Phyre2

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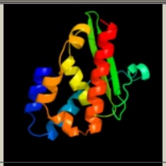
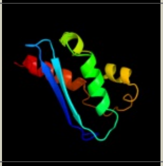
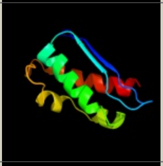
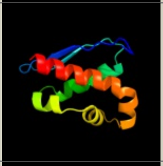
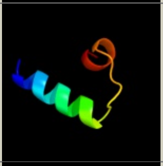
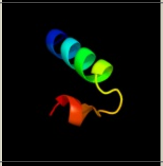
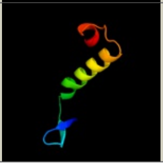
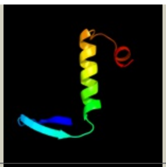
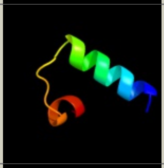
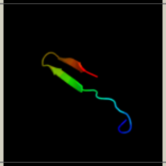
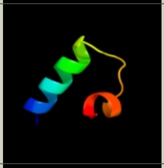
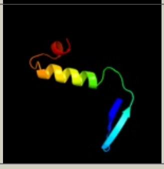
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mzga_	Alignment		100.0	97	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
2	d1ni7a_	Alignment		100.0	33	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
3	c1wloA_	Alignment		100.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sufe protein; **PDBTitle:** solution structure of the hypothetical protein from thermus2 thermophilus hb8
4	d1r9pa_	Alignment		96.2	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
5	d1wfza_	Alignment		94.3	12	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
6	c2z7eB_	Alignment		90.5	11	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
7	d1xjsa_	Alignment		78.7	14	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
8	c1s2nB_	Alignment		55.1	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**extracellular subtilisin-like serine proteinase; **PDBTitle:** crystal strucure of a cold adapted subtilisin-like serine proteinase
9	d1gcia_	Alignment		54.8	21	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
10	c2b6nA_	Alignment		53.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**proteinase k; **PDBTitle:** the 1.8 a crystal structure of a proteinase k like enzyme from a2 psychrotroph serratia species
11	d1r0re_	Alignment		53.1	16	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases

12	c2iy9A_	Alignment		51.7	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**suba; **PDBTitle:** crystal structure of the a-subunit of the ab5 toxin from e.2 coli
13	c2w2qA_	Alignment		49.8	24	**PDB header:**hydrolase/receptor **Chain:** A: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** pcsk9-deltac d374h mutant bound to wt egf-a of ldlr
14	d1su0b_	Alignment		49.6	8	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
15	d1pdaa2	Alignment		45.7	29	**Fold:**dsRBD-like **Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain **Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
16	c3f7oB_	Alignment		45.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine protease; **PDBTitle:** crystal structure of cuticle-degrading protease from paecilomyces2 lilacinus (pl646)
17	c2oxaA_	Alignment		45.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**extracellular serine protease; **PDBTitle:** crystal structure of serine protease of aeromonas sobria
18	c2qq4A_	Alignment		45.0	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster biosynthesis protein iscu; **PDBTitle:** crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (ttha1736) from thermus thermophilus hb8
19	d1p8ja2	Alignment		43.9	24	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
20	d2ixta1	Alignment		42.4	16	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
21	d1gtka2	Alignment	not modelled	41.6	29	**Fold:**dsRBD-like **Superfamily:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain **Family:**Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
22	d1to2e_	Alignment	not modelled	40.4	16	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
23	d2id4a2	Alignment	not modelled	36.8	16	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
24	d1v6ca_	Alignment	not modelled	36.8	12	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
25	c1r64A_	Alignment	not modelled	33.9	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**kexin; **PDBTitle:** the 2.2 a crystal structure of kex2 protease in complex with ac-arg-2 glu-lys-boroarg peptidyl boronic acid inhibitor
26	c1p8jB_	Alignment	not modelled	32.1	24	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**furin precursor; **PDBTitle:** crystal structure of the proprotein convertase furin
27	d1gnsa_	Alignment	not modelled	30.5	14	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
28	d1bh6a_	Alignment	not modelled	29.7	20	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
						Fold: Skp1 dimerisation domain-like

29	d1nexa1	Alignment	not modelled	29.0	17	**Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
30	c3qfhE_	Alignment	not modelled	26.5	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**epidermin leader peptide processing serine protease epip; **PDBTitle:** 2.05 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) from staphylococcus aureus.
31	d1fs1b1	Alignment	not modelled	24.7	30	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
32	c3bpsA_	Alignment	not modelled	23.9	24	**PDB header:**hydrolase/lipid transport **Chain:** A: **PDB Molecule:**proprotein convertase subtilisin/kexin type 9; **PDBTitle:** pcsk9:egf-a complex
33	d1fs2b1	Alignment	not modelled	23.3	30	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
34	c3lpcA_	Alignment	not modelled	22.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprb2; **PDBTitle:** crystal structure of a subtilisin-like protease
35	c3n00A_	Alignment	not modelled	22.0	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**rev-erba-alpha; **PDBTitle:** crystal structure of a deletion mutant of human reverba ligand binding2 domain bound with an ncor id1 peptide determined to 2.60a
36	c2ypnA_	Alignment	not modelled	20.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hydroxymethylbilane synthase); **PDBTitle:** hydroxymethylbilane synthase
37	d2olra2	Alignment	not modelled	19.1	16	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
38	d1tlha_	Alignment	not modelled	18.9	29	**Fold:**Anti-sigma factor AsiA **Superfamily:**Anti-sigma factor AsiA **Family:**Anti-sigma factor AsiA
39	d1ii2a2	Alignment	not modelled	17.9	22	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
40	c2yukA_	Alignment	not modelled	17.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
41	d2pwaa1	Alignment	not modelled	16.8	19	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
42	d2ovra1	Alignment	not modelled	16.4	30	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
43	c2gjvF_	Alignment	not modelled	15.9	15	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** crystal structure of a protein of unknown function from salmonella2 typhimurium
44	d2gjva1	Alignment	not modelled	15.6	15	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**STM4215-like
45	d1meea_	Alignment	not modelled	13.5	16	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
46	d1r6va_	Alignment	not modelled	13.4	28	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
47	d2hh6a1	Alignment	not modelled	12.8	16	**Fold:**Left-handed superhelix **Superfamily:**BH3980-like **Family:**BH3980-like
48	c2w0gA_	Alignment	not modelled	12.0	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** hsp90 co-chaperone cdc37
49	c1us7B_	Alignment	not modelled	10.4	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** complex of hsp90 and p50
50	d1us7b_	Alignment	not modelled	10.4	20	**Fold:**Hsp90 co-chaperone CDC37 **Superfamily:**Hsp90 co-chaperone CDC37 **Family:**Hsp90 co-chaperone CDC37
51	c3gq2B_	Alignment	not modelled	10.3	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general vesicular transport factor p115; **PDBTitle:** crystal structure of the dimer of the p115 tether globular head domain
52	c3lysC_	Alignment	not modelled	10.0	9	**PDB header:**recombination **Chain:** C: **PDB Molecule:**prophage pi2 protein 01, integrase; **PDBTitle:** crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
53	d1gm5a1	Alignment	not modelled	9.4	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**RecG, N-terminal domain **Family:**RecG, N-terminal domain
54	d1n83a_	Alignment	not modelled	9.1	15	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
						PDB header:oxidoreductase

55	c2hl7A_	Alignment	not modelled	9.0	23	**Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
56	d1osha_	Alignment	not modelled	9.0	30	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
57	c3t41B_	Alignment	not modelled	8.2	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**epidermin leader peptide processing serine protease epip; **PDBTitle:** 1.95 angstrom resolution crystal structure of epidermin leader peptide2 processing serine protease (epip) s393a mutant from staphylococcus3 aureus
58	c2w3cA_	Alignment	not modelled	8.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**general vesicular transport factor p115; **PDBTitle:** globular head region of the human general vesicular2 transport factor p115
59	d1vdda_	Alignment	not modelled	7.7	26	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
60	c2kvhA_	Alignment	not modelled	7.1	39	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
61	c3e21A_	Alignment	not modelled	7.0	32	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** crystal structure of faf-1 uba domain
62	c3eq1A_	Alignment	not modelled	6.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
63	d1pq9a_	Alignment	not modelled	6.9	12	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
64	c2kykA_	Alignment	not modelled	6.8	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase itchy homolog; **PDBTitle:** the sandwich region between two lmp2a py motif regulates the2 interaction between aip4ww2domain and py motif
65	c2hc4A_	Alignment	not modelled	6.7	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**vitamin d receptor; **PDBTitle:** crystal structure of the lbd of vdr of danio rerio in2 complex with calcitriol
66	d1t7ra_	Alignment	not modelled	6.7	15	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
67	c3i74B_	Alignment	not modelled	6.4	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**subtilisin-like protease; **PDBTitle:** crystal structure of the plant subtilisin-like protease sbt3 in2 complex with a chloromethylketone inhibitor
68	c3dmbA_	Alignment	not modelled	6.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative general stress protein 26 with a pnp-oxidase like **PDBTitle:** crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
69	c3c18B_	Alignment	not modelled	6.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotidyltransferase-like protein; **PDBTitle:** crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution
70	d1fpoa1	Alignment	not modelled	6.3	8	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
71	d1x40a1	Alignment	not modelled	6.2	22	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
72	c2dl0A_	Alignment	not modelled	6.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1
73	d1coka_	Alignment	not modelled	6.1	15	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
74	d1dbia_	Alignment	not modelled	5.9	21	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
75	c2kg5A_	Alignment	not modelled	5.6	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**arf-gap, rho-gap domain, ank repeat and ph **PDBTitle:** nmr solution structure of arap3-sam
76	c3zqpB_	Alignment	not modelled	5.6	13	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**terminase small subunit; **PDBTitle:** crystal structure of the small terminase oligomerization2 domain from a spp1-like bacteriophage
77	c1z5xE_	Alignment	not modelled	5.5	21	**PDB header:**hormone/growth factor receptor **Chain:** E: **PDB Molecule:**ecdysone receptor ligand binding domain; **PDBTitle:** hemipteran ecdysone receptor ligand-binding domain2 complexed with ponasterone a
78	c2eamA_	Alignment	not modelled	5.5	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative 47 kda protein; **PDBTitle:** solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
						PDB header:nuclear receptor

79	c3lbdA_	Alignment	not modelled	5.4	18	**Chain:** A: **PDB Molecule:**retinoic acid receptor gamma; **PDBTitle:** ligand-binding domain of the human retinoic acid receptor2 gamma bound to 9-cis retinoic acid
80	c2ocfA_	Alignment	not modelled	5.2	11	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**estrogen receptor; **PDBTitle:** human estrogen receptor alpha ligand-binding domain in complex with2 estradiol and the e2#23 fn3 monobody
81	c2kw0A_	Alignment	not modelled	5.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli