Phyre2

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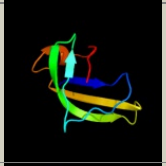
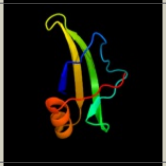
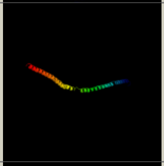
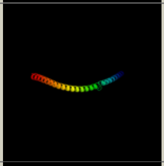
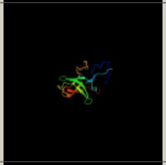
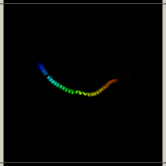
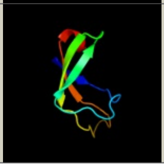
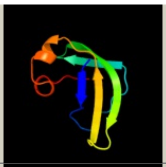
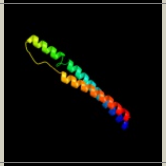
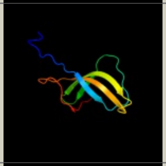
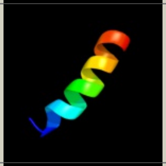
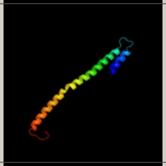
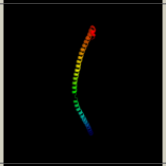
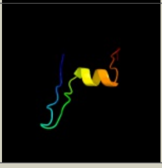
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pj5a1	Alignment		93.4	17	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
2	d1v5va1	Alignment		90.3	17	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
3	d1wosa1	Alignment		87.9	17	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
4	c1v5vA_	Alignment		84.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution
5	c1qu7A_	Alignment		78.6	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i; **PDBTitle:** four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
6	c3girA_	Alignment		75.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of glycine cleavage system2 aminomethyltransferase t from bartonella henselae
7	c1worA_	Alignment		75.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of t-protein of the glycine cleavage2 system
8	c2wpqA_	Alignment		74.7	5	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**trimeric autotransporter adhesin fragment; **PDBTitle:** salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion)
9	c2j5uB_	Alignment		73.9	16	**PDB header:**cell shape regulation **Chain:** B: **PDB Molecule:**mrec protein; **PDBTitle:** mrec lysteria monocytogenes
10	c1ei3C_	Alignment		72.9	13	**PDB header:** **PDB COMPND:**
11	c1yx2B_	Alignment		72.6	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of the probable aminomethyltransferase2 from bacillus subtilis

12	c1pj6A_	Alignment		68.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n,n-dimethylglycine oxidase; **PDBTitle:** crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
13	c2ieqC_	Alignment		67.9	17	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
14	c2qf4A_	Alignment		64.9	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cell shape determining protein mrec; **PDBTitle:** high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
15	d1vloa1	Alignment		63.6	18	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
16	c3tfhB_	Alignment		58.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gcvt-like aminomethyltransferase protein; **PDBTitle:** dmsp-dependent demethylase from p. ubique - apo
17	d1c99a_	Alignment		57.5	28	**Fold:**Transmembrane helix hairpin **Superfamily:**F1F0 ATP synthase subunit C **Family:**F1F0 ATP synthase subunit C
18	c2d4yA_	Alignment		53.0	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 1; **PDBTitle:** crystal structure of a 49k fragment of hap1 (flgk)
19	c3g67A_	Alignment		51.8	5	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima
20	d1txka2	Alignment		50.8	24	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
21	c1kmiZ_	Alignment	not modelled	49.0	12	**PDB header:**signaling protein **Chain:** Z: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of an e.coli chemotaxis protein, chez
22	c1wsrA_	Alignment	not modelled	48.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of human t-protein of glycine cleavage2 system
23	d1fftb2	Alignment	not modelled	46.5	21	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
24	c1txkA_	Alignment	not modelled	46.2	24	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
25	c3lnrA_	Alignment	not modelled	40.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**aerotaxis transducer aer2; **PDBTitle:** crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
26	d1vp7b_	Alignment	not modelled	36.6	17	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
27	c2ch7A_	Alignment	not modelled	35.6	7	**PDB header:**chemotaxis **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
28	c1wyyB_	Alignment	not modelled	35.1	15	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein

29	c1ei3E_	Alignment	not modelled	35.0	9	**PDB header:** **PDB COMPND:**
30	c1deqF_	Alignment	not modelled	31.7	6	**PDB header:** **PDB COMPND:**
31	c2vs0B_	Alignment	not modelled	31.2	9	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
32	d1jz8a3	Alignment	not modelled	30.3	11	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
33	c3gvmA_	Alignment	not modelled	30.1	8	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
34	d1eq1a_	Alignment	not modelled	29.0	10	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
35	d1yq2a3	Alignment	not modelled	27.6	15	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
36	d1szia_	Alignment	not modelled	27.3	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain **Family:**Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
37	c1kqsA_	Alignment	not modelled	27.0	19	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**ribosomal protein l2; **PDBTitle:** the haloarcula marismortui 50s complexed with a2 pretranslocational intermediate in protein synthesis
38	d1ucua_	Alignment	not modelled	26.9	8	**Fold:**Phase 1 flagellin **Superfamily:**Phase 1 flagellin **Family:**Phase 1 flagellin
39	d1g4us1	Alignment	not modelled	25.6	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain
40	d1v58a2	Alignment	not modelled	25.5	17	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
41	c1deqO_	Alignment	not modelled	24.7	14	**PDB header:** **PDB COMPND:**
42	c2kebA_	Alignment	not modelled	24.6	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
43	c3k8wA_	Alignment	not modelled	22.6	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin n20c45
44	c3izcN_	Alignment	not modelled	22.4	16	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
45	c2kbbA_	Alignment	not modelled	21.9	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the talin rod domain, 1655-1822
46	d1im3d_	Alignment	not modelled	21.5	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Cytomegalovirus protein US2
47	d2axte1	Alignment	not modelled	21.3	15	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome b559 subunits **Family:**Cytochrome b559 subunits
48	c2d4xA_	Alignment	not modelled	21.3	6	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 3; **PDBTitle:** crystal structure of a 26k fragment of hap3 (flgl)
49	d1gtra1	Alignment	not modelled	21.0	16	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain
50	c2nrjA_	Alignment	not modelled	21.0	15	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hbl b protein; **PDBTitle:** crystal structure of hemolysin binding component from2 bacillus cereus
51	d1lvfa_	Alignment	not modelled	20.4	11	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
52	c2gl2B_	Alignment	not modelled	20.2	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
53	c3ghgK_	Alignment	not modelled	18.4	8	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
54	c1x31A_	Alignment	not modelled	18.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
						PDB header:structural genomics, unknown function

55	c3o0lB_	Alignment	not modelled	18.1	12	**Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution
56	d1dowa_	Alignment	not modelled	17.9	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
57	c4a19F_	Alignment	not modelled	17.4	19	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl14; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
58	c3k8vB_	Alignment	not modelled	17.0	10	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin n20c20
59	d1wrda1	Alignment	not modelled	16.9	18	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
60	d2zjrs1	Alignment	not modelled	16.3	20	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
61	d1bhua_	Alignment	not modelled	16.1	23	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Streptomyces metalloproteinase inhibitor, SMPI
62	d1dova_	Alignment	not modelled	15.5	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
63	c1vloA_	Alignment	not modelled	15.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminomethyltransferase; **PDBTitle:** crystal structure of aminomethyltransferase (t protein;2 tetrahydrofolate-dependent) of glycine cleavage system (np417381)3 from escherichia coli k12 at 1.70 a resolution
64	c3o5aB_	Alignment	not modelled	15.4	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diheme cytochrome c napb; **PDBTitle:** crystal structure of partially reduced periplasmic nitrate reductase2 from cupriavidus necator using ionic liquids
65	c1rkeA_	Alignment	not modelled	14.9	10	**PDB header:**cell adhesion, structural protein **Chain:** A: **PDB Molecule:**vinculin; **PDBTitle:** human vinculin head (1-258) in complex with human vinculin2 tail (879-1066)
66	c3ojaB_	Alignment	not modelled	14.8	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
67	d2cp5a1	Alignment	not modelled	14.7	11	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
68	d1bhga2	Alignment	not modelled	14.6	16	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
69	c3ls1A_	Alignment	not modelled	13.4	18	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
70	d1pa4a_	Alignment	not modelled	13.0	44	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
71	d1feua_	Alignment	not modelled	13.0	14	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
72	c3iz5N_	Alignment	not modelled	12.8	14	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
73	c2dq3A_	Alignment	not modelled	12.8	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
74	c2kncA_	Alignment	not modelled	12.6	35	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
75	c1vlyA_	Alignment	not modelled	12.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**unknown protein from 2d-page; **PDBTitle:** crystal structure of a putative aminomethyltransferase (ygfz) from2 escherichia coli at 1.30 a resolution
76	c1zvzA_	Alignment	not modelled	12.6	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**vinculin; **PDBTitle:** vinculin head (0-258) in complex with the talin rod residue2 820-844
77	d2cp2a1	Alignment	not modelled	11.9	16	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
78	d1kkga_	Alignment	not modelled	11.8	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Ribosome-binding factor A, RbfA **Family:**Ribosome-binding factor A, RbfA
79	c3nmbA_	Alignment	not modelled	11.0	64	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sugar hydrolase; **PDBTitle:** crystal structure of a putative sugar hydrolase (bacova_03189) from2 bacteroides ovatus at 2.40 a resolution
80	d1wa8a1	Alignment	not modelled	10.8	11	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
						Fold:PEBP-like

81	d1qoua_	Alignment	not modelled	10.5	11	**Superfamily:**PEBP-like **Family:**Phosphatidylethanolamine binding protein
82	c3hd7A_	Alignment	not modelled	10.4	8	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
83	d2coza1	Alignment	not modelled	10.4	14	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
84	d1sj8a2	Alignment	not modelled	10.4	10	**Fold:**I/LWEQ domain **Superfamily:**I/LWEQ domain **Family:**I/LWEQ domain
85	c1exdA_	Alignment	not modelled	10.3	19	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase
86	c1m57H_	Alignment	not modelled	10.1	18	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
87	c3dshA_	Alignment	not modelled	10.0	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**interferon regulatory factor 5; **PDBTitle:** crystal structure of dimeric interferon regulatory factor 5 (irf-5)2 transactivation domain
88	c1urqC_	Alignment	not modelled	9.9	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**synaptosomal-associated protein 25; **PDBTitle:** crystal structure of neuronal q-snares in complex with2 r-snare motif of tomosyn
89	d1t01a1	Alignment	not modelled	9.9	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
90	c3lw9B_	Alignment	not modelled	9.8	24	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**invasion protein inva; **PDBTitle:** structure of a cytoplasmic domain of salmonella inva
91	c1zoqA_	Alignment	not modelled	9.8	25	**PDB header:**transcription/transferase **Chain:** A: **PDB Molecule:**interferon regulatory factor 3; **PDBTitle:** irf3-cbp complex
92	c2kzfA_	Alignment	not modelled	9.7	13	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**ribosome-binding factor a; **PDBTitle:** solution nmr structure of the thermotoga maritima protein tm0855 a2 putative ribosome binding factor a
93	c3h3lB_	Alignment	not modelled	9.7	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sugar hydrolase; **PDBTitle:** crystal structure of putative sugar hydrolase (yp_001304206.1) from2 parabacteroides distasonis atcc 8503 at 1.59 a resolution
94	c2dnxA_	Alignment	not modelled	9.6	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**syntaxin-12; **PDBTitle:** solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
95	d1wgba_	Alignment	not modelled	9.5	13	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
96	c3hbkA_	Alignment	not modelled	9.4	55	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of putative glycosyl hydrolase, was domain of2 unknown function (duf1080) (yp_001302580.1) from parabacteroides3 distasonis atcc 8503 at 2.36 a resolution
97	c1cn3F_	Alignment	not modelled	9.4	25	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fragment of coat protein vp2; **PDBTitle:** interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
98	c1pkvB_	Alignment	not modelled	9.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin
99	c1pkvA_	Alignment	not modelled	9.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin