Phyre^2

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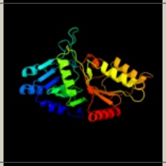
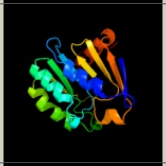
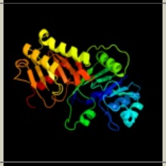
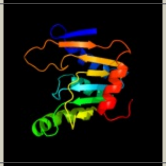
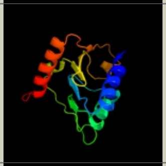
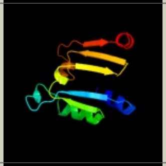
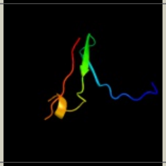
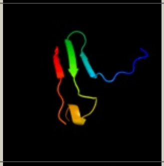
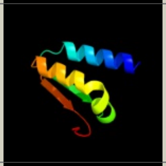
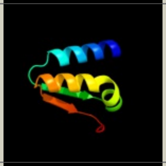
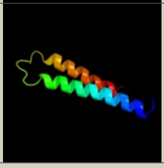
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hsiC_	Alignment		100.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphatidylserine synthase; **PDBTitle:** crystal structure of phosphatidylserine synthase haemophilus2 influenzae rd kw20
2	c1v0sA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase d; **PDBTitle:** uninhibited form of phospholipase d from streptomyces sp.2 strain pmf
3	c1xdoB_	Alignment		100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
4	d1v0wa1	Alignment		100.0	15	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Phospholipase D
5	d1xdpa3	Alignment		99.9	19	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
6	d1byra_	Alignment		99.9	23	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Nuclease
7	c2o8rA_	Alignment		99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
8	d1v0wa2	Alignment		99.9	23	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Phospholipase D
9	d2o8ra3	Alignment		99.1	22	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
10	d1xdpa4	Alignment		99.1	15	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
11	d2o8ra4	Alignment		98.9	11	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain

12	c1q32C_	Alignment		97.7	13	**PDB header:**replication,transcription,hydrolase **Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase; **PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna2 phosphodiesterase
13	c2c1lA_	Alignment		97.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease; **PDBTitle:** structure of the bfii restriction endonuclease
14	c3sq3C_	Alignment		97.2	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure analysis of the yeast tyrosyl-dna phosphodiesterase2 h182a mutant
15	d1jy1a2	Alignment		95.3	18	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
16	c1nopB_	Alignment		95.1	23	**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		94.6	23	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
18	d2f5tx2	Alignment		81.2	23	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**TrmB middle domain-like
19	c2f5tX_	Alignment		75.7	23	**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
20	c3mk7F_	Alignment		69.0	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
21	d1qzqa1	Alignment	not modelled	66.2	36	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
22	d1o98a1	Alignment	not modelled	65.2	10	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
23	d1q32a1	Alignment	not modelled	63.4	13	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
24	d1jy1a1	Alignment	not modelled	61.2	8	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
25	c2a5hC_	Alignment	not modelled	56.7	18	**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).
26	c2l82A_	Alignment	not modelled	56.5	12	**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
27	d1tfra2	Alignment	not modelled	55.7	10	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
						PDB header:chaperone

28	c3kgkA_	Alignment	not modelled	54.1	11	**Chain:** A: **PDB Molecule:**arsenical resistance operon trans-acting repressor arsd; **PDBTitle:** crystal structure of arsd
29	c2b34C_	Alignment	not modelled	45.3	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
30	c1o98A_	Alignment	not modelled	39.9	10	**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
31	d1yaca_	Alignment	not modelled	36.5	21	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
32	c3ktbD_	Alignment	not modelled	35.9	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
33	c2yv5A_	Alignment	not modelled	35.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
34	d2r6gf1	Alignment	not modelled	34.2	18	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
35	c3gbcA_	Alignment	not modelled	27.9	26	**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
36	d1x9ga_	Alignment	not modelled	27.6	14	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
37	c2nytB_	Alignment	not modelled	27.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
38	d1un8a4	Alignment	not modelled	26.9	13	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
39	d1gz0a2	Alignment	not modelled	24.7	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
40	c1yzvA_	Alignment	not modelled	23.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from trypanosoma cruzi
41	d1im5a_	Alignment	not modelled	22.7	16	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
42	d1fftb2	Alignment	not modelled	20.5	17	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
43	c1pt9B_	Alignment	not modelled	20.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase, mitochondrial; **PDBTitle:** crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
44	c2r60A_	Alignment	not modelled	20.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
45	c2bruC_	Alignment	not modelled	20.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p) transhydrogenase subunit beta; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
46	c3l2iB_	Alignment	not modelled	19.8	13	**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.
47	d1d4oa_	Alignment	not modelled	19.5	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
48	d1pnoa_	Alignment	not modelled	19.4	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Transhydrogenase domain III (dIII)
49	d1ueha_	Alignment	not modelled	17.9	16	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
50	d1gz0f2	Alignment	not modelled	17.8	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
51	c2x7mA_	Alignment	not modelled	17.1	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
52	c2q5cA_	Alignment	not modelled	16.6	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
53	c2b8eB_	Alignment	not modelled	16.4	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**cation-transporting atpase; **PDBTitle:** copa atp binding domain

54	c3dy0B_	Alignment	not modelled	16.0	40	**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
55	c2h0rD_	Alignment	not modelled	15.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
56	c1lq8H_	Alignment	not modelled	14.9	40	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**plasma serine protease inhibitor; **PDBTitle:** crystal structure of cleaved protein c inhibitor
57	c2pjuD_	Alignment	not modelled	14.9	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
58	c1s21A_	Alignment	not modelled	14.5	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**orf2; **PDBTitle:** crystal structure of avrpphf orf2, a type iii effector from2 p. syringae
59	d1s21a_	Alignment	not modelled	14.5	23	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**AvrPphF ORF2, a type III effector
60	c1t3gB_	Alignment	not modelled	13.9	11	**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
61	d1ay7b_	Alignment	not modelled	13.9	12	**Fold:**Barstar-like **Superfamily:**Barstar-related **Family:**Barstar-related
62	c2wtaA_	Alignment	not modelled	13.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** acinetobacter baumanii nicotinamidase pyrazinamidease
63	c2yvkA_	Alignment	not modelled	13.8	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
64	c3hu5B_	Alignment	not modelled	13.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
65	d1x94a_	Alignment	not modelled	13.6	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
66	d1pjqa2	Alignment	not modelled	13.6	13	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
67	d1o57a2	Alignment	not modelled	13.5	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	d1t5oa_	Alignment	not modelled	13.4	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
69	c3js3C_	Alignment	not modelled	13.4	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
70	c2rddB_	Alignment	not modelled	13.4	17	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
71	d1nvmb1	Alignment	not modelled	13.4	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
72	d3dtub2	Alignment	not modelled	13.3	7	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
73	c3igzB_	Alignment	not modelled	13.2	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
74	c2iksA_	Alignment	not modelled	13.0	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding transcriptional dual regulator; **PDBTitle:** crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
75	d2fcja1	Alignment	not modelled	12.9	7	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
76	d1t9ka_	Alignment	not modelled	12.7	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
77	d1s4da_	Alignment	not modelled	12.6	10	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
78	c3r2jC_	Alignment	not modelled	12.5	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta-hydrolase-like protein; **PDBTitle:** crystal structure of pnc1 from l. infantum in complex with nicotinate
						PDB header:transcription

79	c2hqbA_	Alignment	not modelled	12.2	8	**Chain:** A: **PDB Molecule:**transcriptional activator of comk gene; **PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
80	c2voyC_	Alignment	not modelled	12.2	38	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
81	c3brqA_	Alignment	not modelled	12.0	5	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg
82	c3zvmA_	Alignment	not modelled	11.9	20	**PDB header:**hydrolase/transferase/dna **Chain:** A: **PDB Molecule:**bifunctional polynucleotide phosphatase/kinase; **PDBTitle:** the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
83	c1hf2A_	Alignment	not modelled	11.8	14	**PDB header:**cell division protein **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the bacterial cell-division inhibitor2 minc from t. maritima
84	c3a11D_	Alignment	not modelled	11.7	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
85	c3h75A_	Alignment	not modelled	11.6	7	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein; **PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
86	d1acoa2	Alignment	not modelled	11.5	10	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
87	d1gpja3	Alignment	not modelled	11.4	15	**Fold:**Ferredoxin-like **Superfamily:**Glutamyl tRNA-reductase catalytic, N-terminal domain **Family:**Glutamyl tRNA-reductase catalytic, N-terminal domain
88	d1nr3a_	Alignment	not modelled	11.4	21	**Fold:**DNA-binding protein Tfx **Superfamily:**DNA-binding protein Tfx **Family:**DNA-binding protein Tfx
89	c2rchA_	Alignment	not modelled	11.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cytochrome p450 74a; **PDBTitle:** crystal structure of arabidopsis thaliana allene oxide synthase (aos,2 cytochrome p450 74a, cyp74a) complexed with 13(s)-hod at 1.85 a3 resolution
90	d1ecfa1	Alignment	not modelled	11.0	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
91	c3ny7A_	Alignment	not modelled	10.9	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sulfate transporter; **PDBTitle:** stas domain of ychm bound to acp
92	d1j5pa4	Alignment	not modelled	10.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
93	c3h5oB_	Alignment	not modelled	10.7	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
94	c3ecsD_	Alignment	not modelled	10.5	13	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
95	c3bblA_	Alignment	not modelled	10.4	11	**PDB header:**regulatory protein **Chain:** A: **PDB Molecule:**regulatory protein of laci family; **PDBTitle:** crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
96	d1qyda_	Alignment	not modelled	10.2	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
97	d1gqna_	Alignment	not modelled	10.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
98	c1o57A_	Alignment	not modelled	10.0	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
99	d1wdea_	Alignment	not modelled	10.0	14	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase