Phyre^2

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Description	P0A8D9
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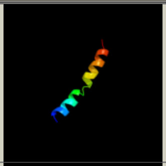
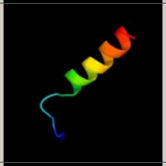
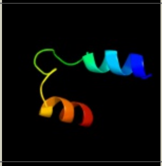
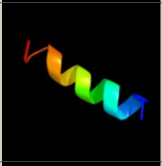
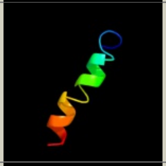
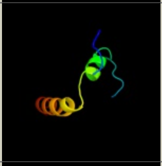
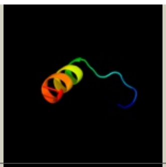
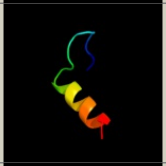
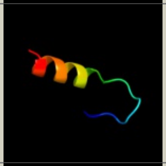
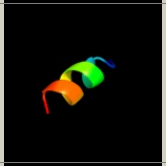
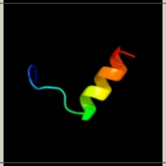
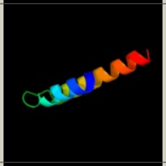
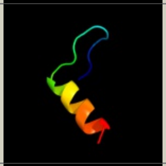
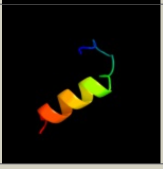
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l9uA_	Alignment		31.7	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3; **PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain
2	c3lwfD_	Alignment		23.2	17	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
3	c3tr7A_	Alignment		17.3	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** structure of a uracil-dna glycosylase (ung) from coxiella burnetii
4	d2osoa1	Alignment		15.8	21	**Fold:**Ligand-binding domain in the NO signalling and Golgi transport **Superfamily:**Ligand-binding domain in the NO signalling and Golgi transport **Family:**MJ1460-like
5	c3ajbB_	Alignment		14.3	31	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** crystal structure of human pex3p in complex with n-terminal pex19p2 peptide
6	c3njcA_	Alignment		13.8	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yslb protein; **PDBTitle:** crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460.
7	c1iojA_	Alignment		13.2	27	**PDB header:**apolipoprotein **Chain:** A: **PDB Molecule:**apoc-i; **PDBTitle:** human apolipoprotein c-i, nmr, 18 structures
8	d2qtva3	Alignment		12.9	9	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
9	c3sibA_	Alignment		12.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ure3-bp sequence specific dna binding protein; **PDBTitle:** crystal structure of ure3-binding protein, wild-type
10	d1tafb_	Alignment		12.2	20	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
11	c1kcfB_	Alignment		11.6	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical 30.2 kd protein c25g10.02 in **PDBTitle:** crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2

12	d3euga_	Alignment		10.4	32	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
13	d1okba_	Alignment		10.0	23	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
14	d2j8xa1	Alignment		9.6	23	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
15	c1p5kA_	Alignment		9.5	55	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution ser to leu11 modification in sds-d252 micelles
16	d1laue_	Alignment		9.2	32	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
17	d1vfga1	Alignment		9.0	33	**Fold:**Poly A polymerase C-terminal region-like **Superfamily:**Poly A polymerase C-terminal region-like **Family:**Poly A polymerase C-terminal region-like
18	c3ls1A_	Alignment		8.7	18	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
19	c3cxmA_	Alignment		8.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil
20	d2hxma1	Alignment		7.6	23	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
21	c2booA_	Alignment	not modelled	7.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** the crystal structure of uracil-dna n-glycosylase (ung)2 from deinococcus radiodurans.
22	d1oeyj_	Alignment	not modelled	7.2	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
23	d1pd0a3	Alignment	not modelled	6.3	9	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
24	d2gykb1	Alignment	not modelled	6.3	27	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**HNH-motif
25	c3eh2B_	Alignment	not modelled	6.1	7	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
26	c3op5B_	Alignment	not modelled	6.0	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase vrk1; **PDBTitle:** human vaccinia-related kinase 1
27	d1miwa1	Alignment	not modelled	6.0	17	**Fold:**Poly A polymerase C-terminal region-like **Superfamily:**Poly A polymerase C-terminal region-like **Family:**Poly A polymerase C-terminal region-like
28	c2akhZ_	Alignment	not modelled	5.9	25	**PDB header:**protein transport **Chain:** Z: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a non-2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
						Fold: Protein kinase-like (PK-like)

29	d1csna_	Alignment	not modelled	5.7	24	**Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
30	c3dinD_	Alignment	not modelled	5.6	50	**PDB header:**membrane protein, protein transport **Chain:** D: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
31	d1rbli_	Alignment	not modelled	5.5	56	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
32	d1kcfa2	Alignment	not modelled	5.2	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Mitochondrial resolvase ydc2 catalytic domain