Phyre2

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Description	Q8BGA5
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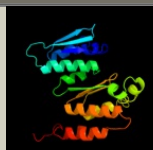
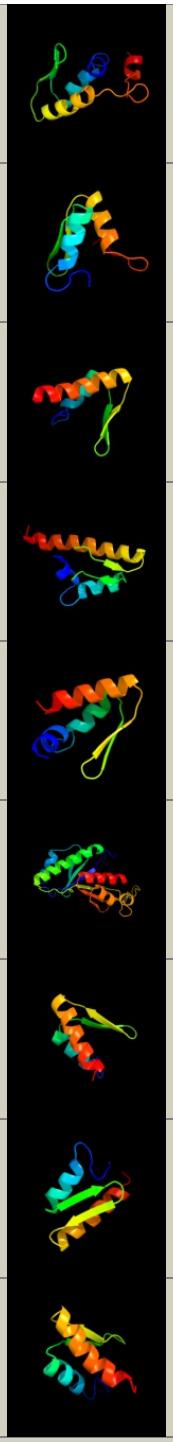
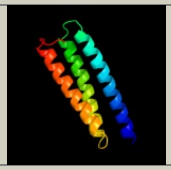
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tuaA_	Alignment		99.9	19	**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		99.8	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)
3	c2e3uA_	Alignment		99.6	28	**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	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)
5	c2yqrA_	Alignment		98.0	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0907 protein; **PDBTitle:** solution structure of the kh domain in kiaa0907 protein
6	c3krmB_	Alignment		97.9	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	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2; **PDBTitle:** pcbp2 kh1-kh2 domains
8	d1k1ga_	Alignment		97.7	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)
9	d1x4na1	Alignment		97.7	9	**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)
10	c1j4wA_	Alignment		97.6	15	**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
11	c2jvzA_	Alignment		97.5	12	**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

12	c4jvhA_	Alignment		97.5	32	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein quaking; **PDBTitle:** structure of the star domain of quaking protein in complex with rna
13	c2hh2A_	Alignment		97.5	20	**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	c4b8tA_	Alignment		97.4	15	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** rna binding protein solution structure of the third kh2 domain of ksrp in complex with the g-rich target sequence.
15	d2ctka1	Alignment		97.4	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)
16	d1khma_	Alignment		97.4	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)
17	c3n89B_	Alignment		97.4	11	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**defective in germ line development protein 3, isoform a; **PDBTitle:** kh domains
18	d1we8a_	Alignment		97.4	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)
19	d2ba0a3	Alignment		97.4	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)
20	c2hh3A_	Alignment		97.4	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the third kh domain of ksrp
21	d1j4wa1	Alignment	not modelled	97.3	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)
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	d2bl5a1	Alignment	not modelled	97.3	33	**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	d1ec6a_	Alignment	not modelled	97.3	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)
25	d2z0sa2	Alignment	not modelled	97.2	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)
26	d2axya1	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)
27	d2ctma1	Alignment	not modelled	97.2	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)
28	c1ztgD_	Alignment	not modelled	97.1	16	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1; **PDBTitle:** human alpha polyc binding protein kh1
29	d1j4wa2	Alignment	not modelled	97.1	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)
30	d1zzka1	Alignment	not modelled	97.1	12	**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)
31	c4jvyA_	Alignment	not modelled	97.1	30	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**female germline-specific tumor suppressor gld-1; **PDBTitle:** structure of the star (signal transduction and activation of rna)2 domain of gld-1 bound to rna
32	d1viga_	Alignment	not modelled	97.0	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)
33	c2anrA_	Alignment	not modelled	97.0	19	**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
34	d1dt4a_	Alignment	not modelled	97.0	22	**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	d1dtja_	Alignment	not modelled	97.0	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)
36	d2ctla1	Alignment	not modelled	97.0	15	**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	d2ctea1	Alignment	not modelled	97.0	28	**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)
38	d1wvna1	Alignment	not modelled	96.8	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)
39	c4am3A_	Alignment	not modelled	96.7	13	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**polyribonucleotide nucleotidyltransferase; **PDBTitle:** crystal structure of c. crescentus pnpase bound to rna
40	d2ctja1	Alignment	not modelled	96.5	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)
41	c4aimA_	Alignment	not modelled	96.5	13	**PDB header:**transferase/peptide **Chain:** A: **PDB Molecule:**polyribonucleotide nucleotidyltransferase; **PDBTitle:** crystal structure of c. crescentus pnpase bound to rnase e2 recognition peptide
42	c2qndA_	Alignment	not modelled	96.5	14	**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
43	c2dgrA_	Alignment	not modelled	96.4	20	**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
44	c3u1kB_	Alignment	not modelled	96.2	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyribonucleotide nucleotidyltransferase 1, mitochondrial; **PDBTitle:** crystal structure of human pnpase
45	d2ctfa1	Alignment	not modelled	95.9	15	**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)
46	c2cy1A_	Alignment	not modelled	91.3	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nusa protein homolog; **PDBTitle:** crystal structure of ape1850
47	c3gkuB_	Alignment	not modelled	90.4	19	**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
48	c1y4cA_	Alignment		88.4	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**maltose binding protein fused with designed **PDBTitle:** designed helical protein fusion mbp
49	d2je6i3	Alignment	not modelled	83.9	43	**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)
50	c2pt7G_	Alignment	not modelled	79.0	41	**PDB header:**hydrolase/protein binding **Chain:** G: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
51	d1wf3a2	Alignment	not modelled	63.4	33	**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	d2asba3	Alignment	not modelled	63.2	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
53	d1egaa2	Alignment	not modelled	59.5	22	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
54	d1hh2p3	Alignment	not modelled	57.3	20	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)

55	d1fe0a_	Alignment	not modelled	57.2	20	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
56	c1egaB_	Alignment	not modelled	49.1	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (gtp-binding protein era); **PDBTitle:** crystal structure of a widely conserved gtpase era
57	c3dxsX_	Alignment	not modelled	49.1	23	**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
58	c1yjrA_	Alignment	not modelled	47.7	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
59	c2rcyB_	Alignment	not modelled	47.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline carboxylate reductase; **PDBTitle:** crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
60	d2ahra1	Alignment	not modelled	45.7	17	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
61	c2d7dA_	Alignment	not modelled	45.2	10	**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
62	d1yqga1	Alignment	not modelled	45.0	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
63	c3nmeA_	Alignment	not modelled	44.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
64	d1p6ta2	Alignment	not modelled	43.0	21	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
65	c2zv4O_	Alignment	not modelled	42.8	13	**PDB header:**structural protein **Chain:** O: **PDB Molecule:**major vault protein; **PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution
66	c1wf3A_	Alignment	not modelled	40.5	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
67	c2ldiA_	Alignment	not modelled	38.6	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** nmr solution structure of ziaan sub mutant
68	d1q8la_	Alignment	not modelled	37.3	7	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
69	d1qh8b_	Alignment	not modelled	37.0	7	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
70	d1ml4a2	Alignment	not modelled	36.1	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
71	d1mwza_	Alignment	not modelled	35.1	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
72	d1vlva2	Alignment	not modelled	35.1	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
73	c2yx0A_	Alignment	not modelled	34.4	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**radical sam enzyme; **PDBTitle:** crystal structure of p. horikoshii tyw1
74	d1afia_	Alignment	not modelled	34.4	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
75	c3gvpB_	Alignment	not modelled	34.1	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
76	c2kgsA_	Alignment	not modelled	33.2	50	**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
77	c3ievA_	Alignment	not modelled	33.1	37	**PDB header:**nucleotide binding protein/rna **Chain:** A: **PDB Molecule:**gtp-binding protein era; **PDBTitle:** crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna
78	d1s6ua_	Alignment	not modelled	32.5	8	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
79	c3v69A_	Alignment	not modelled	31.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein filia; **PDBTitle:** filia-n crystal structure
80	d1qupa2	Alignment	not modelled	31.5	16	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
81	d1vh4a_	Alignment	not modelled	31.1	22	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Stabilizer of iron transporter SufD **Family:**Stabilizer of iron transporter SufD

82	c3fpjA_	Alignment	not modelled	31.0	19	**PDB header:**biosynthetic protein, transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of e81q mutant of mtnas in complex with s-2 adenosylmethionine
83	d2qlvb1	Alignment	not modelled	30.9	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
84	d1pg5a2	Alignment	not modelled	30.6	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
85	d1twla_	Alignment	not modelled	30.2	18	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
86	c2g7zB_	Alignment	not modelled	28.9	13	**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
87	c2l3mA_	Alignment	not modelled	28.7	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**copper-ion-binding protein; **PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames
88	d1kvja_	Alignment	not modelled	28.6	15	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
89	c3canA_	Alignment	not modelled	28.4	12	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
90	d1va0a1	Alignment	not modelled	28.0	37	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
91	d1p6ta1	Alignment	not modelled	27.1	17	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
92	c2ofgX_	Alignment	not modelled	26.9	20	**PDB header:**hydrolase, membrane protein **Chain:** X: **PDB Molecule:**zinc-transporting atpase; **PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form
93	c2ycbA_	Alignment	not modelled	26.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor; **PDBTitle:** structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
94	d1osda_	Alignment	not modelled	26.7	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
95	c2crlA_	Alignment	not modelled	26.5	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase
96	d1ekxa2	Alignment	not modelled	26.5	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
97	c2qlvB_	Alignment	not modelled	26.2	31	**PDB header:**transferase/protein binding **Chain:** B: **PDB Molecule:**protein sip2; **PDBTitle:** crystal structure of the heterotrimer core of the s.2 cerevisiae ampk homolog snf1
98	d1udea_	Alignment	not modelled	25.9	15	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
99	c2jmlA_	Alignment	not modelled	25.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
100	c3n58D_	Alignment	not modelled	25.4	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
101	d2f15a1	Alignment	not modelled	25.0	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
102	c3dhyC_	Alignment	not modelled	24.7	16	**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
103	d2at2a2	Alignment	not modelled	24.1	26	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
104	c2k2pA_	Alignment	not modelled	24.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1203; **PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
105	c3c1qA_	Alignment	not modelled	23.8	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
						Fold:dsRBD-like

106	d1pkpa2	Alignment	not modelled	23.7	29	**Superfamily:**dsRNA-binding domain-like **Family:**Ribosomal S5 protein, N-terminal domain
107	c1k0rB_	Alignment	not modelled	23.6	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nusa; **PDBTitle:** crystal structure of mycobacterium tuberculosis nusa
108	d1pvva2	Alignment	not modelled	23.6	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
109	c2e0kA_	Alignment	not modelled	23.4	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**precorrin-2 c20-methyltransferase; **PDBTitle:** crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
110	d2aw0a_	Alignment	not modelled	23.1	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
111	c3ld3A_	Alignment	not modelled	23.0	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic phosphatase from anaplasma2 phagocytophilum at 1.75a resolution
112	d1vr8a1	Alignment	not modelled	22.7	27	**Fold:**TM1622-like **Superfamily:**TM1622-like **Family:**TM1622-like
113	d2fmra_	Alignment	not modelled	22.6	15	**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)
114	c1ydnA_	Alignment	not modelled	22.6	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
115	d1z0na1	Alignment	not modelled	22.5	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
116	d1z0mb1	Alignment	not modelled	22.4	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
117	c1d4fD_	Alignment	not modelled	22.2	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
118	d2prda_	Alignment	not modelled	22.1	21	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
119	c2kkhA_	Alignment	not modelled	21.9	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**putative heavy metal transporter; **PDBTitle:** structure of the zinc binding domain of the atpase hma4
120	d1ve2a1	Alignment	not modelled	21.7	37	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase