Phyre2

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Description	P0A6M4
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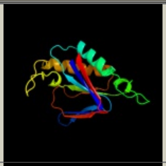
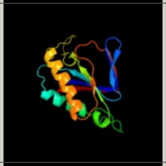
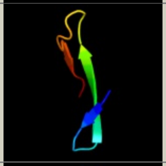
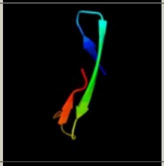
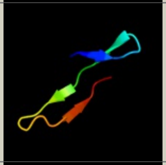
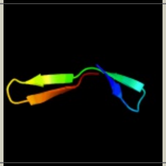
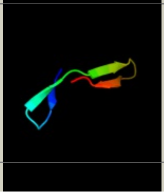
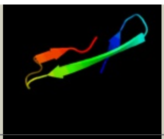
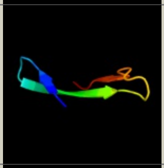
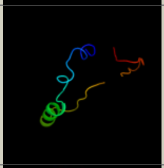
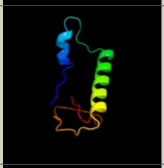
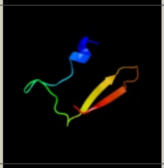
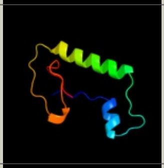
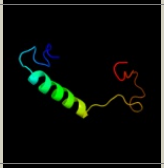
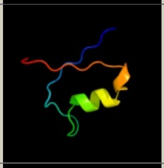
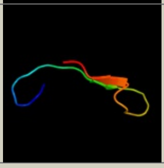
Unique Job ID	4094e3cf6bd409f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jkea_	Alignment		100.0	100	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
2	d1j7ga_	Alignment		100.0	68	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
3	c2dboA_	Alignment		100.0	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus
4	c3ko7E_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** dtd from plasmodium falciparum in complex with d-lysine
5	c2okvC_	Alignment		100.0	41	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable d-tyrosyl-trna(tyr) deacylase 1; **PDBTitle:** c-myc dna unwinding element binding protein
6	d1tc5a_	Alignment		100.0	19	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
7	d2k8ea1	Alignment		68.6	8	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
8	d2k49a2	Alignment		67.1	12	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
9	d3bida1	Alignment		66.5	20	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
10	d2k7ia1	Alignment		61.3	20	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
11	c2k7iB_	Alignment		61.3	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0339 protein atu0232; **PDBTitle:** solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.

12	c2k49A_	Alignment		55.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein so_3888; **PDBTitle:** solution nmr structure of upf0339 protein so3888 from shewanella2 oneidensis. northeast structural genomics consortium target sor190
13	c2k8eA_	Alignment		52.1	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0339 protein yegp; **PDBTitle:** solution nmr structure of protein of unknown function yegp from e.2 coli. ontario center for structural proteomics target ec0640_1_1233 northeast structural genomics consortium target et102.
14	d1s7ia_	Alignment		45.8	8	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
15	c2z8nB_	Alignment		45.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**27.5 kda virulence protein; **PDBTitle:** structural basis for the catalytic mechanism of phosphothreonine lyase
16	d1llna_	Alignment		35.7	23	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Plant cytotoxins
17	c3i0uA_	Alignment		26.4	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphothreonine lyase ospf; **PDBTitle:** structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri
18	c1k6mA_	Alignment		23.3	6	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
19	c2dclB_	Alignment		23.2	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503; **PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3
20	d2k8ea2	Alignment		21.8	26	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
21	c2dgaA_	Alignment	not modelled	19.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of hexameric beta-glucosidase in wheat
22	d1onka_	Alignment	not modelled	19.6	16	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Plant cytotoxins
23	c3gnoA_	Alignment	not modelled	19.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**os03g0212800 protein; **PDBTitle:** crystal structure of a rice os3bglu6 beta-glucosidase
24	d2giab1	Alignment	not modelled	16.3	22	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Guide RNA binding protein gBP
25	c2giaB_	Alignment	not modelled	16.3	22	**PDB header:**translation **Chain:** B: **PDB Molecule:**mitochondrial rna-binding protein 1; **PDBTitle:** crystal structures of trypanosoma bruciei mrp1/mrp2
26	c1bifA_	Alignment	not modelled	15.7	10	**PDB header:**bifunctional enzyme **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; **PDBTitle:** 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
27	d2d6fc3	Alignment	not modelled	15.6	19	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
28	c3tekA_	Alignment	not modelled	14.6	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**thermodbp-single stranded dna binding protein; **PDBTitle:** thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
						Fold: Flavodoxin-like

29	d1a9xb2	Alignment	not modelled	13.4	42	**Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
30	c2d6fC_	Alignment	not modelled	13.3	19	**PDB header:**ligase/rna **Chain:** C: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit e; **PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
31	d1ofua2	Alignment	not modelled	11.6	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
32	c2xtsD_	Alignment	not modelled	10.3	23	**PDB header:**oxidoreductase/electron transport **Chain:** D: **PDB Molecule:**cytochrome; **PDBTitle:** crystal structure of the sulfane dehydrogenase soxcd from paracoccus2 pantotrophus
33	d2k49a1	Alignment	not modelled	10.1	25	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
34	d1ii2a2	Alignment	not modelled	10.0	11	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
35	d1s9ra_	Alignment	not modelled	9.9	21	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
36	c2an7A_	Alignment	not modelled	9.9	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard
37	d1s1ma1	Alignment	not modelled	9.7	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
38	d1nlqa_	Alignment	not modelled	9.7	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Nucleoplasmin-like core domain **Family:**Nucleoplasmin-like core domain
39	d1j3ba2	Alignment	not modelled	9.5	28	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
40	d1rq2a2	Alignment	not modelled	9.3	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
41	d2ftsa1	Alignment	not modelled	9.0	21	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
42	c2hl2A_	Alignment	not modelled	8.9	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
43	d1nm3a2	Alignment	not modelled	8.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
44	d2j44a2	Alignment	not modelled	8.4	13	**Fold:**Prealbumin-like **Superfamily:**Starch-binding domain-like **Family:**PUD-like
45	d1xrua1	Alignment	not modelled	8.2	26	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
46	c3h0mE_	Alignment	not modelled	8.1	20	**PDB header:**ligase **Chain:** E: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
47	c3h16A_	Alignment	not modelled	8.1	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tir protein; **PDBTitle:** crystal structure of a bacteria tir domain, pdtir from2 paracoccus denitrificans
48	c3k6sB_	Alignment	not modelled	7.7	26	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
49	d1k8wa5	Alignment	not modelled	7.7	16	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
50	d2ob5a1	Alignment	not modelled	7.7	21	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
51	d1o51a_	Alignment	not modelled	7.7	15	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
52	c3r84O_	Alignment	not modelled	7.5	19	**PDB header:**transcription **Chain:** O: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 11; **PDBTitle:** structure of the mediator head subcomplex med11/22
53	c2g5xA_	Alignment	not modelled	7.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribosome-inactivating protein; **PDBTitle:** crystal structure of lychnin a type 1 ribosome inactivating2 protein (rip)
54	d1cb0a_	Alignment	not modelled	7.3	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
55	d2f2ab2	Alignment	not modelled	7.3	22	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like

56	d1tf5a1	Alignment	not modelled	7.3	38	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
57	d1a79a1	Alignment	not modelled	7.3	21	**Fold:**Restriction endonuclease-like **Superfamily:**tRNA-intron endonuclease catalytic domain-like **Family:**tRNA-intron endonuclease catalytic domain-like
58	c1keeH_	Alignment	not modelled	7.2	42	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
59	d1ogda_	Alignment	not modelled	7.2	17	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
60	c2v4uA_	Alignment	not modelled	7.1	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthase 2; **PDBTitle:** human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
61	c3epyA_	Alignment	not modelled	7.0	22	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coa-binding domain-containing protein 7; **PDBTitle:** crystal structure of human acyl-coa binding domain 72 complexed with palmitoyl-coa
62	d1wv8a1	Alignment	not modelled	7.0	11	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like **Family:**TTHA1013-like
63	c2dzlA_	Alignment	not modelled	6.7	38	**PDB header:**structural genomics unknown function **Chain:** A: **PDB Molecule:**protein fam100b; **PDBTitle:** solution structure of the uba domain in human protein2 fam100b
64	c2copA_	Alignment	not modelled	6.7	26	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**acyl-coenzyme a binding domain containing 6; **PDBTitle:** solution structure of rsgi ruh-040, an acbp domain from2 human cdna
65	d1ce7a_	Alignment	not modelled	6.5	25	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Plant cytotoxins
66	c2pebB_	Alignment	not modelled	6.4	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative dioxygenase; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f1925) from nostoc2 punctiforme pcc 73102 at 1.46 a resolution
67	c3mk9A_	Alignment	not modelled	6.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ricin; **PDBTitle:** stabilized ricin immunogen 1-33/44-198
68	c3mvkA_	Alignment	not modelled	6.4	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein fucu; **PDBTitle:** the crystal structure of fucu from bifidobacterium longum to 1.65a
69	c1a79B_	Alignment	not modelled	6.3	21	**PDB header:**endonuclease **Chain:** B: **PDB Molecule:**trna endonuclease; **PDBTitle:** crystal structure of the trna splicing endonuclease from2 methanococcus jannaschii
70	d2olra2	Alignment	not modelled	6.1	14	**Fold:**PEP carboxykinase N-terminal domain **Superfamily:**PEP carboxykinase N-terminal domain **Family:**PEP carboxykinase N-terminal domain
71	d1gtfa_	Alignment	not modelled	6.1	32	**Fold:**Double-stranded beta-helix **Superfamily:**TRAP-like **Family:**Trp RNA-binding attenuation protein (TRAP)
72	d1kska3	Alignment	not modelled	6.1	56	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
73	d1i96v_	Alignment	not modelled	6.1	23	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
74	c3icgD_	Alignment	not modelled	6.0	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endoglucanase d; **PDBTitle:** crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
75	c2i1vB_	Alignment	not modelled	5.7	10	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
76	d1rxxa_	Alignment	not modelled	5.7	18	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Arginine deiminase
77	c2z5sN_	Alignment	not modelled	5.6	11	**PDB header:**cell cycle **Chain:** N: **PDB Molecule:**mdm4 protein; **PDBTitle:** molecular basis for the inhibition of p53 by mdmx
78	c2g5iB_	Alignment	not modelled	5.6	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase **PDBTitle:** structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
79	d1t4aa_	Alignment	not modelled	5.4	21	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
80	c3al0B_	Alignment	not modelled	5.3	22	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
						PDB header:structural genomics, unknown function

81	c2yx5A_	Alignment	not modelled	5.2	10	**Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
82	d1p8ja1	Alignment	not modelled	5.2	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Proprotein convertase P-domain
83	d2q3na1	Alignment	not modelled	5.2	13	**Fold:**Ribosome inactivating proteins (RIP) **Superfamily:**Ribosome inactivating proteins (RIP) **Family:**Plant cytotoxins