Phyre^2

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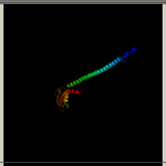
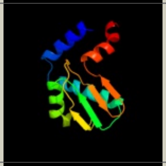
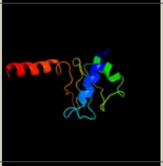
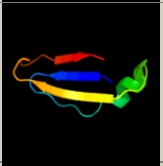
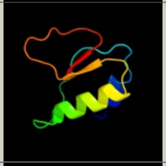
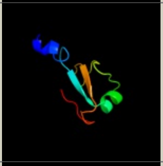
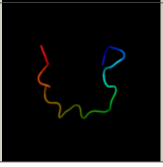
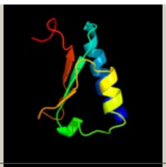
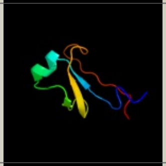
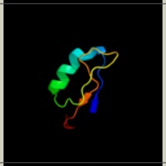
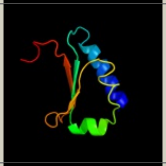
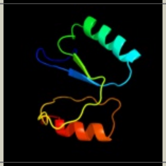
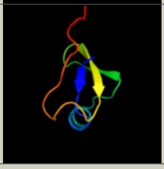
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3k5bE_	Alignment		98.5	14	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
2	d2dm9a1	Alignment		98.3	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**V-type ATPase subunit E-like **Family:**V-type ATPase subunit E
3	c2dm9B_	Alignment		98.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase subunit e; **PDBTitle:** crystal structure of ph1978 from pyrococcus horikoshii ot3
4	c3lg8B_	Alignment		97.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**a-type atp synthase subunit e; **PDBTitle:** crystal structure of the c-terminal part of subunit e (e101-206) from2 methanocaldococcus jannaschii of a1ao atp synthase
5	c2lc0A_	Alignment		90.9	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** rv0020c_nter structure
6	c2c4rL_	Alignment		53.6	17	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
7	c3sftA_	Alignment		23.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
8	c2rrlA_	Alignment		22.6	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar hook-length control protein; **PDBTitle:** solution structure of the c-terminal domain of the flik
9	d3bzka2	Alignment		21.1	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
10	d1y5ia1	Alignment		20.1	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
11	d1zy9a1	Alignment		17.1	22	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**YicI N-terminal domain-like

12	c2e0zA_	Alignment		16.7	10	**PDB header:**virus like particle **Chain:** A: **PDB Molecule:**virus-like particle; **PDBTitle:** crystal structure of virus-like particle from pyrococcus2 furiosus
13	d2jioa1	Alignment		16.5	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
14	d1p9qc3	Alignment		15.8	13	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**Hypothetical protein AF0491, C-terminal domain
15	c2a45J_	Alignment		14.1	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** J: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
16	d1t95a3	Alignment		12.7	13	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**Hypothetical protein AF0491, C-terminal domain
17	c3dktD_	Alignment		12.6	17	**PDB header:**structural protein/virus like particle **Chain:** D: **PDB Molecule:**maritimacin; **PDBTitle:** crystal structure of thermotoga maritima encapsulin
18	c3tr6A_	Alignment		12.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-methyltransferase; **PDBTitle:** structure of a o-methyltransferase from coxiella burnetii
19	c3u7jA_	Alignment		11.5	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
20	d2iv2x1	Alignment		11.2	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
21	d1pkxa1	Alignment	not modelled	10.2	10	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
22	d2q22a1	Alignment	not modelled	8.8	12	**Fold:**Ava3019-like **Superfamily:**Ava3019-like **Family:**Ava3019-like
23	c3h9xB_	Alignment	not modelled	8.2	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein pspto_3016; **PDBTitle:** crystal structure of the pspto_3016 protein from2 pseudomonas syringae, northeast structural genomics3 consortium target psr293
24	c3cagF_	Alignment	not modelled	7.7	16	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
25	d2b0ja2	Alignment	not modelled	7.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
26	c2ki8A_	Alignment	not modelled	7.5	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase, **PDBTitle:** solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
27	c3cbnA_	Alignment	not modelled	7.4	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mth639; **PDBTitle:** crystal structure of a conserved protein (mth639) from2 methanobacterium thermoautotrophicum
						Fold:RRF/tRNA synthetase additional domain-like

28	d1uv7a_	Alignment	not modelled	7.3	12	**Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
29	c1uv7A_	Alignment	not modelled	7.3	12	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
30	d1go3e2	Alignment	not modelled	7.1	21	**Fold:**Dodecin subunit-like **Superfamily:**N-terminal, heterodimerisation domain of RBP7 (RpoE) **Family:**N-terminal, heterodimerisation domain of RBP7 (RpoE)
31	d2c35b2	Alignment	not modelled	7.1	17	**Fold:**Dodecin subunit-like **Superfamily:**N-terminal, heterodimerisation domain of RBP7 (RpoE) **Family:**N-terminal, heterodimerisation domain of RBP7 (RpoE)
32	c3ebrA_	Alignment	not modelled	6.9	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
33	c3sb1B_	Alignment	not modelled	6.8	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hydrogenase expression protein; **PDBTitle:** hydrogenase expression protein huph from thiobacillus denitrificans2 atcc 25259
34	c3ereD_	Alignment	not modelled	6.3	14	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
35	d1chda_	Alignment	not modelled	5.9	17	**Fold:**Methylesterase CheB, C-terminal domain **Superfamily:**Methylesterase CheB, C-terminal domain **Family:**Methylesterase CheB, C-terminal domain
36	d1dmra1	Alignment	not modelled	5.8	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
37	c3a6mB_	Alignment	not modelled	5.8	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**protein grpe; **PDBTitle:** crystal structure of grpe from thermus thermophilus hb8
38	d1tmoa1	Alignment	not modelled	5.6	12	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
39	d1l2pa_	Alignment	not modelled	5.5	11	**Fold:**Single transmembrane helix **Superfamily:**F1F0 ATP synthase subunit B, membrane domain **Family:**F1F0 ATP synthase subunit B, membrane domain
40	d1ogya1	Alignment	not modelled	5.4	17	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
41	d1ou0a_	Alignment	not modelled	5.2	13	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH
42	d1cwpa_	Alignment	not modelled	5.1	13	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
43	d1a8ya3	Alignment	not modelled	5.1	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
44	d1g8ma1	Alignment	not modelled	5.1	10	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
45	c3cxbA_	Alignment	not modelled	5.1	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein sifa; **PDBTitle:** crystal structure of sifa and skip