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Description	P77329
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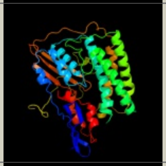
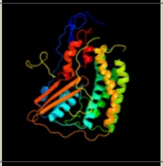
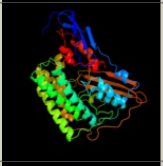
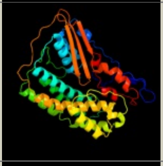
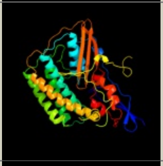
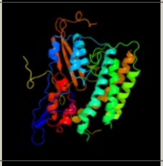
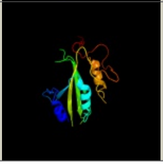
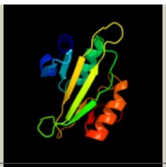
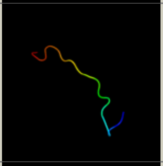
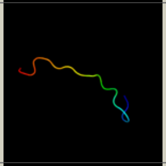
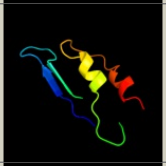
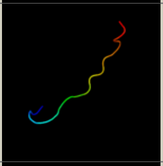
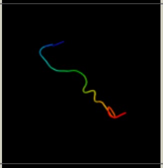
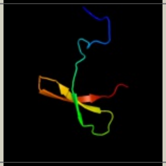
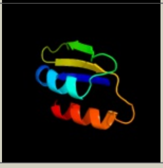
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fug4_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** 4: **PDB Molecule:**nadh-quinone oxidoreductase chain 4; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
2	d2fug41	Alignment		100.0	31	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nqo4-like
3	d1yq9h1	Alignment		100.0	23	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
4	d1frfl_	Alignment		100.0	23	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
5	d1cc1l_	Alignment		100.0	23	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
6	d1e3db_	Alignment		100.0	23	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
7	c1h2aL_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
8	c2wpnB_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic [nifese] hydrogenase, large subunit, **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
9	c3myrB_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nickel-dependent hydrogenase large subunit; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
10	d1wuil1	Alignment		100.0	23	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
11	d2fug51	Alignment		100.0	23	**Fold:**Nqo5-like **Superfamily:**Nqo5-like **Family:**Nqo5-like

12	c3mcrA_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh dehydrogenase, subunit c; **PDBTitle:** crystal structure of nadh dehydrogenase subunit c (tfu_2693) from2 thermobifida fusca yx-er1 at 2.65 a resolution
13	c3cf5G_	Alignment		35.6	17	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
14	d2zjrg1	Alignment		35.6	17	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
15	d1v97a4	Alignment		28.1	8	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
16	c2ftcH_	Alignment		27.5	22	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**39s ribosomal protein l13, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
17	c3bboL_	Alignment		26.3	22	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**ribosomal protein l13; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
18	c3d5bN_	Alignment		25.4	26	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
19	c2dgyA_	Alignment		25.1	10	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
20	d1nh8a2	Alignment		23.7	5	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
21	d1ffvc1	Alignment	not modelled	23.3	15	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
22	c3kwlA_	Alignment	not modelled	20.8	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
23	d1mixa2	Alignment	not modelled	20.5	16	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Third domain of FERM
24	d2j01n1	Alignment	not modelled	19.5	26	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
25	d1ef1a3	Alignment	not modelled	19.3	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
26	c1ufiD_	Alignment	not modelled	18.6	50	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of the dimerization domain of human cenp-b
27	d1ufia_	Alignment	not modelled	18.3	50	**Fold:**ROP-like **Superfamily:**Dimerisation domain of CENP-B **Family:**Dimerisation domain of CENP-B
28	c3mhyC_	Alignment	not modelled	18.3	18	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**pii-like protein pz; **PDBTitle:** a new pii protein structure
						Fold: TolA/TonB C-terminal domain

29	d1u07a_	Alignment	not modelled	18.0	14	**Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
30	d1ni2a3	Alignment	not modelled	17.4	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
31	d2zpya3	Alignment	not modelled	17.0	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
32	c1wvtA_	Alignment	not modelled	16.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st2180; **PDBTitle:** crystal structure of uncharacterized protein st2180 from sulfolobus2 tokodaii
33	d1in0a2	Alignment	not modelled	15.8	20	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
34	d2gych1	Alignment	not modelled	15.7	17	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
35	c2dnwA_	Alignment	not modelled	15.6	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
36	d1gg3a3	Alignment	not modelled	15.3	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
37	c2grxC_	Alignment	not modelled	15.2	8	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**protein tonb; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
38	d1vqza1	Alignment	not modelled	14.6	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
39	d1rtya_	Alignment	not modelled	14.4	11	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Cobalamin adenosyltransferase
40	d2hc5a1	Alignment	not modelled	14.1	13	**Fold:**FlaG-like **Superfamily:**FlaG-like **Family:**FlaG-like
41	c1xx3A_	Alignment	not modelled	13.8	6	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tonb protein; **PDBTitle:** solution structure of escherichia coli tonb-ctd
42	d2ntka1	Alignment	not modelled	13.5	27	**Fold:**Ntn hydrolase-like **Superfamily:**Archaeal IMP cyclohydrolase PurO **Family:**Archaeal IMP cyclohydrolase PurO
43	d1o98a1	Alignment	not modelled	13.3	14	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
44	d2gskb1	Alignment	not modelled	13.1	8	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
45	d1qy7a_	Alignment	not modelled	13.0	10	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
46	d3elna1	Alignment	not modelled	13.0	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
47	c1dpuA_	Alignment	not modelled	12.6	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
48	d1dpua_	Alignment	not modelled	12.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
49	d2piia_	Alignment	not modelled	12.6	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
50	c2oqkA_	Alignment	not modelled	12.1	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
51	d2g40a1	Alignment	not modelled	11.8	24	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**YkgG-like
52	c2g40A_	Alignment	not modelled	11.8	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
53	d3dhxa1	Alignment	not modelled	11.8	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
54	c2z51A_	Alignment	not modelled	11.6	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast; **PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
						PDB header:transferase **Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase,

55	c2zhzC_	Alignment	not modelled	11.6	14	putative; **PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
56	c2w3zA_	Alignment	not modelled	11.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
57	d1d7qa_	Alignment	not modelled	11.3	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
58	d2v4jb2	Alignment	not modelled	11.3	9	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
59	c2ntxB_	Alignment	not modelled	11.2	53	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**emb cab41934.1;
60	d2qswa1	Alignment	not modelled	11.1	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
61	c3echC_	Alignment	not modelled	11.0	36	**PDB header:**transcription, transcription regulation **Chain:** C: **PDB Molecule:**25-mer fragment of protein armr; **PDBTitle:** the marr-family repressor mexr in complex with its antirepressor armr
62	d2r4qa1	Alignment	not modelled	10.5	29	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
63	d1zj8a1	Alignment	not modelled	10.3	17	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
64	c3e7hA_	Alignment	not modelled	10.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** the crystal structure of the beta subunit of the dna-2 directed rna polymerase from vibrio cholerae o1 biovar3 eltor
65	d2qrra1	Alignment	not modelled	10.1	4	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
66	d1yqga2	Alignment	not modelled	10.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
67	c2ibpB_	Alignment	not modelled	9.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**citrate synthase; **PDBTitle:** crystal structure of citrate synthase from pyrobaculum aerophilum
68	d1vfja_	Alignment	not modelled	9.6	10	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
69	d2ns1b1	Alignment	not modelled	9.6	19	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
70	d1r6ta2	Alignment	not modelled	9.6	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
71	d1qxha_	Alignment	not modelled	9.5	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
72	d1llaa3	Alignment	not modelled	9.4	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arthropod hemocyanin, C-terminal domain
73	c2fq2A_	Alignment	not modelled	9.3	14	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
74	d1hc1a3	Alignment	not modelled	9.2	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arthropod hemocyanin, C-terminal domain
75	d2qlvb1	Alignment	not modelled	9.2	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
76	c3ixvG_	Alignment	not modelled	9.1	6	**PDB header:**oxygen binding **Chain:** G: **PDB Molecule:**hemocyanin aa6 chain; **PDBTitle:** scorpion hemocyanin resting state pseudo atomic model built based on2 cryo-em density map
77	c2eceA_	Alignment	not modelled	9.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**462aa long hypothetical selenium-binding protein; **PDBTitle:** x-ray structure of hypothetical selenium-binding protein2 from sulfolobus tokodaii, st0059
78	c3g59A_	Alignment	not modelled	8.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fmn adenylyltransferase; **PDBTitle:** crystal structure of candida glabrata fmn2 adenylyltransferase in complex with atp
79	c3hrdC_	Alignment	not modelled	8.6	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
80	c1bl1A_	Alignment	not modelled	8.6	56	**PDB header:**hormone receptor **Chain:** A: **PDB Molecule:**parathyroid hormone receptor; **PDBTitle:** pth receptor n-terminus fragment, nmr, 1 structure
81	d1es6a2	Alignment	not modelled	8.6	36	**Fold:**EV matrix protein **Superfamily:**EV matrix protein **Family:**EV matrix protein

82	c1es6A_	Alignment	not modelled	8.5	36	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein vp40; **PDBTitle:** crystal structure of the matrix protein of ebola virus
83	c2vgpD_	Alignment	not modelled	8.4	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**inner centromere protein a; **PDBTitle:** crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor
84	d1n62c1	Alignment	not modelled	8.3	15	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
85	d2ic1a1	Alignment	not modelled	8.3	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Cysteine dioxygenase type I
86	c2ip1A_	Alignment	not modelled	8.3	31	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
87	c3jxeB_	Alignment	not modelled	8.1	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
88	d1xhja_	Alignment	not modelled	8.0	36	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
89	c2kzxA_	Alignment	not modelled	8.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
90	c3a05A_	Alignment	not modelled	8.0	31	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
91	d2owna1	Alignment	not modelled	7.9	8	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**Acyl-ACP thioesterase-like
92	c1in0B_	Alignment	not modelled	7.8	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yajq protein; **PDBTitle:** yajq protein (hi1034)
93	d1woha_	Alignment	not modelled	7.8	15	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Arginase-like amidino hydrolases
94	c3hzrD_	Alignment	not modelled	7.8	15	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica
95	c1mbbA_	Alignment	not modelled	7.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uridine diphospho-n-acetylenolpyruvylglucosamine **PDBTitle:** oxidoreductase
96	c1nh7A_	Alignment	not modelled	7.7	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
97	d1vi7a2	Alignment	not modelled	7.6	17	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**YigZ C-terminal domain-like
98	d1h4ra3	Alignment	not modelled	7.6	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
99	c2l4bA_	Alignment	not modelled	7.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a