Phyre^2

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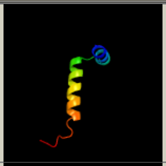
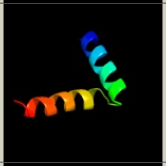
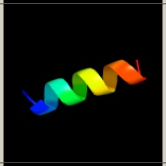
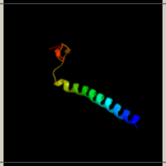
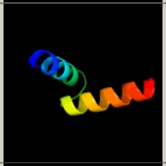
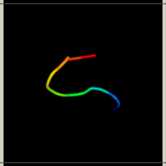
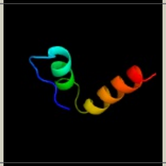
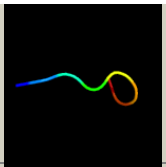
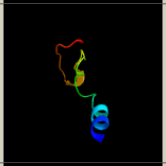
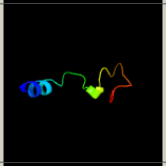
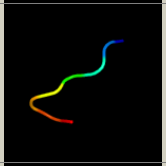
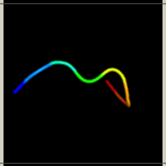
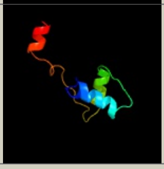
Description	RVBD1982A_(RVBD1982A)_2225849_2226109
Date	Mon Aug 5 13:25:08 BST 2019
Unique Job ID	be3b779c37a42b81

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	Alignment		55.9	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	c6gtsC_	Alignment		44.7	15	**PDB header:**transcription **Chain:** C: **PDB Molecule:**duf1778 domain-containing protein; **PDBTitle:** structure of the atat-atar complex bound dna
3	c6ajnF_	Alignment		42.5	15	**PDB header:**toxin **Chain:** F: **PDB Molecule:**duf1778 domain-containing protein; **PDBTitle:** crystal structure of atatr bound with accoa
4	c6a7vU_	Alignment		40.6	42	**PDB header:**toxin/antitoxin **Chain:** U: **PDB Molecule:**antitoxin vapb11; **PDBTitle:** crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
5	c2kelB_	Alignment		39.8	33	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
6	c4ui9E_	Alignment		36.4	24	**PDB header:**cell cycle **Chain:** E: **PDB Molecule:**anaphase-promoting complex subunit 16; **PDBTitle:** atomic structure of the human anaphase-promoting complex
7	c2q2kB_	Alignment		28.7	31	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of nucleic-acid binding protein
8	d1y9ba1	Alignment		28.4	18	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VCA0319-like
9	c3zifM_	Alignment		25.1	67	**PDB header:**virus **Chain:** M: **PDB Molecule:**penton protein; **PDBTitle:** cryo-em structures of two intermediates provide insight into2 adenovirus assembly and disassembly
10	c2q2kA_	Alignment		24.4	31	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of nucleic-acid binding protein
11	c2k9iB_	Alignment		23.6	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**uncharacterized protein orf56; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus

12	c2ov2O_	Alignment		21.1	25	**PDB header:**protein binding/transferase **Chain:** O: **PDB Molecule:**serine/threonine-protein kinase pak 4; **PDBTitle:** the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
13	c2rt4A_	Alignment		20.9	86	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**af.2a1; **PDBTitle:** nmr structure of designed protein, af.2a1, (ensembles)
14	c4rg9S_	Alignment		19.7	40	**PDB header:**protein binding **Chain:** S: **PDB Molecule:**anaphase-promoting complex subunit 16; **PDBTitle:** crystal structure of apc3-apc16 complex (selenomethionine derivative)
15	c4rg6S_	Alignment		19.6	40	**PDB header:**protein binding **Chain:** S: **PDB Molecule:**anaphase-promoting complex subunit 16; **PDBTitle:** crystal structure of apc3-apc16 complex
16	c2odbB_	Alignment		19.3	38	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
17	c5fmzB_	Alignment		17.9	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rna-directed rna polymerase catalytic subunit; **PDBTitle:** crystal structure of influenza b polymerase with bound 5' vrna
18	c4wsaB_	Alignment		17.7	13	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**rna-directed rna polymerase catalytic subunit; **PDBTitle:** crystal structure of influenza b polymerase bound to the vrna promoter2 (flub1 form)
19	c1e0aB_	Alignment		17.4	50	**PDB header:**signalling protein/kinase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase
20	c1t3mA_	Alignment		15.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
21	d2a4da1	Alignment	not modelled	15.6	33	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
22	c1ceeB_	Alignment	not modelled	15.5	50	**PDB header:**structural protein regulation **Chain:** B: **PDB Molecule:**wiskott-aldrich syndrome protein wasp; **PDBTitle:** solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
23	c2xc7A_	Alignment	not modelled	15.4	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**phosphorylated adapter rna export protein; **PDBTitle:** solution structure of phax-rbd in complex with ssrna
24	d1o4xa1	Alignment	not modelled	14.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
25	c3k0yA_	Alignment	not modelled	13.8	27	**PDB header:**toxin **Chain:** A: **PDB Molecule:**putative toxin related protein; **PDBTitle:** crystal structure of putative toxin related protein (yp_001303978.1)2 from parabacteroides distasonis atcc 8503 at 2.16 a resolution
26	c6cmxA_	Alignment	not modelled	12.5	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**teneurin-2; **PDBTitle:** human teneurin 2 extra-cellular region
27	c4aqqA_	Alignment	not modelled	12.5	56	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**l2 protein iii (penton base); **PDBTitle:** dodecahedron formed of penton base protein from adenovirus ad3
28	c3iynM_	Alignment	not modelled	12.5	67	**PDB header:**virus **Chain:** M: **PDB Molecule:**penton base protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5

29	c2bldD_	Alignment	not modelled	12.3	67	**PDB header:**virus **Chain:** D: **PDB Molecule:**penton protein; **PDBTitle:** the quasi-atomic model of human adenovirus type 52 capsid (part 1)
30	c3eabK_	Alignment	not modelled	12.1	40	**PDB header:**cell cycle **Chain:** K: **PDB Molecule:**chmp1b; **PDBTitle:** crystal structure of spastin mit in complex with escrt iii
31	c4zp3N_	Alignment	not modelled	12.0	25	**PDB header:**signaling protein **Chain:** N: **PDB Molecule:**a-kinase anchor protein 7 isoforms alpha and beta; **PDBTitle:** akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
32	c4zp3M_	Alignment	not modelled	11.9	22	**PDB header:**signaling protein **Chain:** M: **PDB Molecule:**a-kinase anchor protein 7 isoforms alpha and beta; **PDBTitle:** akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
33	d3ctaa2	Alignment	not modelled	10.5	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
34	d2bj7a1	Alignment	not modelled	10.1	12	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
35	c4zp3R_	Alignment	not modelled	9.9	25	**PDB header:**signaling protein **Chain:** R: **PDB Molecule:**a-kinase anchor protein 7 isoforms alpha and beta; **PDBTitle:** akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
36	c4zp3O_	Alignment	not modelled	9.9	25	**PDB header:**signaling protein **Chain:** O: **PDB Molecule:**a-kinase anchor protein 7 isoforms alpha and beta; **PDBTitle:** akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
37	c4zp3Q_	Alignment	not modelled	9.9	25	**PDB header:**signaling protein **Chain:** Q: **PDB Molecule:**a-kinase anchor protein 7 isoforms alpha and beta; **PDBTitle:** akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
38	d2gg2a1	Alignment	not modelled	9.2	15	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
39	c5bsaF_	Alignment	not modelled	9.1	67	**PDB header:**transcription regulator **Chain:** F: **PDB Molecule:**protein spt2 homolog; **PDBTitle:** structure of histone h3/h4 in complex with spt2
40	c5bs7F_	Alignment	not modelled	9.1	67	**PDB header:**transcription regulator **Chain:** F: **PDB Molecule:**protein spt2 homolog; **PDBTitle:** structure of histone h3/h4 in complex with spt2
41	d1ffgb_	Alignment	not modelled	8.2	41	**Fold:**Ferredoxin-like **Superfamily:**CheY-binding domain of CheA **Family:**CheY-binding domain of CheA
42	c2akfB_	Alignment	not modelled	8.1	38	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
43	c2akfC_	Alignment	not modelled	8.1	38	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
44	c2akfA_	Alignment	not modelled	8.1	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**coronin-1a; **PDBTitle:** crystal structure of the coiled-coil domain of coronin 1
45	d2hi6a1	Alignment	not modelled	8.0	50	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
46	c6ci7A_	Alignment	not modelled	7.9	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**ycao; **PDBTitle:** the structure of ycao from methanopyrus kandleri bound with amppcp and2 mg2+
47	d1j74a_	Alignment	not modelled	7.9	35	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
48	c5h7pB_	Alignment	not modelled	7.9	30	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein-sorting-associated protein 46; **PDBTitle:** nmr structure of the vta1ntd-did2(176-204) complex
49	c1a0oH_	Alignment	not modelled	7.8	41	**PDB header:**chemotaxis **Chain:** H: **PDB Molecule:**chea; **PDBTitle:** chey-binding domain of chea in complex with chey
50	c4v1af_	Alignment	not modelled	7.7	16	**PDB header:**ribosome **Chain:** F: **PDB Molecule:** **PDBTitle:** structure of the large subunit of the mammalian mitoribosome, part 22 of 2
51	d2vbua1	Alignment	not modelled	7.6	40	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
52	c4zp3P_	Alignment	not modelled	7.6	19	**PDB header:**signaling protein **Chain:** P: **PDB Molecule:**a-kinase anchor protein 7 isoforms alpha and beta; **PDBTitle:** akap18:pka-riialpha structure reveals crucial anchor points for2 recognition of regulatory subunits of pka
53	c5ydcA_	Alignment	not modelled	7.6	33	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator rv1828; **PDBTitle:** crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis

54	c2bj3D_	Alignment	not modelled	7.4	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
55	d2hzaa1	Alignment	not modelled	7.2	24	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
56	c3g8qA_	Alignment	not modelled	6.8	56	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**predicted rna-binding protein, contains thump **PDBTitle:** a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
57	c6honD_	Alignment	not modelled	6.7	80	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**ccr4-not transcription complex subunit 4, isoform l; **PDBTitle:** drosophila not4 cbm peptide bound to human caf40
58	c6homB_	Alignment	not modelled	6.7	80	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ccr4-not transcription complex subunit 4, isoform l; **PDBTitle:** drosophila not4 cbm peptide bound to human caf40
59	c6honB_	Alignment	not modelled	6.7	80	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**ccr4-not transcription complex subunit 4, isoform l; **PDBTitle:** drosophila not4 cbm peptide bound to human caf40
60	d1efva2	Alignment	not modelled	6.6	44	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
61	c3ol4B_	Alignment	not modelled	6.6	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
62	c6homD_	Alignment	not modelled	6.5	80	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**ccr4-not transcription complex subunit 4, isoform l; **PDBTitle:** drosophila not4 cbm peptide bound to human caf40
63	c4fo7B_	Alignment	not modelled	6.3	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** pseudomonas aeruginosa metap, in mn form
64	c5v2gB_	Alignment	not modelled	6.1	30	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**20-mer peptide; **PDBTitle:** de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
65	c5v2gA_	Alignment	not modelled	6.1	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**20-mer peptide; **PDBTitle:** de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
66	c5v2gC_	Alignment	not modelled	6.1	30	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**20-mer peptide; **PDBTitle:** de novo design of novel covalent constrained meso-size peptide2 scaffolds with unique tertiary structures
67	c3viqC_	Alignment	not modelled	6.1	13	**PDB header:**recombination activator **Chain:** C: **PDB Molecule:**swi5-dependent recombination dna repair protein 1; **PDBTitle:** crystal structure of swi5-sfr1 complex from fission yeast
68	c2gezE_	Alignment	not modelled	6.1	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
69	c1zvvA_	Alignment	not modelled	5.9	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**glucose-resistance amylase regulator; **PDBTitle:** crystal structure of a ccpa-crh-dna complex
70	c5nocA_	Alignment	not modelled	5.9	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**stage 0 sporulation protein j; **PDBTitle:** solution nmr structure of the c-terminal domain of parb (spo0j)
71	d1p94a_	Alignment	not modelled	5.9	22	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
72	c3mx6A_	Alignment	not modelled	5.8	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
73	c2kvcA_	Alignment	not modelled	5.7	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
74	c3iacA_	Alignment	not modelled	5.7	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucuronate isomerase; **PDBTitle:** 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
75	c2wuhB_	Alignment	not modelled	5.6	33	**PDB header:**receptor/peptide **Chain:** B: **PDB Molecule:**collagen peptide; **PDBTitle:** crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
76	c2wuhC_	Alignment	not modelled	5.6	33	**PDB header:**receptor/peptide **Chain:** C: **PDB Molecule:**collagen peptide; **PDBTitle:** crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
77	d1efpa2	Alignment	not modelled	5.3	33	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**C-terminal domain of the electron transfer flavoprotein alpha subunit
78	c3u5eS_	Alignment	not modelled	5.2	21	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l20-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a