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Description P76146
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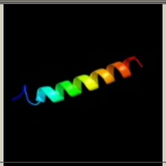
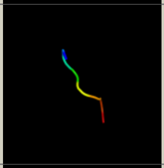
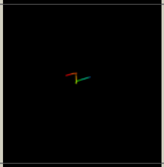
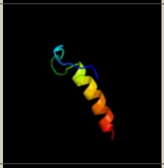
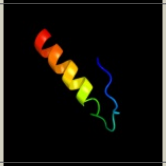
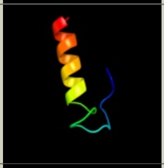
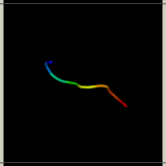
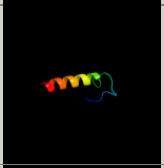
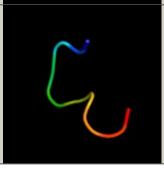
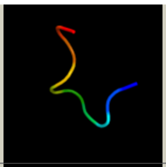
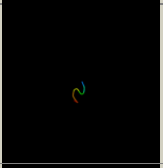
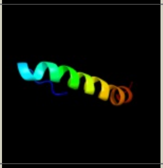
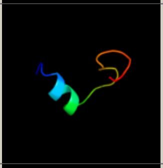
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1kqfb2	Alignment		34.3	7	**Fold:**Single transmembrane helix **Superfamily:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor **Family:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
2	d1h9aa1	Alignment		17.9	63	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
3	d1qkia1	Alignment		17.9	50	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
4	d1u84a_	Alignment		12.5	33	**Fold:**YugE-like **Superfamily:**YugE-like **Family:**YugE-like
5	d1y1la_	Alignment		12.3	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
6	c3rh0A_	Alignment		11.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
7	c2kx2A_	Alignment		11.1	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the solution structure of mth1821
8	d1jf8a_	Alignment		10.9	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
9	c1h9aA_	Alignment		9.6	63	**PDB header:**oxidoreductase (choh(d) - nad(p)) **Chain:** A: **PDB Molecule:**glucose 6-phosphate 1-dehydrogenase; **PDBTitle:** complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from l. mesenteroides with coenzyme nadp
10	d1d1qa_	Alignment		9.3	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
11	c1xviA_	Alignment		9.0	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mannosyl-3-phosphoglycerate phosphatase; **PDBTitle:** crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12

12	d1xvia_	Alignment		9.0	50	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
13	c1qkiE_	Alignment		8.7	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
14	c2bhlB_	Alignment		8.7	50	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
15	d1wzca1	Alignment		8.2	40	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
16	d1p8aa_	Alignment		8.1	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
17	c3ns4A_	Alignment		7.5	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 53; **PDBTitle:** structure of a c-terminal fragment of its vps53 subunit suggests2 similarity of garp to a family of tethering complexes
18	d1gnta_	Alignment		7.5	43	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Hybrid cluster protein (prismane protein)
19	d1s2oa1	Alignment		6.9	40	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
20	d2f76x1	Alignment		6.7	15	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Mason-Pfizer monkey virus matrix protein
21	d1gs0a1	Alignment	not modelled	6.5	12	**Fold:**Domain of poly(ADP-ribose) polymerase **Superfamily:**Domain of poly(ADP-ribose) polymerase **Family:**Domain of poly(ADP-ribose) polymerase
22	d1biaa1	Alignment	not modelled	6.4	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
23	d2rbka1	Alignment	not modelled	6.3	40	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
24	c2cwdA_	Alignment	not modelled	6.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
25	d2amya1	Alignment	not modelled	6.1	40	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
26	c3g9hA_	Alignment	not modelled	6.1	42	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**suppressor of yeast profilin deletion; **PDBTitle:** crystal structure of the c-terminal mu homology domain of2 syp1
27	c3fzqA_	Alignment	not modelled	6.0	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
28	c3niwA_	Alignment	not modelled	5.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron

29	d2izva1	Alignment	not modelled	5.9	25	**Fold:**SOCS box-like **Superfamily:**SOCS box-like **Family:**SOCS box-like
30	d2rd6a1	Alignment	not modelled	5.9	9	**Fold:**Domain of poly(ADP-ribose) polymerase **Superfamily:**Domain of poly(ADP-ribose) polymerase **Family:**Domain of poly(ADP-ribose) polymerase
31	c3gygA_	Alignment	not modelled	5.9	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ntd biosynthesis operon putative hydrolase ntdb; **PDBTitle:** crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
32	c3dnpA_	Alignment	not modelled	5.8	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stress response protein yhax; **PDBTitle:** crystal structure of stress response protein yhax from bacillus2 subtilis
33	d3blhb1	Alignment	not modelled	5.8	13	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
34	c3jvcA_	Alignment	not modelled	5.7	30	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical membrane lipoprotein; **PDBTitle:** crystal structure of the lipoprotein_17 domain from2 q9pra0_urepa protein of ureaplasma parvum. northeast3 structural genomics consortium target uur17a.
35	d1z0kb1	Alignment	not modelled	5.5	11	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
36	c3iynO_	Alignment	not modelled	5.5	25	**PDB header:**virus **Chain:** O: **PDB Molecule:**hexon-associated protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
37	d5pnta_	Alignment	not modelled	5.5	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
38	d1rlma_	Alignment	not modelled	5.4	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
39	c2l18A_	Alignment	not modelled	5.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
40	c3jviA_	Alignment	not modelled	5.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
41	c1s6cB_	Alignment	not modelled	5.3	42	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**potassium voltage-gated channel subfamily d member 2; **PDBTitle:** crystal structure of the complex between kchip1 and kv4.2 n1-30
42	d2aqea1	Alignment	not modelled	5.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**SWIRM domain
43	d1aa7a_	Alignment	not modelled	5.3	38	**Fold:**Influenza virus matrix protein M1 **Superfamily:**Influenza virus matrix protein M1 **Family:**Influenza virus matrix protein M1
44	d1qjta_	Alignment	not modelled	5.2	17	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
45	d1nrwa_	Alignment	not modelled	5.2	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
46	d1dg9a_	Alignment	not modelled	5.2	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
47	c2jvwA_	Alignment	not modelled	5.1	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117
48	d1efya1	Alignment	not modelled	5.1	12	**Fold:**Domain of poly(ADP-ribose) polymerase **Superfamily:**Domain of poly(ADP-ribose) polymerase **Family:**Domain of poly(ADP-ribose) polymerase