Phyre²

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Description	P40711
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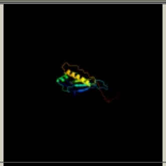
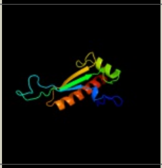
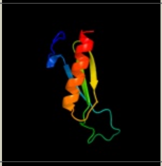
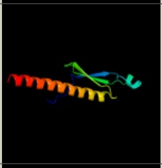
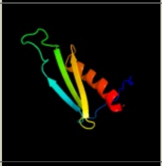
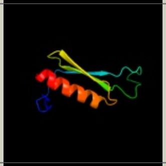
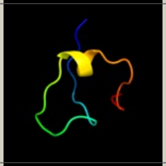
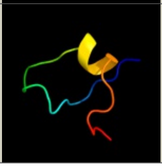
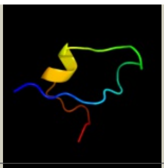
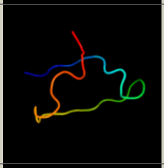
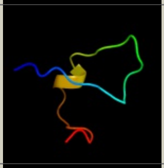
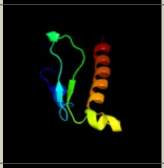
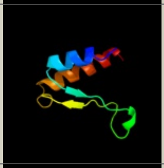
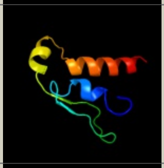
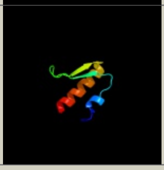
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jy9A_	Alignment		100.0	84	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative trna hydrolase domain; **PDBTitle:** nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220
2	c2jvaA_	Alignment		100.0	62	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase domain protein; **PDBTitle:** nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
3	d1j26a_	Alignment		100.0	26	**Fold:**dsRBD-like **Superfamily:**Peptidyl-tRNA hydrolase domain-like **Family:**Peptidyl-tRNA hydrolase domain
4	c2ihr1_	Alignment		99.9	38	**PDB header:**translation **Chain:** 1: **PDB Molecule:**peptide chain release factor 2; **PDBTitle:** rf2 of thermus thermophilus
5	c3d5cX_	Alignment		99.9	33	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
6	d2b3tb1	Alignment		99.9	35	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
7	d1gqea_	Alignment		99.9	34	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
8	d1rq0a_	Alignment		99.6	35	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
9	c1zbtA_	Alignment		99.2	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution
10	c2z2jA_	Alignment		60.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
11	c3v2iA_	Alignment		59.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis

12	c3neaA_	Alignment		51.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
13	d1ryba_	Alignment		50.5	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
14	d2ptha_	Alignment		46.2	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
15	d2ctka1	Alignment		39.7	25	**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)
16	d2ctla1	Alignment		36.9	19	**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	d1viga_	Alignment		35.9	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)
18	d2ctea1	Alignment		35.8	19	**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)
19	d1x4na1	Alignment		35.2	11	**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)
20	d2ctfa1	Alignment		30.1	25	**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	c2eq9C_	Alignment	not modelled	25.3	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
22	c2eq7C_	Alignment	not modelled	22.5	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
23	d1z2la2	Alignment	not modelled	22.2	11	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
24	d2ctja1	Alignment	not modelled	21.9	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)
25	c3ipjB_	Alignment	not modelled	20.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, iiabc component; **PDBTitle:** the crystal structure of one domain of the pts system, iiabc component2 from clostridium difficile
26	d1wvna1	Alignment	not modelled	20.2	12	**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	d2z0sa2	Alignment	not modelled	17.2	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)
28	d1ysja2	Alignment	not modelled	17.2	9	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain

29	d2ba0a3	Alignment	not modelled	17.0	12	**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)
30	c2yqrA_	Alignment	not modelled	16.6	23	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0907 protein; **PDBTitle:** solution structure of the kh domain in kiaa0907 protein
31	c2jzxA_	Alignment	not modelled	16.5	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2; **PDBTitle:** pcbp2 kh1-kh2 domains
32	d1cg2a2	Alignment	not modelled	15.2	13	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
33	c3dv0I_	Alignment	not modelled	14.2	18	**PDB header:**oxidoreductase/transferase **Chain:** I: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
34	c2eq8C_	Alignment	not modelled	14.1	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
35	d1w4ha1	Alignment	not modelled	13.8	35	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
36	d1w85i_	Alignment	not modelled	13.3	18	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
37	c1ztgD_	Alignment	not modelled	13.3	23	**PDB header:**dna, rna binding protein/dna **Chain:** D: **PDB Molecule:**poly(rc)-binding protein 1; **PDBTitle:** human alpha polyc binding protein kh1
38	c1w3dA_	Alignment	not modelled	13.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
39	d1hh2p3	Alignment	not modelled	13.1	57	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
40	c2e3uA_	Alignment	not modelled	13.0	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein ph1566; **PDBTitle:** crystal structure analysis of dim2p from pyrococcus horikoshii ot3
41	d1g43a_	Alignment	not modelled	12.8	30	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Carbohydrate-binding domain **Family:**Cellulose-binding domain family III
42	d2cyua1	Alignment	not modelled	12.8	35	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
43	c1w4kA_	Alignment	not modelled	12.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase e2; **PDBTitle:** peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
44	c1zwvA_	Alignment	not modelled	11.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
45	d2ctma1	Alignment	not modelled	11.6	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)
46	d2asba3	Alignment	not modelled	11.3	43	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
47	c1rl2A_	Alignment	not modelled	11.0	24	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**protein (ribosomal protein l2); **PDBTitle:** ribosomal protein l2 rna-binding domain from bacillus2 stearothermophilus
48	d1rl2a1	Alignment	not modelled	11.0	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
49	d1ec6a_	Alignment	not modelled	11.0	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)
50	d2axya1	Alignment	not modelled	10.5	25	**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)
51	c2jvzA_	Alignment	not modelled	9.8	13	**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
52	c3a5iB_	Alignment	not modelled	9.6	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**flagellar biosynthesis protein flha;

						PDBTitle: structure of the cytoplasmic domain of flha
53	d1bala_	Alignment	not modelled	8.6	38	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
54	c2g39A_	Alignment	not modelled	7.7	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**acetyl-coa hydrolase; **PDBTitle:** crystal structure of coenzyme a transferase from pseudomonas2 aeruginosa
55	d1g9pa_	Alignment	not modelled	7.6	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
56	c1g9pA_	Alignment	not modelled	7.6	40	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-atracotoxin-hv2a; **PDBTitle:** solution structure of the insecticidal calcium channel2 blocker omega-atracotoxin-hv2a
57	d1tuaa2	Alignment	not modelled	7.4	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)
58	d1ev7a_	Alignment	not modelled	6.9	23	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease NaeI
59	d1wfsa_	Alignment	not modelled	6.3	16	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Cofilin-like
60	d1kn0a_	Alignment	not modelled	6.2	57	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**The homologous-pairing domain of Rad52 recombinase
61	d1r3na2	Alignment	not modelled	5.9	15	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
62	d1khma_	Alignment	not modelled	5.9	25	**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)
63	c2nvvF_	Alignment	not modelled	5.8	50	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetyl-coa hydrolase/transferase family protein; **PDBTitle:** crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
64	c3gk7A_	Alignment	not modelled	5.8	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
65	c3eh7A_	Alignment	not modelled	5.6	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
66	c2rbgB_	Alignment	not modelled	5.5	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein st0493; **PDBTitle:** crystal structure of hypothetical protein(st0493) from2 sulfolobus tokodaii
67	d2g39a2	Alignment	not modelled	5.4	50	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
68	d1x4ma1	Alignment	not modelled	5.4	12	**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)
69	c3on3B_	Alignment	not modelled	5.4	47	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**keto/oxoacid ferredoxin oxidoreductase, gamma subunit; **PDBTitle:** the crystal structure of keto/oxoacid ferredoxin oxidoreductase, gamma2 subunit from geobacter sulfurreducens pca
70	c3mydA_	Alignment	not modelled	5.4	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha from helicobacter pylori
71	c1h2iG_	Alignment	not modelled	5.3	57	**PDB header:**dna-binding protein **Chain:** G: **PDB Molecule:**dna repair protein rad52 homolog; **PDBTitle:** human rad52 protein, n-terminal domain
72	c2cooA_	Alignment	not modelled	5.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
73	d1x2la1	Alignment	not modelled	5.3	15	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
74	c2oasA_	Alignment	not modelled	5.2	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coenzyme a transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.