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Description	P46887
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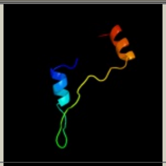
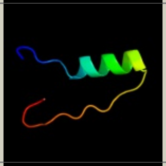
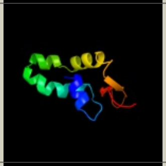
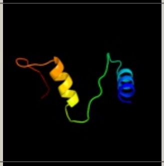
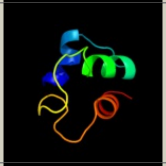
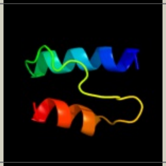
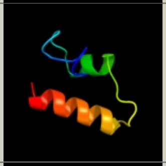
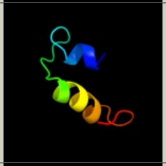
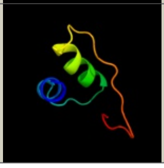
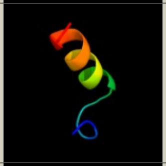
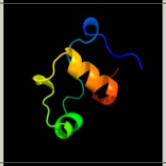
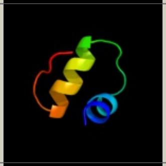
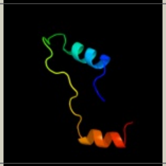
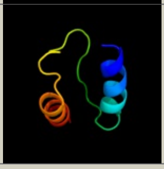
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w2za2	Alignment		35.9	10	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
2	d1sgla_	Alignment		35.7	19	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
3	c2xigA_	Alignment		25.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
4	c3ri6A_	Alignment		24.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-acetylhomoserine sulfhydrylase; **PDBTitle:** a novel mechanism of sulfur transfer catalyzed by o-acetylhomoserine2 sulfhydrylase in methionine biosynthetic pathway of wolinella3 succinogenes
5	d1vqza1	Alignment		24.2	16	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
6	c2l9fA_	Alignment		22.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
7	c3c1dA_	Alignment		21.8	10	**PDB header:**recombination, dna binding protein **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** x-ray crystal structure of recx
8	d2p6ra1	Alignment		21.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like
9	c2o03A_	Alignment		19.2	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
10	c2kw0A_	Alignment		18.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
11	c3d3zA_	Alignment		17.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**actibind; **PDBTitle:** crystal structure of actibind a t2 rnase

12	c3gkxB_	Alignment		17.7	30	**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
13	d2a2pa1	Alignment		17.7	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
14	c3c18B_	Alignment		17.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotidyltransferase-like protein; **PDBTitle:** crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution
15	d1z3ea1	Alignment		17.0	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
16	c3l78A_	Alignment		16.9	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
17	d1bola_	Alignment		16.5	31	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
18	c3r1fO_	Alignment		15.7	35	**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
19	c1ksiA_	Alignment		15.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a eukaryotic (pea seedling) copper-containing2 amine oxidase at 2.2a resolution
20	d1dv5a_	Alignment		15.5	14	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**apo-D-alanyl carrier protein
21	c2kokA_	Alignment	not modelled	15.3	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a.
22	d1qasa1	Alignment	not modelled	14.8	32	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
23	d1rw1a_	Alignment	not modelled	14.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ArsC-like
24	d1pixa2	Alignment	not modelled	14.6	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
25	c3dfgA_	Alignment	not modelled	14.6	29	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris
26	d1rqta_	Alignment	not modelled	13.7	21	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
27	c1rqtB_	Alignment	not modelled	13.7	21	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
28	c1rqtA_	Alignment	not modelled	13.7	21	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**50s ribosomal protein l7/l12;

28	c1rqtA_	Alignment	not modelled	13.7	21	**PDBTitle:** nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
29	d1iyba_	Alignment	not modelled	13.2	25	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
30	c3d5lA_	Alignment	not modelled	13.2	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of regulatory protein recx
31	d3elna1	Alignment	not modelled	12.0	29	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
32	c3ffhA_	Alignment	not modelled	12.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of histidinol-phosphate aminotransferase from2 listeria innocua clip11262.
33	c2hl7A_	Alignment	not modelled	11.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
34	c3fz4A_	Alignment	not modelled	11.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative arsenate reductase; **PDBTitle:** the crystal structure of a possible arsenate reductase from2 streptococcus mutans ua159
35	d1y4ia1	Alignment	not modelled	11.0	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
36	c2pqxA_	Alignment	not modelled	11.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease i; **PDBTitle:** e. coli rnase 1 (in vivo folded)
37	d1c7ga_	Alignment	not modelled	10.8	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
38	d1dixa_	Alignment	not modelled	10.7	26	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
39	c3bv8A_	Alignment	not modelled	10.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tetrahydrodipicolinate acetyltransferase; **PDBTitle:** crystal structure of the n-terminal domain of tetrahydrodipicolinate2 acetyltransferase from staphylococcus aureus
40	d1ucda_	Alignment	not modelled	10.5	21	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
41	c2dbgA_	Alignment	not modelled	10.4	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**myeloid cell nuclear differentiation antigen; **PDBTitle:** solution structure of the pyrin (paad-dapin) domain in2 human myeloid cell nuclear differentiation antigen
42	d1tpla_	Alignment	not modelled	10.4	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Beta-eliminating lyases
43	c3s2xB_	Alignment	not modelled	10.3	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
44	d1bw6a_	Alignment	not modelled	10.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
45	d1y74b1	Alignment	not modelled	9.8	35	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
46	d1kkca2	Alignment	not modelled	9.8	35	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
47	d2ctza1	Alignment	not modelled	9.6	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
48	d1iooa_	Alignment	not modelled	9.3	31	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
49	c2fcdA_	Alignment	not modelled	9.3	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**myosin light chain 1; **PDBTitle:** solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae
50	d1wuua2	Alignment	not modelled	9.1	21	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Galactokinase
51	d1tp6a_	Alignment	not modelled	9.1	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PA1314-like
52	d1dt0a2	Alignment	not modelled	9.0	37	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
53	d1qn2a_	Alignment	not modelled	8.8	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
54	d2nyba2	Alignment	not modelled	8.5	39	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain

						Family: Fe,Mn superoxide dismutase (SOD), C-terminal domain
55	d1jy5a_	Alignment	not modelled	8.3	13	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
56	c3ee4A_	Alignment	not modelled	8.3	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable ribonucleoside-diphosphate reductase; **PDBTitle:** r2-like ligand binding mn/fe oxidase from m. tuberculosis
57	c1vd3A_	Alignment	not modelled	7.9	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rnase ngr3; **PDBTitle:** ribonuclease nt in complex with 2'-ump
58	c3r24A_	Alignment	not modelled	7.8	20	**PDB header:**transferase, viral protein **Chain:** A: **PDB Molecule:**2'-o-methyl transferase; **PDBTitle:** crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible
59	c1fm6V_	Alignment	not modelled	7.8	20	**PDB header:**transcription **Chain:** V: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides.
60	c2hfpB_	Alignment	not modelled	7.7	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**src peptide fragment; **PDBTitle:** crystal structure of ppar gamma with n-sulfonyl-2-indole2 carboxamide ligands
61	c3mwmA_	Alignment	not modelled	7.7	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
62	c3kmgE_	Alignment	not modelled	7.6	20	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator-1; **PDBTitle:** the x-ray crystal structure of ppar-gamma in complex with an indole2 derivative modulator, gsk538, and an src-1 peptide
63	d1kfia3	Alignment	not modelled	7.6	15	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
64	c2f9yB_	Alignment	not modelled	7.6	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
65	d2f9yb1	Alignment	not modelled	7.6	27	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
66	c1fm9E_	Alignment	not modelled	7.6	23	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and gi262570 and co-activator peptides.
67	c1fm6E_	Alignment	not modelled	7.6	23	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.1 angstrom resolution crystal structure of the2 heterodimer of the human rxralpha and ppargamma ligand3 binding domains respectively bound with 9-cis retinoic4 acid and rosiglitazone and co-activator peptides.
68	c1k74E_	Alignment	not modelled	7.6	23	**PDB header:**transcription **Chain:** E: **PDB Molecule:**steroid receptor coactivator; **PDBTitle:** the 2.3 angstrom resolution crystal structure of the2 heterodimer of the human ppargamma and rxralpha ligand3 binding domains respectively bound with gw409544 and 9-cis4 retinoic acid and co-activator peptides.
69	c3ingA_	Alignment	not modelled	7.5	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
70	d1ma1a2	Alignment	not modelled	7.3	33	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
71	c1f93H_	Alignment	not modelled	7.3	37	**PDB header:**transcription **Chain:** H: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
72	d1idsa2	Alignment	not modelled	7.2	37	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
73	c3ff5B_	Alignment	not modelled	7.1	28	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 14; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
74	c3e3vA_	Alignment	not modelled	7.1	21	**PDB header:**recombination **Chain:** A: **PDB Molecule:**regulatory protein recx; **PDBTitle:** crystal structure of recx from lactobacillus salivarius
75	c3s93B_	Alignment	not modelled	7.1	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tudor domain-containing protein 5; **PDBTitle:** crystal structure of conserved motif in tdrd5
76	c1f93G_	Alignment	not modelled	7.1	37	**PDB header:**transcription **Chain:** G: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
77	d1ix9a2	Alignment	not modelled	7.0	46	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain

78	c1g39C_	Alignment	not modelled	6.8	37	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** wild-type hnf-1alpha dimerization domain
79	d1gv3a2	Alignment	not modelled	6.7	23	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
80	c2e7uA_	Alignment	not modelled	6.6	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-aminomutase from2 thermus thermophilus hb8
81	c1gv3B_	Alignment	not modelled	6.6	20	**PDB header:**manganese superoxide dismutase **Chain:** B: **PDB Molecule:**manganese superoxide dismutase; **PDBTitle:** the 2.0 angstrom resolution structure of the catalytic2 portion of a cyanobacterial membrane-bound manganese3 superoxide dismutase
82	d1uera2	Alignment	not modelled	6.4	33	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
83	c3f2hA_	Alignment	not modelled	6.4	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alkylmercury lyase; **PDBTitle:** crystal structure of the mercury-bound form of merb mutant2 c160s, the organomercurial lyase involved in a bacterial3 mercury resistance system
84	c2w85A_	Alignment	not modelled	6.3	28	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19
85	d1tyya_	Alignment	not modelled	6.3	20	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
86	d2hrca1	Alignment	not modelled	6.3	15	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
87	d1qgna_	Alignment	not modelled	6.2	24	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
88	d1vefa1	Alignment	not modelled	6.2	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
89	c2k6sB_	Alignment	not modelled	6.2	21	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**rab11fip2 protein; **PDBTitle:** structure of rab11-fip2 c-terminal coiled-coil domain
90	d1my6a2	Alignment	not modelled	6.2	31	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
91	d1e5ea_	Alignment	not modelled	6.2	24	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
92	c2zsmA_	Alignment	not modelled	6.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
93	d1mnga2	Alignment	not modelled	5.9	30	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
94	d2coba1	Alignment	not modelled	5.9	43	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
95	c2k5eA_	Alignment	not modelled	5.8	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
96	d1vdla_	Alignment	not modelled	5.8	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
97	d2p4ka2	Alignment	not modelled	5.8	37	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
98	d1p7ga2	Alignment	not modelled	5.7	20	**Fold:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Superfamily:**Fe,Mn superoxide dismutase (SOD), C-terminal domain **Family:**Fe,Mn superoxide dismutase (SOD), C-terminal domain
99	c2prgC_	Alignment	not modelled	5.6	23	**PDB header:**complex (thiazolidinedione/receptor) **Chain:** C: **PDB Molecule:**nuclear receptor coactivator src-1; **PDBTitle:** ligand-binding domain of the human peroxisome proliferator2 activated receptor gamma