Email l.a.kelley@imperial.ac.uk
Description P0C0T5
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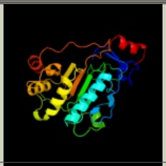
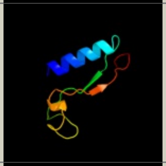
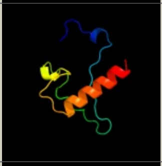
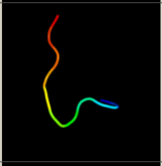
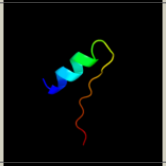
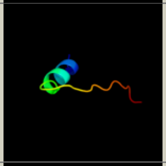
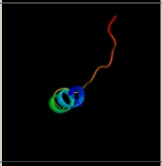
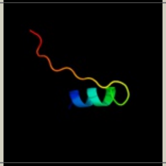
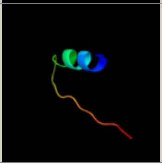
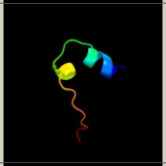
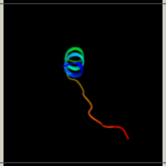
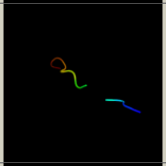
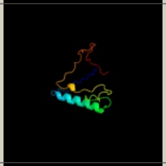
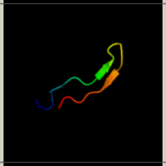
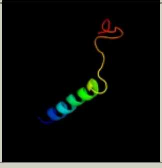
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tzpa_	Alignment		100.0	100	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**MepA-like
2	c2vo9C_	Alignment		80.3	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**l-alanyl-d-glutamate peptidase; **PDBTitle:** crystal structure of the enzymatically active domain of the2 listeria monocytogenes bacteriophage 500 endolysin ply500
3	d2vo9a1	Alignment		41.6	16	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**VanY-like
4	d1r44a_	Alignment		39.2	17	**Fold:**Hedgehog/DD-peptidase **Superfamily:**Hedgehog/DD-peptidase **Family:**VanX-like
5	c1lbuA_	Alignment		33.4	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**muramoyl-pentapeptide carboxypeptidase; **PDBTitle:** hydrolase metallo (zn) dd-peptidase
6	c3ag5A_	Alignment		25.2	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantothenate synthetase from staphylococcus2 aureus
7	d1ihoa_	Alignment		23.3	39	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
8	d1v8fa_	Alignment		22.4	30	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
9	c2faoB_	Alignment		20.9	10	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**probable atp-dependent dna ligase; **PDBTitle:** crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
10	c3innB_	Alignment		20.7	35	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
11	c3uk2B_	Alignment		19.6	48	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** the structure of pantothenate synthetase from burkholderia2 thailandensis

12	c2ejcA_	Alignment		19.3	39	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase; **PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
13	d2a84a1	Alignment		18.6	35	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
14	c3n8hA_	Alignment		18.4	48	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
15	c3mxtA_	Alignment		15.5	44	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
16	c3c7bA_	Alignment		15.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
17	c2iruA_	Alignment		14.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative dna ligase-like protein rv0938/mt0965; **PDBTitle:** crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
18	d2cwza1	Alignment		14.8	4	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**TTHA0967-like
19	d1nkga3	Alignment		12.7	22	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Rhamnogalacturonase B, RhgB, N-terminal domain
20	c1x9vA_	Alignment		12.1	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** dimeric structure of the c-terminal domain of vpr
21	d1ujpa_	Alignment	not modelled	12.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
22	d2o8ra3	Alignment	not modelled	11.8	32	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
23	c2jksA_	Alignment	not modelled	11.4	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**bradyzoite surface antigen bsr4; **PDBTitle:** crystal structure of the the bradyzoite specific antigen2 bsr4 from toxoplasma gondii.
24	c2zuuA_	Alignment	not modelled	9.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lacto-n-biose phosphorylase; **PDBTitle:** crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnac
25	c3kuvB_	Alignment	not modelled	9.7	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fluoroacetyl coenzyme a thioesterase; **PDBTitle:** structural basis of the activity and substrate specificity of the2 fluoroacetyl-coa thioesterase flk - t42s mutant in complex with3 acetate.
26	d2v4ja2	Alignment	not modelled	9.3	50	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
27	c3qooA_	Alignment	not modelled	8.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
28	d1gvia1	Alignment	not modelled	7.3	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes

29	c2x2zE_	Alignment	not modelled	6.6	42	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**apical membrane antigen 1, putative; **PDBTitle:** crystal structure ama1 from toxoplasma gondii
30	c3navB_	Alignment	not modelled	6.5	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
31	d1wzla1	Alignment	not modelled	6.4	33	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
32	d1pvta_	Alignment	not modelled	6.0	17	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
33	d1j0ha1	Alignment	not modelled	6.0	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
34	d1c25a_	Alignment	not modelled	5.8	25	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
35	d1txla_	Alignment	not modelled	5.6	29	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Hypothetical protein YodA
36	c1txlA_	Alignment	not modelled	5.6	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**metal-binding protein yoda; **PDBTitle:** crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149
37	c2q8aA_	Alignment	not modelled	5.5	33	**PDB header:**immune system **Chain:** A: **PDB Molecule:**apical membrane antigen 1; **PDBTitle:** structure of the malaria antigen ama1 in complex with a growth-2 inhibitory antibody
38	c2w82C_	Alignment	not modelled	5.4	45	**PDB header:**replication inhibitor **Chain:** C: **PDB Molecule:**orf18; **PDBTitle:** the structure of arda
39	d1dqaa1	Alignment	not modelled	5.4	8	**Fold:**Ferredoxin-like **Superfamily:**NAD-binding domain of HMG-CoA reductase **Family:**NAD-binding domain of HMG-CoA reductase
40	d1gqpa_	Alignment	not modelled	5.3	27	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**APC10-like
41	c1h4uA_	Alignment	not modelled	5.1	17	**PDB header:**extracellular matrix protein **Chain:** A: **PDB Molecule:**nidogen-1; **PDBTitle:** domain g2 of mouse nidogen-1
42	c2l57A_	Alignment	not modelled	5.1	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
43	d1xuba1	Alignment	not modelled	5.0	17	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like