Phyre2

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Description	Q2MB16
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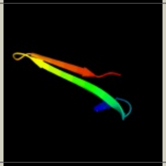
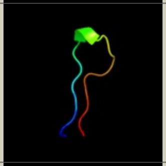
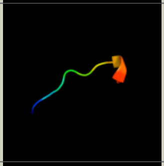
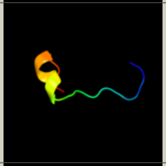
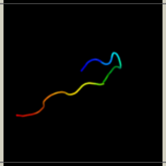
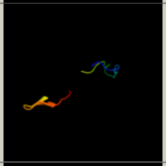
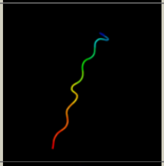
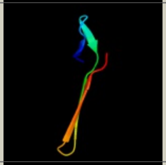
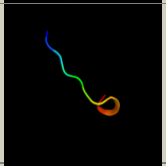
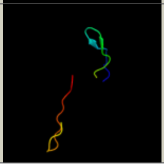
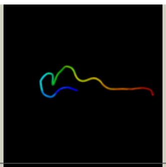
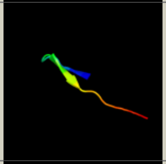
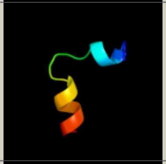
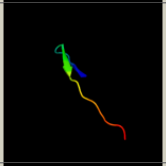
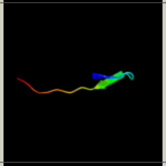
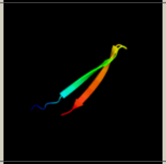
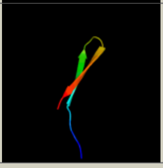
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1w6ta2	Alignment		23.9	30	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
2	c2fymA_	Alignment		21.2	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of e. coli enolase complexed with the2 minimal binding segment of rnase e.
3	d2ivda2	Alignment		20.9	32	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
4	c2a8vA_	Alignment		14.5	27	**PDB header:**protein/rna **Chain:** A: **PDB Molecule:**rna binding domain of rho transcription **PDBTitle:** rho transcription termination factor/rna complex
5	d1seza2	Alignment		14.2	53	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**L-aminoacid/polyamine oxidase
6	d2d13a1	Alignment		13.6	36	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
7	c2oztA_	Alignment		12.3	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tlr1174 protein; **PDBTitle:** crystal structure of o-succinylbenzoate synthase from2 thermosynechococcus elongatus bp-1
8	c3d4cA_	Alignment		11.6	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein, linker, zona pellucida **PDBTitle:** zp-n domain of mammalian sperm receptor zp3 (crystal form i)
9	c3tqpA_	Alignment		11.1	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** structure of an enolase (eno) from coxiella burnetii
10	d1a62a2	Alignment		11.0	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
11	d1wufa2	Alignment		10.6	25	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like

12	d1ru8a_	Alignment		10.2	50	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
13	d1muca2	Alignment		9.6	21	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
14	d1iyxa2	Alignment		9.1	33	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
15	c3qn3B_	Alignment		9.0	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enolase; **PDBTitle:** phosphopyruvate hydratase from campylobacter jejuni.
16	d2ezla_	Alignment		8.8	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
17	d2mnra2	Alignment		8.3	25	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
18	c3tj4B_	Alignment		8.2	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of an enolase from agrobacterium tumefaciens (efi2 target efi-502087) no mg
19	d1bqga2	Alignment		7.6	26	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
20	d1jdfa2	Alignment		7.5	22	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
21	c2pa6A_	Alignment	not modelled	7.2	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of mj0232 from methanococcus jannaschii
22	c3uj2C_	Alignment	not modelled	7.1	26	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** crystal structure of an enolase from anaerostipes caccae (efi target2 efi-502054) with bound mg and sulfate
23	c1iyxA_	Alignment	not modelled	7.1	36	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of enolase from enterococcus hirae
24	d2gtlo1	Alignment	not modelled	7.1	29	**Fold:**Streptavidin-like **Superfamily:**Extracellular hemoglobin linker subunit, receptor domain **Family:**Extracellular hemoglobin linker subunit, receptor domain
25	d1rvka2	Alignment	not modelled	6.9	21	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
26	d2gtln1	Alignment	not modelled	6.6	17	**Fold:**Streptavidin-like **Superfamily:**Extracellular hemoglobin linker subunit, receptor domain **Family:**Extracellular hemoglobin linker subunit, receptor domain
27	d1jpma2	Alignment	not modelled	6.4	29	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
28	d2gl5a2	Alignment	not modelled	6.1	36	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
						PDB header:toxin

29	c1x5vA_	Alignment	not modelled	6.0	50	**Chain:** A: **PDB Molecule:**pcfk1; **PDBTitle:** nmr structure of pcfk1
30	c1ec8B_	Alignment	not modelled	6.0	29	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** e. coli glucarate dehydratase bound to product 2,3-2 dihydroxy-5-oxo-hexanedioate
31	c2pozA_	Alignment	not modelled	5.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dehydratase; **PDBTitle:** crystal structure of a putative dehydratase from mesorhizobium loti
32	c3msyC_	Alignment	not modelled	5.5	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from a marine actinobacterium
33	c2hxtA_	Alignment	not modelled	5.4	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**l-fuconate dehydratase; **PDBTitle:** crystal structure of l-fuconate dehydratase from xanthomonas2 campestris liganded with mg++ and d-erythronohydroxamate
34	c2l35B_	Alignment	not modelled	5.3	13	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**tyro protein tyrosine kinase-binding protein; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
35	c3sjnB_	Alignment	not modelled	5.2	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of enolase spea_3858 (target efi-500646) from2 shewanella pealeana with magnesium bound