

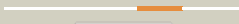






















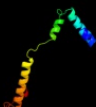







Phyre2

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Description	P29013
Date	Thu Jan 5 11:45:33 GMT 2012
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b7uX_	 Alignment		92.2	19	PDB header: hydrolase Chain: X: PDB Molecule: leukotriene a-4 hydrolase; PDBTitle: leukotriene a4 hydrolase complexed with kelatorphan
2	c3ciaA_	 Alignment		89.9	15	PDB header: hydrolase Chain: A: PDB Molecule: cold-active aminopeptidase; PDBTitle: crystal structure of cold-aminopeptidase from colwellia2 psychrerythraea
3	c3iukB_	 Alignment		89.7	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aureescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
4	c2xpyA_	 Alignment		84.1	20	PDB header: hydrolase Chain: A: PDB Molecule: leukotriene a-4 hydrolase; PDBTitle: structure of native leukotriene a4 hydrolase from saccharomyces2 cerevisiae
5	c3o0yC_	 Alignment		83.6	24	PDB header: lipid binding protein Chain: C: PDB Molecule: lipoprotein; PDBTitle: the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
6	c3se6A_	 Alignment		79.7	16	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 2; PDBTitle: crystal structure of the human endoplasmic reticulum aminopeptidase 2
7	c3qnfA_	 Alignment		65.7	13	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: crystal structure of the open state of human endoplasmic reticulum2 aminopeptidase 1 erap1
8	c1z5hB_	 Alignment		65.4	21	PDB header: hydrolase Chain: B: PDB Molecule: tricorn protease interacting factor f3; PDBTitle: crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
9	c1yewC_	 Alignment		50.4	43	PDB header: oxidoreductase, membrane protein Chain: C: PDB Molecule: particulate methane monooxygenase subunit c2; PDBTitle: crystal structure of particulate methane monooxygenase
10	c3mdjB_	 Alignment		50.1	14	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: er aminopeptidase, erap1, bound to the zinc aminopeptidase inhibitor,2 bestatin
11	d1q8ca_	 Alignment		35.9	23	Fold: NusB-like Superfamily: NusB-like Family: Hypothetical protein MG027

12	d3b7sa3	Alignment		34.3	19	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Leukotriene A4 hydrolase catalytic domain
13	c3chxG_	Alignment		33.0	43	PDB header: membrane protein Chain: G: PDB Molecule: pmoc; PDBTitle: crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
14	c2xdtA_	Alignment		31.0	18	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum aminopeptidase 1; PDBTitle: crystal structure of the soluble domain of human2 endoplasmic reticulum aminopeptidase 1 erap1
15	d1wpba_	Alignment		29.9	9	Fold: YfbU-like Superfamily: YfbU-like Family: YfbU-like
16	c2knaA_	Alignment		29.7	18	PDB header: apoptosis Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 4; PDBTitle: solution structure of uba domain of xiap
17	c2qffA_	Alignment		28.5	19	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of staphylococcal complement inhibitor
18	c2da4A_	Alignment		27.8	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dkfzp686k21156; PDBTitle: solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
19	c1ceuA_	Alignment		24.6	22	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 regulatory protein n-terminal PDBTitle: nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
20	d1dl2a_	Alignment		23.7	17	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1,2-mannosidase, catalytic domain
21	c3t4aG_	Alignment	not modelled	23.4	25	PDB header: immune system Chain: G: PDB Molecule: fibrinogen-binding protein; PDBTitle: structure of a truncated form of staphylococcal complement inhibitor b2 bound to human c3c at 3.4 angstrom resolution
22	d1x9da1	Alignment	not modelled	23.3	20	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1,2-mannosidase, catalytic domain
23	c1x9dA_	Alignment	not modelled	23.3	20	PDB header: hydrolase Chain: A: PDB Molecule: endoplasmic reticulum mannosyl-oligosaccharide 1, PDBTitle: crystal structure of human class i alpha-1,2-mannosidase in2 complex with thio-disaccharide substrate analogue
24	d2zdra2	Alignment	not modelled	23.1	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
25	c2kfvA_	Alignment	not modelled	22.1	13	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 3; PDBTitle: structure of the amino-terminal domain of human fk506-2 binding protein 3 / northeast structural genomics3 consortium target ht99a
26	c2vo9C_	Alignment	not modelled	21.0	16	PDB header: hydrolase Chain: C: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: crystal structure of the enzymatically active domain of the2 listeria monocytogenes bacteriophage 500 endolysin ply500
27	c1g6iA_	Alignment	not modelled	20.6	17	PDB header: hydrolase Chain: A: PDB Molecule: class i alpha-1,2-mannosidase; PDBTitle: crystal structure of the yeast alpha-1,2-mannosidase with bound 1-2 deoxymannojirimycin at 1.59 a resolution PDB header: hydrolase

28	c2gtqA_	Alignment	not modelled	18.4	12	Chain: A: PDB Molecule: aminopeptidase n; PDBTitle: crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
29	d1lvfa_	Alignment	not modelled	18.2	22	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
30	d1x2na1	Alignment	not modelled	17.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
31	d1hcua_	Alignment	not modelled	17.2	11	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
32	d1qd1a2	Alignment	not modelled	17.0	20	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
33	d1nxca_	Alignment	not modelled	16.8	16	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
34	d1m15a1	Alignment	not modelled	16.7	19	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
35	d2vo9a1	Alignment	not modelled	16.6	16	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanY-like
36	c3bpqC_	Alignment	not modelled	16.3	26	PDB header: toxin Chain: C: PDB Molecule: antitoxin relb3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
37	d2oc6a1	Alignment	not modelled	15.8	23	Fold: Secretion chaperone-like Superfamily: YdhG-like Family: YdhG-like
38	c3fpvC_	Alignment	not modelled	15.7	10	PDB header: heme binding protein Chain: C: PDB Molecule: extracellular haem-binding protein; PDBTitle: crystal structure of hbps
39	c2kvrA_	Alignment	not modelled	15.6	4	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 7; PDBTitle: solution nmr structure of human ubiquitin specific protease2 usp7 ubl domain (residues 537-664). nesg target hr4395c/3 sgc-toronto
40	d1du6a_	Alignment	not modelled	15.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
41	d1ndba1	Alignment	not modelled	15.3	23	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
42	c2nrzB_	Alignment	not modelled	14.9	19	PDB header: hydrolase Chain: B: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal half of uvrc bound to2 its catalytic divalent cation
43	c3ayhA_	Alignment	not modelled	14.7	22	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase iii subunit rpc9; PDBTitle: crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
44	d2ri9a1	Alignment	not modelled	14.3	13	Fold: alpha/alpha toroid Superfamily: Seven-hairpin glycosidases Family: Class I alpha-1;2-mannosidase, catalytic domain
45	d3cx5i1	Alignment	not modelled	13.9	6	Fold: Single transmembrane helix Superfamily: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
46	c1krfA_	Alignment	not modelled	13.8	13	PDB header: hydrolase Chain: A: PDB Molecule: mannosyl-oligosaccharide alpha-1,2-mannosidase; PDBTitle: structure of p. citrinum alpha 1,2-mannosidase reveals the basis for2 differences in specificity of the er and golgi class i enzymes
47	c2xr9A_	Alignment	not modelled	13.8	26	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2)
48	c3izbU_	Alignment	not modelled	12.9	20	PDB header: ribosome Chain: U: PDB Molecule: 40s ribosomal protein s24; PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
49	d1mv8a1	Alignment	not modelled	12.8	28	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
50	d1miaa2	Alignment	not modelled	12.8	8	Fold: BRCA2 tower domain Superfamily: BRCA2 tower domain Family: BRCA2 tower domain
51	d1fra2	Alignment	not modelled	12.7	86	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
52	c3mlcC_	Alignment	not modelled	12.6	20	PDB header: isomerase Chain: C: PDB Molecule: fg41 malonate semialdehyde decarboxylase;

						PDBTitle: crystal structure of fg41msad inactivated by 3-chloropropiolate
53	d2g1da1	Alignment	not modelled	12.2	9	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
54	d1m5sa2	Alignment	not modelled	12.1	86	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
55	d1mylb_	Alignment	not modelled	12.1	62	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
56	d1m5ha2	Alignment	not modelled	12.0	86	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
57	c3ezkB_	Alignment	not modelled	12.0	29	PDB header: hydrolase Chain: B: PDB Molecule: dna packaging protein gp17; PDBTitle: bacteriophage t4 gp17 motor assembly based on crystal2 structures and cryo-em reconstructions
58	d1eg1a_	Alignment	not modelled	12.0	26	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
59	c2vzaD_	Alignment	not modelled	11.9	29	PDB header: cell adhesion Chain: D: PDB Molecule: cell filamentation protein; PDBTitle: type iv secretion system effector protein bepa
60	c3pbpL_	Alignment	not modelled	11.7	80	PDB header: transport protein, structural protein Chain: L: PDB Molecule: nucleoporin nup159; PDBTitle: structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex
61	d1x6ma_	Alignment	not modelled	11.5	18	Fold: Mss4-like Superfamily: Mss4-like Family: Glutathione-dependent formaldehyde-activating enzyme, Gfa
62	c3pg8B_	Alignment	not modelled	11.5	13	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
63	d1zxoal	Alignment	not modelled	11.2	57	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
64	c2xrgA_	Alignment	not modelled	11.2	26	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleotide pyrophosphatase/phosphodiesterase family PDBTitle: crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
65	c2dmnA_	Alignment	not modelled	11.1	24	PDB header: transcription Chain: A: PDB Molecule: homeobox protein tgif2lx; PDBTitle: the solution structure of the homeobox domain of human2 homeobox protein tgif2lx
66	d2a21a1	Alignment	not modelled	11.1	10	Fold: Profilin-like Superfamily: GlcG-like Family: GlcG-like
67	d1crka1	Alignment	not modelled	10.8	19	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
68	c3bbnR_	Alignment	not modelled	10.8	38	PDB header: ribosome Chain: R: PDB Molecule: ribosomal protein s18; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
69	c3e38A_	Alignment	not modelled	10.6	29	PDB header: hydrolase Chain: A: PDB Molecule: two-domain protein containing predicted php-like metal- PDBTitle: crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bv_u_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
70	d1myla_	Alignment	not modelled	10.6	62	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
71	c3mgwA_	Alignment	not modelled	10.5	25	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme g; PDBTitle: thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
72	c3cezA_	Alignment	not modelled	10.4	29	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
73	c1w9iA_	Alignment	not modelled	10.3	13	PDB header: myosin Chain: A: PDB Molecule: myosin ii heavy chain; PDBTitle: myosin ii dictyostelium discoideum motor domain s456y bound2 with mgadp-befx
74	d1tlua1	Alignment	not modelled	10.2	23	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
75	c2y8pA_	Alignment	not modelled	10.2	8	PDB header: lyase Chain: A: PDB Molecule: endo-type membrane-bound lytic murein transglycosylase a; PDBTitle: crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
76	c2ktrA_	Alignment	not modelled	10.2	7	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs

77	d1bazb_	Alignment	not modelled	10.1	62	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
78	c2nrrA_	Alignment	not modelled	10.1	25	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal rnaseh endonuclease2 domain of uvrbc
79	c2l1uA_	Alignment	not modelled	10.0	50	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b2, mitochondrial; PDBTitle: structure-functional analysis of mammalian msrb2 protein
80	c3c65A_	Alignment	not modelled	10.0	12	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearothermophilus uvrC 5'2 endonuclease domain
81	c3mnwP_	Alignment	not modelled	9.9	30	PDB header: immune system Chain: P: PDB Molecule: gp41; PDBTitle: crystal structure of the non-neutralizing hiv antibody 13h11 fab2 fragment with a gp41 mper-derived peptide in a helical conformation
82	d1xrsb2	Alignment	not modelled	9.9	16	Fold: Dodecin subunit-like Superfamily: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain Family: D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
83	d1atia2	Alignment	not modelled	9.9	10	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
84	d1b28a_	Alignment	not modelled	9.7	62	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
85	d1qh4a1	Alignment	not modelled	9.6	13	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
86	c2p58C_	Alignment	not modelled	9.5	26	PDB header: transport protein/chaperone Chain: C: PDB Molecule: putative type iii secretion protein yscg; PDBTitle: structure of the yersinia pestis type iii secretion system2 needle protein yscf in complex with its chaperones3 ysce/yscg
87	d1jjcb2	Alignment	not modelled	9.4	22	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
88	d2ctda1	Alignment	not modelled	9.4	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
89	d1xm0a1	Alignment	not modelled	9.4	50	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
90	d2qkwa1	Alignment	not modelled	9.3	32	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Avirulence protein AvrPto Family: Avirulence protein AvrPto
91	c2qkwa_	Alignment	not modelled	9.3	32	PDB header: transferase Chain: A: PDB Molecule: avirulence protein; PDBTitle: structural basis for activation of plant immunity by2 bacterial effector protein avrpto
92	c3kztB_	Alignment	not modelled	9.3	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
93	c2k8dA_	Alignment	not modelled	9.2	43	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msrb; PDBTitle: solution structure of a zinc-binding methionine sulfoxide reductase
94	c1l6jA_	Alignment	not modelled	9.2	60	PDB header: hydrolase Chain: A: PDB Molecule: matrix metalloproteinase-9; PDBTitle: crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
95	d1myka_	Alignment	not modelled	9.2	62	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
96	c1xuzA_	Alignment	not modelled	9.2	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siac; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminol
97	c3mnzP_	Alignment	not modelled	9.1	30	PDB header: immune system Chain: P: PDB Molecule: gp41 mper-derived peptide; PDBTitle: crystal structure of the non-neutralizing hiv antibody 13h11 fab2 fragment with a gp41 mper-derived peptide bearing ala substitutions3 in a helical conformation
98	d1bdta_	Alignment	not modelled	9.0	62	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
99	c2kl4A_	Alignment	not modelled	9.0	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2032 protein; PDBTitle: nmr structure of the protein nb7804a