Phyre^2

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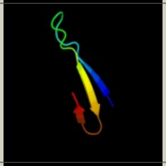
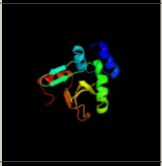
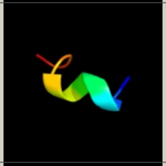
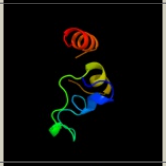
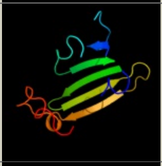
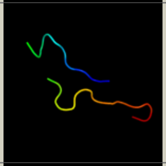
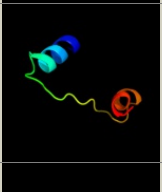
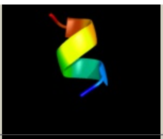
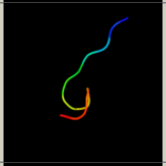
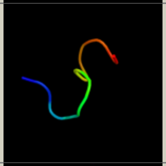
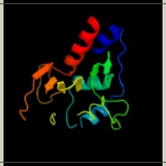
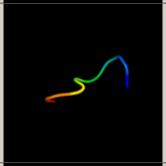
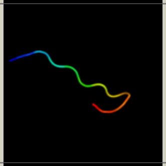
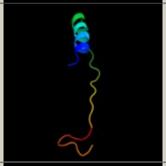
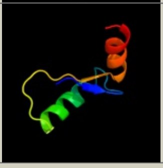
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2prva1	Alignment		83.6	10	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
2	c3dsmA_	Alignment		64.3	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bacuni_02894; **PDBTitle:** crystal structure of the surface layer protein bacuni_02894 from2 bacteroides uniformis, northeast structural genomics consortium3 target btr193d.
3	d2paga1	Alignment		49.3	23	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
4	c3d5pB_	Alignment		23.1	10	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**putative glucan synthesis regulator of smi1/knr4 family; **PDBTitle:** crystal structure of a putative glucan synthesis regulator of2 smi1/knr4 family (bf1740) from bacteroides fragilis nctc 9343 at 1.453 a resolution
5	c1jrjA_	Alignment		23.1	33	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
6	c1d0rA_	Alignment		21.7	40	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
7	d2hy5c1	Alignment		17.7	27	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like
8	c2vt8B_	Alignment		15.4	20	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**proteasome inhibitor pi31 subunit; **PDBTitle:** structure of a conserved dimerisation domain within fbox72 and pi31
9	c2dk7A_	Alignment		14.8	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation regulator 1; **PDBTitle:** solution structure of ww domain in transcription elongation2 regulator 1
10	c3mbqC_	Alignment		14.3	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase; **PDBTitle:** crystal structure of deoxyuridine 5-triphosphate nucleotidohydrolase2 from brucella melitensis, orthorhombic crystal form
11	c1r0lD_	Alignment		13.9	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph

12	c1nauA_	Alignment		13.6	38	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
13	d2rm0w1	Alignment		13.6	42	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
14	c1zr7A_	Alignment		13.1	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**huntingtin-interacting protein hypa/fbp11; **PDBTitle:** solution structure of the first ww domain of fbp11
15	d2icga1	Alignment		13.0	13	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
16	c2uuvC_	Alignment		12.9	33	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase; **PDBTitle:** alkyldihydroxyacetonephosphate synthase in p1
17	d1ywia1	Alignment		12.5	33	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
18	c1ywjA_	Alignment		12.4	33	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**formin-binding protein 3; **PDBTitle:** structure of the fbp11ww1 domain
19	c3iuzA_	Alignment		12.2	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative glyoxalase superfamily protein; **PDBTitle:** crystal structure of putative glyoxalase superfamily protein2 (yp_299723.1) from ralstonia eutropha jmp134 at 1.90 a resolution
20	d1zxoa1	Alignment		12.1	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
21	d1zr7a1	Alignment	not modelled	11.5	33	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
22	c1bh0A_	Alignment	not modelled	11.3	50	**PDB header:**synthetic hormone **Chain:** A: **PDB Molecule:**glucagon; **PDBTitle:** structure of a glucagon analog
23	d1o6wa2	Alignment	not modelled	11.2	50	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
24	d1qw9a2	Alignment	not modelled	11.1	47	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
25	c3ks8D_	Alignment	not modelled	11.1	16	**PDB header:**viral protein/rna **Chain:** D: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** crystal structure of reston ebolavirus vp35 rna binding2 domain in complex with 18bp dsrna
26	d1zbsa2	Alignment	not modelled	10.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
27	c3fkeB_	Alignment	not modelled	10.7	16	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**polymerase cofactor vp35; **PDBTitle:** structure of the ebola vp35 interferon inhibitory domain
28	c2eghA_	Alignment	not modelled	10.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
						PDB header:translation regulation/hydrolase

29	c3mcaA_	Alignment	not modelled	10.7	22	**Chain:** A: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
30	d1o6wa1	Alignment	not modelled	10.5	27	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
31	c3a14B_	Alignment	not modelled	10.4	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
32	c3e53A_	Alignment	not modelled	10.2	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**fatty-acid-coa ligase fadd28; **PDBTitle:** crystal structure of n-terminal domain of a fatty acyl amp2 ligase faal28 from mycobacterium tuberculosis
33	d1xdpa3	Alignment	not modelled	9.8	18	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
34	d1iloa_	Alignment	not modelled	9.8	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
35	c2zxqA_	Alignment	not modelled	9.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** crystal structure of endo-alpha-n-acetylgalactosaminidase2 from bifidobacterium longum (engbf)
36	c3gafF_	Alignment	not modelled	9.6	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**7-alpha-hydroxysteroid dehydrogenase; **PDBTitle:** 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
37	d2c7fa2	Alignment	not modelled	9.3	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
38	d1r0ka3	Alignment	not modelled	9.0	30	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
39	d2dk1a1	Alignment	not modelled	8.8	25	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
40	c2qkmG_	Alignment	not modelled	8.4	22	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**spbc3b9.21 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
41	d1q67a_	Alignment	not modelled	8.3	22	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Dcp1
42	c2dk1A_	Alignment	not modelled	8.0	25	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**ww domain-binding protein 4; **PDBTitle:** solution structure of ww domain in ww domain binding2 protein 4 (wbp-4)
43	c2w4lC_	Alignment	not modelled	8.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** human dcmp deaminase
44	c1q67B_	Alignment	not modelled	7.9	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**decapping protein involved in mrna degradation- **PDBTitle:** crystal structure of dcp1p
45	c2y3rC_	Alignment	not modelled	7.9	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**taml; **PDBTitle:** structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
46	c3muwE_	Alignment	not modelled	7.9	67	**PDB header:**virus **Chain:** E: **PDB Molecule:**structural polyprotein; **PDBTitle:** pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
47	c1bmxA_	Alignment	not modelled	7.9	44	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**human immunodeficiency virus type 1 capsid; **PDBTitle:** hiv-1 capsid protein major homology region peptide analog,2 nmr, 8 structures
48	c1z8yE_	Alignment	not modelled	7.8	67	**PDB header:**virus **Chain:** E: **PDB Molecule:**spike glycoprotein e1; **PDBTitle:** mapping the e2 glycoprotein of alphaviruses
49	c1ld4O_	Alignment	not modelled	7.8	67	**PDB header:**virus **Chain:** O: **PDB Molecule:**spike glycoprotein e1; **PDBTitle:** placement of the structural proteins in sindbis virus
50	c2alaA_	Alignment	not modelled	7.4	67	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**structural polyprotein (p130); **PDBTitle:** crystal structure of the semliki forest virus envelope protein e1 in2 its monomeric conformation.
51	d2alaa2	Alignment	not modelled	7.4	67	**Fold:**Viral glycoprotein, central and dimerisation domains **Superfamily:**Viral glycoprotein, central and dimerisation domains **Family:**Viral glycoprotein, central and dimerisation domains
52	c1t5qA_	Alignment	not modelled	7.3	38	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**gastric inhibitory polypeptide; **PDBTitle:** solution structure of gip(1-30)amide in tfe/water
53	c3n42F_	Alignment	not modelled	7.3	67	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**e1 envelope glycoprotein; **PDBTitle:** crystal structures of the mature envelope glycoprotein complex (furin2 cleavage) of chikungunya virus.
54	c2xfcD_	Alignment	not modelled	7.3	67	**PDB header:**virus **Chain:** D: **PDB Molecule:**e1 envelope glycoprotein; **PDBTitle:** the chikungunya e1 e2 envelope glycoprotein complex fit into2 the semliki forest virus cryo-em map
						PDB header:virus

55	c2xfbF_	Alignment	not modelled	7.2	67	**Chain:** F: **PDB Molecule:**e1 envelope glycoprotein; **PDBTitle:** the chikungunya e1 e2 envelope glycoprotein complex fit into2 the sindbis virus cryo-em map
56	d1q0qa3	Alignment	not modelled	7.2	24	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
57	c3tu8A_	Alignment	not modelled	7.2	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**burkholderia lethal factor 1 (blf1); **PDBTitle:** crystal structure of the burkholderia lethal factor 1 (blf1)
58	c3j0cG_	Alignment	not modelled	7.1	67	**PDB header:**virus **Chain:** G: **PDB Molecule:**e1 envelope glycoprotein; **PDBTitle:** models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
59	d1ccwb_	Alignment	not modelled	6.7	37	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Glutamate mutase, large subunit
60	c3mzlH_	Alignment	not modelled	6.6	22	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**protein transport protein sec31; **PDBTitle:** sec13/sec31 edge element, loop deletion mutant
61	c2xhfA_	Alignment	not modelled	6.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin 5; **PDBTitle:** crystal structure of peroxiredoxin 5 from alvinella pompejana
62	c3muuA_	Alignment	not modelled	6.5	67	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**structural polyprotein; **PDBTitle:** crystal structure of the sindbis virus e2-e1 heterodimer at low ph
63	c6rlxB_	Alignment	not modelled	6.5	58	**PDB header:**hormone(muscle relaxant) **Chain:** B: **PDB Molecule:**relaxin, b-chain; **PDBTitle:** x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
64	d3er7a1	Alignment	not modelled	6.5	24	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Exig0174-like
65	c2hvwC_	Alignment	not modelled	6.5	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deoxycytidylate deaminase; **PDBTitle:** crystal structure of dcmp deaminase from streptococcus2 mutans
66	d1y9ia_	Alignment	not modelled	6.3	19	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
67	d1yt3a2	Alignment	not modelled	6.2	13	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
68	d1cqqa_	Alignment	not modelled	6.2	36	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
69	d1twfb_	Alignment	not modelled	6.1	50	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta
70	c3eukL_	Alignment	not modelled	5.9	14	**PDB header:**cell cycle **Chain:** L: **PDB Molecule:**chromosome partition protein muke; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
71	d1vq2a_	Alignment	not modelled	5.6	33	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
72	c2l5aA_	Alignment	not modelled	5.6	20	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein cse4, protein scm3, **PDBTitle:** structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
73	d2bsya1	Alignment	not modelled	5.5	25	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
74	c2kruA_	Alignment	not modelled	5.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** solution nmr structure of the pcp_red domain of light-2 independent protochlorophyllide reductase subunit b from3 chlorobium tepidum. northeast structural genomics4 consortium target ctr69a (casp target)
75	c2obuA_	Alignment	not modelled	5.2	38	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**gastric inhibitory polypeptide; **PDBTitle:** solution structure of gip in tfe/water
76	d2arca_	Alignment	not modelled	5.1	15	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
77	c3fqgA_	Alignment	not modelled	5.1	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein din1; **PDBTitle:** crystal structure of the s. pombe rai1
78	d2a8na1	Alignment	not modelled	5.1	24	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
79	d1rfza_	Alignment	not modelled	5.1	42	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
						PDB header:unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein g8a1p1:

80	c1zxoB_	Alignment	not modelled	5.1	16	**PDBTitle:** x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.