Phyre^2

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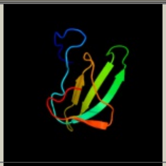
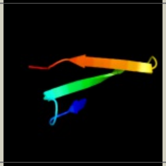
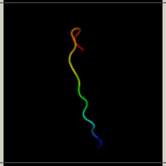
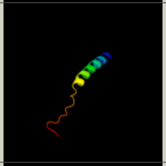
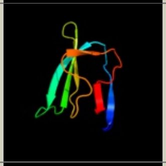
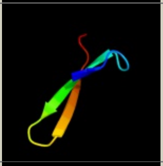
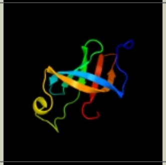
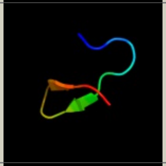
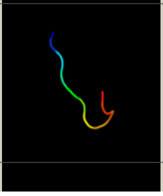
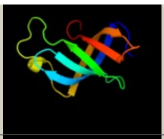
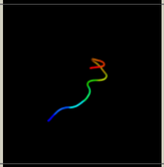
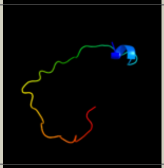
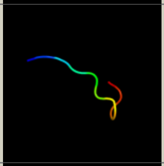
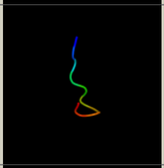
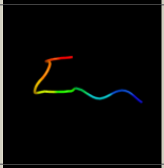
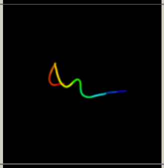
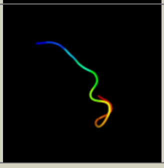
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gu1A_	Alignment		49.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
2	c3k8rA_	Alignment		48.0	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution
3	d1q46a2	Alignment		47.5	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
4	d1e32a1	Alignment		39.5	25	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
5	c2dk6A_	Alignment		39.3	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**parp11 protein; **PDBTitle:** solution structure of wwe domain in poly (adp-ribose)2 polymerase family, member 11 (parp 11)
6	d1k75a_	Alignment		35.1	14	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
7	c2hsiB_	Alignment		33.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
8	c2x8nA_	Alignment		26.2	25	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**cv0863; **PDBTitle:** solution nmr structure of uncharacterized protein cv08632 from chromobacterium violaceum. northeast structural3 genomics target (nesg) target cvt3. ocsp4 target cv0863.
9	c1q46A_	Alignment		26.1	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 alpha subunit; **PDBTitle:** crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
10	d2d8xa2	Alignment		17.1	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
11	c1yc0I_	Alignment		16.0	45	**PDB header:**hydrolase/inhibitor **Chain:** I: **PDB Molecule:**kunitz-type protease inhibitor 1; **PDBTitle:** short form hgfa with first kunitz domain from hai-1

12	c1yz6A_	Alignment		15.5	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 alpha **PDBTitle:** crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
13	d1dema_	Alignment		15.0	18	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
14	d1faki_	Alignment		14.9	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
15	c2kkuA_	Alignment		14.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein af2351 from archaeoglobus2 fulgidus. northeast structural genomics consortium target3 att9/ontario center for structural proteomics target af2351
16	d1tfxc_	Alignment		13.8	18	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
17	d1bika1	Alignment		13.7	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
18	d1bika2	Alignment		13.2	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
19	d1brbi_	Alignment		13.0	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
20	d1bpia_	Alignment		12.7	18	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
21	d1w36b3	Alignment	not modelled	12.5	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
22	d1dtxa_	Alignment	not modelled	12.2	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
23	c3bpjD_	Alignment	not modelled	12.0	24	**PDB header:**translation **Chain:** D: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit j; **PDBTitle:** crystal structure of human translation initiation factor 3, subunit 12 alpha
24	c1y62E_	Alignment	not modelled	11.7	30	**PDB header:**toxin **Chain:** E: **PDB Molecule:**conkunitzin-s1; **PDBTitle:** a 2.4 crystal structure of conkunitzin-s1, a novel kunitz-2 fold cone snail neurotoxin.
25	d1irha_	Alignment	not modelled	10.5	30	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
26	d1dtka_	Alignment	not modelled	10.5	18	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
27	d1shpa_	Alignment	not modelled	10.4	29	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
28	d1uuba_	Alignment	not modelled	10.1	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
29	d1p2ji_	Alignment	not modelled	10.1	18	**Fold:**BPTI-like **Superfamily:**BPTI-like

						Family: Small Kunitz-type inhibitors & BPTI-like toxins
30	d1go3e1	Alignment	not modelled	10.0	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
31	c1tocR_	Alignment	not modelled	10.0	30	**PDB header:**complex (hydrolase/inhibitor) **Chain:** R: **PDB Molecule:**ornithodorin; **PDBTitle:** structure of serine proteinase
32	d2brfa1	Alignment	not modelled	9.8	22	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
33	d2j7ja3	Alignment	not modelled	9.8	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
34	d1bunb_	Alignment	not modelled	9.7	30	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
35	d1jc6a_	Alignment	not modelled	9.1	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
36	d2z0sa1	Alignment	not modelled	9.1	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
37	d1n7oa3	Alignment	not modelled	9.0	60	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hyaluronate lyase-like, central domain
38	d1g6xa_	Alignment	not modelled	8.7	18	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
39	c3bybB_	Alignment	not modelled	8.7	18	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**textilinin; **PDBTitle:** crystal structure of textilinin-1, a kunitz-type serine2 protease inhibitor from the australian common brown snake3 venom
40	d1hn0a4	Alignment	not modelled	8.6	40	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hyaluronate lyase-like, central domain
41	d1aapa_	Alignment	not modelled	8.6	40	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
42	c3hizB_	Alignment	not modelled	8.5	22	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
43	d1f1sa4	Alignment	not modelled	8.3	40	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hyaluronate lyase-like, central domain
44	d2ahob2	Alignment	not modelled	8.3	9	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
45	d1ujra_	Alignment	not modelled	8.2	23	**Fold:**WWE domain **Superfamily:**WWE domain **Family:**WWE domain
46	d1x1ia3	Alignment	not modelled	8.1	60	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hyaluronate lyase-like, central domain
47	d3ctka1	Alignment	not modelled	7.9	24	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Plant cytotoxins
48	d1zr0b1	Alignment	not modelled	7.8	40	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
49	d1wjia_	Alignment	not modelled	7.7	41	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
50	c3kyeC_	Alignment	not modelled	7.7	26	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**roadblock/lc7 domain, robl_lc7; **PDBTitle:** crystal structure of roadblock/lc7 domain from streptomyces2 avermitilis
51	d1rwha3	Alignment	not modelled	7.7	60	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hyaluronate lyase-like, central domain
52	d1cb8a3	Alignment	not modelled	7.6	60	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Hyaluronate lyase-like, central domain
53	d1ld6a_	Alignment	not modelled	7.6	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
54	d1ejmb_	Alignment	not modelled	7.5	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
55	c2ba1B_	Alignment	not modelled	7.5	15	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
56	d1di2a_	Alignment	not modelled	7.4	11	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)

57	d1adza_	Alignment	not modelled	7.4	20	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
58	d2b2ca1	Alignment	not modelled	7.3	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Spermidine synthase
59	d1ktha_	Alignment	not modelled	7.1	40	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
60	c3tekA_	Alignment	not modelled	7.0	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
61	c2l3iA_	Alignment	not modelled	7.0	100	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**aoxki4a, antimicrobial peptide in spider venom; **PDBTitle:** oxki4a, spider derived antimicrobial peptide
62	d2ba0a1	Alignment	not modelled	6.8	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	d1f2fa_	Alignment	not modelled	6.6	22	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
64	d1bf0a_	Alignment	not modelled	6.6	10	**Fold:**BPTI-like **Superfamily:**BPTI-like **Family:**Small Kunitz-type inhibitors & BPTI-like toxins
65	c2kcrA_	Alignment	not modelled	6.6	30	**PDB header:**toxin **Chain:** A: **PDB Molecule:**anntoxin; **PDBTitle:** solution structure of anntoxin
66	d1kl9a2	Alignment	not modelled	6.6	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
67	c3tr9A_	Alignment	not modelled	6.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
68	c2ddiA_	Alignment	not modelled	6.5	30	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wap, follistatin/kazal, immunoglobulin, kunitz **PDBTitle:** nmr structure of the second kunitz domain of human wfikkn1
69	d1sdda2	Alignment	not modelled	6.3	50	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
70	d2je6i1	Alignment	not modelled	6.2	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
71	c2odyF_	Alignment	not modelled	6.1	27	**PDB header:**blood clotting/blood clotting inhibitor **Chain:** F: **PDB Molecule:**boophilin; **PDBTitle:** thrombin-bound boophilin displays a functional and accessible2 reactive-site loop
72	d1bz7a1	Alignment	not modelled	6.1	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
73	d1mnda2	Alignment	not modelled	5.9	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
74	c1q8kA_	Alignment	not modelled	5.9	11	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2 **PDBTitle:** solution structure of alpha subunit of human eif2
75	c2jufA_	Alignment	not modelled	5.8	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**p53-associated parkin-like cytoplasmic protein; **PDBTitle:** nmr solution structure of parc cph domain. nesg target2 hr3443b/sgc-toronto
76	d2eyva1	Alignment	not modelled	5.5	22	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
77	c2jo7A_	Alignment	not modelled	5.4	24	**PDB header:**surface active protein **Chain:** A: **PDB Molecule:**glycosylphosphatidylinositol-anchored merozoite **PDBTitle:** solution structure of the adhesion protein bd37 from2 babesia divergens
78	c1facA_	Alignment	not modelled	5.4	50	**PDB header:**coagulation factor **Chain:** A: **PDB Molecule:**coagulation factor viii; **PDBTitle:** coagulation factor viii, nmr, 1 structure
79	d1qe3a_	Alignment	not modelled	5.4	33	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
80	c3ayhA_	Alignment	not modelled	5.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc9; **PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
81	d1d0xa2	Alignment	not modelled	5.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
82	d2i27n1	Alignment	not modelled	5.2	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin

						Family:V set domains (antibody variable domain-like)
83	d1il1b1	Alignment	not modelled	5.1	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
84	c2kz5A_	Alignment	not modelled	5.1	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor nf-e2 45 kda subunit; **PDBTitle:** solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
85	d1ouoa_	Alignment	not modelled	5.0	14	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Endonuclease I