Phyre2

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Description	P75933
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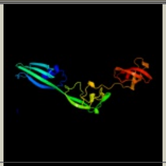
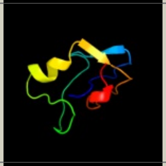
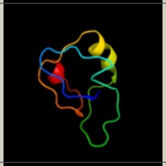
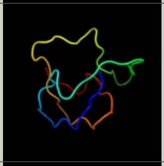
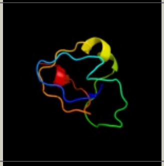
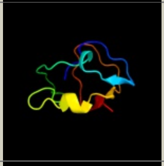
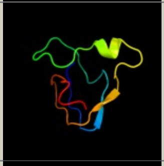
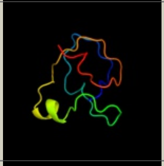
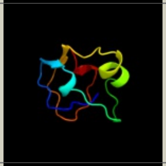
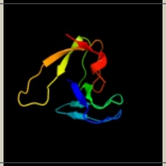
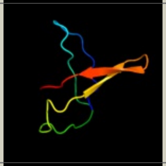
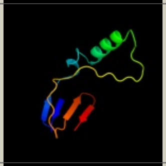
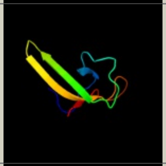
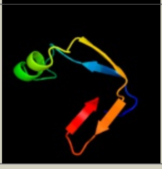
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3frnA_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flga; **PDBTitle:** crystal structure of flagellar protein flga from thermotoga maritima2 msb8
2	d2zdra1	Alignment		97.9	21	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
3	d1vlia1	Alignment		97.8	15	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
4	c3g8rA_	Alignment		97.6	22	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
5	c1xuzA_	Alignment		97.6	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
6	c1vliA_	Alignment		97.3	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
7	d1opsa_	Alignment		97.2	19	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
8	d1c8aa2	Alignment		97.0	23	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
9	c1wvoA_	Alignment		96.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sialic acid synthase; **PDBTitle:** solution structure of rsgi ruh-029, an antifreeze protein2 like domain in human n-acetylneuraminic acid phosphate3 synthase gene.
10	d3nlaa_	Alignment		96.6	19	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
11	c1c8aA_	Alignment		96.3	23	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**protein (antifreeze protein type iii); **PDBTitle:** nmr structure of intramolecular dimer antifreeze protein2 rd3, 40 sa structures

12	d1ucsa_	Alignment		86.7	19	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
13	d1hg7a_	Alignment		86.3	19	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
14	c3k3sG_	Alignment		48.4	19	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**altronate hydrolase; **PDBTitle:** crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
15	c1iq8B_	Alignment		44.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**archaeosine trna-guanine transglycosylase; **PDBTitle:** crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
16	d1yloa1	Alignment		43.8	19	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
17	d1sv6a_	Alignment		40.1	18	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
18	c2eb5D_	Alignment		36.4	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2-oxo-hept-3-ene-1,7-dioate hydratase; **PDBTitle:** crystal structure of hpcg complexed with oxalate
19	d2q07a1	Alignment		34.7	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
20	c4a1cS_	Alignment		33.4	19	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rpl26; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
21	c3l53F_	Alignment	not modelled	32.2	16	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative fumarylacetoacetate isomerase/hydrolase; **PDBTitle:** crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
22	d2zjrr1	Alignment	not modelled	31.3	23	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
23	d1vqot1	Alignment	not modelled	30.1	23	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
24	c3iz5Y_	Alignment	not modelled	29.5	19	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l26 (l24p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
25	c3f9xA_	Alignment	not modelled	26.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd8; **PDBTitle:** structural insights into lysine multiple methylation by set2 domain methyltransferases, set8-y334f / h4-lys20me2 /3 adohcy
26	d2g46a1	Alignment	not modelled	21.8	27	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Viral histone H3 Lysine 27 Methyltransferase
27	d2f69a2	Alignment	not modelled	21.1	7	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
28	c2w5zA_	Alignment	not modelled	20.7	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase hrx; **PDBTitle:** ternary complex of the mixed lineage leukaemia (mll1) set2 domain with the cofactor product s-adenosylhomocysteine3

						and histone peptide.
29	d1nr9a_	Alignment	not modelled	20.0	13	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
30	c3opeA_	Alignment	not modelled	19.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable histone-lysine n-methyltransferase ash1l; **PDBTitle:** structural basis of auto-inhibitory mechanism of histone2 methyltransferase
31	c3n71A_	Alignment	not modelled	18.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone lysine methyltransferase smyd1; **PDBTitle:** crystal structure of cardiac specific histone methyltransferase smyd1
32	d2grea1	Alignment	not modelled	18.6	18	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
33	d1vhea1	Alignment	not modelled	18.5	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
34	d1h3ia2	Alignment	not modelled	17.8	7	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
35	d1pgsa1	Alignment	not modelled	16.7	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**PHM/PNGase F **Family:**Glycosyl-asparaginase
36	c3cw1D_	Alignment	not modelled	16.2	18	**PDB header:**splicing **Chain:** D: **PDB Molecule:**small nuclear ribonucleoprotein sm d3; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
37	c3bw1A_	Alignment	not modelled	16.1	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm3; **PDBTitle:** crystal structure of homomeric yeast lsm3 exhibiting novel octameric2 ring organisation
38	c3h6lA_	Alignment	not modelled	15.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd2; **PDBTitle:** methyltransferase domain of human set domain-containing protein 2
39	c3ooiA_	Alignment	not modelled	15.6	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-36 and h4 **PDBTitle:** crystal structure of human histone-lysine n-methyltransferase nsd1 set2 domain in complex with s-adenosyl-l-methionine
40	c1xqhE_	Alignment	not modelled	13.8	7	**PDB header:**transferase **Chain:** E: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-4 **PDBTitle:** crystal structure of a ternary complex of the2 methyltransferase set9 (also known as set7/9) with a p533 peptide and sah
41	d1ml9a_	Alignment	not modelled	13.7	27	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
42	c3s8pA_	Alignment	not modelled	13.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv420h1; **PDBTitle:** crystal structure of the set domain of human histone-lysine n-2 methyltransferase suv420h1 in complex with s-adenosyl-l-methionine
43	d1u6ea2	Alignment	not modelled	13.3	25	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
44	c2o8jC_	Alignment	not modelled	13.0	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-9 **PDBTitle:** human euchromatic histone methyltransferase 2
45	c3pgwB_	Alignment	not modelled	12.8	19	**PDB header:**splicing/dna/rna **Chain:** B: **PDB Molecule:**sm b; **PDBTitle:** crystal structure of human u1 snrnp
46	d1d3bb_	Alignment	not modelled	12.6	19	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
47	c1b34A_	Alignment	not modelled	12.5	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (small nuclear ribonucleoprotein sm d1); **PDBTitle:** crystal structure of the d1d2 sub-complex from the human snrnp core2 domain
48	d1b34a_	Alignment	not modelled	12.5	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
49	c3rq4A_	Alignment	not modelled	12.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv420h2; **PDBTitle:** crystal structure of suppressor of variegation 4-20 homolog 2
50	c3bo5A_	Alignment	not modelled	12.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setmar; **PDBTitle:** crystal structure of methyltransferase domain of human histone-lysine2 n-methyltransferase setmar
51	c2pn0D_	Alignment	not modelled	12.1	21	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea

52	d1vcpa_	Alignment	not modelled	12.0	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
53	c3swnA_	Alignment	not modelled	11.8	23	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
54	d1cxla3	Alignment	not modelled	11.8	20	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
55	c3swnC_	Alignment	not modelled	11.5	14	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**u6 snrna-associated sm-like protein lsm7; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
56	d2fwka1	Alignment	not modelled	11.4	23	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
57	c3mekA_	Alignment	not modelled	11.3	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 3; **PDBTitle:** crystal structure of human histone-lysine n-2 methyltransferase smyd3 in complex with s-adenosyl-l-3 methionine
58	c2qpwA_	Alignment	not modelled	11.2	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pr domain zinc finger protein 2; **PDBTitle:** methyltransferase domain of human pr domain-containing2 protein 2
59	d1i4k1_	Alignment	not modelled	11.0	23	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
60	c2r3aA_	Alignment	not modelled	11.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv39h2; **PDBTitle:** methyltransferase domain of human suppressor of variegation2 3-9 homolog 2
61	c1mvhA_	Alignment	not modelled	10.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cryptic loci regulator 4; **PDBTitle:** structure of the set domain histone lysine2 methyltransferase clr4
62	d1mvha_	Alignment	not modelled	10.5	20	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Histone lysine methyltransferases
63	d1d3ba_	Alignment	not modelled	10.4	18	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
64	d1wyka_	Alignment	not modelled	10.3	22	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
65	c3qwvA_	Alignment	not modelled	10.2	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 2; **PDBTitle:** crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy
66	c3pgwQ_	Alignment	not modelled	10.0	19	**PDB header:**splicing/dna/rna **Chain:** Q: **PDB Molecule:**sm b; **PDBTitle:** crystal structure of human u1 snrnp
67	d1i8fa_	Alignment	not modelled	9.8	10	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
68	c3rayA_	Alignment	not modelled	9.7	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pr domain-containing protein 11; **PDBTitle:** crystal structure of methyltransferase domain of human pr domain-2 containing protein 11
69	d1u0ma2	Alignment	not modelled	9.5	22	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
70	c3ep0A_	Alignment	not modelled	9.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pr domain zinc finger protein 12; **PDBTitle:** methyltransferase domain of human pr domain-containing2 protein 12
71	d1mgqa_	Alignment	not modelled	9.2	9	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
72	c1kxfA_	Alignment	not modelled	9.1	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sindbis virus capsid protein; **PDBTitle:** sindbis virus capsid, (wild-type) residues 1-264,2 tetragonal crystal form (form ii)
73	d1ep5a_	Alignment	not modelled	9.0	16	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
74	d1r3ea1	Alignment	not modelled	8.7	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
75	c3cw1Z_	Alignment	not modelled	8.7	14	**PDB header:**splicing **Chain:** Z: **PDB Molecule:**small nuclear ribonucleoprotein f; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
76	c3cw1A_	Alignment	not modelled	8.6	19	**PDB header:**splicing **Chain:** A: **PDB Molecule:**small nuclear ribonucleoprotein-associated proteins b and **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
						PDB header:rna binding protein **Chain:** T: **PDB Molecule:**u6 snrna-associated sm-like protein

77	c3swnT_	Alignment	not modelled	8.5	18	lsm6; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
78	d1svdm1	Alignment	not modelled	8.5	12	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
79	d1qexa_	Alignment	not modelled	8.5	15	**Fold:**gp9 **Superfamily:**gp9 **Family:**gp9
80	d1d3bl_	Alignment	not modelled	8.2	19	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
81	d1y0ya1	Alignment	not modelled	8.2	21	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
82	d1jbma_	Alignment	not modelled	8.0	9	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
83	d1bxni_	Alignment	not modelled	8.0	27	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
84	d2h2ja2	Alignment	not modelled	7.9	31	**Fold:**beta-clip **Superfamily:**SET domain **Family:**RuBisCo LSMT catalytic domain
85	d1th7a1	Alignment	not modelled	7.9	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
86	c3lazB_	Alignment	not modelled	7.8	32	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-galactarate dehydratase; **PDBTitle:** the crystal structure of the n-terminal domain of d-2 galactarate dehydratase from escherichia coli cft073
87	d1bwvs_	Alignment	not modelled	7.6	27	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
88	c3cw15_	Alignment	not modelled	7.5	14	**PDB header:**splicing **Chain:** 5: **PDB Molecule:**small nuclear ribonucleoprotein g; **PDB Fragment:**residues 1-215; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
89	d3bmva3	Alignment	not modelled	7.4	23	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
90	d1h641_	Alignment	not modelled	7.4	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Sm motif of small nuclear ribonucleoproteins, SNRNP
91	c3izcs_	Alignment	not modelled	7.3	16	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein rpl20 (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
92	d1gtta1	Alignment	not modelled	7.3	32	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
93	d1lcka1	Alignment	not modelled	7.1	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
94	c3bboW_	Alignment	not modelled	7.0	29	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**ribosomal protein l24; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
95	d1pama3	Alignment	not modelled	7.0	21	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
96	d1gtta2	Alignment	not modelled	6.8	26	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
97	d1wh3a_	Alignment	not modelled	6.8	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
98	d1sawa_	Alignment	not modelled	6.5	14	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
99	c2dxcG_	Alignment	not modelled	6.4	20	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form