Phyre^2

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Description	Q46898
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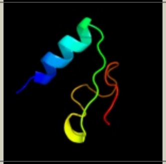
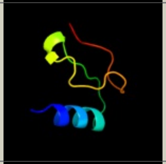
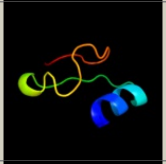
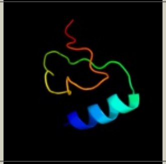
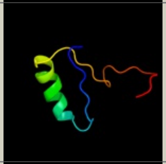
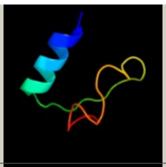
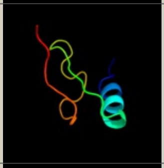
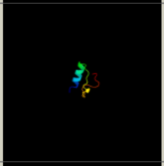
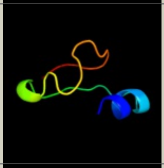
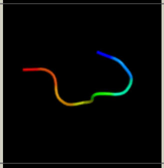
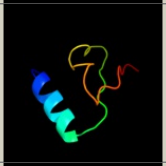
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kg4A_	Alignment		99.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from mannheimia2 succiniciproducens
2	d2ihta1	Alignment		64.8	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
3	d1ovma1	Alignment		63.5	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
4	d1t9ba1	Alignment		52.7	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
5	d2ez9a1	Alignment		51.5	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
6	d1zpda1	Alignment		51.2	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
7	d1pvda1	Alignment		49.7	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
8	d2djia1	Alignment		41.4	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
9	d2ji7a1	Alignment		35.2	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
10	d1fyva_	Alignment		29.3	17	**Fold:**Flavodoxin-like **Superfamily:**Toll/Interleukin receptor TIR domain **Family:**Toll/Interleukin receptor TIR domain
11	c3h16A_	Alignment		26.2	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tir protein; **PDBTitle:** crystal structure of a bacteria tir domain, pdtir from2 paracoccus denitrificans

12	d1ozha1	Alignment		24.9	8	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
13	d1q6za1	Alignment		23.9	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
14	c3oziB_	Alignment		22.9	8	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**l6tr; **PDBTitle:** crystal structure of the tir domain from the flax disease resistance2 protein l6
15	c2vbgB_	Alignment		22.1	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**branched-chain alpha-ketoacid decarboxylase; **PDBTitle:** the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
16	c2panF_	Alignment		18.0	18	**PDB header:**lyase **Chain:** F: **PDB Molecule:**glyoxylate carboligase; **PDBTitle:** crystal structure of e. coli glyoxylate carboligase
17	c1powA_	Alignment		14.5	21	**PDB header:**oxidoreductase(oxygen as acceptor) **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
18	c1wxnA_	Alignment		12.3	50	**PDB header:**toxin **Chain:** A: **PDB Molecule:**toxin apetx2; **PDBTitle:** solution structure of apetx2, a specific peptide inhibitor2 of asic3 proton-gated channels
19	c2vbiF_	Alignment		11.2	15	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
20	d2nzwa1	Alignment		11.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**FucT-like
21	d1fyxa_	Alignment	not modelled	10.4	4	**Fold:**Flavodoxin-like **Superfamily:**Toll/Interleukin receptor TIR domain **Family:**Toll/Interleukin receptor TIR domain
22	c2ap7A_	Alignment	not modelled	10.2	60	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bombinin h2; **PDBTitle:** solution structure of bombinin h2 in dpc micelles
23	c3pdiG_	Alignment	not modelled	10.1	13	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nife; **PDBTitle:** precursor bound nifen
24	c2ap8A_	Alignment	not modelled	10.1	60	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bombinin h4; **PDBTitle:** solution structure of bombinin h4 in dpc micelles
25	c2w93A_	Alignment	not modelled	9.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pyruvate decarboxylase isozyme 1; **PDBTitle:** crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate3 pyruvamide
26	c2djiA_	Alignment	not modelled	9.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate oxidase; **PDBTitle:** crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
27	c2z5vA_	Alignment	not modelled	8.6	16	**PDB header:**immune system **Chain:** A: **PDB Molecule:**myeloid differentiation primary response protein **PDBTitle:** solution structure of the tir domain of human myd88
28	c2pgnA_	Alignment	not modelled	7.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclohexane-1,2-dione hydrolase (cdh); **PDBTitle:** the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-

						1,2-dione
29	d1m1na_	Alignment	not modelled	7.6	7	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
30	d2fug61	Alignment	not modelled	7.1	17	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nq06-like
31	d1vkya_	Alignment	not modelled	7.0	28	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
32	d1qh8a_	Alignment	not modelled	6.9	7	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
33	c3le4A_	Alignment	not modelled	6.8	27	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**microprocessor complex subunit dgcr8; **PDBTitle:** crystal structure of the dgcr8 dimerization domain
34	c1jscA_	Alignment	not modelled	6.6	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**acetohydroxy-acid synthase; **PDBTitle:** crystal structure of the catalytic subunit of yeast2 acetohydroxyacid synthase: a target for herbicidal3 inhibitors
35	c1ovmC_	Alignment	not modelled	5.9	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**indole-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
36	d1wdia_	Alignment	not modelled	5.5	38	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
37	c3cf4G_	Alignment	not modelled	5.2	9	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**acetyl-coa decarboxylase/synthase epsilon subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex