

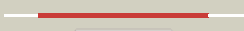















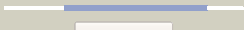
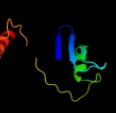





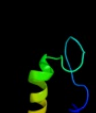




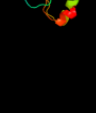


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AAT2
Date	Thu Jan 5 11:13:45 GMT 2012
Unique Job ID	1bc5d1759b5739f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2fkia1</a>	 Alignment		100.0	23	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YjbR-like <b>Family:</b> YjbR-like
2	<a href="#">d2a1va1</a>	 Alignment		100.0	33	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YjbR-like <b>Family:</b> YjbR-like
3	<a href="#">c3h9xB_</a>	 Alignment		100.0	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein pspto_3016; <b>PDBTitle:</b> crystal structure of the pspto_3016 protein from2 pseudomonas syringae, northeast structural genomics3 consortium target psr293
4	<a href="#">d2oc6a1</a>	 Alignment		97.3	13	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YdhG-like <b>Family:</b> YdhG-like
5	<a href="#">d2i8da1</a>	 Alignment		97.2	14	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YdhG-like <b>Family:</b> YdhG-like
6	<a href="#">d2od0a1</a>	 Alignment		96.8	17	<b>Fold:</b> Secretion chaperone-like <b>Superfamily:</b> YgaC/TfoX-N like <b>Family:</b> TfoX N-terminal domain-like
7	<a href="#">c2kl4A_</a>	 Alignment		96.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bh2032 protein; <b>PDBTitle:</b> nmr structure of the protein nb7804a
8	<a href="#">c3n0kA_</a>	 Alignment		39.2	14	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> serine protease inhibitor 1; <b>PDBTitle:</b> proteinase inhibitor from coprinopsis cinerea
9	<a href="#">c3s83A_</a>	 Alignment		21.5	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ggdef family protein; <b>PDBTitle:</b> crystal structure of eal domain from caulobacter crescentus cb15
10	<a href="#">d2j7qa1</a>	 Alignment		21.2	11	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> M48USP-like
11	<a href="#">c2raxY_</a>	 Alignment		18.0	17	<b>PDB header:</b> cell cycle <b>Chain:</b> Y: <b>PDB Molecule:</b> borealin; <b>PDBTitle:</b> crystal structure of borealin (20-78) bound to survivin (1-120)

12	<a href="#">d1lq9a_</a>	Alignment		15.7	5	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Actinorhodin biosynthesis monooxygenase ActVa-Orf6
13	<a href="#">d1pu1a_</a>	Alignment		14.6	4	<b>Fold:</b> Hypothetical protein MTH677 <b>Superfamily:</b> Hypothetical protein MTH677 <b>Family:</b> Hypothetical protein MTH677
14	<a href="#">d1xx6a1</a>	Alignment		12.7	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Type II thymidine kinase
15	<a href="#">d2i0ka1</a>	Alignment		11.8	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> FAD-linked oxidases, C-terminal domain <b>Family:</b> Cholesterol oxidase
16	<a href="#">c3cb4D_</a>	Alignment		11.5	13	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> the crystal structure of lepa
17	<a href="#">c1ybxA_</a>	Alignment		10.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> conserved hypothetical protein cth-383 from clostridium thermocellum
18	<a href="#">d1igna1</a>	Alignment		7.9	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> DNA-binding domain of rap1
19	<a href="#">c1gmuB_</a>	Alignment		7.0	17	<b>PDB header:</b> metallochaperone <b>Chain:</b> B: <b>PDB Molecule:</b> uree; <b>PDBTitle:</b> structure of uree
20	<a href="#">d1nyra3</a>	Alignment		6.9	12	<b>Fold:</b> RRF/tRNA synthetase additional domain-like <b>Superfamily:</b> ThrRS/AlaRS common domain <b>Family:</b> Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
21	<a href="#">c1xnwD_</a>	Alignment	not modelled	6.9	15	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> propionyl-coa carboxylase complex b subunit; <b>PDBTitle:</b> apo-coa carboxylase beta subunit from s. coelicolor (pccb),2 apo form #2, mutant d422i
22	<a href="#">d1na6a2</a>	Alignment	not modelled	6.8	24	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Type II restriction endonuclease catalytic domain
23	<a href="#">c3rpjA_</a>	Alignment	not modelled	6.5	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> curlin genes transcriptional regulator; <b>PDBTitle:</b> structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
24	<a href="#">c1ij3A_</a>	Alignment	not modelled	6.3	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
25	<a href="#">c1ws1A_</a>	Alignment	not modelled	6.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide deformylase 1; <b>PDBTitle:</b> structure analysis of peptide deformylase from bacillus2 cereus
26	<a href="#">d1o4sa_</a>	Alignment	not modelled	6.1	17	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> AAT-like
27	<a href="#">d1ix1a_</a>	Alignment	not modelled	6.1	17	<b>Fold:</b> Peptide deformylase <b>Superfamily:</b> Peptide deformylase <b>Family:</b> Peptide deformylase
28	<a href="#">d2glz1a1</a>	Alignment	not modelled	6.0	5	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> FwdE-like <b>Family:</b> FwdE-like

29	<a href="#">c3qu1B_</a>	Alignment	not modelled	6.0	17	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> peptide deformylase 2; <b>PDBTitle:</b> peptide deformylase from vibrio cholerae
30	<a href="#">dliwga1</a>	Alignment	not modelled	6.0	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains <b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
31	<a href="#">c2w3tA_</a>	Alignment	not modelled	5.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide deformylase; <b>PDBTitle:</b> chloro complex of the ni-form of e.coli deformylase
32	<a href="#">c2i06A_</a>	Alignment	not modelled	5.7	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> phycobilisome lcm core-membrane linker polypeptide; <b>PDBTitle:</b> solution nmr structure of the pbs linker polypeptide domain (fragment2 254-400) of phycobilisome linker protein apce from synechocystis sp.3 pcc 6803. northeast structural genomics consortium target sgr209c
33	<a href="#">c2fyfB_</a>	Alignment	not modelled	5.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoserine aminotransferase; <b>PDBTitle:</b> structure of a putative phosphoserine aminotransferase from2 mycobacterium tuberculosis
34	<a href="#">d1pixa3</a>	Alignment	not modelled	5.5	10	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain