Phyre^2

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Description	P0ADS9
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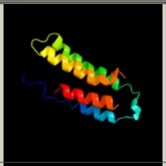
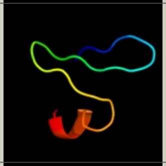
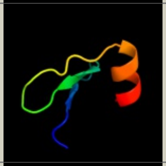
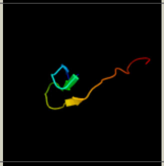
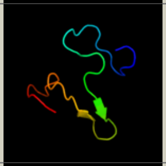
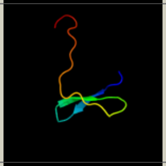
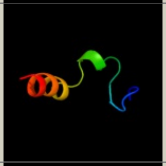
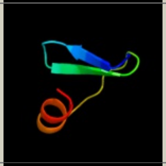
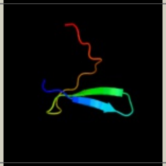
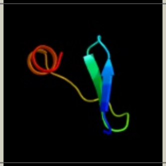
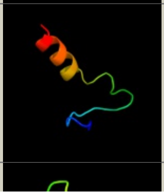
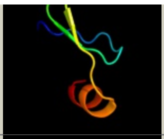
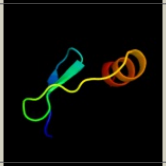
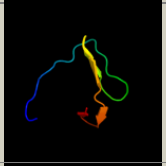
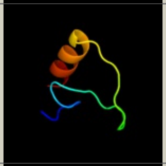
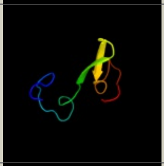
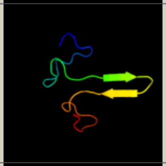
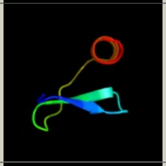
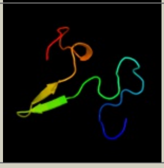
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1eq1a_	Alignment		60.9	13	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
2	c2pfuA_	Alignment		54.9	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**biopolymer transport exbd protein; **PDBTitle:** nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
3	d1kgsa1	Alignment		53.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
4	d1eeja2	Alignment		52.0	26	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
5	c3poaA_	Alignment		46.2	14	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
6	d1t3ba2	Alignment		42.9	24	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
7	c6paxA_	Alignment		38.4	22	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
8	c2pmuD_	Alignment		38.3	14	**PDB header:**transcription regulation **Chain:** D: **PDB Molecule:**response regulator phop; **PDBTitle:** crystal structure of the dna-binding domain of phop
9	c2iyjA_	Alignment		38.2	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol disulfide interchange protein dsbc; **PDBTitle:** crystal structure of the n-terminal dimer domain of e.coli2 dsbc
10	d1opca_	Alignment		35.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
11	d1pdnc_	Alignment		35.5	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain

12	c2hwvA_	Alignment		31.1	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding response regulator vicr; **PDBTitle:** crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
13	c2jzyA_	Alignment		30.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein pcor; **PDBTitle:** solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
14	d1smpi_	Alignment		30.7	18	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
15	d1p2fa1	Alignment		30.2	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
16	d1g3ga_	Alignment		29.6	15	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
17	c3fm8A_	Alignment		25.7	14	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
18	d1ys7a1	Alignment		24.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
19	c2zxjB_	Alignment		23.0	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein walr; **PDBTitle:** crystal structure of yycf dna-binding domain from staphylococcus2 aureus
20	c2kklA_	Alignment		22.9	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of the fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
21	d1pcfa_	Alignment	not modelled	22.0	21	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
22	d1wlna1	Alignment	not modelled	22.0	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
23	c2raxY_	Alignment	not modelled	21.8	13	**PDB header:**cell cycle **Chain:** Y: **PDB Molecule:**borealin; **PDBTitle:** crystal structure of borealin (20-78) bound to survivin (1-120)
24	d1d6za4	Alignment	not modelled	19.7	18	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Copper amine oxidase, domain N **Family:**Copper amine oxidase, domain N
25	c3gmgB_	Alignment	not modelled	19.1	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
26	c2hqnA_	Alignment	not modelled	18.9	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
27	d1gxqa_	Alignment	not modelled	18.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
28	c2xu6B_	Alignment	not modelled	18.5	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**mdv1 coiled coil; **PDBTitle:** mdv1 coiled coil domain
						Fold: Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment

29	d1oisa_	Alignment	not modelled	18.4	30	**Superfamily:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Family:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
30	c2k27A_	Alignment	not modelled	17.9	21	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
31	c1nl3B_	Alignment	not modelled	17.6	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase seca 1 subunit; **PDBTitle:** crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
32	d1k78a1	Alignment	not modelled	17.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
33	c2jv8A_	Alignment	not modelled	17.3	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ne1242; **PDBTitle:** solution structure of protein ne1242 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net4
34	c1r21A_	Alignment	not modelled	16.7	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**antigen ki-67; **PDBTitle:** solution structure of human ki67 fha domain
35	c3prlD_	Alignment	not modelled	16.3	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadp-dependent glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of nadp-dependent glyceraldehyde-3-phosphate2 dehydrogenase from bacillus halodurans c-125
36	d6paxa1	Alignment	not modelled	15.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
37	c1lq7A_	Alignment	not modelled	15.0	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**alpha3w; **PDBTitle:** de novo designed protein model of radical enzymes
38	d1k4ta3	Alignment	not modelled	15.0	26	**Fold:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Superfamily:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment **Family:**Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment
39	d1ywya1	Alignment	not modelled	14.8	15	**Fold:**PH domain-like barrel **Superfamily:**PA2021-like **Family:**PA2021-like
40	d1b63a1	Alignment	not modelled	14.1	9	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
41	c3v4cB_	Alignment	not modelled	13.8	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
42	d1azca_	Alignment	not modelled	13.4	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
43	d2hgsa1	Alignment	not modelled	13.3	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Eukaryotic glutathione synthetase, substrate-binding domain
44	d2o8ra2	Alignment	not modelled	13.0	6	**Fold:**PHP14-like **Superfamily:**PHP14-like **Family:**PPK middle domain-like
45	c2b9sA_	Alignment	not modelled	12.9	18	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**topoisomerase i-like protein; **PDBTitle:** crystal structure of heterodimeric l. donovani2 topoisomerase i-vanadate-dna complex
46	d1rz4a1	Alignment	not modelled	12.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
47	d1cc3a_	Alignment	not modelled	11.8	24	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
48	d1wnda_	Alignment	not modelled	11.8	21	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
49	d2ccwa1	Alignment	not modelled	11.2	18	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
50	c1gk9A_	Alignment	not modelled	10.7	8	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**penicillin g acylase alpha subunit; **PDBTitle:** crystal structures of penicillin acylase enzyme-substrate2 complexes: structural insights into the catalytic mechanism
51	d2g1la1	Alignment	not modelled	10.3	13	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
52	c2ae3A_	Alignment	not modelled	9.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
53	c1a31A_	Alignment	not modelled	9.6	27	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**protein (topoisomerase i); **PDBTitle:** human reconstituted dna topoisomerase i in covalent complex2 with a 22 base pair dna duplex
						Fold: Cupredoxin-like

54	d1joia_	Alignment	not modelled	9.4	21	**Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
55	c3nrlB_	Alignment	not modelled	9.3	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rumgna_01417; **PDBTitle:** crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
56	c1nh3A_	Alignment	not modelled	9.3	27	**PDB header:**isomerase/dna **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** human topoisomerase i ara-c complex
57	c2h47C_	Alignment	not modelled	9.2	15	**PDB header:**oxidoreductase/electron transport **Chain:** C: **PDB Molecule:**azurin; **PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1)
58	d2v4jc1	Alignment	not modelled	9.0	29	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
59	c2p2uA_	Alignment	not modelled	9.0	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**host-nuclease inhibitor protein gam, putative; **PDBTitle:** crystal structure of putative host-nuclease inhibitor2 protein gam from desulfovibrio vulgaris
60	c3uotB_	Alignment	not modelled	8.8	17	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
61	c3k3wA_	Alignment	not modelled	8.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**penicillin g acylase; **PDBTitle:** thermostable penicillin g acylase from alcaligence faecalis2 in orthorhombic form
62	d1jzga_	Alignment	not modelled	8.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Plastocyanin/azurin-like
63	d1uhta_	Alignment	not modelled	8.5	17	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
64	d2ff4a3	Alignment	not modelled	8.4	18	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
65	c2k4jA_	Alignment	not modelled	8.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** arsr dna binding domain
66	d1h7sa1	Alignment	not modelled	8.2	14	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
67	c1t3jA_	Alignment	not modelled	8.1	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mitofusin 1; **PDBTitle:** mitofusin domain hr2 v686m/i708m mutant
68	d2affa1	Alignment	not modelled	7.9	14	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
69	c3i38D_	Alignment	not modelled	7.8	16	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
70	d2g82a1	Alignment	not modelled	7.5	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	d1g6ga_	Alignment	not modelled	7.5	20	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
72	c3gqsB_	Alignment	not modelled	7.4	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**adenylate cyclase-like protein; **PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis
73	d1ggaa1	Alignment	not modelled	7.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
74	c3swfA_	Alignment	not modelled	7.2	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
75	d1oaia_	Alignment	not modelled	7.0	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
76	c3iwkB_	Alignment	not modelled	7.0	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
77	d1o04a_	Alignment	not modelled	7.0	8	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
78	c3i38L_	Alignment	not modelled	7.0	15	**PDB header:**chaperone **Chain:** L: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
79	d1f32a_	Alignment	not modelled	7.0	9	**Fold:**Pepsin inhibitor-3 **Superfamily:**Pepsin inhibitor-3 **Family:**Pepsin inhibitor-3

80	c3b4wA_	Alignment	not modelled	6.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
81	c2wybA_	Alignment	not modelled	6.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-homoserine lactone acylase pvdq subunit **PDBTitle:** the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
82	d1tg7a5	Alignment	not modelled	6.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Glycosyl hydrolases family 35 catalytic domain
83	c2ve5H_	Alignment	not modelled	6.6	7	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
84	c3ho6B_	Alignment	not modelled	6.4	16	**PDB header:**toxin **Chain:** B: **PDB Molecule:**toxin a; **PDBTitle:** structure-function analysis of inositol hexakisphosphate-2 induced autoprocessing in clostridium difficile toxin a
85	d1xdpa2	Alignment	not modelled	6.4	19	**Fold:**PHP14-like **Superfamily:**PHP14-like **Family:**PPK middle domain-like
86	c1jzdA_	Alignment	not modelled	6.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
87	d1hloa_	Alignment	not modelled	6.3	23	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
88	c2kz6A_	Alignment	not modelled	6.3	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2
89	d2ff4a1	Alignment	not modelled	6.1	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
90	c1fi4A_	Alignment	not modelled	6.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate 5-diphosphate decarboxylase; **PDBTitle:** the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
91	c3nepX_	Alignment	not modelled	6.0	16	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
92	c1ajnA_	Alignment	not modelled	5.9	8	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**penicillin amidohydrolase; **PDBTitle:** penicillin acylase complexed with p-nitrophenylacetic acid
93	d1n62a2	Alignment	not modelled	5.9	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
94	c1m5iA_	Alignment	not modelled	5.8	14	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**apc protein; **PDBTitle:** crystal structure of the coiled coil region 129-250 of the2 tumor suppressor gene product apc
95	c2pnvA_	Alignment	not modelled	5.8	32	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
96	d1ag8a_	Alignment	not modelled	5.7	8	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
97	c1t3bA_	Alignment	not modelled	5.7	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
98	d1bhga3	Alignment	not modelled	5.7	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
99	d1lgpa_	Alignment	not modelled	5.6	13	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain