Phyre^2

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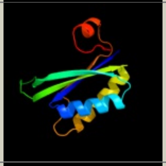
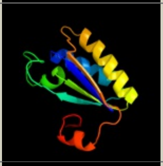
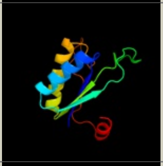
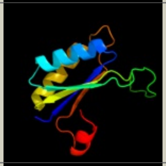
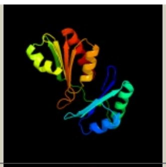
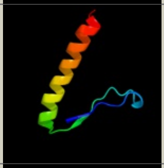
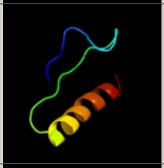
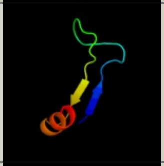
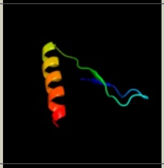
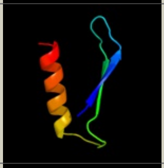
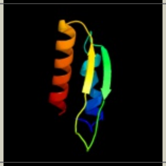
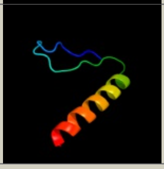
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i82A_	Alignment		100.0	100	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**ethanolamine utilization protein eutl; **PDBTitle:** ethanolamine utilization microcompartment shell subunit, eutl closed2 form
2	c3io0A_	Alignment		100.0	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**etub protein; **PDBTitle:** crystal structure of etub from clostridium kluyveri
3	c3nwgA_	Alignment		100.0	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microcompartments protein; **PDBTitle:** the crystal structure of a microcomparments protein from2 desulfitobacterium hafniense dcb
4	c3n79A_	Alignment		100.0	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**pdut; **PDBTitle:** pdut c38s mutant from salmonella enterica typhimurium
5	c3ia0c_	Alignment		99.8	25	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein euts; **PDBTitle:** ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
6	c3cgiD_	Alignment		99.8	26	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
7	d2a10a1	Alignment		99.6	15	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
8	d2a1ba1	Alignment		99.6	20	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
9	c3ngkA_	Alignment		99.5	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**propanediol utilization protein pdua; **PDBTitle:** pdua from salmonella enterica typhimurium
10	d2ewha1	Alignment		99.5	24	**Fold:**Ferredoxin-like **Superfamily:**CcmK-like **Family:**CcmK-like
11	c3i6pF_	Alignment		99.5	23	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**ethanolamine utilization protein eutm; **PDBTitle:** ethanolamine utilization microcompartment shell subunit, eutm

12	c3f56F_	Alignment		98.9	18	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**csos1d; **PDBTitle:** the structure of a previously undetected carboxysome shell2 protein: csos1d from prochlorococcus marinus med4
13	d2ctka1	Alignment		37.5	20	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
14	c2hh3A_	Alignment		25.1	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the third kh domain of ksrp
15	c2jnvA_	Alignment		23.6	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
16	d1dtja_	Alignment		23.0	29	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
17	d1khma_	Alignment		21.9	16	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
18	d1xhja_	Alignment		20.8	15	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
19	d1qd1a1	Alignment		18.9	17	**Fold:**Ferredoxin-like **Superfamily:**Formiminotransferase domain of formiminotransferase-cyclodeaminase. **Family:**Formiminotransferase domain of formiminotransferase-cyclodeaminase.
20	d2ctea1	Alignment		18.8	13	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
21	d1aisa2	Alignment	not modelled	15.7	6	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
22	d1j4wa2	Alignment	not modelled	15.6	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
23	c2hh2A_	Alignment	not modelled	15.5	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh-type splicing regulatory protein; **PDBTitle:** solution structure of the fourth kh domain of ksrp
24	d1zzka1	Alignment	not modelled	14.2	16	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
25	c2jzxA_	Alignment	not modelled	14.0	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2; **PDBTitle:** pcbp2 kh1-kh2 domains
26	d2ctma1	Alignment	not modelled	13.1	14	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
27	d1j4wa1	Alignment	not modelled	12.9	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
28	c1qd1A_	Alignment	not modelled	12.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**formiminotransferase-cyclodeaminase; **PDBTitle:** the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
29	c1ztgD_	Alignment	not modelled	12.3	19	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1;

						PDBTitle: human alpha polyc binding protein kh1
30	d2axya1	Alignment	not modelled	11.6	17	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
31	d1ec6a_	Alignment	not modelled	11.2	26	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
32	c2z51A_	Alignment	not modelled	11.1	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
33	d1veha_	Alignment	not modelled	9.6	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
34	d1nh2a2	Alignment	not modelled	9.1	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
35	d1ftra2	Alignment	not modelled	8.6	13	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
36	c3krmB_	Alignment	not modelled	8.4	14	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**insulin-like growth factor 2 mrna-binding protein **PDBTitle:** imp1 kh34
37	d1qnaa2	Alignment	not modelled	8.3	11	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
38	d1wvna1	Alignment	not modelled	7.9	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
39	c2jvzA_	Alignment	not modelled	7.7	10	**PDB header:**splicing **Chain:** A: **PDB Molecule:**far upstream element-binding protein 2; **PDBTitle:** solution nmr structure of the second and third kh domains2 of ksrp
40	d1dt4a_	Alignment	not modelled	6.9	24	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
41	d1cdwa2	Alignment	not modelled	6.4	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
42	c3dclC_	Alignment	not modelled	6.3	11	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**tm1086; **PDBTitle:** crystal structure of tm1086
43	d2ctla1	Alignment	not modelled	6.3	20	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
44	d1mp9a2	Alignment	not modelled	6.2	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
45	c2wqfA_	Alignment	not modelled	6.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper induced nitroreductase d; **PDBTitle:** crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fmn
46	d1vq3a_	Alignment	not modelled	5.9	20	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
47	c2e1mC_	Alignment	not modelled	5.9	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
48	d1u0ta_	Alignment	not modelled	5.6	15	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
49	d1nh2a1	Alignment	not modelled	5.4	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
50	d1xpma1	Alignment	not modelled	5.3	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
51	d2h9ec1	Alignment	not modelled	5.3	18	**Fold:**Serine protease inhibitors **Superfamily:**Serine protease inhibitors **Family:**ATI-like
52	d1iuha_	Alignment	not modelled	5.2	14	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**2'-5' RNA ligase LigT
53	d1u0ua2	Alignment	not modelled	5.1	13	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like