsB_	Alignment	not modelled	8.3	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 aquifex aeolicus
93	d1ixrc1	Alignment	not modelled	8.0	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
94	d1kyha_	Alignment	not modelled	7.9	30	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
95	d1a4ia2	Alignment	not modelled	7.8	10	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
96	c3edpB_	Alignment	not modelled	7.6	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lin2111 protein; **PDBTitle:** the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
97	d1j9ba_	Alignment	not modelled	7.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
98	d1t1va_	Alignment	not modelled	7.4	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
99	c3pv9D_	Alignment	not modelled	7.4	17	**PDB header:**immune system **Chain:** D: **PDB Molecule:**putative uncharacterized protein ph1245; **PDBTitle:** structure of ph1245, a cas1 from pyrococcus horikoshii