Phyre^2

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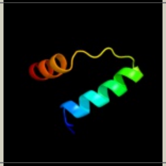
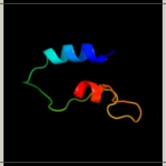
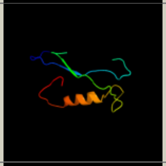
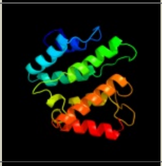
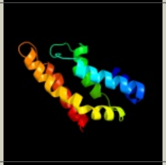
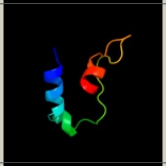
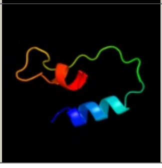
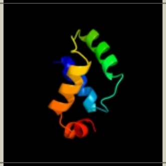
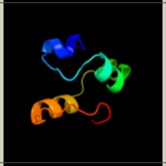
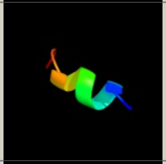
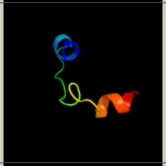
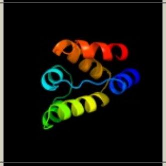
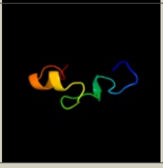
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1x5bA_	Alignment		75.9	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2; **PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
2	d1dvpa1	Alignment		61.5	9	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
3	c3zyqA_	Alignment		47.8	17	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
4	d1elka_	Alignment		42.7	10	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
5	d2ezha_	Alignment		42.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
6	c2w36B_	Alignment		40.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
7	c3i26C_	Alignment		39.9	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hemagglutinin-esterase; **PDBTitle:** structure of bovine torovirus hemagglutinin-esterase
8	d1ujka_	Alignment		37.9	12	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
9	c3onlB_	Alignment		37.1	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**epsin-3; **PDBTitle:** yeast ent3_enth-vti1p_habc complex structure
10	c3gocB_	Alignment		36.9	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
11	c3ga2A_	Alignment		36.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624

12	d1oz9a_	Alignment		34.1	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
13	d2ezia_	Alignment		33.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
14	c2r18A_	Alignment		31.5	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid assembly protein vp3; **PDBTitle:** structural insights into the multifunctional protein vp3 of2 birnaviruses
15	d1xm5a_	Alignment		31.1	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
16	d1tvia_	Alignment		30.3	42	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
17	d1dp7p_	Alignment		29.3	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**P4 origin-binding domain-like
18	d1cy5a_	Alignment		28.9	7	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**Caspase recruitment domain, CARD
19	c1xaxA_	Alignment		27.1	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
20	c3sqgE_	Alignment		23.1	27	**PDB header:**transferase **Chain:** E: **PDB Molecule:**methyl-coenzyme m reductase, beta subunit; **PDBTitle:** crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats
21	d1t1ua2	Alignment	not modelled	22.0	19	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
22	c2eqoA_	Alignment	not modelled	21.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 3-interacting **PDBTitle:** solution structure of the stn_traf3ip1_nd domain of2 interleukin 13 receptor alpha 1-binding protein-1 [homo3 sapiens]
23	d1dmga_	Alignment	not modelled	21.2	14	**Fold:**Ribosomal protein L4 **Superfamily:**Ribosomal protein L4 **Family:**Ribosomal protein L4
24	c3pvlA_	Alignment	not modelled	20.5	14	**PDB header:**motor protein/protein transport **Chain:** A: **PDB Molecule:**myosin viia isoform 1; **PDBTitle:** structure of myosin viia myth4-ferm-sh3 in complex with the cen1 of2 sans
25	c3ghgK_	Alignment	not modelled	20.0	31	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
26	d2opla1	Alignment	not modelled	19.5	19	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
27	d1ndba2	Alignment	not modelled	19.3	20	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
28	c1h0mD_	Alignment	not modelled	19.2	10	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
						PDB header:transcription

29	c1zljE_	Alignment	not modelled	19.0	7	**Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
30	c1hbmE_	Alignment	not modelled	18.0	33	**PDB header:**methanogenesis **Chain:** E: **PDB Molecule:**methyl-coenzyme m reductase i beta subunit; **PDBTitle:** methyl-coenzyme m reductase enzyme product complex
31	c3edeB_	Alignment	not modelled	18.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cyclomaltodextrinase; **PDBTitle:** structural base for cyclodextrin hydrolysis
32	d1a04a1	Alignment	not modelled	17.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
33	d1h3ga3	Alignment	not modelled	17.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
34	d1hbnb1	Alignment	not modelled	17.7	33	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
35	c2vgqA_	Alignment	not modelled	17.3	19	**PDB header:**immune system/transport **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, **PDBTitle:** crystal structure of human ips-1 card
36	c1deqO_	Alignment	not modelled	17.2	33	**PDB header:** **PDB COMPND:**
37	d1nm8a2	Alignment	not modelled	17.0	20	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
38	d1fs1b2	Alignment	not modelled	16.6	33	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
39	c2gdvA_	Alignment	not modelled	16.1	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sucrose phosphorylase; **PDBTitle:** sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
40	d1puza_	Alignment	not modelled	15.7	15	**Fold:**YgfY-like **Superfamily:**YgfY-like **Family:**YgfY-like
41	d1or7a1	Alignment	not modelled	15.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
42	c2vdcF_	Alignment	not modelled	15.0	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glutamate synthase [nadph] large chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
43	d1nexa2	Alignment	not modelled	14.9	33	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
44	d2i3oa1	Alignment	not modelled	14.5	10	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
45	c2w31A_	Alignment	not modelled	13.9	7	**PDB header:**oxygen transport **Chain:** A: **PDB Molecule:**globin; **PDBTitle:** globin domain of geobacter sulfurreducens globin-coupled2 sensor
46	c1e6yE_	Alignment	not modelled	13.9	33	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**methyl-coenzyme m reductase i beta subunit; **PDBTitle:** methyl-coenzyme m reductase from methanosarcina barkeri
47	d1xl7a2	Alignment	not modelled	13.8	21	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
48	d2hc5a1	Alignment	not modelled	13.8	13	**Fold:**FlaG-like **Superfamily:**FlaG-like **Family:**FlaG-like
49	c2rnqA_	Alignment	not modelled	13.6	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation factor iie subunit **PDBTitle:** solution structure of the c-terminal acidic domain of tfiie2 alpha
50	c2jtxA_	Alignment	not modelled	13.6	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation factor iie subunit **PDBTitle:** nmr structure of the tfiie-alpha carboxyl terminus
51	c1dvpA_	Alignment	not modelled	13.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
52	c2lcvA_	Alignment	not modelled	13.1	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
53	d1e6yb1	Alignment	not modelled	13.1	33	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-

						terminal domain
54	c3g5bA_	Alignment	not modelled	13.0	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**netrin receptor unc5b; **PDBTitle:** the structure of unc5b cytoplasmic domain
55	c3jroC_	Alignment	not modelled	13.0	19	**PDB header:**transport protein, structural protein **Chain:** C: **PDB Molecule:**nucleoporin nup84; **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
56	c1xrxD_	Alignment	not modelled	12.9	29	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
57	d1xrxa1	Alignment	not modelled	12.9	29	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
58	c3qp5C_	Alignment	not modelled	12.7	12	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
59	d1e6vb1	Alignment	not modelled	12.6	33	**Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain **Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
60	d1v74b_	Alignment	not modelled	12.3	25	**Fold:**Four-helical up-and-down bundle **Superfamily:**Colicin D immunity protein **Family:**Colicin D immunity protein
61	d1hw6a_	Alignment	not modelled	12.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
62	d1l3la1	Alignment	not modelled	12.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
63	c2krfB_	Alignment	not modelled	12.0	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
64	d1fsea_	Alignment	not modelled	11.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
65	c3lvzA_	Alignment	not modelled	11.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**blr6230 protein; **PDBTitle:** new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
66	c3sztB_	Alignment	not modelled	11.8	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
67	c2jq6A_	Alignment	not modelled	11.3	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**eh domain-containing protein 1; **PDBTitle:** structure of eh-domain of ehd1
68	d1q5ma_	Alignment	not modelled	11.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
69	c2jpcA_	Alignment	not modelled	11.1	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
70	c2hpcF_	Alignment	not modelled	11.1	38	**PDB header:**blood clotting **Chain:** F: **PDB Molecule:**fibrinogen, gamma polypeptide; **PDBTitle:** crystal structure of fragment d from human fibrinogen complexed with2 gly-pro-arg-pro-amide.
71	d1gvia3	Alignment	not modelled	11.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
72	c3fiaA_	Alignment	not modelled	10.9	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**intersectin-1; **PDBTitle:** crystal structure of the eh 1 domain from human intersectin-2 1 protein. northeast structural genomics consortium target3 hr3646e.
73	c1qhoA_	Alignment	not modelled	10.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
74	d2pbea1	Alignment	not modelled	10.8	18	**Fold:**PAP/OAS1 substrate-binding domain **Superfamily:**PAP/OAS1 substrate-binding domain **Family:**AadK C-terminal domain-like
75	c3kblA_	Alignment	not modelled	10.8	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**female germline-specific tumor suppressor gld-1; **PDBTitle:** crystal structure of the gld-1 homodimerization domain from2 caenorhabditis elegans n169a mutant at 2.28 a resolution
76	d2ve8a1	Alignment	not modelled	10.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
77	c2qy7A_	Alignment	not modelled	10.6	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**clathrin interactor 1; **PDBTitle:** crystal structure of human epsinr enth domain
78	d1q7ha2	Alignment	not modelled	10.6	46	**Fold:**Cystatin-like **Superfamily:**Pre-PUA domain **Family:**Hypothetical protein Ta1423, N-terminal domain
						Fold: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin

79	d1tuka1	Alignment	not modelled	10.6	27	**Superfamily:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin **Family:**Plant lipid-transfer and hydrophobic proteins
80	d1c01a_	Alignment	not modelled	10.5	27	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Plant antimicrobial protein MIAMP1
81	d1nn7a_	Alignment	not modelled	10.3	14	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
82	d1j20a2	Alignment	not modelled	10.3	17	**Fold:**Argininosuccinate synthetase, C-terminal domain **Superfamily:**Argininosuccinate synthetase, C-terminal domain **Family:**Argininosuccinate synthetase, C-terminal domain
83	d1s1ga_	Alignment	not modelled	10.3	14	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
84	d2esha1	Alignment	not modelled	10.3	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
85	c3bvhC_	Alignment	not modelled	10.2	31	**PDB header:**blood clotting **Chain:** C: **PDB Molecule:**fibrinogen gamma chain; **PDBTitle:** crystal structure of recombinant gammad364a fibrinogen fragment d with2 the peptide ligand gly-pro-arg-pro-amide
86	c2kmgA_	Alignment	not modelled	10.2	26	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**klca; **PDBTitle:** the structure of the klca and ardb proteins show a novel2 fold and antirestriction activity against type i dna3 restriction systems in vivo but not in vitro
87	c2rnjA_	Alignment	not modelled	10.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
88	d1ofda3	Alignment	not modelled	10.1	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
89	c1nexC_	Alignment	not modelled	10.0	36	**PDB header:**ligase, cell cycle **Chain:** C: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
90	c2q0oA_	Alignment	not modelled	10.0	2	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
91	d2c9wc1	Alignment	not modelled	10.0	36	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**BTB/POZ domain
92	c1llm1A_	Alignment	not modelled	9.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-dependent glutamate synthase; **PDBTitle:** structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
93	d1ug7a_	Alignment	not modelled	9.8	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain from hypothetical 2610208m17rik protein **Family:**Domain from hypothetical 2610208m17rik protein
94	c3k8kB_	Alignment	not modelled	9.8	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
95	d1ht6a2	Alignment	not modelled	9.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
96	c2cblA_	Alignment	not modelled	9.8	15	**PDB header:**complex (proto-oncogene/peptide) **Chain:** A: **PDB Molecule:**proto-oncogene cbl; **PDBTitle:** n-terminal domain of cbl in complex with its binding site2 on zap-70
97	d1inza_	Alignment	not modelled	9.8	13	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**ENTH domain
98	d1ea9c3	Alignment	not modelled	9.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
99	c3excX_	Alignment	not modelled	9.7	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of the rna'se sso8090 from sulfolobus solfataricus