Phyre^2

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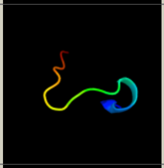
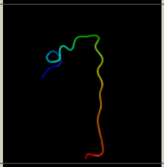
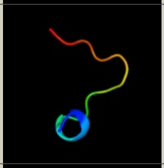
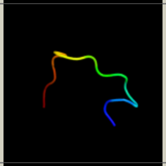
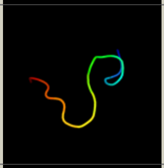
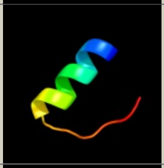
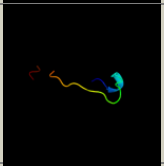
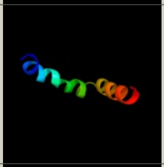
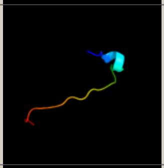
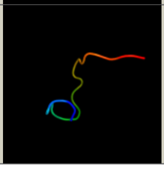
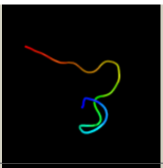
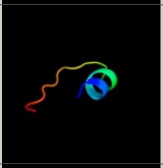
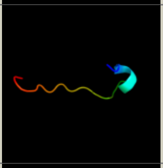
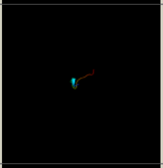
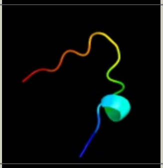
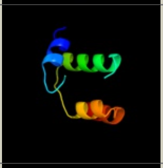
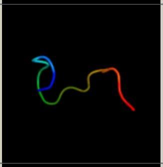
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kuzA_	Alignment		38.4	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**plexin-c1; **PDBTitle:** crystal structure of the ubiquitin like domain of plxnc1
2	c2jphA_	Alignment		38.0	53	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**plexin-b1; **PDBTitle:** nmr solution structure of the rho gtpase binding domain of2 human plexin-b1
3	d1wjna_	Alignment		34.3	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
4	c3h6nA_	Alignment		34.2	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**plexin-d1; **PDBTitle:** crystal structure of the ubiquitin-like domain of plexin d1
5	c3q3jA_	Alignment		33.3	47	**PDB header:**membrane protein/protein binding **Chain:** A: **PDB Molecule:**plexin-a2; **PDBTitle:** crystal structure of plexin a2 rbd in complex with rnd1
6	d1z2ma1	Alignment		21.7	35	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
7	d2odgc1	Alignment		17.2	22	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
8	d1we7a_	Alignment		16.2	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
9	c2wx3A_	Alignment		14.2	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mrna-decapping enzyme 1a; **PDBTitle:** asymmetric trimer of the human dcp1a c-terminal domain
10	d1we6a_	Alignment		14.1	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
11	c1wziA_	Alignment		13.6	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus

12	c3su8X_	Alignment		13.3	53	**PDB header:**apoptosis/signaling protein **Chain:** X: **PDB Molecule:**plexin-b1; **PDBTitle:** crystal structure of a truncated intracellular domain of plexin-b1 in2 complex with rac1
13	d157la_	Alignment		12.9	17	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
14	c2agaA_	Alignment		12.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**machado-joseph disease protein 1; **PDBTitle:** de-ubiquitinating function of ataxin-3: insights from the2 solution structure of the josephin domain
15	d1ogwa_	Alignment		12.1	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
16	c3ig3A_	Alignment		10.1	44	**PDB header:**signaling protein, membrane protein **Chain:** A: **PDB Molecule:**plxna3 protein; **PDBTitle:** crystal strucure of mouse plexin a3 intracellular domain
17	d1zkha1	Alignment		9.7	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
18	d1p37a_	Alignment		9.7	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
19	d1y7ta2	Alignment		9.4	31	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
20	d1i0za2	Alignment		9.4	31	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
21	c3m62B_	Alignment	not modelled	9.2	25	**PDB header:**ligase/protein binding **Chain:** B: **PDB Molecule:**uv excision repair protein rad23; **PDBTitle:** crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of rad23
22	d2f2qa1	Alignment	not modelled	9.1	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
23	c3hm6X_	Alignment	not modelled	9.0	50	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**plexin-b1; **PDBTitle:** crystal structure of the cytoplasmic domain of human plexin b1
24	d1v5oa_	Alignment	not modelled	8.3	44	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
25	d1j8ca_	Alignment	not modelled	8.3	35	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
26	d1b8pa2	Alignment	not modelled	8.0	31	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
27	c3jrnA_	Alignment	not modelled	7.6	27	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**at1g72930 protein; **PDBTitle:** crystal structure of tir domain from arabidopsis thaliana
28	d1oqya4	Alignment	not modelled	7.3	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
29	d9ldta2	Alignment	not modelled	7.0	25	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like

						Family: Lactate & malate dehydrogenases, C-terminal domain
30	d2c5lc1	Alignment	not modelled	6.8	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
31	c2o4wA_	Alignment	not modelled	6.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** t4 lysozyme circular permutant
32	d1wxva1	Alignment	not modelled	6.7	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
33	d1v5ta_	Alignment	not modelled	6.7	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
34	d1icha_	Alignment	not modelled	6.4	29	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
35	c1ichA_	Alignment	not modelled	6.4	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
36	c3pbpL_	Alignment	not modelled	6.1	25	**PDB header:**transport protein,structural protein **Chain:** L: **PDB Molecule:**nucleoporin nup159; **PDBTitle:** structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex
37	d1z2ma2	Alignment	not modelled	6.1	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
38	d1sifa_	Alignment	not modelled	6.1	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
39	d2ihoa2	Alignment	not modelled	6.0	50	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**MOA C-terminal domain-like
40	d1uela_	Alignment	not modelled	6.0	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
41	c2kj6A_	Alignment	not modelled	5.9	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**tubulin folding cofactor b; **PDBTitle:** nmr solution structure of a tubulin folding cofactor b2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3436a
42	c2k25A_	Alignment	not modelled	5.9	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ubb; **PDBTitle:** automated nmr structure of the ubb by fapsy
43	d1l64a_	Alignment	not modelled	5.7	16	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
44	c2l7rA_	Alignment	not modelled	5.7	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin-like protein fubi; **PDBTitle:** solution nmr structure of n-terminal ubiquitin-like domain of fubi, a2 ribosomal protein s30 precursor from homo sapiens. northeast3 structural genomics consortium (nesg) target hr6166
45	d1ldma2	Alignment	not modelled	5.7	25	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
46	d2bh1a1	Alignment	not modelled	5.6	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Cyto-EpsL domain
47	c2kanA_	Alignment	not modelled	5.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ar3433a; **PDBTitle:** solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
48	d1wx8a1	Alignment	not modelled	5.6	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
49	d2ldxa2	Alignment	not modelled	5.4	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
50	d1jtma_	Alignment	not modelled	5.4	18	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
51	c1yx5B_	Alignment	not modelled	5.3	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
52	d1qbaa2	Alignment	not modelled	5.3	12	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Bacterial chitobiase, n-terminal domain
53	d2g7ja1	Alignment	not modelled	5.1	30	**Fold:**Secretion chaperone-like **Superfamily:**YgaC/TfoX-N like **Family:**YgaC-like
54	d1bt0a_	Alignment	not modelled	5.1	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related