Phyre^2

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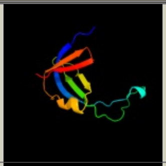
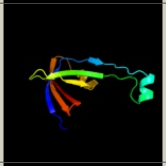
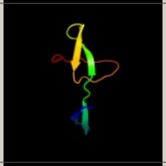
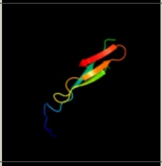
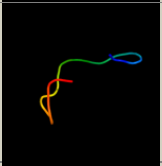
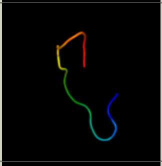
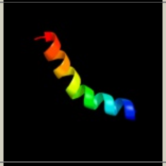
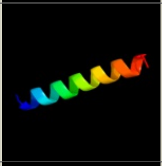
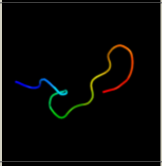
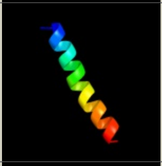
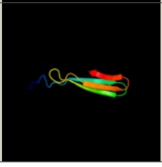
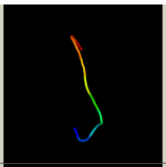
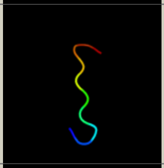
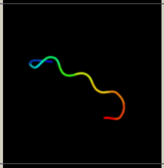
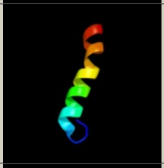
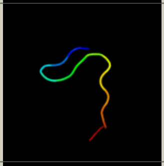
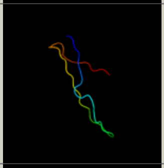
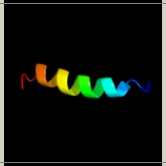
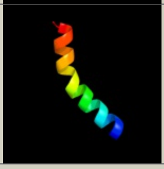
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l0cA_	Alignment		100.0	85	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** solution nmr structure of protein sty4237 (residues 36-120) from2 salmonella enterica, northeast structural genomics consortium target3 slr115
2	c3rd4A_	Alignment		98.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of propen_03304 from proteus penneri atcc 351982 northeast structural genomics consortium target id pvr55
3	c2jysA_	Alignment		70.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protease/reverse transcriptase; **PDBTitle:** solution structure of simian foamy virus (mac) protease
4	c3uajA_	Alignment		18.5	11	**PDB header:**viral protein/immune system **Chain:** A: **PDB Molecule:**envelope protein; **PDBTitle:** crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
5	c2pm5B_	Alignment		17.7	38	**PDB header:**antimicrobial protein **Chain:** B: **PDB Molecule:**neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha **PDBTitle:** human alpha-defensin 1 derivative (hnp1)
6	c2pm5A_	Alignment		17.7	38	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha **PDBTitle:** human alpha-defensin 1 derivative (hnp1)
7	c3sokB_	Alignment		16.5	17	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**fimbrial protein; **PDBTitle:** dichelobacter nodosus pilin fima
8	d2axti1	Alignment		15.4	17	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
9	c2pm1A_	Alignment		14.8	38	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**neutrophil defensin 1 (hnp-1) (hp-1) (hp1) **PDBTitle:** derivative of human alpha-defensin 1 (hnp1)
10	d1oqwa_	Alignment		14.3	17	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
11	c1urzC_	Alignment		13.7	20	**PDB header:**virus/viral protein **Chain:** C: **PDB Molecule:**envelope protein; **PDBTitle:** low ph induced, membrane fusion conformation of the2 envelope protein of tick-borne encephalitis virus

12	c3msuA_	Alignment		12.3	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from francisella tularensis
13	c2h12C_	Alignment		11.9	60	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** structure of acetobacter aceti citrate synthase complexed2 with oxaloacetate and carboxymethyldethia coenzyme a (cmx)
14	d1k3pa_	Alignment		11.4	50	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
15	c3mk7B_	Alignment		11.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit o; **PDBTitle:** the structure of cbb3 cytochrome oxidase
16	c2jufA_	Alignment		10.9	27	**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
17	d1l3wa5	Alignment		10.3	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cadherin-like **Family:**Cadherin
18	d2axtk1	Alignment		9.3	23	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein K, PsbK **Family:**PsbK-like
19	c3a0bk_	Alignment		9.3	19	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
20	d2pila_	Alignment		8.8	17	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**Pilin
21	c3a0bK_	Alignment	not modelled	8.6	19	**PDB header:**electron transport **Chain:** K: **PDB Molecule:**photosystem ii reaction center protein k; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
22	c3pqsA_	Alignment	not modelled	8.6	22	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**transferrin-binding protein; **PDBTitle:** the crystal structures of porcine pathogen aph87_tbpb
23	c2k21A_	Alignment	not modelled	8.1	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
24	d1bdta_	Alignment	not modelled	8.1	71	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
25	c1pi7A_	Alignment	not modelled	8.1	5	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
26	c2gohA_	Alignment	not modelled	8.1	5	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles
27	c1pi8A_	Alignment	not modelled	8.1	5	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** structure of the channel-forming trans-membrane domain of2 virus protein "u" (vpu) from hiv-1
28	c2gofA_	Alignment	not modelled	8.1	5	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** three-dimensional structure of the trans-membrane domain of2 vpu from hiv-1 in aligned phospholipid bicelles

29	c1pjeA_	Alignment	not modelled	8.1	5	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpu protein; **PDBTitle:** structure of the channel-forming trans-membrane domain of2 virus protein "u"(vpu) from hiv-1
30	d1xnea_	Alignment	not modelled	7.8	30	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
31	d1x6va1	Alignment	not modelled	7.5	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
32	c2ky9A_	Alignment	not modelled	7.5	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ydhk; **PDBTitle:** solution nmr structure of ydhk c-terminal domain from b.subtilis,2 northeast structural genomics consortium target target sr518
33	d1b28a_	Alignment	not modelled	7.5	71	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
34	d2jnga1	Alignment	not modelled	7.1	25	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**CPH domain
35	c2ibpB_	Alignment	not modelled	6.7	60	**PDB header:**transferase **Chain:** B: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from pyrobaculum aerophilum
36	d2qqsa2	Alignment	not modelled	6.6	14	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
37	c2l2tA_	Alignment	not modelled	6.4	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
38	c3hoeA_	Alignment	not modelled	6.3	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tbpb; **PDBTitle:** crystal structure of surface lipoprotein
39	c2rddB_	Alignment	not modelled	6.3	9	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
40	d2qqra2	Alignment	not modelled	6.3	16	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
41	d1m56d_	Alignment	not modelled	6.2	19	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
42	c2j7aC_	Alignment	not modelled	6.1	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytochrome c quinol dehydrogenase nrfh; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris
43	d1czpa_	Alignment	not modelled	5.9	4	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
44	d1tula_	Alignment	not modelled	5.8	14	**Fold:**beta-clip **Superfamily:**Tlp20, baculovirus telokin-like protein **Family:**Tlp20, baculovirus telokin-like protein
45	c3pquB_	Alignment	not modelled	5.6	44	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**transferrin binding protein b; **PDBTitle:** the crystal structures of porcine pathogen ash57_tbpb
46	d1x68a1	Alignment	not modelled	5.5	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
47	d1igub_	Alignment	not modelled	5.5	29	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
48	d1o7xa_	Alignment	not modelled	5.4	60	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
49	d1igqa_	Alignment	not modelled	5.4	29	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
50	c2r26C_	Alignment	not modelled	5.3	60	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum