Phyre2

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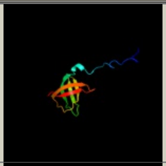
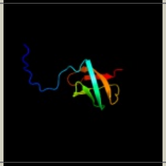
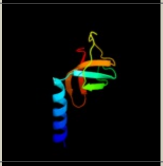
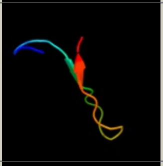
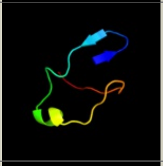
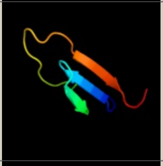
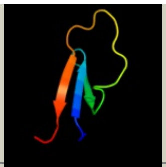
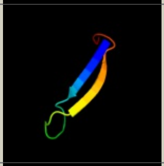
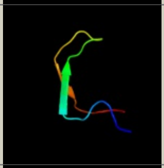
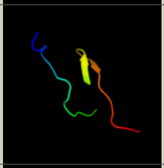
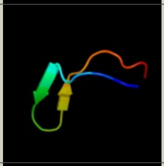
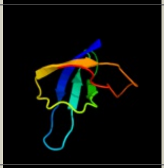
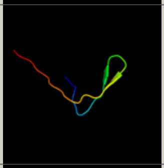
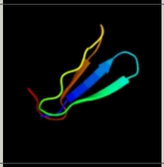
Description	P0AAS3
Date	Thu Jan 5 11:13:40 GMT 2012
Unique Job ID	4573f68575a02432

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5hA_	Alignment		99.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
2	d2exda1	Alignment		99.5	17	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
3	c3cp0A_	Alignment		99.4	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
4	c2k14A_	Alignment		99.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**yuaf protein; **PDBTitle:** solution structure of the soluble domain of the nfed2 protein yuaf from bacillus subtilis
5	c3fjsC_	Alignment		42.6	26	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like cupin fold; **PDBTitle:** crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
6	d1mvfd_	Alignment		42.6	29	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/Peml addiction antidote
7	c3e0eA_	Alignment		41.3	28	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a; **PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
8	d1xrua1	Alignment		36.9	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
9	c2nv4A_	Alignment		35.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0066 protein af_0241; **PDBTitle:** crystal structure of upf0066 protein af0241 in complex with2 s-adenosylmethionine. northeast structural genomics3 consortium target gr27
10	c1ywkE_	Alignment		35.5	14	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**4-deoxy-l-threo-5-hexosulose-uronate ketol- **PDBTitle:** crystal structure of 4-deoxy-1-threo-5-hexosulose-uronate2 ketol-isomerase from enterococcus faecalis
11	c3a5zF_	Alignment		32.3	22	**PDB header:**ligase **Chain:** F: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of escherichia coli genx in complex with elongation2 factor p

12	d1ywka1	Alignment		28.4	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**KduI-like
13	c2p0pA_	Alignment		27.0	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**alr1010 protein; **PDBTitle:** calcium binding protein in the free form
14	d1nppa2	Alignment		26.5	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
15	c2e6zA_	Alignment		26.0	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
16	c3okxA_	Alignment		24.9	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yaeb-like protein rpa0152; **PDBTitle:** crystal structure of yaeb-like protein from rhodopseudomonas palustris
17	c2yv5A_	Alignment		24.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
18	d1ueba1	Alignment		24.4	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
19	c2ozjB_	Alignment		24.2	8	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel; **PDBTitle:** crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
20	d1nnxa_	Alignment		23.9	13	**Fold:**OB-fold **Superfamily:**Hypothetical protein YgiW **Family:**Hypothetical protein YgiW
21	d1nz9a_	Alignment	not modelled	23.9	18	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
22	d1x6oa1	Alignment	not modelled	23.7	18	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
23	d2huha1	Alignment	not modelled	23.7	8	**Fold:**C2 domain-like **Superfamily:**Smr-associated domain-like **Family:**Smr-associated domain
24	d1ub4c_	Alignment	not modelled	21.8	22	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
25	c2qjlA_	Alignment	not modelled	21.8	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
26	d1vfsa1	Alignment	not modelled	21.5	18	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
27	c2k6pA_	Alignment	not modelled	21.1	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
28	d1v43a2	Alignment	not modelled	20.9	26	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
29	d2fo0a1	Alignment	not modelled	20.9	13	**Fold:**SH3-like barrel **Superfamily:**SH3-domain

						Family:SH3-domain
30	d1tkea1	Alignment	not modelled	20.8	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
31	d1u0la1	Alignment	not modelled	20.7	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
32	d1wgka_	Alignment	not modelled	20.0	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
33	d1xo3a_	Alignment	not modelled	19.7	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
34	d1orua_	Alignment	not modelled	19.6	16	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**MOSC (MOCO sulphurase C-terminal) domain
35	d1k25a2	Alignment	not modelled	19.5	8	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
36	c2kvqG_	Alignment	not modelled	19.2	16	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
37	c2jvvA_	Alignment	not modelled	19.2	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
38	c1xtdA_	Alignment	not modelled	18.5	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic initiation factor 5a; **PDBTitle:** structural analysis of leishmania mexicana eukaryotic initiation2 factor 5a
39	d1wfwa_	Alignment	not modelled	18.5	16	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
40	d1tq5a1	Alignment	not modelled	17.9	7	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Pirin-like
41	d1yhfa1	Alignment	not modelled	17.7	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
42	c1bkbA_	Alignment	not modelled	17.6	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 5a; **PDBTitle:** initiation factor 5a from archebacterium pyrobaculum2 aerophilum
43	d1whoa_	Alignment	not modelled	17.3	14	**Fold:**C2 domain-like **Superfamily:**PHL pollen allergen **Family:**PHL pollen allergen
44	d2vv5a1	Alignment	not modelled	17.3	22	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
45	c2pfwB_	Alignment	not modelled	17.2	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
46	c2k9xA_	Alignment	not modelled	17.0	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
47	c3b9bA_	Alignment	not modelled	16.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
48	c3di4A_	Alignment	not modelled	16.3	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein duf1989; **PDBTitle:** crystal structure of a duf1989 family protein (spo0365) from2 silicibacter pomeroyi dss-3 at 1.60 a resolution
49	c3oyyA_	Alignment	not modelled	16.2	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of pseudomonas aeruginosa elongation factor p
50	c2i0nA_	Alignment	not modelled	15.8	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**class vii unconventional myosin; **PDBTitle:** structure of dictyostelium discoideum myosin vii sh3 domain2 with adjacent proline rich region
51	c3fn2A_	Alignment	not modelled	15.3	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative sensor histidine kinase domain; **PDBTitle:** crystal structure of a putative sensor histidine kinase domain from2 clostridium symbiosum atcc 14940
52	d2pi2a1	Alignment	not modelled	15.1	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
53	c3treA_	Alignment	not modelled	14.9	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of a translation elongation factor p (efp) from coxiella2 burnetii
54	d1ue9a_	Alignment	not modelled	14.7	22	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
55	c1vftA_	Alignment	not modelled	14.7	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of l-cycloserine-bound form of alanine2

						racemase from d-cycloserine-producing streptomyces3 lavendulae
56	c3e0jG_	Alignment	not modelled	14.2	13	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
57	c3oruA_	Alignment	not modelled	14.1	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**duf1989 family protein; **PDBTitle:** crystal structure of a duf1989 family protein (tm1040_0329) from2 silicibacter sp. tm1040 at 1.11 a resolution
58	d2gcxa1	Alignment	not modelled	14.0	0	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
59	c2jw4A_	Alignment	not modelled	13.8	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cytoplasmic protein nck1; **PDBTitle:** nmr solution structure of the n-terminal sh3 domain of2 human nckalpha
60	d1dm9a_	Alignment	not modelled	13.6	11	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
61	c1dm9A_	Alignment	not modelled	13.6	11	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
62	d1zud21	Alignment	not modelled	13.3	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
63	c3hksB_	Alignment	not modelled	13.1	19	**PDB header:**translation, rna binding protein **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 5a-2; **PDBTitle:** crystal structure of eukaryotic translation initiation2 factor eif-5a2 from arabidopsis thaliana
64	d1tygb_	Alignment	not modelled	12.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
65	d1nyra2	Alignment	not modelled	12.8	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
66	c2j6kE_	Alignment	not modelled	12.4	4	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**cd2-associated protein; **PDBTitle:** n-terminal sh3 domain of cms (cd2ap human homolog)
67	c2dy3B_	Alignment	not modelled	12.2	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from corynebacterium glutamicum
68	c3lwcA_	Alignment	not modelled	12.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
69	d1wlpb1	Alignment	not modelled	11.9	26	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
70	c2eifA_	Alignment	not modelled	11.5	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (eukaryotic translation initiation factor 5a); **PDBTitle:** eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
71	c3cwiA_	Alignment	not modelled	11.1	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
72	d1j3ta_	Alignment	not modelled	11.1	7	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
73	c3dwmA_	Alignment	not modelled	10.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
74	c1ybyB_	Alignment	not modelled	10.8	15	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation elongation factor p; **PDBTitle:** conserved hypothetical protein cth-95 from clostridium2 thermocellum
75	c1uebB_	Alignment	not modelled	10.6	15	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of translation elongation factor p from2 thermus thermophilus hb8
76	d1ueba3	Alignment	not modelled	10.4	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
77	c3gf5A_	Alignment	not modelled	10.3	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**major vault protein; **PDBTitle:** crystal structure of the p21 r1-r7 n-terminal domain of murine mvp
78	d1bkba1	Alignment	not modelled	10.2	20	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
79	d1iz6a1	Alignment	not modelled	10.2	19	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
80	c3k3sG_	Alignment	not modelled	10.1	20	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**altronate hydrolase; **PDBTitle:** crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
						PDB header:biosynthetic protein

81	c1iz6B_	Alignment	not modelled	10.0	19	**Chain:** B: **PDB Molecule:**initiation factor 5a; **PDBTitle:** crystal structure of translation initiation factor 5a from pyrococcus2 horikoshii
82	c3i4oA_	Alignment	not modelled	10.0	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
83	d2as0a1	Alignment	not modelled	10.0	35	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
84	d1oqka_	Alignment	not modelled	10.0	13	**Fold:**Rof/RNase P subunit-like **Superfamily:**Rof/RNase P subunit-like **Family:**RNase P subunit p29-like
85	d1vqot1	Alignment	not modelled	9.5	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
86	c2rqrA_	Alignment	not modelled	9.3	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**engulfment and cell motility protein 1, linker, dedicator **PDBTitle:** the solution structure of human dock2 sh3 domain - elmo1 peptide2 chimera complex
87	c2kymA_	Alignment	not modelled	9.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**bud emergence protein 1; **PDBTitle:** solution structure of the bem1p sh3-ci domain from l.elongisporus in2 complex with ste20p peptide
88	d1psea_	Alignment	not modelled	9.2	23	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
89	c1y7xA_	Alignment	not modelled	9.2	11	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**major vault protein; **PDBTitle:** solution structure of a two-repeat fragment of major vault2 protein
90	d2d40a1	Alignment	not modelled	9.2	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Gentisate 1,2-dioxygenase-like
91	c1tygG_	Alignment	not modelled	9.2	14	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
92	c2jlnA_	Alignment	not modelled	9.1	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
93	c1zlmA_	Alignment	not modelled	9.1	5	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**osteoclast stimulating factor 1; **PDBTitle:** crystal structure of the sh3 domain of human osteoclast2 stimulating factor
94	c3p8bB_	Alignment	not modelled	9.0	30	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
95	d1m1ha1	Alignment	not modelled	8.9	15	**Fold:**N-utilization substance G protein NusG, insert domain **Superfamily:**N-utilization substance G protein NusG, insert domain **Family:**N-utilization substance G protein NusG, insert domain
96	d1uhfa_	Alignment	not modelled	8.9	14	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
97	c4a1cS_	Alignment	not modelled	8.8	10	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rpl26; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
98	c2kq8A_	Alignment	not modelled	8.7	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell wall hydrolase; **PDBTitle:** solution nmr structure of a domain from bt9727_4915 from2 bacillus thuringiensis, northeast structural genomics3 consortium target bur95a
99	c2k6dA_	Alignment	not modelled	8.5	14	**PDB header:**sh3 domain/ubiquitin **Chain:** A: **PDB Molecule:**sh3 domain-containing kinase-binding protein 1; **PDBTitle:** cin85 sh3-c domain in complex with ubiquitin