Phyre^2

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Description	P39385
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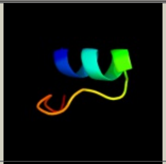
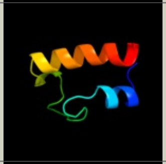
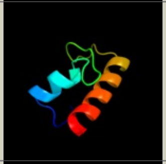
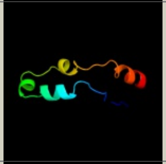
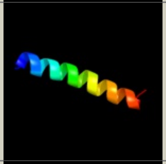
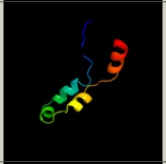
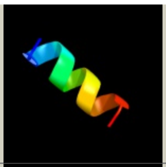
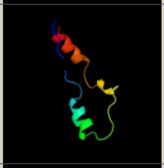
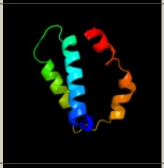
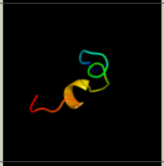
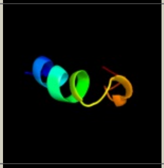
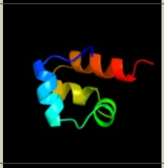
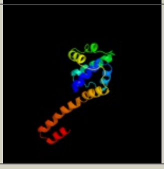
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xg7a_	Alignment		48.1	30	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like
2	d1ee8a1	Alignment		44.6	21	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
3	d1k3xa1	Alignment		42.5	13	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
4	d1tdza1	Alignment		37.5	17	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
5	d1r2za1	Alignment		37.5	19	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
6	c3edyA_	Alignment		36.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1; **PDBTitle:** crystal structure of the precursor form of human tripeptidyl-peptidase2 1
7	d1k82a1	Alignment		35.3	10	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
8	d1xqoa_	Alignment		30.6	30	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like
9	c2kncA_	Alignment		29.9	28	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
10	c3ee6A_	Alignment		29.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidyl-peptidase 1; **PDBTitle:** crystal structure analysis of tripeptidyl peptidase -i
11	d1ug3a1	Alignment		29.0	15	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like

12	c2lbgA_	Alignment		27.8	46	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**major prion protein; **PDBTitle:** structure of the chr of the prion protein in dpc micelles
13	d1t1ea2	Alignment		25.9	12	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
14	c2k1aA_	Alignment		25.9	28	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
15	c3h2zA_	Alignment		25.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol-1-phosphate 5-dehydrogenase; **PDBTitle:** the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
16	d1t5ja_	Alignment		24.6	18	**Fold:**ADP-ribosylglycohydrolase **Superfamily:**ADP-ribosylglycohydrolase **Family:**ADP-ribosylglycohydrolase
17	c3g9dB_	Alignment		24.3	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dinitrogenase reductase activacting **PDBTitle:** crystal structure glycohydrolase
18	d2aq0a1	Alignment		23.6	8	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
19	c2qtyB_	Alignment		22.1	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(adp-ribose) glycohydrolase arh3; **PDBTitle:** crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
20	c2r6cG_	Alignment		21.6	15	**PDB header:**replication **Chain:** G: **PDB Molecule:**dnag primase, helicase binding domain; **PDBTitle:** crystal form bh2
21	c2k7rA_	Alignment	not modelled	20.3	16	**PDB header:**replication **Chain:** A: **PDB Molecule:**primosomal protein dnai; **PDBTitle:** n-terminal domain of the bacillus subtilis helicase-loading2 protein dnai
22	c2wocA_	Alignment	not modelled	19.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosyl-[dinitrogen reductase] glycohydrolase; **PDBTitle:** crystal structure of the dinitrogenase reductase-activating2 glycohydrolase (drag) from rhodospirillum rubrum
23	c2yzwA_	Alignment	not modelled	19.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosylglycohydrolase; **PDBTitle:** adp-ribosylglycohydrolase-related protein complex
24	c1b9uA_	Alignment	not modelled	17.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
25	d2gp4a2	Alignment	not modelled	16.9	13	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**IvD/EDD N-terminal domain-like
26	d1rh5b_	Alignment	not modelled	16.8	22	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
27	c1ug3A_	Alignment	not modelled	15.7	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic protein synthesis initiation factor **PDBTitle:** c-terminal portion of human eif4gi
28	d2piha1	Alignment	not modelled	15.0	5	**Fold:**YheA-like **Superfamily:**YheA/YmcA-like **Family:**YmcA-like

29	c2pihA_	Alignment	not modelled	15.0	5	**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
30	c2kncB_	Alignment	not modelled	14.8	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
31	c2f5qA_	Alignment	not modelled	14.6	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
32	c3hd7A_	Alignment	not modelled	13.9	6	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
33	d1v54d_	Alignment	not modelled	13.9	13	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
34	c3qnqD_	Alignment	not modelled	13.8	16	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
35	c2y69Q_	Alignment	not modelled	13.7	13	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
36	d2a1ja1	Alignment	not modelled	13.6	8	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
37	d2crga1	Alignment	not modelled	13.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
38	c2kluA_	Alignment	not modelled	12.8	26	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
39	c2w2eA_	Alignment	not modelled	12.7	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin; **PDBTitle:** 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
40	d1xi8a3	Alignment	not modelled	12.5	20	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
41	c3hfwA_	Alignment	not modelled	12.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
42	c2opfA_	Alignment	not modelled	12.2	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
43	c2gp4A_	Alignment	not modelled	12.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
44	c3a46B_	Alignment	not modelled	11.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of mvnei1/thf complex
45	c2l23A_	Alignment	not modelled	11.0	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 25; **PDBTitle:** nmr structure of the acid (activator interacting domain) of the human2 mediator med25 protein
46	c1wazA_	Alignment	not modelled	11.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
47	c3h3pT_	Alignment	not modelled	10.8	43	**PDB header:**immune system **Chain:** T: **PDB Molecule:**4e10_s0_1tjlc_004_n; **PDBTitle:** crystal structure of hiv epitope-scaffold 4e10 fv complex
48	c1q90L_	Alignment	not modelled	10.7	30	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**cytochrome b6f complex subunit petl; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
49	d1q90l_	Alignment	not modelled	10.7	30	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
50	c3kvhA_	Alignment	not modelled	10.7	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
51	c1ee8A_	Alignment	not modelled	10.7	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
52	c1nnjA_	Alignment	not modelled	10.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
53	d1ymga1	Alignment	not modelled	10.1	28	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like

54	c1ymgA_	Alignment	not modelled	10.1	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
55	c2hjmB_	Alignment	not modelled	9.8	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pf1176; **PDBTitle:** crystal structure of a singleton protein pf1176 from p. furiosus
56	d1k6za_	Alignment	not modelled	9.7	26	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
57	c2vt2A_	Alignment	not modelled	9.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** structure and functional properties of the bacillus2 subtilis transcriptional repressor rex
58	c3d9sB_	Alignment	not modelled	9.4	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin-5; **PDBTitle:** human aquaporin 5 (aqp5) - high resolution x-ray structure
59	d1rfza_	Alignment	not modelled	9.4	11	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
60	c2zu6E_	Alignment	not modelled	9.4	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** crystal structure of the eif4a-pdcd4 complex
61	c1k82D_	Alignment	not modelled	9.3	10	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
62	c2kqzA_	Alignment	not modelled	9.3	4	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**proteasomal ubiquitin receptor adrm1; **PDBTitle:** fragment of proteasome protein
63	d1xova2	Alignment	not modelled	9.1	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
64	d1jlja_	Alignment	not modelled	9.1	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
65	c2qtqB_	Alignment	not modelled	9.0	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** crystal structure of a predicted dna-binding transcriptional regulator2 (saro_1072) from novosphingobium aromaticivorans dsm at 1.85 a3 resolution
66	c3c02A_	Alignment	not modelled	8.9	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaglyceroporin; **PDBTitle:** x-ray structure of the aquaglyceroporin from plasmodium falciparum
67	d1ug8a_	Alignment	not modelled	8.8	22	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
68	c2bcxB_	Alignment	not modelled	8.8	86	**PDB header:**calcium binding protein **Chain:** B: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of calmodulin in complex with a ryanodine2 receptor peptide
69	d1jyaa_	Alignment	not modelled	8.6	26	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
70	d2a4ha1	Alignment	not modelled	8.6	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
71	c2zmeA_	Alignment	not modelled	8.5	5	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
72	c3cuqA_	Alignment	not modelled	8.3	5	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
73	d2cdxa_	Alignment	not modelled	8.3	20	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
74	d1rc2a_	Alignment	not modelled	8.3	33	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
75	d1y0na_	Alignment	not modelled	8.2	11	**Fold:**YehU-like **Superfamily:**YehU-like **Family:**YehU-like
76	c1u0bB_	Alignment	not modelled	8.2	13	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
77	d1dd4c_	Alignment	not modelled	8.2	18	**Fold:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Superfamily:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain **Family:**Ribosomal protein L7/12, oligomerisation (N-terminal) domain
78	c1amlA_	Alignment	not modelled	8.1	27	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**amyloid a4; **PDBTitle:** the alzheimer`s disease amyloid a4 peptide (residues 1-40)
79	d1j4na_	Alignment	not modelled	8.1	22	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like

						Family: Aquaporin-like
80	d1cksa_	Alignment	not modelled	8.1	67	**Fold:**Cell cycle regulatory proteins **Superfamily:**Cell cycle regulatory proteins **Family:**Cell cycle regulatory proteins
81	c2dzrA_	Alignment	not modelled	8.1	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
82	c1dvpA_	Alignment	not modelled	8.0	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
83	c2jesG_	Alignment	not modelled	8.0	20	**PDB header:**viral protein **Chain:** G: **PDB Molecule:**portal protein; **PDBTitle:** portal protein from bacteriophage spp1
84	d1u5ta1	Alignment	not modelled	8.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
85	d2hxja1	Alignment	not modelled	7.9	22	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
86	c2f2bA_	Alignment	not modelled	7.9	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**aquaporin aqpm; **PDBTitle:** crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
87	c3ahhA_	Alignment	not modelled	7.8	12	**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
88	c1m5iA_	Alignment	not modelled	7.8	13	**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
89	d1hq1a_	Alignment	not modelled	7.7	35	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
90	c2yqkA_	Alignment	not modelled	7.7	26	**PDB header:**transcription/apoptosis **Chain:** A: **PDB Molecule:**arginine-glutamic acid dipeptide repeats protein; **PDBTitle:** solution structure of the sant domain in arginine-glutamic2 acid dipeptide (re) repeats
91	c1zaxZ_	Alignment	not modelled	7.7	18	**PDB header:**structural protein **Chain:** Z: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
92	c1zawV_	Alignment	not modelled	7.7	18	**PDB header:**structural protein **Chain:** V: **PDB Molecule:**50s ribosomal protein l7/l12; **PDBTitle:** ribosomal protein l10-l12(ntd) complex, space group p212121,2 form a
93	d1rkta2	Alignment	not modelled	7.6	12	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
94	c1dfwA_	Alignment	not modelled	7.6	54	**PDB header:**immune system **Chain:** A: **PDB Molecule:**lung surfactant protein b; **PDBTitle:** conformational mapping of the n-terminal segment of2 surfactant protein b in lipid using 13c-enhanced fourier3 transform infrared spectroscopy (ftir)
95	d1qb2a_	Alignment	not modelled	7.6	18	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
96	d1sb0a_	Alignment	not modelled	7.6	14	**Fold:**Kix domain of CBP (creb binding protein) **Superfamily:**Kix domain of CBP (creb binding protein) **Family:**Kix domain of CBP (creb binding protein)
97	c3llqB_	Alignment	not modelled	7.5	25	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**aquaporin z 2; **PDBTitle:** aquaporin structure from plant pathogen agrobacterium tumerfaciens
98	c2krxA_	Alignment	not modelled	7.5	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asl3597 protein; **PDBTitle:** solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
99	c1jauA_	Alignment	not modelled	7.5	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**transmembrane glycoprotein (gp41); **PDBTitle:** nmr solution structure of the trp-rich peptide of hiv gp412 bound to dpc micelles