Phyre^2

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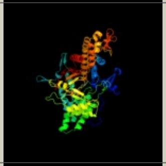
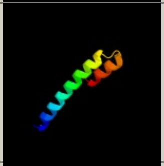
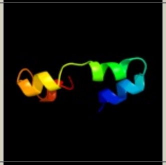
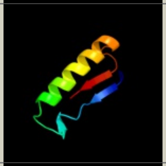
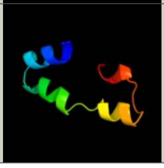
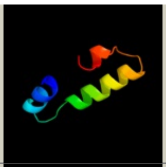
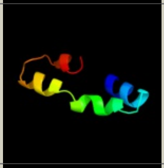
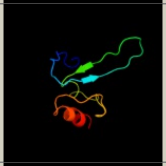
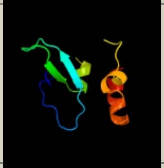
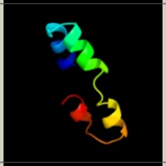
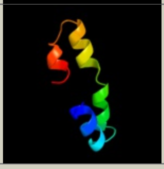
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r9da_	Alignment		100.0	38	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
2	c2y8nC_	Alignment		100.0	28	**PDB header:**lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate decarboxylase large subunit; **PDBTitle:** crystal structure of glycyl radical enzyme
3	c2f3oB_	Alignment		100.0	32	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
4	d1h16a_	Alignment		100.0	26	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
5	d1qhma_	Alignment		100.0	22	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
6	d1hk8a_	Alignment		99.4	18	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
7	c1hk8A_	Alignment		99.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
8	d1qkra_	Alignment		71.1	24	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
9	d1r0ka1	Alignment		63.9	28	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
10	c3gr1A_	Alignment		63.2	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
11	d1q0qa1	Alignment		48.6	21	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain

12	c2jcyA_	Alignment		45.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
13	c3au9A_	Alignment		44.5	23	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
14	c1r0lD_	Alignment		44.1	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
15	c1v9xA_	Alignment		42.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase; **PDBTitle:** solution structure of the first zn-finger domain of2 poly(adp-ribose) polymerase-1
16	c3odeA_	Alignment		38.5	18	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** human parp-1 zinc finger 2 (zn2) bound to dna
17	c3gr0D_	Alignment		32.4	18	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-362)
18	c2cs2A_	Alignment		30.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of the second zn-finger domain of2 poly(adp-ribose) polymerase-1
19	c2eghA_	Alignment		29.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
20	c1k5hB_	Alignment		29.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase
21	c1aq5C_	Alignment	not modelled	26.9	32	**PDB header:**coiled-coil **Chain:** C: **PDB Molecule:**cartilage matrix protein; **PDBTitle:** high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
22	c2f40A_	Alignment	not modelled	25.9	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf1455; **PDBTitle:** structure of a novel protein from backbone-centered nmr data and nmr-2 assisted structure prediction
23	c2dmjA_	Alignment	not modelled	24.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly (adp-ribose) polymerase family, member 1; **PDBTitle:** solution structure of the first zf-parp domain of human2 poly(adp-ribose)polymerase-1
24	d1vioa2	Alignment	not modelled	24.3	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
25	d1jvaa3	Alignment	not modelled	21.2	11	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
26	c2z4tA_	Alignment	not modelled	20.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-galactoside alpha-2,6-sialyltransferase; **PDBTitle:** crystal structure of vibrionaceae photobacterium sp. jt-ish-224 2,6-2 sialyltransferase in a ternary complex with donor product cmp and3 accepter substrate lactose
27	d1u5tb1	Alignment	not modelled	19.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
						Fold:N domain of copper amine oxidase-like

28	d1v5ra1	Alignment	not modelled	18.9	44	**Superfamily:**GAS2 domain-like **Family:**GAS2 domain
29	d1p9ka_	Alignment	not modelled	18.2	14	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
30	d2i9ia1	Alignment	not modelled	17.7	20	**Fold:**Anticodon-binding domain-like **Superfamily:**XCC0632-like **Family:**NLBH-like
31	c2i9iA_	Alignment	not modelled	17.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of helicobacter pylori protein hp0492
32	d1nh2a2	Alignment	not modelled	17.3	21	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
33	c2jobA_	Alignment	not modelled	17.1	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
34	c1fuiB_	Alignment	not modelled	16.9	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
35	d1pgja1	Alignment	not modelled	16.7	27	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
36	d1aisa1	Alignment	not modelled	16.5	9	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
37	d1nh2a1	Alignment	not modelled	16.5	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
38	d1i36a1	Alignment	not modelled	16.4	18	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Conserved hypothetical protein MTH1747
39	c2q01A_	Alignment	not modelled	16.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uronate isomerase; **PDBTitle:** crystal structure of glucuronate isomerase from caulobacter crescentus
40	d1qnaa2	Alignment	not modelled	16.1	21	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
41	d1irxa1	Alignment	not modelled	15.8	13	**Fold:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Superfamily:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Family:**C-terminal domain of class I lysyl-tRNA synthetase
42	d1r0ka3	Alignment	not modelled	15.8	30	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
43	d1mp9a1	Alignment	not modelled	15.8	36	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
44	d1aisa2	Alignment	not modelled	15.6	33	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
45	c2knjA_	Alignment	not modelled	15.4	17	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**microplusin preprotein; **PDBTitle:** nmr structure of microplusin a antimicrobial peptide from2 rhipicephalus (boophilus) microplus
46	d2i15a1	Alignment	not modelled	15.2	40	**Fold:**MG296-like **Superfamily:**MG296-like **Family:**MG296-like
47	c3inpA_	Alignment	not modelled	14.9	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
48	d1uj8a1	Alignment	not modelled	14.7	12	**Fold:**Another 3-helical bundle **Superfamily:**IscX-like **Family:**IscX-like
49	c3eagA_	Alignment	not modelled	14.6	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- **PDBTitle:** the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
50	d1qnaa1	Alignment	not modelled	14.4	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
51	d1dq3a4	Alignment	not modelled	14.4	19	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Intein endonuclease
52	d1mp9a2	Alignment	not modelled	14.3	33	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
53	c2khvA_	Alignment	not modelled	14.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.

54	d1rlfa_	Alignment	not modelled	13.8	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
55	d1q5qh_	Alignment	not modelled	13.4	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
56	d1fi3a_	Alignment	not modelled	13.3	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
57	d1nj1a3	Alignment	not modelled	13.3	17	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
58	d1cdwa2	Alignment	not modelled	13.3	16	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
59	c3a14B_	Alignment	not modelled	13.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
60	d1rypi_	Alignment	not modelled	12.9	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
61	c1r8jB_	Alignment	not modelled	12.9	26	**PDB header:**circadian clock protein **Chain:** B: **PDB Molecule:**kaia; **PDBTitle:** crystal structure of circadian clock protein kaia from2 synechococcus elongatus
62	d2bm3a1	Alignment	not modelled	12.9	17	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
63	d1cdwa1	Alignment	not modelled	12.8	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
64	d1tyja1	Alignment	not modelled	12.5	22	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
65	d1yuaa2	Alignment	not modelled	12.5	44	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
66	c3ol0C_	Alignment	not modelled	12.3	17	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
67	c2b59A_	Alignment	not modelled	12.3	17	**PDB header:**hydrolase/structural protein **Chain:** A: **PDB Molecule:**cog1196: chromosome segregation atpases; **PDBTitle:** the type ii cohesin dockerin complex
68	c3d36B_	Alignment	not modelled	12.2	13	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**sporulation kinase b; **PDBTitle:** how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
69	d1ciia1	Alignment	not modelled	12.2	28	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
70	c2vpmB_	Alignment	not modelled	12.1	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
71	c3ghpA_	Alignment	not modelled	12.1	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** structure of the second type ii cohesin module from the2 adaptor scaa scaffoldin of acetivibrio cellulolyticus3 (including long c-terminal linker)
72	c3thgA_	Alignment	not modelled	12.0	31	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** crystal structure of the creosote rubisco activase c-domain
73	c2a7oA_	Alignment	not modelled	12.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**huntingtin interacting protein b; **PDBTitle:** solution structure of the hset2/hypb sri domain
74	c2kwvA_	Alignment	not modelled	11.9	36	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution structure of ubm1 of murine polymerase iota in complex with2 ubiquitin
75	d1w7pd1	Alignment	not modelled	11.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
76	c3fnkA_	Alignment	not modelled	11.6	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** crystal structure of the second type ii cohesin module from2 the cellulosomal adaptor scaa scaffoldin of acetivibrio3 cellulolyticus
77	c1u57A_	Alignment	not modelled	11.6	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gag polyprotein; **PDBTitle:** nmr structure of the (345-392)gag sequence from hiv-1
78	c2hx6A	Alignment	not modelled	11.5	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease;

78	[illegible]	Alignment	not modelled	[illegible]	[illegible]	**PDBTitle:** solution structure analysis of the phage t42 endoribonuclease regb
79	c3nzwH_	Alignment	not modelled	11.3	19	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** H: **PDB Molecule:**proteasome component pup1; **PDBTitle:** crystal structure of the yeast 20s proteasome in complex with 2b
80	d1aoya_	Alignment	not modelled	11.1	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
81	d1zv9a1	Alignment	not modelled	11.1	30	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
82	c3vjjA_	Alignment	not modelled	11.1	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**p9-1; **PDBTitle:** crystal structure analysis of the p9-1
83	c3oryA_	Alignment	not modelled	11.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
84	d1st6a7	Alignment	not modelled	11.0	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
85	d1uw0a_	Alignment	not modelled	10.9	9	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**PARP-type zinc finger
86	c2i6lB_	Alignment	not modelled	10.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mitogen-activated protein kinase 6; **PDBTitle:** crystal structure of human mitogen activated protein kinase2 6 (mapk6)
87	c2d2rA_	Alignment	not modelled	10.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
88	d1hx8a1	Alignment	not modelled	10.7	13	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**Phosphoinositide-binding clathrin adaptor, domain 2
89	d2gykb1	Alignment	not modelled	10.6	22	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
90	d2g39a2	Alignment	not modelled	10.6	20	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
91	c3ltiA_	Alignment	not modelled	10.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains
92	c2fhgC_	Alignment	not modelled	10.2	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome, beta subunit; **PDBTitle:** crystal structure of mycobacterial tuberculosis proteasome
93	d2jb0b1	Alignment	not modelled	10.0	17	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
94	d1x9na2	Alignment	not modelled	10.0	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
95	c3kh0A_	Alignment	not modelled	9.8	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ral guanine nucleotide dissociation stimulator; **PDBTitle:** crystal structure of the ras-association (ra) domain of2 ralgds
96	c7ceiB_	Alignment	not modelled	9.8	18	**PDB header:**immune system **Chain:** B: **PDB Molecule:**protein (colicin e7 immunity protein); **PDBTitle:** the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
97	d1r6oc1	Alignment	not modelled	9.6	26	**Fold:**ClpS-like **Superfamily:**ClpS-like **Family:**Adaptor protein ClpS (YljA)
98	d1sj8a2	Alignment	not modelled	9.5	17	**Fold:**I/LWEQ domain **Superfamily:**I/LWEQ domain **Family:**I/LWEQ domain
99	d1lfda_	Alignment	not modelled	9.4	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD