Phyre^2

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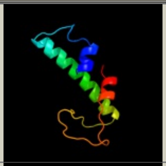
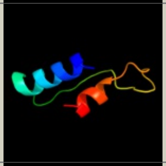
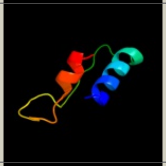
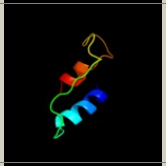
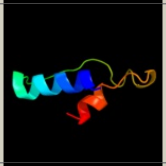
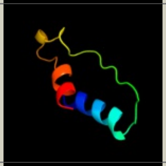
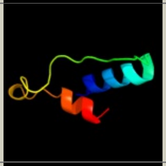
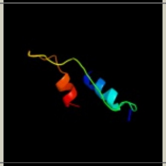
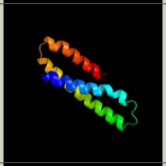
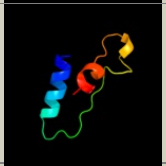
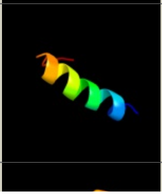
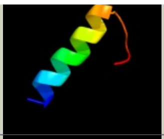
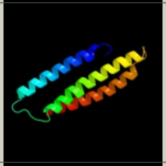
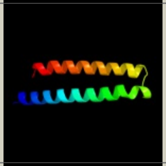
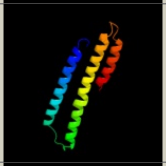
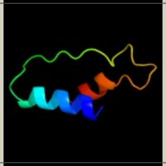
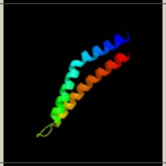
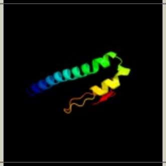
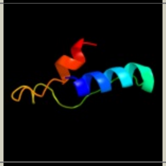
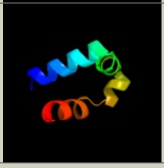
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u2ma_	Alignment		99.3	81	**Fold:**OmpH-like **Superfamily:**OmpH-like **Family:**OmpH-like
2	d1di6a_	Alignment		85.1	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
3	d2f7wa1	Alignment		80.2	24	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
4	d1mkza_	Alignment		75.3	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
5	d1uuya_	Alignment		74.9	22	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
6	c2is8A_	Alignment		72.8	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
7	d1jlja_	Alignment		71.3	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
8	d1y5ea1	Alignment		68.5	22	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
9	c2v8sV_	Alignment		64.6	16	**PDB header:**protein transport **Chain:** V: **PDB Molecule:**vesicle transport through interaction with **PDBTitle:** vti1b habc domain - epsinr enth domain complex
10	c2pjkA_	Alignment		64.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
11	c2kruA_	Alignment		49.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** solution nmr structure of the pcp_red domain of light-2 independent protochlorophyllide reductase subunit b from3 chlorobium tepidum. northeast structural genomics4 consortium target ctr69a (casp target)

12	c2l09A_	Alignment		46.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**asr4154 protein; **PDBTitle:** solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
13	c1nfoA_	Alignment		42.1	10	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein e2; **PDBTitle:** apolipoprotein e2 (apoe2, d154a mutation)
14	d2gtsa1	Alignment		41.3	13	**Fold:**Ferritin-like **Superfamily:**HP0062-like **Family:**HP0062-like
15	d1gs9a_	Alignment		39.5	6	**Fold:**Four-helical up-and-down bundle **Superfamily:**Apolipoprotein **Family:**Apolipoprotein
16	c3rfqC_	Alignment		38.0	20	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
17	c3layF_	Alignment		30.9	11	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
18	c2qhkA_	Alignment		26.9	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of methyl-accepting chemotaxis protein from vibrio2 parahaemolyticus rimd 2210633
19	d2g2ca1	Alignment		22.5	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
20	d2pu9a1	Alignment		22.3	24	**Fold:**Ferredoxin thioredoxin reductase (FTR), catalytic beta chain **Superfamily:**Ferredoxin thioredoxin reductase (FTR), catalytic beta chain **Family:**Ferredoxin thioredoxin reductase (FTR), catalytic beta chain
21	c3huuC_	Alignment	not modelled	21.4	4	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcription regulator like protein; **PDBTitle:** crystal structure of transcription regulator like protein from2 staphylococcus haemolyticus
22	c3l49D_	Alignment	not modelled	20.7	4	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc sugar (ribose) transporter, periplasmic **PDBTitle:** crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
23	d2iaza1	Alignment	not modelled	20.5	11	**Fold:**YheA-like **Superfamily:**YheA/YmcA-like **Family:**YheA-like
24	c3rotA_	Alignment	not modelled	19.5	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc sugar transporter, periplasmic sugar binding protein; **PDBTitle:** crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
25	c1deqO_	Alignment	not modelled	18.2	10	**PDB header:** **PDB COMPND:**
26	c2xpdC_	Alignment	not modelled	17.1	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thiol peroxidase; **PDBTitle:** reduced thiol peroxidase (tpx) from yersinia pseudotuberculosis
27	d1guda_	Alignment	not modelled	16.9	4	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
28	c2vk2A_	Alignment	not modelled	16.8	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
						PDB header:transport protein

29	c2qvcC_	Alignment	not modelled	15.6	13	**Chain:** C: **PDB Molecule:**sugar abc transporter, periplasmic sugar-binding **PDBTitle:** crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
30	c3brsA_	Alignment	not modelled	15.5	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of sugar transporter from clostridium2 phytofermentans
31	c3ghgK_	Alignment	not modelled	14.9	9	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
32	c1jyeA_	Alignment	not modelled	14.7	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
33	d1jyea_	Alignment	not modelled	14.7	25	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
34	d1tlfa_	Alignment	not modelled	13.6	29	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
35	c3dbiA_	Alignment	not modelled	12.8	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from escherichia coli complexed with phosphate
36	d1fxkc_	Alignment	not modelled	12.7	10	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
37	d8abpa_	Alignment	not modelled	12.4	4	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
38	d1byka_	Alignment	not modelled	12.2	9	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
39	c3g1wB_	Alignment	not modelled	12.1	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sugar abc transporter; **PDBTitle:** crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
40	c3jy6B_	Alignment	not modelled	11.9	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci transcriptional regulator from lactobacillus2 brevis
41	c3bblA_	Alignment	not modelled	11.8	4	**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
42	c3kbqA_	Alignment	not modelled	11.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
43	c3fosA_	Alignment	not modelled	11.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
44	d1myla_	Alignment	not modelled	11.4	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
45	c2jugB_	Alignment	not modelled	11.2	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
46	c3l6uA_	Alignment	not modelled	11.2	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system periplasmic **PDBTitle:** crystal structure of abc-type sugar transport system,2 periplasmic component from exiguobacterium sibiricum
47	c3clkB_	Alignment	not modelled	11.1	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcription regulator; **PDBTitle:** crystal structure of a transcription regulator from lactobacillus2 plantarum
48	d2etda1	Alignment	not modelled	10.9	11	**Fold:**Bromodomain-like **Superfamily:**LemA-like **Family:**LemA-like
49	c3khnB_	Alignment	not modelled	10.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**motb protein, putative; **PDBTitle:** crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris.
50	c3hcwB_	Alignment	not modelled	10.8	3	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**maltose operon transcriptional repressor; **PDBTitle:** crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus areus
51	c3bilA_	Alignment	not modelled	10.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable laci-family transcriptional regulator; **PDBTitle:** crystal structure of a probable laci family transcriptional2 regulator from corynebacterium glutamicum
52	c2rgyA_	Alignment	not modelled	10.5	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum
53	c3ksmA_	Alignment	not modelled	10.3	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system,

						periplasmic2 component from hahella chejuensis
54	c3d02A_	Alignment	not modelled	10.1	9	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative laci-type transcriptional regulator; **PDBTitle:** crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
55	c3ma0A_	Alignment	not modelled	9.8	13	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**d-xylose-binding periplasmic protein; **PDBTitle:** closed liganded crystal structure of xylose binding protein from2 escherichia coli
56	c1deqF_	Alignment	not modelled	9.8	4	**PDB header:** **PDB COMPND:**
57	d1b28a_	Alignment	not modelled	9.6	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
58	d1u00a1	Alignment	not modelled	9.4	6	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
59	d1mylb_	Alignment	not modelled	9.4	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
60	c1ei3E_	Alignment	not modelled	9.0	11	**PDB header:** **PDB COMPND:**
61	d2nqra3	Alignment	not modelled	8.9	23	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
62	c3kkeA_	Alignment	not modelled	8.8	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**laci family transcriptional regulator; **PDBTitle:** crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
63	c2g4rB_	Alignment	not modelled	8.8	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
64	c3brqA_	Alignment	not modelled	8.7	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg
65	c2o20H_	Alignment	not modelled	8.7	13	**PDB header:**transcription **Chain:** H: **PDB Molecule:**catabolite control protein a; **PDBTitle:** crystal structure of transcription regulator ccpa of lactococcus2 lactis
66	d2nzug1	Alignment	not modelled	8.6	4	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
67	d1qb5d_	Alignment	not modelled	8.5	24	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
68	c2h0aA_	Alignment	not modelled	8.3	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of probable transcription regulator from2 thermus thermophilus
69	d1st6a6	Alignment	not modelled	8.2	8	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
70	c3ixrA_	Alignment	not modelled	8.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
71	c3k4hA_	Alignment	not modelled	8.2	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
72	c2y3mA_	Alignment	not modelled	8.2	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein hofq; **PDBTitle:** structure of the extra-membranous domain of the secretin2 hofq from actinobacillus actinomycetemcomitans
73	c1u00A_	Alignment	not modelled	8.2	8	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
74	c3e61A_	Alignment	not modelled	8.1	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional repressor of ribose operon; **PDBTitle:** crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
75	c2fn9A_	Alignment	not modelled	7.9	8	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**ribose abc transporter, periplasmic ribose-binding protein; **PDBTitle:** thermotoga maritima ribose binding protein unliganded form
76	c3gybB_	Alignment	not modelled	7.9	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulators (laci-family **PDBTitle:** crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
77	d2piha1	Alignment	not modelled	7.9	8	**Fold:**YheA-like **Superfamily:**YheA/YmcA-like **Family:**YmcA-like
78	c2pihA_	Alignment	not modelled	7.9	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ymca; **PDBTitle:** crystal structure of protein ymca from bacillus subtilis,2 northeast structural genomics target sr375

79	c2ja9A_	Alignment	not modelled	7.8	10	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40
80	c2eq7C_	Alignment	not modelled	7.6	7	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
81	c3hnwB_	Alignment	not modelled	7.6	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
82	c3o74A_	Alignment	not modelled	7.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fructose transport system repressor frur; **PDBTitle:** crystal structure of cra transcriptional dual regulator from2 pseudomonas putida
83	c3g85A_	Alignment	not modelled	7.6	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (laci family); **PDBTitle:** crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
84	c3cs3A_	Alignment	not modelled	7.5	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
85	c2ywnA_	Alignment	not modelled	7.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin-like protein; **PDBTitle:** crystal structure of peroxiredoxin-like protein from2 sulfolobus tokodaii
86	c2rjoA_	Alignment	not modelled	7.5	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
87	c3e3mA_	Alignment	not modelled	7.4	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
88	c2eq8C_	Alignment	not modelled	7.3	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
89	c3gknA_	Alignment	not modelled	7.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
90	d2oeea1	Alignment	not modelled	7.1	10	**Fold:**YheA-like **Superfamily:**YheA/YmcA-like **Family:**YheA-like
91	c3onjA_	Alignment	not modelled	7.0	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**t-snare vti1; **PDBTitle:** crystal structure of yeast vti1p_habc domain
92	c2eq9C_	Alignment	not modelled	7.0	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
93	c3h75A_	Alignment	not modelled	7.0	13	**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
94	d1sx5a_	Alignment	not modelled	7.0	6	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoRV
95	d1dbqa_	Alignment	not modelled	7.0	17	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
96	d1tjya_	Alignment	not modelled	6.9	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
97	c2kngA_	Alignment	not modelled	6.8	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** solution structure of c-domain of lsr2
98	d2nn6h3	Alignment	not modelled	6.6	6	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
99	c3liaA_	Alignment	not modelled	6.6	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical sensory transduction histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase mmhk1s-z2