Phyre^2

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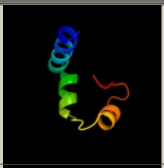
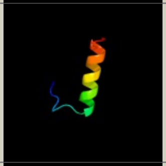
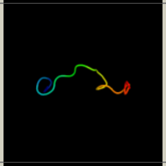
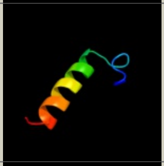
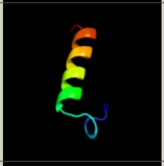
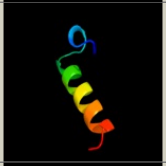
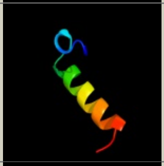
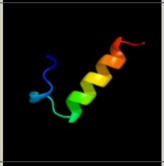
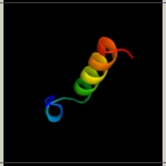
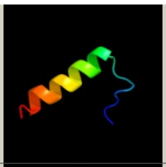
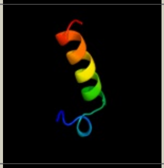
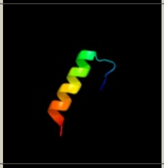
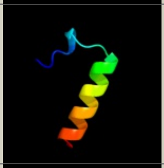
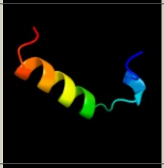
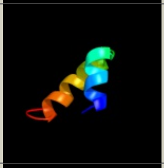
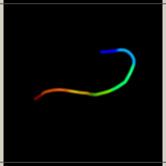
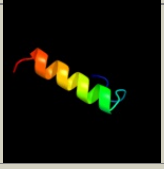
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s4ka_	Alignment		21.4	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**YdiL-like
2	c3pueA_	Alignment		11.7	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
3	d1ploa_	Alignment		10.8	32	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Extracellular domain of cell surface receptors
4	c3fkkA_	Alignment		10.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
5	d2gsca1	Alignment		10.3	40	**Fold:**Bromodomain-like **Superfamily:**IVS-encoded protein-like **Family:**IVS-encoded protein-like
6	c3h5dD_	Alignment		9.5	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
7	c3g0sA_	Alignment		9.4	36	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
8	c3qfeB_	Alignment		9.1	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative dihydrodipicolinate synthase family protein; **PDBTitle:** crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
9	d2a6na1	Alignment		9.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
10	d1f74a_	Alignment		8.8	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
11	c3d0cB_	Alignment		8.7	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution

12	c3bi8A_	Alignment		8.5	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
13	c3na8A_	Alignment		8.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
14	d1hl2a_	Alignment		8.2	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
15	c2v9dB_	Alignment		7.9	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
16	c3n2xB_	Alignment		7.9	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uncharacterized protein yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
17	c3b4uB_	Alignment		7.7	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
18	d1z3xa1	Alignment		7.5	17	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**GUN4-associated domain
19	d1ki1b2	Alignment		7.2	57	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
20	c3si9B_	Alignment		7.1	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
21	c3qwmA_	Alignment	not modelled	6.9	57	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**iq motif and sec7 domain-containing protein 1; **PDBTitle:** crystal structure of gep100, the plextrin homology domain of iq motif2 and sec7 domain-containing protein 1 isoform a
22	d1xkya1	Alignment	not modelled	6.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
23	c3eb2A_	Alignment	not modelled	6.8	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
24	c3fluD_	Alignment	not modelled	6.3	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
25	c3noeA_	Alignment	not modelled	6.2	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
26	c2yxgD_	Alignment	not modelled	5.6	28	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
27	c2vc6A_	Alignment	not modelled	5.6	40	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
28	c2jnsA_	Alignment	not modelled	5.6	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bromodomain-containing protein 4; **PDBTitle:** solution structure of the bromodomain-containing protein 42 et domain

29	d1o5ka_	Alignment	not modelled	5.6	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
30	d1txda2	Alignment	not modelled	5.6	33	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
31	d1xcga2	Alignment	not modelled	5.6	33	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)