Phyre^2

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Description	P33345
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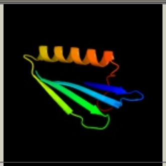
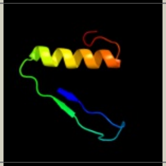
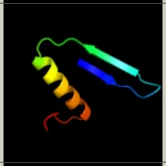
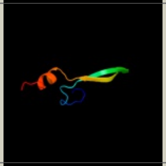
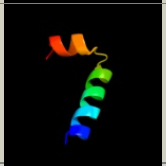
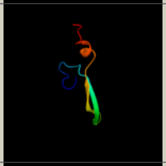
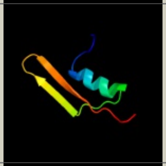
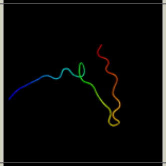
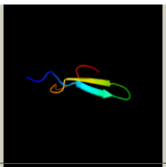
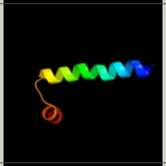
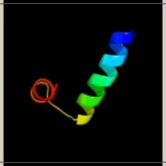
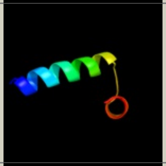
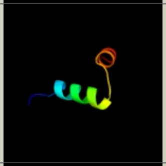
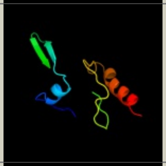
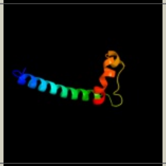
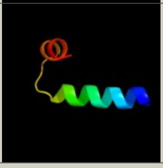
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ra8A_	Alignment		99.8	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein q64v53_bacfr; **PDBTitle:** crystal structure of the q64v53_bacfr protein from bacteroides2 fragilis. northeast structural genomics consortium target bfr43
2	c2eocA_	Alignment		98.2	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 3; **PDBTitle:** solution structure of the wgr domain from human poly [adp-2 ribose] polymerase-3
3	d2cr9a1	Alignment		97.5	28	**Fold:**WGR domain-like **Superfamily:**WGR domain-like **Family:**WGR domain
4	c3u5gB_	Alignment		41.6	13	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s1-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
5	c1y9qA_	Alignment		38.6	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
6	c2xzm4_	Alignment		37.1	13	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**40s ribosomal protein s3a; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
7	c2bnoA_	Alignment		34.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
8	c1yzxB_	Alignment		33.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase kappa 1; **PDBTitle:** crystal structure of human kappa class glutathione2 transferase
9	d1jjcb1	Alignment		30.5	16	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
10	d2awna1	Alignment		29.8	15	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
11	d1te4a_	Alignment		28.7	13	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**PBS lyase HEAT-like repeat

12	d2hf3a1	Alignment		28.6	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
13	c3ooxA_	Alignment		24.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 2og-fe(ii) oxygenase family protein; **PDBTitle:** crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
14	c3f6wE_	Alignment		23.2	23	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
15	c2o38A_	Alignment		22.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
16	d2o38a1	Alignment		22.7	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
17	c3op9A_	Alignment		21.0	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
18	c3gknA_	Alignment		20.1	14	**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
19	d1xvla1	Alignment		19.8	20	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
20	d2a6ca1	Alignment		18.5	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
21	d1vb5a_	Alignment	not modelled	18.1	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
22	c3qb0C_	Alignment	not modelled	17.2	16	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**actin-related protein 4; **PDBTitle:** crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
23	d2phcb1	Alignment	not modelled	17.2	22	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
24	c3clcC_	Alignment	not modelled	16.7	19	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
25	d1iwga6	Alignment	not modelled	16.2	17	**Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
26	d1r69a_	Alignment	not modelled	16.2	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
27	d2nrac1	Alignment	not modelled	16.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
						PDB header:virus **Chain:** B: **PDB Molecule:**vp3a, the building block protein of inner

28	c3k1qB_	Alignment	not modelled	15.8	15	shell; **PDBTitle:** backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
29	c3hpbA_	Alignment	not modelled	15.7	22	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**snx5 protein; **PDBTitle:** crystal structure of snx5-px domain in p212121 space group
30	c1o1aP_	Alignment	not modelled	15.7	20	**PDB header:**contractile protein **Chain:** P: **PDB Molecule:**skeletal muscle myosin ii; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
31	d1yt3a2	Alignment	not modelled	15.6	20	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
32	d1z67a1	Alignment	not modelled	15.5	9	**Fold:**YidB-like **Superfamily:**YidB-like **Family:**YidB-like
33	d1c0fa1	Alignment	not modelled	14.8	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
34	c2cseW_	Alignment	not modelled	14.8	24	**PDB header:**virus **Chain:** W: **PDB Molecule:**major core protein lambda 1; **PDBTitle:** features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
35	d1vbka2	Alignment	not modelled	14.7	29	**Fold:**THUMP domain **Superfamily:**THUMP domain-like **Family:**THUMP domain
36	d2cyya1	Alignment	not modelled	14.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
37	d2cg4a1	Alignment	not modelled	14.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
38	d1ep5a_	Alignment	not modelled	13.8	15	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
39	d1y9qa1	Alignment	not modelled	13.2	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
40	c3f52A_	Alignment	not modelled	13.1	19	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
41	c2zp2B_	Alignment	not modelled	13.0	22	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
42	c3mfqB_	Alignment	not modelled	12.9	9	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
43	d2croa_	Alignment	not modelled	12.5	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
44	c3k1qC_	Alignment	not modelled	12.5	15	**PDB header:**virus **Chain:** C: **PDB Molecule:**vp3b, the building block protein of inner shell; **PDBTitle:** backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
45	d2cfxa1	Alignment	not modelled	12.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
46	c2dbbA_	Alignment	not modelled	11.8	21	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph0061; **PDBTitle:** crystal structure of ph0061
47	c3kblA_	Alignment	not modelled	11.8	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**female germline-specific tumor suppressor gld-1; **PDBTitle:** crystal structure of the gld-1 homodimerization domain from2 caenorhabditis elegans n169a mutant at 2.28 a resolution
48	c6rlxC_	Alignment	not modelled	11.8	56	**PDB header:**hormone(muscle relaxant) **Chain:** C: **PDB Molecule:**relaxin, a-chain; **PDBTitle:** x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
49	c6rlxA_	Alignment	not modelled	11.8	56	**PDB header:**hormone(muscle relaxant) **Chain:** A: **PDB Molecule:**relaxin, a-chain; **PDBTitle:** x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
50	d1yaga1	Alignment	not modelled	11.6	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
51	c1vbkA_	Alignment	not modelled	11.5	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
52	d2fxua1	Alignment	not modelled	11.5	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
						Fold: Isocitrate/Isopropylmalate dehydrogenase-like

53	d1itwa_	Alignment	not modelled	11.4	25	**Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Monomeric isocitrate dehydrogenase
54	d1sq8a_	Alignment	not modelled	11.3	27	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
55	d1i1ga1	Alignment	not modelled	11.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
56	c3bjxB_	Alignment	not modelled	11.1	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**halocarboxylic acid dehalogenase dehi; **PDBTitle:** structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
57	c2b0tA_	Alignment	not modelled	11.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp isocitrate dehydrogenase; **PDBTitle:** structure of monomeric nadp isocitrate dehydrogenase
58	c4proD_	Alignment	not modelled	10.9	11	**PDB header:**serine protease **Chain:** D: **PDB Molecule:**alpha-lytic protease; **PDBTitle:** alpha-lytic protease complexed with pro region
59	c2xskA_	Alignment	not modelled	10.9	55	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**csgc; **PDBTitle:** e. coli curli protein csgc - secys
60	c2cfxD_	Alignment	not modelled	10.8	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hth-type transcriptional regulator lrpc; **PDBTitle:** structure of b.subtilis lrpc
61	c3pppA_	Alignment	not modelled	10.8	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline-binding protein; **PDBTitle:** structures of the substrate-binding protein provide insights into the2 multiple compatible solutes binding specificities of bacillus3 subtilis abc transporter opuc
62	d1pc6a_	Alignment	not modelled	10.8	10	**Fold:**NinB **Superfamily:**NinB **Family:**NinB
63	c3ltjA_	Alignment	not modelled	10.6	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**alpharep-4; **PDBTitle:** structure of a new family of artificial alpha helicoidal repeat2 proteins (alpha-rep) based on thermostable heat-like repeats
64	c2rajA_	Alignment	not modelled	10.1	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**sorting nexin-9; **PDBTitle:** so4 bound px-bar membrane remodeling unit of sorting nexin 9
65	d1llib_	Alignment	not modelled	10.1	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
66	c2phcB_	Alignment	not modelled	10.0	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
67	c1pbyA_	Alignment	not modelled	9.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**quinohemoprotein amine dehydrogenase 60 kda **PDBTitle:** structure of the phenylhydrazine adduct of the2 quinohemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
68	c3eusB_	Alignment	not modelled	9.9	23	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
69	c2l4aA_	Alignment	not modelled	9.8	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
70	c1i1gA_	Alignment	not modelled	9.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator lrpa; **PDBTitle:** crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
71	c2kpjA_	Alignment	not modelled	9.5	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
72	d2fbea1	Alignment	not modelled	9.3	13	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**SPRY domain
73	d2ofya1	Alignment	not modelled	9.3	3	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
74	c3lisB_	Alignment	not modelled	9.2	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**csp231i c protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
75	c3bs3A_	Alignment	not modelled	9.1	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
76	c3b7hA_	Alignment	not modelled	9.0	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
77	c2e1cA_	Alignment	not modelled	9.0	24	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex

78	c2lbaA_	Alignment	not modelled	8.9	28	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**babp protein; **PDBTitle:** solution structure of chicken ileal babp in complex with2 glycochenodeoxycholic acid
79	c2rliA_	Alignment	not modelled	8.9	7	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sco2 protein homolog, mitochondrial; **PDBTitle:** solution structure of cu(i) human sco2
80	c1ocuA_	Alignment	not modelled	8.9	18	**PDB header:**sorting protein **Chain:** A: **PDB Molecule:**sorting nexin; **PDBTitle:** crystal structure of the yeast px-domain protein grd19p2 (sorting nexin 3) complexed to3 phosphatidylinosytol-3-phospahte.
81	c1jmxA_	Alignment	not modelled	8.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
82	d1sbqa_	Alignment	not modelled	8.8	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
83	c3d3kD_	Alignment	not modelled	8.7	23	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
84	c3o66A_	Alignment	not modelled	8.7	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine/carnitine/choline abc transporter; **PDBTitle:** crystal structure of glycine betaine/carnitine/choline abc transporter
85	d1rioa_	Alignment	not modelled	8.7	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
86	d1soua_	Alignment	not modelled	8.6	21	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**Methenyltetrahydrofolate synthetase
87	c3bdnB_	Alignment	not modelled	8.6	15	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
88	c3d3jA_	Alignment	not modelled	8.6	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
89	c2ewtA_	Alignment	not modelled	8.5	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
90	c1f8vE_	Alignment	not modelled	8.4	40	**PDB header:**virus/rna **Chain:** E: **PDB Molecule:**mature capsid protein gamma; **PDBTitle:** the structure of pariacoto virus reveals a dodecahedral2 cage of duplex rna
91	d2hy5a1	Alignment	not modelled	8.4	22	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
92	d1f1sa2	Alignment	not modelled	8.3	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
93	c1wwuA_	Alignment	not modelled	8.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein flj21935; **PDBTitle:** solution structure of the sam_pnt domain of human protein2 flj21935
94	d1y7ya1	Alignment	not modelled	8.3	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
95	c3r0eC_	Alignment	not modelled	8.3	18	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
96	d3clsd2	Alignment	not modelled	8.2	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
97	d1k8ka1	Alignment	not modelled	8.2	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
98	d1ixsa_	Alignment	not modelled	8.1	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
99	c2p6tH_	Alignment	not modelled	8.0	24	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis