Phyre^2

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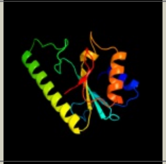
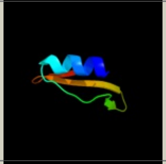
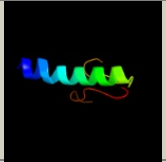
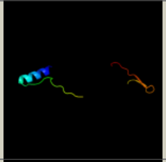
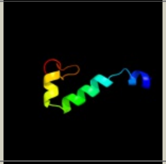
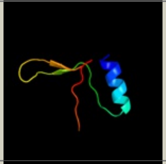
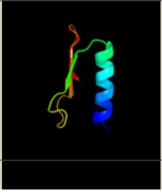
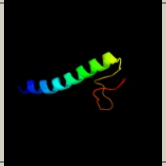
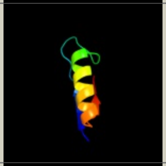
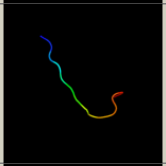
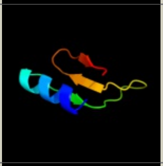
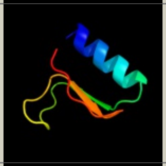
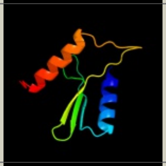
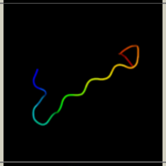
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cw0a_	Alignment		100.0	100	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
2	d1vsra_	Alignment		100.0	100	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
3	c3hrlA_	Alignment		99.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endonuclease-like protein; **PDBTitle:** crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
4	c3fovA_	Alignment		84.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0102 protein rpa0323; **PDBTitle:** crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
5	c2fqzC_	Alignment		82.7	26	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**r.ecl18ki; **PDBTitle:** metal-depleted ecl18ki in complex with uncleaved dna
6	d1m0da_	Alignment		81.9	22	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
7	d1na6a2	Alignment		60.3	26	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Type II restriction endonuclease catalytic domain
8	d1y88a2	Alignment		55.5	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**MRR-like
9	c3hxkB_	Alignment		54.1	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sugar hydrolase; **PDBTitle:** crystal structure of a sugar hydrolase (yeeb) from2 lactococcus lactis, northeast structural genomics3 consortium target kr108
10	d1uxoa_	Alignment		52.8	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**YdeN-like
11	d1gefa_	Alignment		47.5	21	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like

12	c3o3nA_	Alignment		45.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
13	c3bm3A_	Alignment		33.8	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**pspgi restriction endonuclease; **PDBTitle:** restriction endonuclease pspgi-substrate dna complex
14	c2o2gA_	Alignment		33.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dienelactone hydrolase; **PDBTitle:** crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
15	d1ff3c_	Alignment		32.5	31	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
16	c1y88A_	Alignment		30.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1548; **PDBTitle:** crystal structure of protein of unknown function af1548
17	d1hh1a_	Alignment		29.7	28	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
18	c1fokA_	Alignment		29.4	11	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (foki restriction endonucleas); **PDBTitle:** structure of restriction endonuclease foki bound to dna
19	c2j89A_	Alignment		29.2	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine sulfoxide reductase a; **PDBTitle:** functional and structural aspects of poplar cytosolic and2 plastidial type a methionine sulfoxide reductases
20	c2hihB_	Alignment		29.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase 46 kda form; **PDBTitle:** crystal structure of staphylococcus hyicus lipase
21	c3pilA_	Alignment	not modelled	27.5	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of mxr1 from saccharomyces cerevisiae in reduced2 form
22	c2wj0B_	Alignment	not modelled	27.0	25	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**archaeal hjc; **PDBTitle:** crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
23	d1fvga_	Alignment	not modelled	26.2	36	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
24	c3mn1B_	Alignment	not modelled	24.4	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase; **PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
25	c1na6B_	Alignment	not modelled	24.1	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**restriction endonuclease ecorii; **PDBTitle:** crystal structure of restriction endonuclease ecorii mutant2 r88a
26	c2qruA_	Alignment	not modelled	22.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
27	d2je8a5	Alignment	not modelled	22.3	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
28	d2qlva1	Alignment	not modelled	22.2	12	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Ssp2 C-terminal domain-like
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase

29	c3bqhA_	Alignment	not modelled	21.2	42	msra/msrb; **PDBTitle:** structure of the central domain (msra) of neisseria meningitidis pilb2 (oxidized form)
30	d1ji3a_	Alignment	not modelled	20.9	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
31	d2v8qa1	Alignment	not modelled	19.1	7	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Ssp2 C-terminal domain-like
32	c1fvaA_	Alignment	not modelled	18.3	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** crystal structure of bovine methionine sulfoxide reductase
33	d1ob8a_	Alignment	not modelled	18.1	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
34	c2qjwA_	Alignment	not modelled	17.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein xcc1541; **PDBTitle:** crystal structure of a putative hydrolase of the alpha/beta2 superfamily (xcc1541) from xanthomonas campestris pv. campestris at3 1.35 a resolution
35	c3ahhA_	Alignment	not modelled	17.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**xylulose 5-phosphate/fructose 6-phosphate phosphoketolase; **PDBTitle:** h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
36	d1ff3a_	Alignment	not modelled	17.6	31	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
37	d1jg5a_	Alignment	not modelled	17.5	40	**Fold:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Superfamily:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Family:**GTP cyclohydrolase I feedback regulatory protein, GFRP
38	c1nwaA_	Alignment	not modelled	16.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msra; **PDBTitle:** structure of mycobacterium tuberculosis methionine2 sulfoxide reductase a in complex with protein-bound3 methionine
39	d1nwaa_	Alignment	not modelled	16.9	33	**Fold:**Ferredoxin-like **Superfamily:**Peptide methionine sulfoxide reductase **Family:**Peptide methionine sulfoxide reductase
40	d2pbla1	Alignment	not modelled	16.6	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
41	d2qrda1	Alignment	not modelled	16.3	19	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Ssp2 C-terminal domain-like
42	c3gzjB_	Alignment	not modelled	15.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polyneuridine-aldehyde esterase; **PDBTitle:** crystal structure of polyneuridine aldehyde esterase2 complexed with 16-epi-vellosimine
43	c3hl4B_	Alignment	not modelled	14.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline-phosphate cytidylyltransferase a; **PDBTitle:** crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
44	c3llcA_	Alignment	not modelled	14.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution
45	c3dqzB_	Alignment	not modelled	14.4	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein; **PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis2 thaliana
46	d1rila_	Alignment	not modelled	14.3	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
47	c2p14A_	Alignment	not modelled	14.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**heterodimeric restriction endonuclease r.bspd6i small **PDBTitle:** crystal structure of small subunit (r.bspd6i2) of the heterodimeric2 restriction endonuclease r.bspd6i
48	c2wtmC_	Alignment	not modelled	13.3	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**est1e; **PDBTitle:** est1e from butyrivibrio proteoclasticus
49	c3ic8D_	Alignment	not modelled	13.2	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized gst-like proteinprotein; **PDBTitle:** the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
50	c3bjrA_	Alignment	not modelled	12.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxylesterase; **PDBTitle:** crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
51	d1xkla_	Alignment	not modelled	12.7	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
52	c2qipA_	Alignment	not modelled	12.6	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function vpa0982; **PDBTitle:** crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
53	c3ksrA_	Alignment	not modelled	12.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative serine hydrolase; **PDBTitle:** crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
54	c2je8B_	Alignment	not modelled	11.3	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2

						thetaiotaomicron
55	d1r0va1	Alignment	not modelled	11.1	13	**Fold:**Restriction endonuclease-like **Superfamily:**tRNA-intron endonuclease catalytic domain-like **Family:**tRNA-intron endonuclease catalytic domain-like
56	d1h70a_	Alignment	not modelled	10.5	19	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Dimethylarginine dimethylaminohydrolase DDAH
57	c3elbA_	Alignment	not modelled	10.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ethanolamine-phosphate cytidylyltransferase; **PDBTitle:** human ctp: phosphoethanolamine cytidylyltransferase in complex with2 cmp
58	c2i3dA_	Alignment	not modelled	10.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu1826; **PDBTitle:** crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
59	d2i3da1	Alignment	not modelled	10.3	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
60	c3n07B_	Alignment	not modelled	10.2	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
61	d1z9ha2	Alignment	not modelled	10.1	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
62	d2fuka1	Alignment	not modelled	10.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Atu1826-like
63	d1vjza_	Alignment	not modelled	9.6	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
64	d2d5ua1	Alignment	not modelled	9.5	14	**Fold:**PUG domain-like **Superfamily:**PUG domain-like **Family:**PUG domain
65	d1dina_	Alignment	not modelled	9.5	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Dienelactone hydrolase
66	d1v2aa2	Alignment	not modelled	9.5	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
67	d1jl2a_	Alignment	not modelled	9.3	36	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
68	d1gpla2	Alignment	not modelled	9.3	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
69	d1jl1a_	Alignment	not modelled	8.9	36	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
70	d1ufoa_	Alignment	not modelled	8.8	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
71	c2omkB_	Alignment	not modelled	8.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of the bacteroides thetaiotaomicron thiamin2 pyrophosphokinase
72	c2hb5A_	Alignment	not modelled	8.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**reverse transcriptase/ribonuclease h; **PDBTitle:** crystal structure of the moloney murine leukemia virus2 rnase h domain
73	d2vzsa5	Alignment	not modelled	8.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
74	c2jw1A_	Alignment	not modelled	8.0	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lipoprotein mxim; **PDBTitle:** structural characterization of the type iii pilotin-2 secretin interaction in shigella flexneri by nmr3 spectroscopy
75	c2qkkI_	Alignment	not modelled	7.9	44	**PDB header:**hydrolase/dna/rna **Chain:** I: **PDB Molecule:**ribonuclease h1; **PDBTitle:** human rnase h catalytic domain mutant d210n in complex with2 14-mer rna/dna hybrid
76	d1zs8a2	Alignment	not modelled	7.7	12	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
77	d1vmea1	Alignment	not modelled	7.5	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
78	d2gvia1	Alignment	not modelled	7.5	38	**Fold:**FwdE/GAPDH domain-like **Superfamily:**FwdE-like **Family:**FwdE-like
79	d1r7ha_	Alignment	not modelled	7.5	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
80	d1vkha_	Alignment	not modelled	7.4	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Putative serine hydrolase Ydr428c
81	c2rniA	Alignment	not modelled	7.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease h;

81	c2rpiA_	Alignment	not modelled	[illegible]	[illegible]	**PDBTitle:** the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
82	c1qgeD_	Alignment	not modelled	7.1	46	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
83	d1qzua_	Alignment	not modelled	6.9	25	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
84	c3e0mB_	Alignment	not modelled	6.9	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
85	c1fuiB_	Alignment	not modelled	6.8	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
86	d2glza1	Alignment	not modelled	6.6	38	**Fold:**FwdE/GAPDH domain-like **Superfamily:**FwdE-like **Family:**FwdE-like
87	d1g5qa_	Alignment	not modelled	6.1	18	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
88	c2ykqC_	Alignment	not modelled	6.0	19	**PDB header:**rna-binding protein **Chain:** C: **PDB Molecule:**line-1 orf1p; **PDBTitle:** structure of the human line-1 orf1p trimer
89	c2gviA_	Alignment	not modelled	5.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a putative formylmethanofuran dehydrogenase2 subunit e (ta1109) from thermoplasma acidophilum at 1.87 a resolution
90	c3hstD_	Alignment	not modelled	5.8	30	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein rv2228c/mt2287; **PDBTitle:** n-terminal rnase h domain of rv2228c from mycobacterium tuberculosis2 as a fusion protein with maltose binding protein
91	d1pn9a2	Alignment	not modelled	5.8	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
92	c3ihkC_	Alignment	not modelled	5.8	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83
93	d1whza_	Alignment	not modelled	5.7	19	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
94	d1e89a_	Alignment	not modelled	5.7	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
95	c3rqrA_	Alignment	not modelled	5.6	22	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of the ryr domain of the rabbit ryanodine receptor
96	c3uoaB_	Alignment	not modelled	5.5	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** crystal structure of the malt1 paracaspase (p21 form)
97	d2c2la2	Alignment	not modelled	5.4	18	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
98	c1pq1B_	Alignment	not modelled	5.3	38	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl2-like protein 11; **PDBTitle:** crystal structure of bcl-xl/bim
99	d1cuka1	Alignment	not modelled	5.3	19	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain