Phyre2

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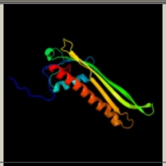
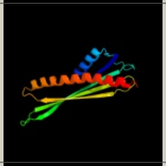
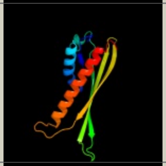
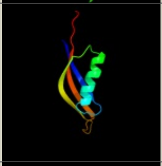
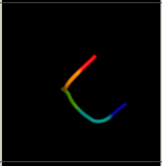
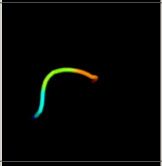
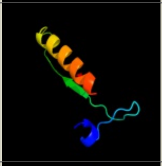
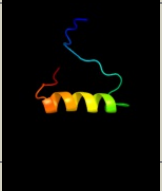
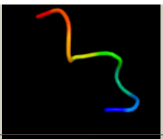
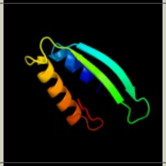
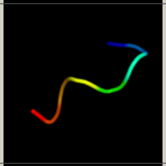
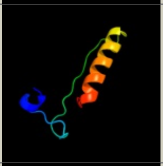
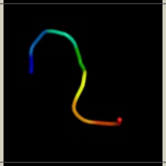
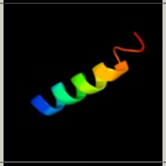
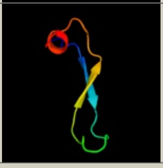
Description	P0ADC1
Date	Thu Jan 5 11:20:33 GMT 2012
Unique Job ID	59d823930f1c55c5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jxpA_	Alignment		100.0	16	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein b; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
2	c2r76A_	Alignment		100.0	34	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**rare lipoprotein b; **PDBTitle:** crystal structure of the rare lipoprotein b (so_1173) from shewanella2 oneidensis, northeast structural genomics consortium target sor91a
3	c3bf2A_	Alignment		100.0	27	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of the a1ksw9_neimf protein from2 neisseria meningitidis. northeast structural genomics3 consortium target mr36a
4	c3oqtP_	Alignment		35.9	17	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
5	c2x5eA_	Alignment		35.3	60	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0271 protein pa4511; **PDBTitle:** crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
6	d1xw8a_	Alignment		34.6	60	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
7	c3onrI_	Alignment		30.2	14	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
8	c2vxaL_	Alignment		30.0	24	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
9	d2ux9a1	Alignment		29.4	19	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
10	d1zlqa1	Alignment		18.4	12	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
11	d2dfaa1	Alignment		18.2	29	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like

12	c2obkE_	Alignment		17.7	50	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**selt/selw/selh selenoprotein domain; **PDBTitle:** x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
13	d1v6ta_	Alignment		17.6	13	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
14	c3mgjA_	Alignment		16.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1480; **PDBTitle:** crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
15	c2ojlB_	Alignment		16.5	50	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
16	c2grvC_	Alignment		15.7	17	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**lpqw; **PDBTitle:** crystal structure of lpqw
17	d1a6ca3	Alignment		15.7	36	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
18	c3dexA_	Alignment		15.5	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sav_2001; **PDBTitle:** crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
19	c2kncA_	Alignment		15.2	35	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
20	c2vsvB_	Alignment		14.6	30	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2
21	d2fa8a1	Alignment	not modelled	14.1	50	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
22	d1b8qa_	Alignment	not modelled	14.0	17	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
23	c2p0gB_	Alignment	not modelled	13.9	50	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**selenoprotein w-related protein; **PDBTitle:** crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75
24	c3od1A_	Alignment	not modelled	13.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase regulatory subunit; **PDBTitle:** the crystal structure of an atp phosphoribosyltransferase regulatory2 subunit/histidyl-trna synthetase from bacillus halodurans c
25	c2pxgA_	Alignment	not modelled	13.3	50	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein; **PDBTitle:** nmr solution structure of omla
26	d1x61a2	Alignment	not modelled	13.1	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
27	d2fnea1	Alignment	not modelled	13.1	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
28	d1nn4a_	Alignment	not modelled	12.7	26	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
						PDB header:isomerase

29	c3s5pA_	Alignment	not modelled	12.1	24	**Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
30	c2a40F_	Alignment	not modelled	11.8	60	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**wiskott-aldrich syndrome protein family member 2; **PDBTitle:** ternary complex of the wh2 domain of wave with actin-dnase i
31	c2a40C_	Alignment	not modelled	11.8	60	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**wiskott-aldrich syndrome protein family member 2; **PDBTitle:** ternary complex of the wh2 domain of wave with actin-dnase i
32	c2v90E_	Alignment	not modelled	10.4	26	**PDB header:**protein-binding **Chain:** E: **PDB Molecule:**pdz domain-containing protein 3; **PDBTitle:** crystal structure of the 3rd pdz domain of intestine- and2 kidney-enriched pdz domain ikepp (pdzd3)
33	d2ex2a1	Alignment	not modelled	9.8	11	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
34	c1iclA_	Alignment	not modelled	9.6	42	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**th1ox; **PDBTitle:** solution structure of designed beta-sheet mini-protein th1ox
35	c3ol0C_	Alignment	not modelled	9.0	50	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**de novo designed monomer trefoil-fold sub-domain which **PDBTitle:** crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
36	d1qbea_	Alignment	not modelled	8.9	21	**Fold:**RNA bacteriophage capsid protein **Superfamily:**RNA bacteriophage capsid protein **Family:**RNA bacteriophage capsid protein
37	c3lvuB_	Alignment	not modelled	8.5	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
38	d2c7na1	Alignment	not modelled	8.3	75	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**A20-like zinc finger
39	c2db5A_	Alignment	not modelled	8.3	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the first pdz domain of inad-like2 protein
40	c2c7mA_	Alignment	not modelled	7.9	75	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**rab guanine nucleotide exchange factor 1; **PDBTitle:** human rabex-5 residues 1-74 in complex with ubiquitin
41	c3v2gA_	Alignment	not modelled	7.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of a dehydrogenase/reductase from sinorhizobium2 meliloti 1021
42	d1hu3a_	Alignment	not modelled	7.7	13	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
43	c3ghfA_	Alignment	not modelled	7.7	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
44	c2kzyA_	Alignment	not modelled	7.2	75	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zfand5 protein (zinc finger protein 216 (predicted), **PDBTitle:** solution nmr structure of the znf216 a20 zinc finger
45	d1vpta_	Alignment	not modelled	7.1	38	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap methylase
46	d2ccqa1	Alignment	not modelled	7.1	13	**Fold:**PUG domain-like **Superfamily:**PUG domain-like **Family:**PUG domain
47	d1g9oa_	Alignment	not modelled	7.1	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
48	c2fgyA_	Alignment	not modelled	6.9	38	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxysome shell polypeptide; **PDBTitle:** beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csosca)
49	d1uf2c1	Alignment	not modelled	6.8	67	**Fold:**A virus capsid protein alpha-helical domain **Superfamily:**A virus capsid protein alpha-helical domain **Family:**Phytoreovirus capsid
50	c1vp3A_	Alignment	not modelled	6.6	38	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**vp39; **PDBTitle:** vaccinia virus protein vp39 in complex with s-adenosylhomocysteine
51	c1v39A_	Alignment	not modelled	6.6	38	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**vp39; **PDBTitle:** dc26 mutant of vaccinia virus protein vp39 in complex with s-2 adenosylhomocysteine and m7g(5')pppg
52	c2k1aA_	Alignment	not modelled	6.6	32	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
53	c3k7pA_	Alignment	not modelled	6.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.

54	c3m1pA_	Alignment	not modelled	6.6	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
55	c3l3bA_	Alignment	not modelled	6.6	67	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
56	c2iwnA_	Alignment	not modelled	6.3	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 3rd pdz domain of multiple pdz domain protein mpdz (casp2 target)
57	c3ftoA_	Alignment	not modelled	6.3	15	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**oligopeptide-binding protein oppa; **PDBTitle:** crystal structure of oppa in a open conformation
58	c3ry3B_	Alignment	not modelled	6.3	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative solute-binding protein; **PDBTitle:** putative solute-binding protein from yersinia pestis.
59	d1w5da1	Alignment	not modelled	6.3	12	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
60	d1ncfa3	Alignment	not modelled	6.1	43	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**TNF receptor-like
61	c1ztyA_	Alignment	not modelled	6.1	12	**PDB header:**sugar binding protein, signaling protein **Chain:** A: **PDB Molecule:**chitin oligosaccharide binding protein; **PDBTitle:** crystal structure of the chitin oligasaccharide binding2 protein
62	c2ogpA_	Alignment	not modelled	5.8	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** solution structure of the second pdz domain of par-3
63	c3j00Z_	Alignment	not modelled	5.8	18	**PDB header:**ribosome/ribosomal protein **Chain:** Z: **PDB Molecule:**cell division protein ftsq; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
64	d1um1a_	Alignment	not modelled	5.7	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
65	d1vp8a_	Alignment	not modelled	5.7	30	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
66	d1jjcb5	Alignment	not modelled	5.6	25	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
67	c1vdfB_	Alignment	not modelled	5.6	13	**PDB header:**extracellular matrix protein **Chain:** B: **PDB Molecule:**cartilage oligomeric matrix protein; **PDBTitle:** assembly domain of cartilage oligomeric matrix protein
68	d2d5ua1	Alignment	not modelled	5.6	13	**Fold:**PUG domain-like **Superfamily:**PUG domain-like **Family:**PUG domain
69	c2npbA_	Alignment	not modelled	5.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw
70	c2iwoA_	Alignment	not modelled	5.5	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** 12th pdz domain of multiple pdz domain protein mpdz (casp2 target)
71	d1k32a1	Alignment	not modelled	5.5	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
72	d2vvpa1	Alignment	not modelled	5.4	20	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
73	c3he8A_	Alignment	not modelled	5.1	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
74	c2kr1A_	Alignment	not modelled	5.1	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin protein ligase e3a; **PDBTitle:** solution nmr structure of zinc binding n-terminal domain of ubiquitin-2 protein ligase e3a from homo sapiens. northeast structural genomics3 consortium (nesg) target hr3662
75	d2d9ia1	Alignment	not modelled	5.1	21	**Fold:**IF3-like **Superfamily:**SMR domain-like **Family:**Smr domain