Phyre^2

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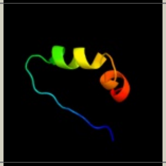
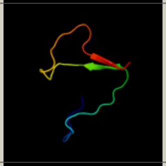
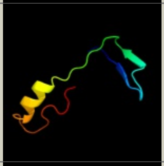
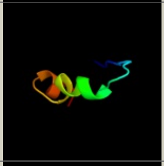
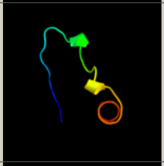
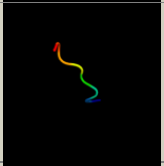
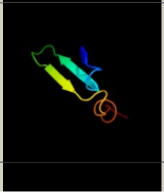
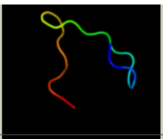
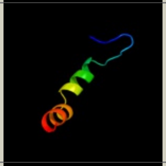
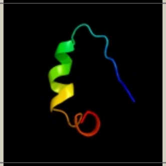
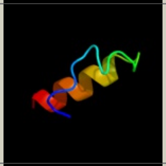
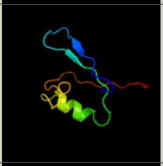
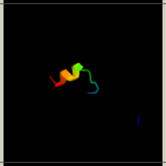
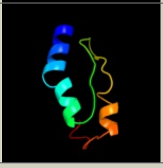
Description	P33353
Date	Thu Jan 5 11:51:54 GMT 2012
Unique Job ID	a1ceb9407ef865e4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oy5a_	Alignment		57.6	33	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
2	c1oy5B_	Alignment		56.7	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
3	d2b5id2	Alignment		35.6	21	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
4	d1s6la2	Alignment		25.7	14	**Fold:**NosL/MerB-like **Superfamily:**NosL/MerB-like **Family:**MerB-like
5	d1p9pa_	Alignment		20.4	22	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
6	d1nfga1	Alignment		19.5	10	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
7	d1uala_	Alignment		18.2	22	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
8	c3quvB_	Alignment		17.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
9	c3knuD_	Alignment		16.7	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
10	d1dx5i2	Alignment		14.0	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
11	c2l6nA_	Alignment		13.4	15	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_001092504.1; **PDBTitle:** nmr solution structure of the protein yp_001092504.1

12	d1zaka2	Alignment		13.1	50	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
13	d2ih2a2	Alignment		12.9	24	**Fold:**DNA methylase specificity domain **Superfamily:**DNA methylase specificity domain **Family:**TaqI C-terminal domain-like
14	c3ky7A_	Alignment		12.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
15	c1v85A_	Alignment		11.7	33	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**similar to ring finger protein 36; **PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator
16	d1nh8a2	Alignment		11.6	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
17	d2akja4	Alignment		11.6	20	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
18	c3pvcA_	Alignment		11.3	38	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of apo mnmc from yersinia pestis
19	c2e58D_	Alignment		10.5	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**mnmc2; **PDBTitle:** crystal structure of mnmc2 from aquifex aeolicus
20	d1veha_	Alignment		10.4	20	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
21	c3luuA_	Alignment	not modelled	10.3	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein with unknown function which belongs to2 pfam duf971 family (afe_2189) from acidithiobacillus ferrooxidans3 atcc 23270 at 1.93 a resolution
22	d2bt6a1	Alignment	not modelled	10.1	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
23	d1zj8a4	Alignment	not modelled	9.6	10	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
24	c3pghD_	Alignment	not modelled	9.3	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cyclooxygenase-2; **PDBTitle:** cyclooxygenase-2 (prostaglandin synthase-2) complexed with a non-2 selective inhibitor, flurbiprofen
25	c2jdjB_	Alignment	not modelled	9.3	7	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**redy-like protein; **PDBTitle:** crystal structure of hapk from hahella chejuensis
26	d1nkia_	Alignment	not modelled	9.2	30	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
27	c1ddxA_	Alignment	not modelled	8.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (prostaglandin h2 synthase-2); **PDBTitle:** crystal structure of a mixture of arachidonic acid and prostaglandin2 bound to the cyclooxygenase active site of cox-2: prostaglandin3 structure
28	d3cu0a1	Alignment	not modelled	8.4	25	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase

29	d1m7xa1	Alignment	not modelled	8.3	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
30	d3proc2	Alignment	not modelled	8.0	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
31	c1pggB_	Alignment	not modelled	7.8	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin h2 synthase-1; **PDBTitle:** prostaglandin h2 synthase-1 complexed with 1-(4-iodobenzoyl)-5-2 methoxy-2-methylindole-3-acetic acid (iodoindomethacin), trans model
32	c1ht8B_	Alignment	not modelled	7.8	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin h2 synthase-1; **PDBTitle:** the 2.7 angstrom resolution model of ovine cox-1 complexed with2 alclofenac
33	c2oyuP_	Alignment	not modelled	7.7	38	**PDB header:**oxidoreductase **Chain:** P: **PDB Molecule:**prostaglandin g/h synthase 1; **PDBTitle:** indomethacin-(s)-alpha-ethyl-ethanolamide bound to cyclooxygenase-1
34	d1xr4a2	Alignment	not modelled	7.5	16	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
35	d2r7da1	Alignment	not modelled	7.3	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
36	c2d0jD_	Alignment	not modelled	7.2	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
37	d1v82a_	Alignment	not modelled	7.1	25	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
38	c2lkjA_	Alignment	not modelled	7.1	44	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-m; **PDBTitle:** structures and interaction analyses of the integrin alpha-m beta-22 cytoplasmic tails
39	d1wgya_	Alignment	not modelled	7.1	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
40	c2ofqA_	Alignment	not modelled	7.0	11	**PDB header:**protein transport/protein transport **Chain:** A: **PDB Molecule:**trao; **PDBTitle:** nmr solution structure of a complex between the virb9/virb72 interaction domains of the pkm101 type iv secretion system
41	c2kakA_	Alignment	not modelled	6.8	47	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ec protein i/ii; **PDBTitle:** solution structure of the beta-e-domain of wheat ec-12 metallothionein
42	d1xhja_	Alignment	not modelled	6.7	17	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
43	d1bxni_	Alignment	not modelled	6.7	4	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
44	d1npba_	Alignment	not modelled	6.7	30	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
45	c2kvhA_	Alignment	not modelled	6.6	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
46	c2k49A_	Alignment	not modelled	6.4	19	**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
47	c2x8nA_	Alignment	not modelled	6.4	11	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**cv0863; **PDBTitle:** solution nmr structure of uncharacterized protein cv08632 from chromobacterium violaceum. northeast structural3 genomics target (nesg) target cvt3. ocsp4 target cv0863.
48	d1uzhc1	Alignment	not modelled	6.4	9	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
49	c3iefA_	Alignment	not modelled	6.4	19	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
50	c3n5nX_	Alignment	not modelled	6.2	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase; **PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
51	c2d2aA_	Alignment	not modelled	6.1	25	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**sufa protein; **PDBTitle:** crystal structure of escherichia coli sufa involved in2 biosynthesis of iron-sulfur clusters
52	c2k8oA_	Alignment	not modelled	6.1	78	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-l; **PDBTitle:** solution structure of integrin alpha l
53	c2k7iB_	Alignment	not modelled	6.1	25	**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.
54	d2k7ia1	Alignment	not modelled	6.1	25	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
55	c1aqsA_	Alignment	not modelled	6.1	43	**PDB header:**metallothionein **Chain:** A: **PDB Molecule:**cu-metallothionein; **PDBTitle:** cu-metallothionein from saccharomyces cerevisiae, nmr, 102 structures
56	d3bida1	Alignment	not modelled	6.0	6	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
57	d2a2pa1	Alignment	not modelled	5.9	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
58	d1tkea1	Alignment	not modelled	5.9	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
59	c3ps9A_	Alignment	not modelled	5.9	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
60	c2p58B_	Alignment	not modelled	5.8	42	**PDB header:**transport protein/chaperone **Chain:** B: **PDB Molecule:**putative type iii secretion protein yscf; **PDBTitle:** structure of the yersinia pestis type iii secretion system2 needle protein yscf in complex with its chaperones3 ysce/yscg
61	d1rbli_	Alignment	not modelled	5.7	9	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
62	c2p0tA_	Alignment	not modelled	5.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0307 protein pspto_4464; **PDBTitle:** structural genomics, the crystal structure of a conserved putative2 protein from pseudomonas syringae pv. tomato str. dc3000
63	d2p0ta1	Alignment	not modelled	5.5	14	**Fold:**PSPTO4464-like **Superfamily:**PSPTO4464-like **Family:**PSPTO4464-like
64	d1wxma1	Alignment	not modelled	5.5	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
65	d1w7ja1	Alignment	not modelled	5.5	27	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
66	c3jqoH_	Alignment	not modelled	5.4	11	**PDB header:**transport protein **Chain:** H: **PDB Molecule:**trao protein; **PDBTitle:** crystal structure of the outer membrane complex of a type iv2 secretion system
67	c2k8eA_	Alignment	not modelled	5.4	16	**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.
68	c2apnA_	Alignment	not modelled	5.3	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein hi1723; **PDBTitle:** hi1723 solution structure
69	c2vncB_	Alignment	not modelled	5.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycogen operon protein glgx; **PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
70	d1q4ga2	Alignment	not modelled	5.3	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
71	c3fqmA_	Alignment	not modelled	5.2	38	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural protein 5a; **PDBTitle:** crystal structure of a novel dimeric form of hcv ns5a domain i protein
72	d1xrta1	Alignment	not modelled	5.2	19	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
73	c1q40C_	Alignment	not modelled	5.1	19	**PDB header:**translation **Chain:** C: **PDB Molecule:**mrna transport regulator mtr2; **PDBTitle:** crystal structure of the c. albicans mtr2-mex67 m domain complex
74	d1wjpa2	Alignment	not modelled	5.1	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2