Phyre^2

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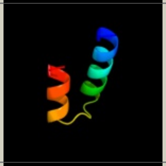
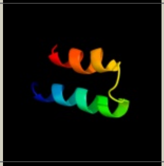
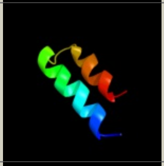
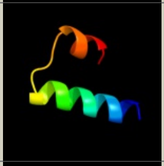
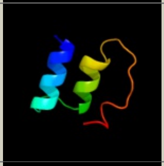
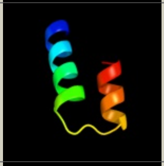
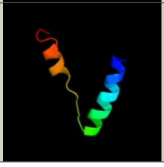
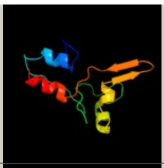
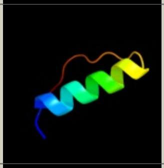
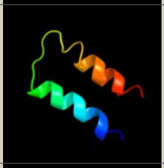
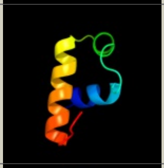
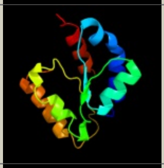
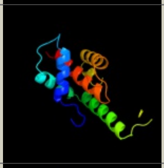
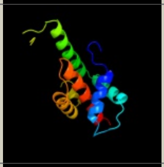
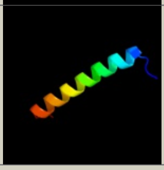
Description	P0ADD5
Date	Thu Jan 5 11:20:41 GMT 2012
Unique Job ID	566998bd5e61f6a6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jvdA_	Alignment		49.2	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynzc from bacillus subtilis. northeast3 structural genomics target sr384-1-46
2	c3bhpA_	Alignment		47.2	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** crystal structure of upf0291 protein ynzc from bacillus2 subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
3	d1vp7a_	Alignment		45.7	14	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
4	c2y0sJ_	Alignment		43.6	10	**PDB header:**transferase **Chain:** J: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
5	c2y0sQ_	Alignment		43.6	10	**PDB header:**transferase **Chain:** Q: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
6	c2hepA_	Alignment		42.6	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0291 protein ynzc; **PDBTitle:** solution nmr structure of the upf0291 protein ynzc from2 bacillus subtilis. northeast structural genomics target3 sr384.
7	d2hepa1	Alignment		42.6	4	**Fold:**Long alpha-hairpin **Superfamily:**YnzC-like **Family:**YznC-like
8	d2pp4a1	Alignment		40.4	13	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
9	d1vp7b_	Alignment		37.3	14	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
10	c3hkzY_	Alignment		33.0	9	**PDB header:**transferase **Chain:** Y: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
11	d1w53a_	Alignment		31.7	12	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Phosphoserine phosphatase RsbU, N-terminal domain

12	d1vd6a1	Alignment		31.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
13	d1qd1a2	Alignment		31.4	23	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
14	d1o1za_	Alignment		29.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
15	c3hkzZ_	Alignment		27.6	9	**PDB header:**transferase **Chain:** Z: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
16	c3sztB_	Alignment		27.0	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
17	d1wo8a1	Alignment		26.7	12	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
18	d1tlqa_	Alignment		25.7	15	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
19	c1tlqA_	Alignment		25.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ypjq; **PDBTitle:** crystal structure of protein ypjq from bacillus subtilis, pfam duf64
20	d1ml8a_	Alignment		24.4	10	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**YhfA-like
21	c2yvxD_	Alignment	not modelled	24.0	9	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
22	c2ql8A_	Alignment	not modelled	23.6	3	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative redox protein; **PDBTitle:** crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
23	c2wb1Q_	Alignment	not modelled	23.1	8	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
24	c2bjoA_	Alignment	not modelled	22.1	3	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**organic hydroperoxide resistance protein ohrb; **PDBTitle:** crystal structure of the organic hydroperoxide resistance2 protein ohrb of bacillus subtilis
25	c2wb1J_	Alignment	not modelled	21.9	8	**PDB header:**transcription **Chain:** J: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
26	c2waqQ_	Alignment	not modelled	20.9	6	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
27	c3cjeA_	Alignment	not modelled	20.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**osmc-like protein; **PDBTitle:** crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution

28	d1lqla_	Alignment	not modelled	20.1	10	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
29	c1lqlE_	Alignment	not modelled	20.1	10	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**osmotical inducible protein c like family; **PDBTitle:** crystal structure of osmc like protein from mycoplasma2 pneumoniae
30	d1uspa_	Alignment	not modelled	18.2	3	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
31	c2egtA_	Alignment	not modelled	18.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein aq_1549; **PDBTitle:** crystal structure of hypothetical protein (aq1549) from aquifex2 aeolicus
32	d1n2fa_	Alignment	not modelled	16.9	7	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
33	d1q8la_	Alignment	not modelled	16.7	8	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
34	c3eerA_	Alignment	not modelled	16.5	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**organic hydroperoxide resistance protein, putative; **PDBTitle:** high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961
35	d1qwia_	Alignment	not modelled	16.2	7	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
36	d2pn2a1	Alignment	not modelled	16.2	13	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
37	d1vlaa_	Alignment	not modelled	15.4	13	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**YhfA-like
38	d2p6va1	Alignment	not modelled	15.2	15	**Fold:**TAFH domain-like **Superfamily:**TAFH domain-like **Family:**TAFH domain-like
39	c2i88A_	Alignment	not modelled	15.2	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**colicin-e1; **PDBTitle:** crystal structure of the channel-forming domain of colicin2 e1
40	c2j6yB_	Alignment	not modelled	14.3	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphoserine phosphatase rsbu; **PDBTitle:** structural and functional characterisation of partner2 switching regulating the environmental stress response in3 bacillus subtilis
41	d1jt6a2	Alignment	not modelled	14.1	7	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
42	c2bezC_	Alignment	not modelled	14.1	11	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** structure of a proteolitically resistant core from the2 severe acute respiratory syndrome coronavirus s2 fusion3 protein
43	c1ciiA_	Alignment	not modelled	13.6	15	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
44	d1nyed_	Alignment	not modelled	12.8	10	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
45	c2qdqA_	Alignment	not modelled	11.1	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** crystal structure of the talin dimerisation domain
46	d2opla1	Alignment	not modelled	10.7	7	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
47	c3ks6A_	Alignment	not modelled	10.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens3 str. c58 (dupont) at 1.80 a resolution
48	d1whra_	Alignment	not modelled	10.3	11	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
49	c2kkhA_	Alignment	not modelled	10.3	10	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
50	c3no5C_	Alignment	not modelled	9.7	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
51	d2oa4a1	Alignment	not modelled	9.4	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
52	c3b47A_	Alignment	not modelled	9.4	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0582
53	c3bd7A_	Alignment	not modelled	9.4	5	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2;

53	c3hd7A_	Alignment	not modelled	9.4	5	**PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
54	d2o38a1	Alignment	not modelled	9.3	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
55	c2o38A_	Alignment	not modelled	9.3	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
56	c2fxpA_	Alignment	not modelled	9.2	9	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**spike glycoprotein; **PDBTitle:** solution structure of the sars-coronavirus hr2 domain
57	d2jf2a1	Alignment	not modelled	9.1	13	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
58	c3i10A_	Alignment	not modelled	9.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (np_812074.1) from bacteroides thetaiotaomicron3 vpi-5482 at 1.35 a resolution
59	c3c6cA_	Alignment	not modelled	9.0	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
60	c2jrtA_	Alignment	not modelled	8.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
61	d2v4jb2	Alignment	not modelled	8.8	12	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
62	d1xmba2	Alignment	not modelled	8.7	12	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
63	c2pz0B_	Alignment	not modelled	8.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
64	c2y7eA_	Alignment	not modelled	8.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
65	c3lotC_	Alignment	not modelled	8.4	17	**PDB header:**structure genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
66	c3qvqB_	Alignment	not modelled	8.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase olei02445; **PDBTitle:** the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate
67	c2otdC_	Alignment	not modelled	8.2	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a
68	c2kyzA_	Alignment	not modelled	7.7	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**heavy metal binding protein; **PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
69	c3e02A_	Alignment	not modelled	7.4	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849; **PDBTitle:** crystal structure of a duf849 family protein (bxe_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
70	c1y3kA_	Alignment	not modelled	7.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein
71	d1x4pa1	Alignment	not modelled	7.3	20	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
72	c3r1fO_	Alignment	not modelled	7.1	13	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
73	c1yg0A_	Alignment	not modelled	7.0	8	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
74	c3e49A_	Alignment	not modelled	7.0	6	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf849 with a tim barrel fold; **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bxe_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
75	c2uwjF_	Alignment	not modelled	6.9	23	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**type iii export protein pscf; **PDBTitle:** structure of the heterotrimeric complex which regulates2 type iii secretion needle formation
76	c1wyyB_	Alignment	not modelled	6.9	11	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 glycoprotein;

76	c1wyyB_	Alignment	not modelled	6.9	11	**PDBTitle:** post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
77	d1iiba_	Alignment	not modelled	6.8	9	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
78	d2ieaa3	Alignment	not modelled	6.7	21	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
79	c3ipdB_	Alignment	not modelled	6.7	10	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
80	d1otsa_	Alignment	not modelled	6.6	11	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
81	d1kpla_	Alignment	not modelled	6.6	13	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
82	c3chvA_	Alignment	not modelled	6.5	7	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
83	c2lkyA_	Alignment	not modelled	6.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of msmeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
84	c2l2qA_	Alignment	not modelled	6.4	3	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
85	c2v4iA_	Alignment	not modelled	6.4	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate n-acetyltransferase 2 alpha chain; **PDBTitle:** structure of a novel n-acyl-enzyme intermediate of an n-2 terminal nucleophile (ntn) hydrolase, oat2
86	c2ofhX_	Alignment	not modelled	6.2	10	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
87	d1osda_	Alignment	not modelled	6.1	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
88	d2axta1	Alignment	not modelled	6.1	20	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
89	c3ck4K_	Alignment	not modelled	6.0	14	**PDB header:**protein binding **Chain:** K: **PDB Molecule:**gcn4 leucine zipper; **PDBTitle:** a heterospecific leucine zipper tetramer
90	d1cpza_	Alignment	not modelled	5.9	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
91	c3cqbB_	Alignment	not modelled	5.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable protease htpx homolog; **PDBTitle:** crystal structure of heat shock protein htpx domain from vibrio2 parahaemolyticus rimd 2210633
92	d2ofya1	Alignment	not modelled	5.7	13	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
93	c2b2hA_	Alignment	not modelled	5.7	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
94	d1e0ga_	Alignment	not modelled	5.7	15	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
95	d1mwza_	Alignment	not modelled	5.7	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
96	c1qd1A_	Alignment	not modelled	5.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**formiminotransferase-cyclodeaminase; **PDBTitle:** the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
97	c3a1yF_	Alignment	not modelled	5.6	24	**PDB header:**ribosomal protein **Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p); **PDBTitle:** the structure of protein complex
98	c1yjrA_	Alignment	not modelled	5.5	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
99	c1izlJ_	Alignment	not modelled	5.5	20	**PDB header:**photosynthesis **Chain:** J: **PDB Molecule:**photosystem ii: subunit psba; **PDBTitle:** crystal structure of photosystem ii