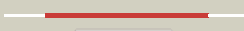
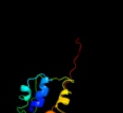
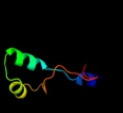
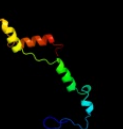
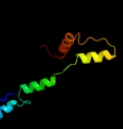


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P46022
Date	Thu Jan 5 12:03:55 GMT 2012
Unique Job ID	a0f16afa0265c34b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dwkC_	 Alignment		100.0	30	PDB header: transferase Chain: C: PDB Molecule: penicillin-binding protein 2; PDBTitle: identification of dynamic structural motifs involved in2 peptidoglycan glycosyltransfer
2	c2olva_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding protein 2; PDBTitle: structural insight into the transglycosylation step of bacterial cell2 wall biosynthesis : donor ligand complex
3	c3hzsA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
4	d2oqoa1	 Alignment		100.0	40	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
5	d2olua1	 Alignment		100.0	30	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
6	c3fwlA_	 Alignment		100.0	30	PDB header: transferase, hydrolase Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: crystal structure of the full-length transglycosylase pbp1b2 from escherichia coli
7	c3udiA_	 Alignment		100.0	32	PDB header: penicillin-binding protein/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
8	c2wadB_	 Alignment		98.5	7	PDB header: peptide binding protein Chain: B: PDB Molecule: penicillin-binding protein 2b; PDBTitle: penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204)
9	c1pmdA_	 Alignment		90.7	13	PDB header: peptidoglycan synthesis Chain: A: PDB Molecule: peptidoglycan synthesis multifunctional enzyme; PDBTitle: penicillin-binding protein 2x (pbp-2x)
10	d1mv8a1	 Alignment		49.4	16	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
11	d1dlja1	 Alignment		37.4	16	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: UDP-glucose/GDP-mannose dehydrogenase dimerisation domain

12	c3zriA	Alignment		28.4	15	PDB header: chaperone Chain: A: PDB Molecule: clpb protein; PDBTitle: n-domain of clpv from vibrio cholerae
13	d1qvra1	Alignment		28.3	15	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
14	d2ieaa3	Alignment		27.7	17	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
15	d2guka1	Alignment		27.1	25	Fold: PG1857-like Superfamily: PG1857-like Family: PG1857-like
16	c2k77A	Alignment		26.9	11	PDB header: chaperone, protein binding Chain: A: PDB Molecule: negative regulator of genetic competence PDBTitle: nmr solution structure of the bacillus subtilis clpc n-2 domain
17	c3fesB	Alignment		26.3	22	PDB header: atp binding protein Chain: B: PDB Molecule: atp-dependent clp endopeptidase; PDBTitle: crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile
18	d1e6vb2	Alignment		26.1	21	Fold: Ferredoxin-like Superfamily: Methyl-coenzyme M reductase subunits Family: Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
19	d1hbnb2	Alignment		24.3	17	Fold: Ferredoxin-like Superfamily: Methyl-coenzyme M reductase subunits Family: Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
20	d3broa1	Alignment		17.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
21	d2iyva1	Alignment	not modelled	15.9	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
22	d2fbha1	Alignment	not modelled	15.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
23	c3kaeC	Alignment	not modelled	13.9	30	PDB header: protein binding Chain: C: PDB Molecule: possible protein of nuclear scaffold; PDBTitle: cdc27 n-terminus
24	c3gg2B	Alignment	not modelled	13.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
25	c2cv8A	Alignment	not modelled	13.1	29	PDB header: hydrolase Chain: A: PDB Molecule: trna-splicing endonuclease; PDBTitle: crystal structure of trna-intron endonuclease from2 sulfobolus tokodaii
26	d1q3ta	Alignment	not modelled	12.4	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
27	c2kvrA	Alignment	not modelled	11.7	33	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
28	c3sqgE	Alignment	not modelled	11.4	21	PDB header: transferase Chain: E: PDB Molecule: methyl-coenzyme m reductase, beta subunit;

						PDBTitle: crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats PDB header: methanogenesis Chain: E: PDB Molecule: methyl-coenzyme m reductase i beta subunit; PDBTitle: methyl-coenzyme m reductase enzyme product complex
29	c1hbmE_	Alignment	not modelled	11.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fr253; PDBTitle: crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.
30	c3fdfA_	Alignment	not modelled	11.4	17	Fold: Inhibitor of vertebrate lysozyme, lvy Superfamily: Inhibitor of vertebrate lysozyme, lvy Family: Inhibitor of vertebrate lysozyme, lvy
31	d1gpga_	Alignment	not modelled	11.3	26	PDB header: cell cycle/protein-binding Chain: B: PDB Molecule: 26s protease regulatory subunit 6b; PDBTitle: structure of the oncoprotein gankyrin in complex with s62 atpase of the 26s proteasome
32	c2dvwB_	Alignment	not modelled	11.3	13	PDB header: hydrolase Chain: D: PDB Molecule: trna-splicing endonuclease; PDBTitle: splicing endonuclease from aeropyrum pernix
33	c3ajvD_	Alignment	not modelled	11.1	33	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, marr family; PDBTitle: crystal structure of marr family transcription regulator sp03579
34	c3bj6B_	Alignment	not modelled	11.0	17	PDB header: apoptosis inhibitor Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 2; PDBTitle: structure of ciap1 card
35	c2l9mA_	Alignment	not modelled	10.7	16	PDB header: isomerase Chain: A: PDB Molecule: inositol-3-phosphate synthase; PDBTitle: myo-inositol 1-phosphate synthase from mycobacterium2 tuberculosis in complex with nad and zinc.
36	c1gr0A_	Alignment	not modelled	9.9	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
37	d1e6ca_	Alignment	not modelled	9.7	24	PDB header: protein binding Chain: D: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: crystal structure analysis of yeast nas6p complexed with2 the proteasome subunit, rpt3
38	c2dzoD_	Alignment	not modelled	9.6	14	PDB header: transcription Chain: F: PDB Molecule: mediator of rna polymerase ii transcription subunit 22; PDBTitle: structure of the mediator head subcomplex med11/22
39	c3r84F_	Alignment	not modelled	9.5	30	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
40	c3o2qB_	Alignment	not modelled	9.4	17	Fold: DEATH domain Superfamily: DEATH domain Family: Caspase recruitment domain, CARD
41	d1dгна_	Alignment	not modelled	9.3	16	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
42	c3r0aB_	Alignment	not modelled	9.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: gdp-mannose 6-dehydrogenase; PDBTitle: 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from pseudomonas aeruginosa
43	c1mv8A_	Alignment	not modelled	8.8	16	PDB header: transcription Chain: B: PDB Molecule: marr-family transcriptional regulator; PDBTitle: crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
44	c3nqoB_	Alignment	not modelled	8.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
45	d1k6ma1	Alignment	not modelled	8.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain
46	d1m8pa3	Alignment	not modelled	8.5	14	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
47	c3csqC_	Alignment	not modelled	8.1	11	PDB header: transferase Chain: A: PDB Molecule: shikimate kinase; PDBTitle: structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
48	c1zuiA_	Alignment	not modelled	8.1	19	PDB header: hydrolase Chain: B: PDB Molecule: glutaminase; PDBTitle: probable glutaminase from geobacillus kaustophilus hta426
49	c2pbyB_	Alignment	not modelled	8.1	20	PDB header: transferase Chain: C: PDB Molecule: xanthosine methyltransferase; PDBTitle: the structure of xanthosine methyltransferase
50	c2eg5C_	Alignment	not modelled	8.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: SWIRM domain
51	d2dw4a1	Alignment	not modelled	8.0	19	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
52	d1tdza1	Alignment	not modelled	7.9	13	Fold: P-loop containing nucleoside triphosphate hydrolases

53	d1rkba_	Alignment	not modelled	7.9	14	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
54	d1kaga_	Alignment	not modelled	7.8	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
55	d1k82a1	Alignment	not modelled	7.8	8	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
56	c3prjB_	Alignment	not modelled	7.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
57	d1m6ex_	Alignment	not modelled	7.6	37	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Salicylic acid carboxyl methyltransferase (SAMT)
58	d2grrb1	Alignment	not modelled	7.5	17	Fold: alpha-alpha superhelix Superfamily: Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain Family: Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain
59	d2htja1	Alignment	not modelled	7.5	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FaeA-like
60	d1gr0a1	Alignment	not modelled	7.4	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
61	c3o2sB_	Alignment	not modelled	7.2	17	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72 complex
62	d1b79a_	Alignment	not modelled	7.1	18	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
63	d1r2za1	Alignment	not modelled	6.7	17	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
64	c2h2wA_	Alignment	not modelled	6.6	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
65	d1b7go2	Alignment	not modelled	6.5	32	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
66	c2rh5B_	Alignment	not modelled	6.4	19	PDB header: transferase Chain: B: PDB Molecule: adenylate kinase; PDBTitle: structure of apo adenylate kinase from aquifex aeolicus
67	c2wgoA_	Alignment	not modelled	6.3	43	PDB header: surfactant protein Chain: A: PDB Molecule: ranaspumin-2; PDBTitle: structure of ranaspumin-2, a surfactant protein from the2 foam nests of a tropical frog
68	c1x1qA_	Alignment	not modelled	6.3	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
69	c3cugD_	Alignment	not modelled	6.3	12	PDB header: protein transport Chain: D: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
70	c1rqtB_	Alignment	not modelled	6.3	22	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
71	c1rqtA_	Alignment	not modelled	6.3	22	PDB header: ribosome Chain: A: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: nmr structure of dimeric n-terminal domain of ribosomal2 protein l7 from e.coli
72	d1rqta_	Alignment	not modelled	6.3	22	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
73	c3imkA_	Alignment	not modelled	6.2	14	PDB header: metal binding protein Chain: A: PDB Molecule: putative molybdenum carrier protein; PDBTitle: crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
74	d1jeqa1	Alignment	not modelled	6.2	23	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
75	d1jwea_	Alignment	not modelled	6.2	19	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
76	c2q3eH_	Alignment	not modelled	6.1	11	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
77	d1rz4a2	Alignment	not modelled	6.1	18	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Eukaryotic translation initiation factor 3 subunit 12, eIF3k, N-terminal domain

78	c3omdB_	Alignment	not modelled	6.1	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of unknown function protein from leptospirillum2 rubarum
79	c3akcA_	Alignment	not modelled	6.0	21	PDB header: transferase Chain: A: PDB Molecule: cytidylate kinase; PDBTitle: crystal structure of cmp kinase in complex with cdp and adp from2 thermus thermophilus hb8
80	c3cwbQ_	Alignment	not modelled	6.0	24	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
81	c2a6eF_	Alignment	not modelled	5.9	15	PDB header: transferase Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: crystal structure of the t. thermophilus rna polymerase2 holoenzyme
82	c3fh2A_	Alignment	not modelled	5.8	11	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent protease (heat shock protein); PDBTitle: the crystal structure of the probable atp-dependent protease (heat2 shock protein) from corynebacterium glutamicum
83	d1lk3a_	Alignment	not modelled	5.8	13	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
84	d1vhxa_	Alignment	not modelled	5.8	24	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
85	c3fdiA_	Alignment	not modelled	5.6	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
86	d2czca1	Alignment	not modelled	5.6	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
87	c3b5iB_	Alignment	not modelled	5.6	16	PDB header: transferase Chain: B: PDB Molecule: s-adenosyl-l-methionine:salicylic acid carboxyl PDBTitle: crystal structure of indole-3-acetic acid methyltransferase
88	c1jirA_	Alignment	not modelled	5.6	23	PDB header: dna binding protein Chain: A: PDB Molecule: thyroid autoantigen; PDBTitle: the three-dimensional structure of the c-terminal dna2 binding domain of human ku70
89	d1mkia_	Alignment	not modelled	5.5	15	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Glutaminase
90	d1ee8a1	Alignment	not modelled	5.5	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
91	c3uo9B_	Alignment	not modelled	5.5	24	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: crystal structure of human gac in complex with glutamate and bptes
92	c2nyxB_	Alignment	not modelled	5.5	9	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
93	d1tfra1	Alignment	not modelled	5.3	17	Fold: SAM domain-like Superfamily: 5' to 3' exonuclease, C-terminal subdomain Family: 5' to 3' exonuclease, C-terminal subdomain
94	d1ux8a_	Alignment	not modelled	5.3	17	Fold: Globin-like Superfamily: Globin-like Family: Truncated hemoglobin
95	c3nw0B_	Alignment	not modelled	5.3	23	PDB header: metal binding protein Chain: B: PDB Molecule: melanoma-associated antigen g1; PDBTitle: crystal structure of mageg1 and nse1 complex
96	c1z1sA_	Alignment	not modelled	5.3	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa3332; PDBTitle: crystal structure of putative isomerase pa3332 from2 pseudomonas aeruginosa
97	c3iz6M_	Alignment	not modelled	5.2	37	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s18 (s13p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
98	c3ss4C_	Alignment	not modelled	5.2	24	PDB header: hydrolase Chain: C: PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form
99	c3g79A_	Alignment	not modelled	5.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; PDBTitle: crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1