Phyre2

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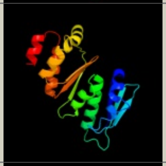
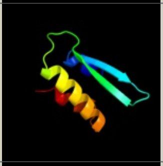
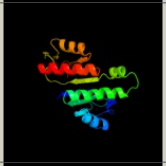
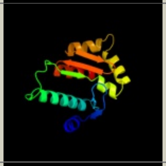
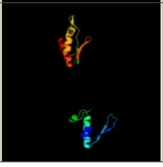
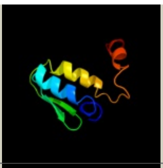
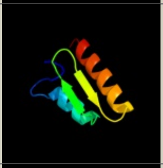
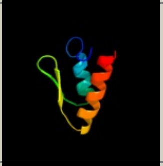
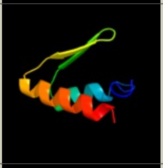
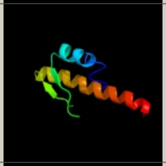
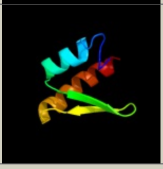
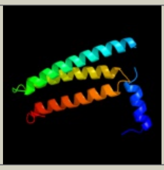
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tuaA_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ape0754; **PDBTitle:** 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix
2	d1tuaa2	Alignment		99.9	24	**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)
3	c2e3uA_	Alignment		99.7	26	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein ph1566; **PDBTitle:** crystal structure analysis of dim2p from pyrococcus horikoshii ot3
4	d1tuaa1	Alignment		98.3	17	**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)
5	c2yqrA_	Alignment		98.1	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0907 protein; **PDBTitle:** solution structure of the kh domain in kiaa0907 protein
6	c3krmB_	Alignment		98.0	17	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**insulin-like growth factor 2 mrna-binding protein **PDBTitle:** imp1 kh34
7	c2jzxA_	Alignment		97.8	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2; **PDBTitle:** pcbp2 kh1-kh2 domains
8	d1k1ga_	Alignment		97.8	27	**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)
9	c2jvzA_	Alignment		97.8	13	**PDB header:**splicing **Chain:** A: **PDB Molecule:**far upstream element-binding protein 2; **PDBTitle:** solution nmr structure of the second and third kh domains2 of ksrp
10	d1x4na1	Alignment		97.7	11	**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)
11	c1j4wA_	Alignment		97.7	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**fuse binding protein; **PDBTitle:** complex of the kh3 and kh4 domains of fbp with a2 single_stranded 29mer dna oligonucleotide from the fuse3 element of the c-myc oncogene

12	d2bl5a1	Alignment		97.6	35	**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)
13	c2hh2A_	Alignment		97.5	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the fourth kh domain of ksrp
14	d2ba0a3	Alignment		97.5	25	**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)
15	c2hh3A_	Alignment		97.5	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the third kh domain of ksrp
16	d1we8a_	Alignment		97.4	18	**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)
17	d1khma_	Alignment		97.4	14	**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)
18	c2anrA_	Alignment		97.4	14	**PDB header:**rna-binding protein/rna **Chain:** A: **PDB Molecule:**neuro-oncological ventral antigen 1; **PDBTitle:** crystal structure (ii) of nova-1 kh1/kh2 domain tandem with 25nt rna2 hairpin
19	d2ctka1	Alignment		97.4	20	**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)
20	d1j4wa1	Alignment		97.4	19	**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)
21	d1ec6a_	Alignment	not modelled	97.4	20	**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)
22	d1x4ma1	Alignment	not modelled	97.3	20	**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)
23	d2ctma1	Alignment	not modelled	97.3	20	**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)
24	d2axya1	Alignment	not modelled	97.3	19	**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)
25	d1zzka1	Alignment	not modelled	97.3	14	**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)
26	c3n89B_	Alignment	not modelled	97.2	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**defective in germ line development protein 3, isoform a; **PDBTitle:** kh domains
27	d2z0sa2	Alignment	not modelled	97.2	26	**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)
28	d1j4wa2	Alignment	not modelled	97.2	17	**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)
29	d1dt4a_	Alignment	not modelled	97.2	26	**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)
30	c1ztgD_	Alignment	not modelled	97.1	18	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1; **PDBTitle:** human alpha polyc binding protein kh1
31	d2ctla1	Alignment	not modelled	97.1	16	**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)
32	d1dtja_	Alignment	not modelled	97.1	23	**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)
33	d2ctea1	Alignment	not modelled	97.0	30	**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)
34	d1wvna1	Alignment	not modelled	97.0	16	**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)
35	d1viga_	Alignment	not modelled	97.0	16	**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)
36	d2ctja1	Alignment	not modelled	96.4	24	**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)
37	c2qndA_	Alignment	not modelled	96.3	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**fmr1 protein; **PDBTitle:** crystal structure of the kh1-kh2 domains from human fragile x mental2 retardation protein
38	c2dgrA_	Alignment	not modelled	95.8	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ring finger and kh domain-containing protein 1; **PDBTitle:** solution structure of the second kh domain in ring finger2 and kh domain containing protein 1
39	c3u1kB_	Alignment	not modelled	95.7	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyribonucleotide nucleotidyltransferase 1, mitochondrial; **PDBTitle:** crystal structure of human pnpase
40	d2ctfa1	Alignment	not modelled	95.7	17	**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)
41	c2cy1A_	Alignment	not modelled	91.3	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nusa protein homolog; **PDBTitle:** crystal structure of ape1850
42	c1y4cA_	Alignment		88.7	10	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
43	c3gkuB_	Alignment	not modelled	85.3	26	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**probable rna-binding protein; **PDBTitle:** crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
44	d2je6i3	Alignment	not modelled	84.9	48	**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)
45	c2pt7G_	Alignment	not modelled	80.9	45	**PDB header:**hydrolase/protein binding **Chain:** G: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
46	d1wf3a2	Alignment	not modelled	65.2	29	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
47	d1egaa2	Alignment	not modelled	64.9	21	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
48	d2asba3	Alignment	not modelled	57.7	24	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
49	d1fe0a_	Alignment	not modelled	52.9	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
50	c2rcyB_	Alignment	not modelled	49.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline carboxylate reductase; **PDBTitle:** crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
51	d1hh2p3	Alignment	not modelled	48.0	25	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
52	c1wf3A_	Alignment	not modelled	46.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
53	c1hh2P_	Alignment	not modelled	46.8	21	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
54	c3dxsX_	Alignment	not modelled	44.1	20	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**copper-transporting atpase ran1; **PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase
						PDB header:nucleotide binding protein/rna

55	c3ievA_	Alignment	not modelled	41.9	37	**Chain:** A: **PDB Molecule:**gtp-binding protein era; **PDBTitle:** crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna
56	c2g7zB_	Alignment	not modelled	39.1	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
57	c3nmeA_	Alignment	not modelled	38.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
58	c1egaB_	Alignment	not modelled	37.7	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (gtp-binding protein era); **PDBTitle:** crystal structure of a widely conserved gtpase era
59	c1l2fA_	Alignment	not modelled	37.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
60	d2ahra1	Alignment	not modelled	36.3	17	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
61	d1mwza_	Alignment	not modelled	35.4	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
62	c2d7dA_	Alignment	not modelled	32.1	11	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
63	d1yqga1	Alignment	not modelled	31.1	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
64	d1a5ca_	Alignment	not modelled	30.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
65	c1k0rB_	Alignment	not modelled	30.4	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa
66	c3i4tA_	Alignment	not modelled	30.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**diphthine synthase; **PDBTitle:** crystal structure of putative diphthine synthase from2 entamoeba histolytica
67	c3kx6C_	Alignment	not modelled	29.8	23	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose-1,6-bisphosphate aldolase from babesia2 bovis at 2.1a resolution
68	d1pixa3	Alignment	not modelled	28.9	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
69	c3u97A_	Alignment	not modelled	28.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease toxin brnt; **PDBTitle:** 1.1 angstrom-resolution crystal structure of the brucella abortus2 ribonuclease toxin, brnt
70	c1yjrA_	Alignment	not modelled	28.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein
71	c3d64A_	Alignment	not modelled	27.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
72	c3gvpB_	Alignment	not modelled	27.8	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
73	d1q8la_	Alignment	not modelled	27.1	8	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
74	c3v69A_	Alignment	not modelled	27.0	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein filia; **PDBTitle:** filia-n crystal structure
75	c3c1qA_	Alignment	not modelled	26.8	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**general secretion pathway protein f; **PDBTitle:** the three-dimensional structure of the cytoplasmic domains of epsf2 from the type 2 secretion system of vibrio cholerae
76	c2pc4B_	Alignment	not modelled	26.8	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
77	c2ldiA_	Alignment	not modelled	26.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
78	d1ml4a2	Alignment	not modelled	26.6	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
79	c2wbyC_	Alignment	not modelled	26.5	18	**PDB header:**hydrolase/hormone **Chain:** C: **PDB Molecule:**insulin a chain; **PDBTitle:** crystal structure of human insulin-degrading enzyme in2 complex with insulin
80	c2wc0C_	Alignment	not modelled	26.5	18	**PDB header:**hydrolase/hormone **Chain:** C: **PDB Molecule:**insulin a chain; **PDBTitle:** crystal structure of human insulin degrading enzyme in2 complex with iodinated insulin
						PDB header:hormone

81	c2ws7E_	Alignment	not modelled	26.5	18	**Chain:** E: **PDB Molecule:**insulin a chain; **PDBTitle:** semi-synthetic analogue of human insulin prob26-dti
82	c2wbyE_	Alignment	not modelled	26.5	18	**PDB header:**hydrolase/hormone **Chain:** E: **PDB Molecule:**insulin a chain; **PDBTitle:** crystal structure of human insulin-degrading enzyme in2 complex with insulin
83	c2wc0E_	Alignment	not modelled	26.5	18	**PDB header:**hydrolase/hormone **Chain:** E: **PDB Molecule:**insulin a chain; **PDBTitle:** crystal structure of human insulin degrading enzyme in2 complex with iodinated insulin
84	c1jcaA_	Alignment	not modelled	26.4	24	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**insulin a; **PDBTitle:** non-standard design of unstable insulin analogues with enhanced2 activity
85	c1tujA_	Alignment	not modelled	26.2	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**odorant binding protein asp2; **PDBTitle:** solution structure of the honey bee general odorant binding2 protein asp2 in complex with trimethylsilyl-d4 propionate
86	d1va0a1	Alignment	not modelled	26.1	33	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
87	c2kgsA_	Alignment	not modelled	25.9	57	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** solution structure of the amino-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
88	c1jcaC_	Alignment	not modelled	25.3	24	**PDB header:**hormone/growth factor **Chain:** C: **PDB Molecule:**insulin a; **PDBTitle:** non-standard design of unstable insulin analogues with enhanced2 activity
89	d2at2a2	Alignment	not modelled	24.0	26	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
90	d1vlva2	Alignment	not modelled	23.0	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
91	d1ekxa2	Alignment	not modelled	23.0	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
92	c3zs2A_	Alignment	not modelled	23.0	18	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin a chain; **PDBTitle:** tyrb25,nmepheb26,lysb28,prob29-insulin analogue crystal2 structure
93	c2ws7A_	Alignment	not modelled	23.0	18	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin a chain; **PDBTitle:** semi-synthetic analogue of human insulin prob26-dti
94	c1os4G_	Alignment	not modelled	23.0	18	**PDB header:**hormone/growth factor **Chain:** G: **PDB Molecule:**insulin; **PDBTitle:** dehydrated t6 human insulin at 295 k
95	c3zs2G_	Alignment	not modelled	23.0	18	**PDB header:**hormone **Chain:** G: **PDB Molecule:**insulin a chain; **PDBTitle:** tyrb25,nmepheb26,lysb28,prob29-insulin analogue crystal2 structure
96	c2ws7K_	Alignment	not modelled	22.5	18	**PDB header:**hormone **Chain:** K: **PDB Molecule:**insulin a chain; **PDBTitle:** semi-synthetic analogue of human insulin prob26-dti
97	c2jmlA_	Alignment	not modelled	22.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
98	c1rweC_	Alignment	not modelled	22.2	18	**PDB header:**hormone/growth factor **Chain:** C: **PDB Molecule:**insulin; **PDBTitle:** enhancing the activity of insulin at receptor edge: crystal structure2 and photo-cross-linking of a8 analogues
99	c1rweA_	Alignment	not modelled	22.2	18	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**insulin; **PDBTitle:** enhancing the activity of insulin at receptor edge: crystal structure2 and photo-cross-linking of a8 analogues
100	c2e0kA_	Alignment	not modelled	22.1	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
101	d1s6ua_	Alignment	not modelled	21.6	8	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
102	c2yx0A_	Alignment	not modelled	21.6	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
103	c3dhyC_	Alignment	not modelled	21.5	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
104	c2kkhA_	Alignment	not modelled	21.2	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
105	d1pg5a2	Alignment	not modelled	21.2	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
106	c3gkyC_	Alignment	not modelled	21.1	18	**PDB header:**hormone **Chain:** C: **PDB Molecule:**insulin a chain; **PDBTitle:** the structural basis of an er stress-associated bottleneck2 in a protein folding landscape
						PDB header:hormone

107	c3q6eC_	Alignment	not modelled	20.9	18	**Chain:** C: **PDB Molecule:**insulin a chain; **PDBTitle:** human insulin in complex with cucurbit[7]uril
108	c2zv4O_	Alignment	not modelled	20.8	11	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
109	c3gkyA_	Alignment	not modelled	20.2	18	**PDB header:**hormone **Chain:** A: **PDB Molecule:**insulin a chain; **PDBTitle:** the structural basis of an er stress-associated bottleneck2 in a protein folding landscape