Phyre^2

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Description	RVBD3528c_(-)_3964658_3965371
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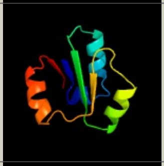
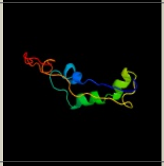
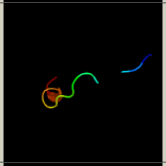
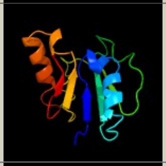
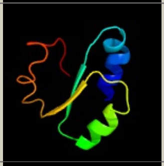
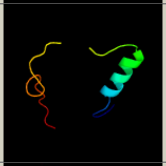
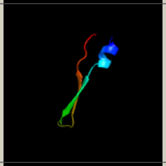
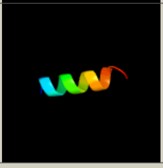
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3tkaA_	Alignment		39.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase h; **PDBTitle:** crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
2	c4er3A_	Alignment		29.3	20	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-79 specific; **PDBTitle:** crystal structure of human dot1l in complex with inhibitor epz004777
3	c1nw3A_	Alignment		28.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone methyltransferase dot1l; **PDBTitle:** structure of the catalytic domain of human dot1l, a non-set domain2 nucleosomal histone methyltransferase
4	d1nw3a_	Alignment		28.7	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l
5	c2bg5C_	Alignment		28.6	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase; **PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
6	c3u21B_	Alignment		28.3	38	**PDB header:**transcription regulation, dna binding **Chain:** B: **PDB Molecule:**nuclear factor related to kappa-b-binding protein; **PDBTitle:** crystal structure of a fragment of nuclear factor related to kappa-b-2 binding protein (residues 370-495) (nfrkb) from homo sapiens at 2.183 a resolution
7	c1fpqA_	Alignment		27.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoliquiritigenin 2'-o-methyltransferase; **PDBTitle:** crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase
8	c1m6yA_	Alignment		25.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah
9	d1fp1d2	Alignment		24.0	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
10	c4qdkB_	Alignment		22.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**magnesium-protoporphyrin o-methyltransferase; **PDBTitle:** crystal structure of magnesium protoporphyrin ix methyltransferase2 (chlm) from synechocystis pcc 6803 with bound sah
11	c4p7cB_	Alignment		22.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (mo5u34)-methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato

12	c1fp2A_	Alignment		22.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isoflavone o-methyltransferase; **PDBTitle:** crystal structure analysis of isoflavone o-methyltransferase
13	c6ecvB_	Alignment		20.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**stid protein; **PDBTitle:** stid o-mt residues 976-1266
14	d2fpwa1	Alignment		20.2	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Histidinol phosphatase-like
15	c3lw6A_	Alignment		19.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7
16	c4a6dA_	Alignment		18.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydroxyindole o-methyltransferase; **PDBTitle:** crystal structure of human n-acetylserotonin2 methyltransferase (asmt) in complex with sam
17	c6i5zA_	Alignment		18.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-methyltransferase 1; **PDBTitle:** papaver somniferum o-methyltransferase
18	c6gkvB_	Alignment		18.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**coclaurine n-methyltransferase; **PDBTitle:** crystal structure of coclaurine n-methyltransferase (cnmt) bound to n-2 methylheliamine and sah
19	c3udsA_	Alignment		17.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inositol-pentakisphosphate 2-kinase; **PDBTitle:** inositol 1,3,4,5,6-pentakisphosphate 2-kinase from a. thaliana in2 complex with adp.
20	c3f1iH_	Alignment		17.6	38	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** human escrt-0 core complex
21	c3p2kA_	Alignment	not modelled	17.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of an antibiotic related methyltransferase
22	c3mq2A_	Alignment	not modelled	17.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methyltransferase; **PDBTitle:** crystal structure of 16s rrna methyltranferase kamb
23	d2bo4a1	Alignment	not modelled	17.2	29	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**MGS-like
24	d1vmda_	Alignment	not modelled	16.3	29	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
25	c6ec3C_	Alignment	not modelled	16.2	21	**PDB header:**transferase, oxidoreductase **Chain:** C: **PDB Molecule:**methyltransferase domain-containing protein; **PDBTitle:** crystal structure of evdmo1
26	c2zufA_	Alignment	not modelled	15.7	24	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
27	c3gqqD_	Alignment	not modelled	15.7	26	**PDB header:**splicing **Chain:** D: **PDB Molecule:**protein unc-119 homolog a; **PDBTitle:** crystal structure of the human retinal protein 4 (unc-1192 homolog a). northeast structural genomics consortium3 target hr3066a
28	c5wp5A_	Alignment	not modelled	15.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphomethylethanolamine n-methyltransferase 2; **PDBTitle:** arabidopsis thaliana phosphoethanolamine n-methyltransferase 22 (atpmt2) in complex with sah

29	c1f7uA_	Alignment	not modelled	15.2	26	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
30	d1gg3a3	Alignment	not modelled	13.1	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
31	d1fp2a2	Alignment	not modelled	13.1	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
32	c4m8nB_	Alignment	not modelled	11.6	25	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**plexinc1 intracellular region; **PDBTitle:** crystal structure of plexinc1/rap1b complex
33	c3d9oB_	Alignment	not modelled	10.3	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rna-binding protein 16; **PDBTitle:** snapshots of the rna processing factor scaf8 bound to different2 phosphorylated forms of the carboxy-terminal domain of rna-polymerase3 ii
34	d1ef1a3	Alignment	not modelled	10.3	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
35	d2p7ja1	Alignment	not modelled	9.9	12	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**YkuI C-terminal domain-like
36	c4kdcA_	Alignment	not modelled	9.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-demethylubiquinone-9 3-methyltransferase; **PDBTitle:** crystal structure of ubig
37	c2zkqb_	Alignment	not modelled	9.7	12	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
38	c1x1aA_	Alignment	not modelled	9.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**crtf-related protein; **PDBTitle:** crystal structure of bchu complexed with s-adenosyl-l-methionine
39	c1kyzC_	Alignment	not modelled	9.5	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**caffeic acid 3-o-methyltransferase; **PDBTitle:** crystal structure analysis of caffeic acid/5-hydroxyferulic2 acid 3/5-o-methyltransferase ferulic acid complex
40	d2ge7a1	Alignment	not modelled	9.5	50	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
41	d1skyb1	Alignment	not modelled	9.4	10	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
42	c4xcxA_	Alignment	not modelled	9.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**small rna 2'-o-methyltransferase; **PDBTitle:** methyltransferase domain of small rna 2'-o-methyltransferase
43	d1f7ua2	Alignment	not modelled	9.4	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
44	d2nefa_	Alignment	not modelled	9.3	16	**Fold:**Regulatory factor Nef **Superfamily:**Regulatory factor Nef **Family:**Regulatory factor Nef
45	c4uw2D_	Alignment	not modelled	9.2	24	**PDB header:**immune system **Chain:** D: **PDB Molecule:**csm1; **PDBTitle:** crystal structure of csm1 in t.onnurineus
46	c5kn4B_	Alignment	not modelled	9.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pavine n-methyltransferase; **PDBTitle:** pavine n-methyltransferase apoenzyme ph 6.0
47	c4gokG_	Alignment	not modelled	9.0	26	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**protein unc-119 homolog a; **PDBTitle:** the crystal structure of arl2gppnhp in complex with unc119a
48	c3lwgB_	Alignment	not modelled	9.0	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hp0420 homologue; **PDBTitle:** crystal structure of hp0420-homologue c46a from helicobacter felis
49	c2ifsA_	Alignment	not modelled	9.0	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protien interacting protein and **PDBTitle:** structure of the n-wasp evh1 domain in complex with an extended wip2 peptide
50	d1b93a_	Alignment	not modelled	8.8	29	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
51	d2uubb1	Alignment	not modelled	8.8	32	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
52	d2zpya3	Alignment	not modelled	8.8	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
53	d1f6va_	Alignment	not modelled	8.7	17	**Fold:**C-terminal domain of B transposition protein **Superfamily:**C-terminal domain of B transposition protein **Family:**C-terminal domain of B transposition protein
54			not modelled	8.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of the sam-dependent methyltransferase

		Alignment	not modelled			cg3271 from2 corynebacterium glutamicum in complex with s-adenosyl-l-homocysteine3 and pyrophosphate. northeast structural genomics consortium target4 cgr113a
55	d2cjra1	Alignment	not modelled	8.5	50	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
56	d2f43a1	Alignment	not modelled	8.4	18	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
57	d3b5ha2	Alignment	not modelled	8.2	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
58	d1ni2a3	Alignment	not modelled	8.1	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
59	c5v75E_	Alignment	not modelled	8.0	25	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**microcompartments protein; **PDBTitle:** structure of haliangium ochraceum bmc-t ho-5816
60	d2bcgg2	Alignment	not modelled	7.8	27	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
61	c6g13B_	Alignment	not modelled	7.7	42	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**nucleoprotein; **PDBTitle:** c-terminal domain of mers-cov nucleocapsid
62	d1xzpa3	Alignment	not modelled	7.6	29	**Fold:**Folate-binding domain **Superfamily:**Folate-binding domain **Family:**TrmE formyl-THF-binding domain
63	c1xzqB_	Alignment	not modelled	7.6	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
64	d2ca1a1	Alignment	not modelled	7.6	50	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
65	c1s1hB_	Alignment	not modelled	7.5	10	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
66	c4krhB_	Alignment	not modelled	7.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoethanolamine n-methyltransferase 2; **PDBTitle:** semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine
67	c3p9kD_	Alignment	not modelled	7.4	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**caffeic acid o-methyltransferase; **PDBTitle:** crystal structure of perennial ryegrass lpomt1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
68	c1s4pA_	Alignment	not modelled	7.3	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycolipid 2-alpha-mannosyltransferase; **PDBTitle:** crystal structure of yeast alpha1,2-mannosyltransferase kre2p/mnt1p:2 ternary complex with gdp/mn and methyl-alpha-mannoside acceptor
69	c5a08A_	Alignment	not modelled	7.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable mannosyltransferase ktr4; **PDBTitle:** x-ray structure of the mannosyltransferase ktr4p from s. cerevisiae
70	d1s4na_	Alignment	not modelled	7.3	35	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycolipid 2-alpha-mannosyltransferase
71	c4irqB_	Alignment	not modelled	7.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**beta-1,4-galactosyltransferase 7; **PDBTitle:** crystal structure of catalytic domain of human beta1,2 4galactosyltransferase 7 in closed conformation in complex with3 manganese and udp
72	d2giba1	Alignment	not modelled	7.2	50	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
73	c5v76A_	Alignment	not modelled	7.1	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microcompartments protein; **PDBTitle:** structure of haliangium ochraceum bmc-t ho-3341
74	c2vxdA_	Alignment	not modelled	7.1	71	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** the structure of the c-terminal domain of nucleophosmin
75	c6em5w_	Alignment	not modelled	7.1	20	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**ribosome assembly factor mrt4; **PDBTitle:** state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
76	c3f56F_	Alignment	not modelled	7.0	25	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**csos1d; **PDBTitle:** the structure of a previously undetected carboxysome shell protein:2 csos1d from prochlorococcus marinus med4
77	d1h4ra3	Alignment	not modelled	7.0	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
78	c3k1lA_	Alignment	not modelled	6.9	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fancl; **PDBTitle:** crystal structure of fancl
79	d2k0bx1	Alignment	not modelled	6.8	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like

						Family:UBA domain
80	c3bbnB_	Alignment	not modelled	6.6	24	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
81	c4ineB_	Alignment	not modelled	6.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein pmt-2; **PDBTitle:** crystal structure of n-methyl transferase (pmt-2) from caenorhabditis2 elegant complexed with s-adenosyl homocysteine and3 phosphoethanolamine
82	c5epwB_	Alignment	not modelled	6.6	25	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**nucleoprotein; **PDBTitle:** c-terminal domain of human coronavirus nl63 nucleocapsid protein
83	c3j6vB_	Alignment	not modelled	6.6	10	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**28s ribosomal protein s2, mitochondrial; **PDBTitle:** cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
84	c5o5jV_	Alignment	not modelled	6.6	28	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**30s ribosomal protein s2; **PDBTitle:** structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
85	d1pzta_	Alignment	not modelled	6.3	22	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**beta 1,4 galactosyltransferase (b4GalT1)
86	c3dh0B_	Alignment	not modelled	6.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam dependent methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 aquifex aeolicus
87	c1zgaA_	Alignment	not modelled	6.2	21	**PDB header:**plant protein, transferase **Chain:** A: **PDB Molecule:**isoflavanone 4'-o-methyltransferase'; **PDBTitle:** crystal structure of isoflavanone 4'-o-methyltransferase complexed2 with (+)-6a-hydroxymaackiain
88	c3noyA_	Alignment	not modelled	6.2	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
89	c2llhA_	Alignment	not modelled	6.2	71	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**nucleophosmin; **PDBTitle:** nmr structure of npm1_c70
90	c3vjfA_	Alignment	not modelled	6.2	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wa20; **PDBTitle:** crystal structure of de novo 4-helix bundle protein wa20
91	d1yuba_	Alignment	not modelled	6.2	9	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
92	d1fx0a1	Alignment	not modelled	6.1	13	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
93	c2v6yA_	Alignment	not modelled	6.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aaa family atpase, p60 katanin; **PDBTitle:** structure of the mit domain from a s. solfataricus vps4-2 like atpase
94	c4ht7G_	Alignment	not modelled	6.0	25	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**co2 concentrating mechanism protein p; **PDBTitle:** co2 concentrating mechanism protein p, ccmp form 2
95	c3egbA_	Alignment	not modelled	6.0	50	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein pellino homolog 2; **PDBTitle:** structure of pellino2 fha domain at 3.3 angstroms resolution.
96	d2dk8a1	Alignment	not modelled	5.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RPO3F domain-like
97	d1lj8a4	Alignment	not modelled	5.7	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
98	c5l39D_	Alignment	not modelled	5.7	25	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**rmm microcompartment shell protein msm0275; **PDBTitle:** the structure of the fused permuted hexameric shell protein msm02752 from the rmm microcompartment
99	c6n2oB_	Alignment	not modelled	5.6	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyruvate ferredoxin/flavodoxin oxidoreductase, beta **PDBTitle:** 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound