
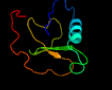
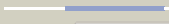



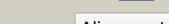


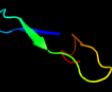

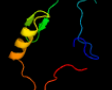



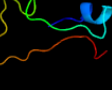
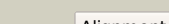





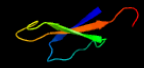
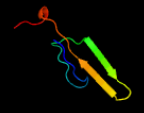



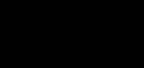





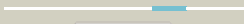


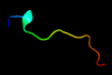

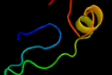

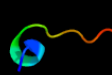

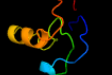





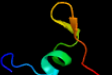



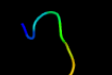



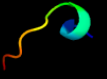



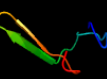



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uf0a_	 Alignment		29.3	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
2	c4atul_	 Alignment		25.5	15	PDB header: hydrolase Chain: I: PDB Molecule: neuronal migration protein doublecortin; PDBTitle: human doublecortin n-dc repeat plus linker, and tubulin (2xrp) docked2 into an 8a cryo-em map of doublecortin-stabilised microtubules3 reconstructed in absence of kinesin
3	c5mslA_	 Alignment		22.0	23	PDB header: transcription Chain: A: PDB Molecule: anti-sigma-f factor fin; PDBTitle: solution structure of the b. subtilis anti-sigma-f factor, fin
4	cli26A_	 Alignment		19.5	75	PDB header: toxin Chain: A: PDB Molecule: ptu-1; PDBTitle: solution structure of ptu-1, a toxin from the assassin bugs2 peirates turpis that blocks the voltage sensitive calcium3 channel n-type
5	c5zjlA_	 Alignment		18.5	33	PDB header: allergen Chain: A: PDB Molecule: der f 23 allergen; PDBTitle: crystal structure of the dust mite allergen der f 23 from2 dermatophagoides farinae
6	d1pn0a2	 Alignment		15.7	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
7	d1t1ja_	 Alignment		15.2	20	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: Hypothetical protein PA1492
8	c5nmpF_	 Alignment		14.3	30	PDB header: hydrolase Chain: F: PDB Molecule: isatin hydrolase; PDBTitle: isatin hydrolase a (iha) from ralstonia solanacearum
9	d1sxje1	 Alignment		14.3	27	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
10	c3d23A_	 Alignment		14.1	45	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 3c-like proteinase; PDBTitle: main protease of hcov-hku1
11	c6e7kB_	 Alignment		13.8	32	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis

12	d1nsla_	Alignment		13.8	28	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
13	c6erdD_	Alignment		13.4	19	PDB header: transferase Chain: D: PDB Molecule: aminoglycoside n6'-acetyltransferase; PDBTitle: crystal structure of a putative acetyltransferase from bacillus cereus2 species.
14	c2q6fB_	Alignment		12.6	45	PDB header: hydrolase Chain: B: PDB Molecule: infectious bronchitis virus (ibv) main protease; PDBTitle: crystal structure of infectious bronchitis virus (ibv) main protease2 in complex with a michael acceptor inhibitor n3
15	c6f2rK_	Alignment		12.5	40	PDB header: chaperone Chain: K: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
16	d1lvaa_	Alignment		12.5	45	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
17	d1mjda_	Alignment		12.3	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
18	c4xfqB_	Alignment		11.8	45	PDB header: hydrolase Chain: B: PDB Molecule: pedv main protease; PDBTitle: crystal structure basis for pedv 3c like protease
19	c2ynbA_	Alignment		11.7	45	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like proteinase; PDBTitle: crystal structure of the main protease of coronavirus hku4 in complex2 with a michael acceptor sg85
20	c3tloA_	Alignment		11.4	45	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like proteinase; PDBTitle: crystal structure of hcov-nl63 3c-like protease
21	d1p9sa_	Alignment	not modelled	11.3	45	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
22	c1y6uA_	Alignment	not modelled	10.7	27	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
23	c6fb3A_	Alignment	not modelled	10.7	20	PDB header: cell adhesion Chain: A: PDB Molecule: teneurin-2; PDBTitle: teneurin 2 partial extracellular domain
24	d1mg4a_	Alignment	not modelled	10.6	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
25	c6b4aB_	Alignment	not modelled	9.9	18	PDB header: structural protein Chain: B: PDB Molecule: doublecortin; PDBTitle: crystal structure of the c-terminal domain of doublecortin (tgdcx)2 from toxoplasma gondii me49
26	d2duca1	Alignment	not modelled	9.8	36	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
27	c2d2aA_	Alignment	not modelled	9.3	19	PDB header: metal transport Chain: A: PDB Molecule: sufa protein; PDBTitle: crystal structure of escherichia coli sufa involved in biosynthesis of2 iron-sulfur clusters
28	c5yq7C_	Alignment	not modelled	8.6	32	PDB header: photosynthesis Chain: C: PDB Molecule: cytochrome subunit of photosynthetic reaction center; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii

29	c1pn0A_	Alignment	not modelled	8.5	28	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum
30	c6f2rE_	Alignment	not modelled	8.5	40	PDB header: chaperone Chain: E: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
31	c2q9kA_	Alignment	not modelled	8.4	29	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
32	d1qnta2	Alignment	not modelled	8.2	33	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
33	c2k4zA_	Alignment	not modelled	7.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsrr; PDBTitle: solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
34	c5nnaB_	Alignment	not modelled	7.9	31	PDB header: hydrolase Chain: B: PDB Molecule: isatin hydrolase a; PDBTitle: isatin hydrolase a (iha) from labrenzia aggregata bound to benzyl2 benzoate
35	c2jynA_	Alignment	not modelled	7.4	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0368 protein ypl225w; PDBTitle: a novel solution nmr structure of protein yst0336 from2 saccharomyces cerevisiae. northeast structural genomics3 consortium target yt51/ontario centre for structural4 proteomics target yst0336
36	c4rt0B_	Alignment	not modelled	7.2	32	PDB header: protein binding Chain: B: PDB Molecule: alginate biosynthesis protein alg44; PDBTitle: structure of the alg44 pilz domain from pseudomonas aeruginosa pao1 in2 complex with c-di-gmp
37	c3entB_	Alignment	not modelled	7.1	47	PDB header: structural protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of nitrollin, a betagamma-crystallin from2 nitrospira multiformis-in alternate space group (p65)
38	c2knnA_	Alignment	not modelled	7.0	57	PDB header: plant protein Chain: A: PDB Molecule: cycloviolacin-o2; PDBTitle: solution structure of the cyclotide cycloviolacin o2 with2 glu6 methylated (cyo2me)
39	c2mdwA_	Alignment	not modelled	7.0	100	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of a strand-swapped dimer of the ww domain
40	c4m6rA_	Alignment	not modelled	6.9	28	PDB header: lyase Chain: A: PDB Molecule: methylthioribulose-1-phosphate dehydratase; PDBTitle: structural and biochemical basis for the inhibition of cell death by2 apip, a methionine salvage enzyme
41	c2kfdA_	Alignment	not modelled	6.6	42	PDB header: nuclear protein Chain: A: PDB Molecule: pre-mrna-processing protein prp40; PDBTitle: prp40 ff4 domain
42	c3eukC_	Alignment	not modelled	6.4	29	PDB header: cell cycle Chain: C: PDB Molecule: chromosome partition protein mukb, linker; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammas complex, asymmetric dimer
43	c2mixA_	Alignment	not modelled	6.3	46	PDB header: toxin Chain: A: PDB Molecule: venom peptide toxin; PDBTitle: structure of a novel venom peptide toxin from sample limited terebrid2 marine snail
44	c3berA_	Alignment	not modelled	6.3	20	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx47; PDBTitle: human dead-box rna-helicase ddx47, conserved domain i in complex with2 amp
45	c5l82A_	Alignment	not modelled	6.2	47	PDB header: antibiotic Chain: A: PDB Molecule: enterococcin k1; PDBTitle: nmr structure of enterocin k1 in 50%/50% tfe/water
46	d2cg7a1	Alignment	not modelled	6.1	29	Fold: Fnl-like domain Superfamily: Fnl-like domain Family: Fibronectin type I module
47	c1z9vA_	Alignment	not modelled	6.1	86	PDB header: unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth0776; PDBTitle: solution structure of mth0776 from methanobacterium2 thermoautotrophicum (strain h)
48	c3mi6A_	Alignment	not modelled	5.9	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
49	c4k1rA_	Alignment	not modelled	5.9	25	PDB header: hydrolase Chain: A: PDB Molecule: amsh-like protease sst2; PDBTitle: crystal structure of schizosaccharomyces pombe sst2 catalytic domain2 and ubiquitin
50	c2qjvB_	Alignment	not modelled	5.5	44	PDB header: isomerase Chain: B: PDB Molecule: uncharacterized iolb-like protein; PDBTitle: crystal structure of an iolb-like protein (stm4420) from salmonella2 typhimurium lt2 at 1.90 a resolution
51	c3vg8F_	Alignment	not modelled	5.4	78	PDB header: unknown function Chain: F: PDB Molecule: hypothetical protein tthb210; PDBTitle: crystal structure of hypothetical protein tthb210 from thermus2 thermophilus hb8
52	c5ijlA_	Alignment	not modelled	5.4	21	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
						PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase

53	c3fe2B_	Alignment	not modelled	5.4	24	ddx5; PDBTitle: human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp
54	c6c0fp_	Alignment	not modelled	5.2	39	PDB header: ribosome Chain: P; PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 2)
55	d1e8ca2	Alignment	not modelled	5.2	18	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
56	c2kfwA_	Alignment	not modelled	5.2	20	PDB header: isomerase Chain: A; PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase PDBTitle: solution structure of full-length slyd from e.coli
57	c6f2rA_	Alignment	not modelled	5.1	40	PDB header: chaperone Chain: A; PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
58	c4j0nA_	Alignment	not modelled	5.1	31	PDB header: hydrolase Chain: A; PDB Molecule: isatin hydrolase b; PDBTitle: crystal structure of a manganese dependent isatin hydrolase
59	d1r11a3	Alignment	not modelled	5.1	60	Fold: MutS N-terminal domain-like Superfamily: tRNA-intron endonuclease N-terminal domain-like Family: tRNA-intron endonuclease N-terminal domain-like
60	d1veca_	Alignment	not modelled	5.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain


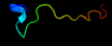
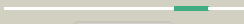
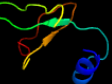







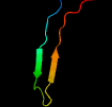
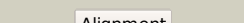
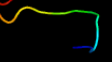



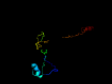

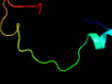

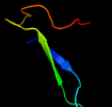
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1jegB_	 Alignment		45.1	67	PDB header: transferase/hydrolase Chain: B: PDB Molecule: hematopoietic cell protein-tyrosine phosphatase PDBTitle: solution structure of the sh3 domain from c-terminal src2 kinase complexed with a peptide from the tyrosine3 phosphatase pep
2	c5m8pA_	 Alignment		39.4	17	PDB header: unknown function Chain: A: PDB Molecule: 5,6-dihydroxyindole-2-carboxylic acid oxidase; PDBTitle: crystal structure of human tyrosinase related protein 1 in complex2 with tyrosine
3	c2ifsA_	 Alignment		27.7	56	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protien interacting protein and PDBTitle: structure of the n-wasp evh1 domain in complex with an extended wip2 peptide
4	c6igzK_	 Alignment		24.4	45	PDB header: plant protein Chain: K: PDB Molecule: psak; PDBTitle: structure of psi-lhci
5	c1e2vB_	 Alignment		21.5	36	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
6	c6f07B_	 Alignment		21.2	19	PDB header: cell cycle Chain: B: PDB Molecule: centromere dna-binding protein complex cbf3 subunit b; PDBTitle: cbf3 core complex
7	c1ctmA_	 Alignment		18.0	27	PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
8	d1hcza1	 Alignment		17.6	30	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
9	c2c1dC_	 Alignment		16.3	31	PDB header: oxidoreductase Chain: C: PDB Molecule: soxa; PDBTitle: crystal structure of soxxa from p. pantotrophus
10	d1vf5c1	 Alignment		16.0	30	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
11	d1e2wa1	 Alignment		15.9	40	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain

12	d1ci3m1	Alignment		15.5	30	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
13	c2jxmB_	Alignment		15.4	27	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
14	c2ml7A_	Alignment		15.1	71	PDB header: unknown function Chain: A: PDB Molecule: specific abundant protein 3; PDBTitle: ginsentides: characterization, structure and application of a new2 class of highly stable cystine knot peptides in ginseng
15	c2e75C_	Alignment		14.1	27	PDB header: photosynthesis Chain: C: PDB Molecule: apocytochrome f; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
16	d2qj2a1	Alignment		14.0	20	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain
17	c6ah3K_	Alignment		13.5	10	PDB header: hydrolase/rna Chain: K: PDB Molecule: ribonuclease p protein subunit rpr2; PDBTitle: cryo-em structure of yeast ribonuclease p with pre-trna substrate
18	d1zfoa_	Alignment		13.2	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LASP-1
19	c6ijoG_	Alignment		13.1	44	PDB header: photosynthesis Chain: G: PDB Molecule: psag; PDBTitle: photosystem i of chlamydomonas reinhardtii
20	c6ijjK_	Alignment		12.7	36	PDB header: membrane protein Chain: K: PDB Molecule: psak; PDBTitle: photosystem i of chlamydomonas reinhardtii
21	d1xu6a_	Alignment	not modelled	12.4	41	Fold: Trefoil/Plexin domain-like Superfamily: Variant surface glycoprotein MITAT 1.2, VSG 221, C-terminal domain Family: Variant surface glycoprotein MITAT 1.2, VSG 221, C-terminal domain
22	c1xu6A_	Alignment	not modelled	12.4	41	PDB header: immune system, membrane protein Chain: A: PDB Molecule: variant surface glycoprotein mitat 1.2; PDBTitle: structure of the c-terminal domain from trypanosoma brucei variant2 surface glycoprotein mitat1.2
23	c1q90A_	Alignment	not modelled	12.4	36	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
24	c2l09A_	Alignment	not modelled	12.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: asr4154 protein; PDBTitle: solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
25	c1tu2B_	Alignment	not modelled	11.9	27	PDB header: electron transport Chain: B: PDB Molecule: apocytochrome f; PDBTitle: the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
26	d1jg5a_	Alignment	not modelled	11.8	40	Fold: GTP cyclohydrolase I feedback regulatory protein, GFRP Superfamily: GTP cyclohydrolase I feedback regulatory protein, GFRP Family: GTP cyclohydrolase I feedback regulatory protein, GFRP
27	d1tu2b1	Alignment	not modelled	11.3	27	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
28	c3cguB_	Alignment	not modelled	10.6	25	PDB header: hormone/signaling protein Chain: B: PDB Molecule: protein giant-lens;

					PDBTitle: crystal structure of unliganded argos
29	c2mixA	Alignment	not modelled	9.8	29 PDB header: toxin Chain: A: PDB Molecule: venom peptide toxin; PDBTitle: structure of a novel venom peptide toxin from sample limited terebrid2 marine snail
30	d2glia1	Alignment	not modelled	9.8	33 Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
31	c6dgaA	Alignment	not modelled	9.7	14 PDB header: unknown function Chain: A: PDB Molecule: rpfr; PDBTitle: cronobacter turicensis rpfr quorum-sensing receptor rpff interaction2 domain
32	c2kvsA	Alignment	not modelled	8.9	75 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mw0776; PDBTitle: nmr solution structure of q7a1e8 protein from staphylococcus2 aureus: northeast structural genomics consortium target:3 zr215
33	d1dq7a	Alignment	not modelled	8.8	48 Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
34	d1omya	Alignment	not modelled	8.5	48 Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
35	c2wsfG	Alignment	not modelled	8.5	56 PDB header: photosynthesis Chain: G: PDB Molecule: photosystem i reaction center subunit v, chloroplastic; PDBTitle: improved model of plant photosystem i
36	d1rrha1	Alignment	not modelled	8.5	15 Fold: Lipoxigenase Superfamily: Lipoxigenase Family: Plant lipoxigenases
37	d1mo9a3	Alignment	not modelled	8.4	21 Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
38	d1a0da	Alignment	not modelled	8.3	14 Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
39	d1uwva2	Alignment	not modelled	8.2	19 Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: (Uracil-5-)-methyltransferase
40	d1h32a2	Alignment	not modelled	8.2	27 Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c SoxA
41	d1q7ha2	Alignment	not modelled	8.1	47 Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Hypothetical protein Ta1423, N-terminal domain
42	c2wscK	Alignment	not modelled	8.1	56 PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit psak, chloroplastic; PDBTitle: improved model of plant photosystem i
43	d1a0ca	Alignment	not modelled	8.1	16 Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
44	c5m4tA	Alignment	not modelled	7.9	32 PDB header: membrane protein Chain: A: PDB Molecule: variant surface glycoprotein mitat 1.1; PDBTitle: c-terminal domain structure of vsg m1.1
45	d1xlma	Alignment	not modelled	7.9	20 Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
46	d1ywva1	Alignment	not modelled	7.7	16 Fold: PH domain-like barrel Superfamily: PA2021-like Family: PA2021-like
47	c6exnc	Alignment	not modelled	7.7	33 PDB header: splicing Chain: C: PDB Molecule: pre-mrna-splicing factor snu114; PDBTitle: post-catalytic p complex spliceosome with 3' splice site docked
48	d1rrpb	Alignment	not modelled	7.7	32 Fold: PH domain-like barrel Superfamily: PH domain-like Family: Ran-binding domain
49	c5gvdB	Alignment	not modelled	7.5	36 PDB header: protein binding Chain: B: PDB Molecule: tudor domain-containing protein 3; PDBTitle: human tdrd3 duf1767-ob domains
50	c5z47A	Alignment	not modelled	7.2	9 PDB header: hydrolase Chain: A: PDB Molecule: pyrrolidone-carboxylate peptidase; PDBTitle: crystal structure of pyrrolidone carboxylate peptidase i with2 disordered loop a from deinococcus radiodurans r1
51	d1ogmx1	Alignment	not modelled	7.2	31 Fold: Dextranase, N-terminal domain Superfamily: Dextranase, N-terminal domain Family: Dextranase, N-terminal domain
52	d1znpa1	Alignment	not modelled	7.1	20 Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like
53	d1dkca	Alignment	not modelled	7.0	40 Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Gurmarin-like Family: Antifungal peptide
54	c3kf6B	Alignment	not modelled	7.0	42 PDB header: structural protein Chain: B: PDB Molecule: protein ten1; PDBTitle: crystal structure of s. pombe stn1-ten1 complex
					PDB header: unknown function

55	c5xbdA	Alignment	not modelled	6.9	36	Chain: A: PDB Molecule: pb1; PDBTitle: disulfide-constrained wound healing peptide derived from pereskia bleo
56	d1yuda1	Alignment	not modelled	6.8	20	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like
57	c3lzzB	Alignment	not modelled	6.8	10	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structures of cupin superfamily bbduf985 from branchiostoma2 belcheri tsingtauense in apo and gdp-bound forms
58	c6hmsB	Alignment	not modelled	6.8	38	PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna polymerase ii large PDBTitle: cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
59	c6k0bH	Alignment	not modelled	6.7	17	PDB header: rna binding protein/rna Chain: H: PDB Molecule: ribonuclease p protein component 4; PDBTitle: cryo-em structure of archaeal ribonuclease p with mature trna
60	d1hlqa	Alignment	not modelled	6.7	22	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
61	d1h32a1	Alignment	not modelled	6.6	27	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c SoxA
62	d5gata	Alignment	not modelled	6.6	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
63	d1a0ea	Alignment	not modelled	6.5	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
64	d2gp4a2	Alignment	not modelled	6.4	21	Fold: IlvD/EDD N-terminal domain-like Superfamily: IlvD/EDD N-terminal domain-like Family: IlvD/EDD N-terminal domain-like
65	c3f6qB	Alignment	not modelled	6.4	29	PDB header: signaling protein/signaling protein Chain: B: PDB Molecule: lim and senescent cell antigen-like-containing PDBTitle: crystal structure of integrin-linked kinase ankyrin repeat2 domain in complex with pinch1 lim1 domain
66	c4naeA	Alignment	not modelled	6.4	39	PDB header: transferase Chain: A: PDB Molecule: heptaprenylglyceryl phosphate synthase; PDBTitle: pcrb from geobacillus kaustophilus, with bound g1p
67	c4yn3B	Alignment	not modelled	6.4	29	PDB header: hydrolase Chain: B: PDB Molecule: cucumisin; PDBTitle: crystal structure of cucumisin complex with pro-peptide
68	c2e5rA	Alignment	not modelled	6.4	29	PDB header: dna binding protein Chain: A: PDB Molecule: dystrobrevin alpha; PDBTitle: solution structure of the zz domain of dystrobrevin alpha2 (dystrobrevin-alpha)
69	c3lw5K	Alignment	not modelled	6.4	22	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x psak; PDBTitle: improved model of plant photosystem i
70	c5owgA	Alignment	not modelled	6.3	29	PDB header: oxidoreductase Chain: A: PDB Molecule: pcyx_ebk42635; PDBTitle: structure of pcyx_ebk42635
71	c5m73H	Alignment	not modelled	6.3	60	PDB header: rna binding protein Chain: H: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain
72	d1x63a2	Alignment	not modelled	6.3	80	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
73	c5ijlA	Alignment	not modelled	6.2	38	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
74	d1hroa	Alignment	not modelled	6.1	20	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
75	c2o01G	Alignment	not modelled	5.9	56	PDB header: photosynthesis Chain: G: PDB Molecule: photosystem i reaction center subunit v, chloroplast; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
76	d2if1a	Alignment	not modelled	5.9	28	Fold: elF1-like Superfamily: elF1-like Family: elF1-like
77	c6iczz	Alignment	not modelled	5.8	44	PDB header: splicing Chain: Z: PDB Molecule: pre-mrna-splicing factor slu7; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
78	d2j9ga1	Alignment	not modelled	5.8	25	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
79	d1gu2a	Alignment	not modelled	5.7	26	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
80	c4ce41	Alignment	not modelled	5.7	28	PDB header: ribosome Chain: 1: PDB Molecule: mrpl28; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
						PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease p protein component 4;




















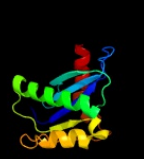

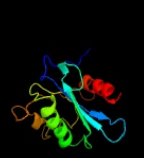
81	c2zaeB_	Alignment	not modelled	5.7	27	PDBTitle: crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
82	c4xkmB_	Alignment	not modelled	5.6	14	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of xylose isomerase from an human intestinal tract2 microbe bacteroides thetaiotaomicron
83	d1ebda3	Alignment	not modelled	5.5	14	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
84	c2h2mA_	Alignment	not modelled	5.5	20	PDB header: metal transport Chain: A: PDB Molecule: comm domain-containing protein 1; PDBTitle: solution structure of the n-terminal domain of commd12 (murr1)
85	c2pbzC_	Alignment	not modelled	5.4	18	PDB header: ligase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis
86	d2f6ua1	Alignment	not modelled	5.4	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
87	d1hwtc1	Alignment	not modelled	5.3	22	Fold: Zn2/Cys6 DNA-binding domain Superfamily: Zn2/Cys6 DNA-binding domain Family: Zn2/Cys6 DNA-binding domain
88	d2c42a2	Alignment	not modelled	5.3	38	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
89	d1rkta1	Alignment	not modelled	5.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
90	c4ncpF_	Alignment	not modelled	5.3	19	PDB header: unknown function Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 4-hbt like thioesterase sav1878 from2 staphylococcus aureus subsp. aureus mu50
91	d1h9hi_	Alignment	not modelled	5.2	23	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant inhibitors of proteinases and amylases Family: Plant inhibitors of proteinases and amylases
92	c5mpwA_	Alignment	not modelled	5.2	17	PDB header: plant protein Chain: A: PDB Molecule: multiple organellar rna editing factor 1, mitochondrial; PDBTitle: crystal structure of arabidopsis thaliana rna editing factor morf1
93	c4n0oC_	Alignment	not modelled	5.2	17	PDB header: hydrolase/dna Chain: C: PDB Molecule: replicase polypeptide 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
94	d1xhja_	Alignment	not modelled	5.1	38	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
95	c4ienB_	Alignment	not modelled	5.1	18	PDB header: hydrolase Chain: B: PDB Molecule: putative acyl-coa hydrolase; PDBTitle: crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
96	c2qq2C_	Alignment	not modelled	5.1	22	PDB header: hydrolase Chain: C: PDB Molecule: cytosolic acyl coenzyme a thioester hydrolase; PDBTitle: crystal structure of c-terminal domain of human acyl-coa thioesterase2 7
97	c4g7wB_	Alignment	not modelled	5.1	40	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of the minor coat protein2 piii from ctxphi
98	c4g7xA_	Alignment	not modelled	5.1	40	PDB header: protein binding/protein binding Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a complex between the ctxphi piii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
99	d2b1ya1	Alignment	not modelled	5.0	21	Fold: Atu1913-like Superfamily: Atu1913-like Family: Atu1913-like

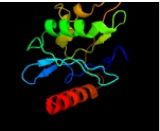

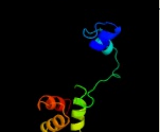



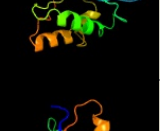
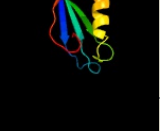

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2aklA_	 Alignment		49.2	48	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
2	d1k8rb_	 Alignment		44.8	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
3	c3fzeA_	 Alignment		36.5	39	PDB header: protein binding Chain: A: PDB Molecule: protein ste5; PDBTitle: structure of the 'minimal scaffold' (ms) domain of ste5 that2 cocatalyzes fus3 phosphorylation by ste7
4	d1ogyb_	 Alignment		29.9	30	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
5	c5u0pN_	 Alignment		28.3	21	PDB header: transcription Chain: N: PDB Molecule: mediator complex subunit 14; PDBTitle: cryo-em structure of the transcriptional mediator
6	c1fpvA_	 Alignment		22.0	36	PDB header: virus Chain: A: PDB Molecule: feline panleukopenia virus (strain b) viral PDBTitle: structure determination of feline panleukopenia virus empty2 particles
7	d1cta1	 Alignment		21.5	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
8	c3wmmY_	 Alignment		17.3	45	PDB header: photosynthesis Chain: Y: PDB Molecule: lh1 alpha polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
9	c5l1xH_	 Alignment		17.2	31	PDB header: viral protein Chain: H: PDB Molecule: hmpv f1 subunit; PDBTitle: structure of the human metapneumovirus fusion protein in the2 postfusion conformation
10	c4aq2I_	 Alignment		16.3	30	PDB header: oxidoreductase Chain: I: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: resting state of homogentisate 1,2-dioxygenase
11	c5d74B_	 Alignment		14.6	31	PDB header: hydrolase Chain: B: PDB Molecule: putative phage lysin; PDBTitle: the crystal structure of ly7917

29	d1g8kb_	Alignment	not modelled	8.8	27	Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
30	d2r85a1	Alignment	not modelled	8.8	67	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: PurP N-terminal domain-like
31	c4mbyB_	Alignment	not modelled	8.2	33	PDB header: viral protein Chain: B: PDB Molecule: major capsid protein vp1; PDBTitle: structure of b-lymphotropic polyomavirus vp1 in complex with 3'-2 sialyllactose
32	d1imla1	Alignment	not modelled	8.1	75	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
33	c3s7xC_	Alignment	not modelled	8.0	33	PDB header: viral protein Chain: C: PDB Molecule: major capsid protein vp1; PDBTitle: unassembled washington university polyomavirus vp1 pentamer r198k2 mutant
34	c5e9fD_	Alignment	not modelled	7.9	57	PDB header: lyase Chain: D: PDB Molecule: isocitrate lyase; PDBTitle: structural insights of isocitrate lyases from magnaporthe oryzae
35	d2pbza1	Alignment	not modelled	7.8	78	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: PurP N-terminal domain-like
36	d2r7ka1	Alignment	not modelled	7.3	67	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: PurP N-terminal domain-like
37	d2bfdal	Alignment	not modelled	7.3	24	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
38	c2vbgB_	Alignment	not modelled	7.2	25	PDB header: lyase Chain: B: PDB Molecule: branched-chain alpha-ketoacid decarboxylase; PDBTitle: the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
39	d1cixa_	Alignment	not modelled	7.1	75	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
40	c1cixA_	Alignment	not modelled	7.1	75	PDB header: antimicrobial peptide Chain: A: PDB Molecule: protein (tachystatin a); PDBTitle: three-dimensional structure of antimicrobial peptide2 tachystatin a isolated from horseshoe crab
41	c6btcA_	Alignment	not modelled	7.0	30	PDB header: dna binding protein Chain: A: PDB Molecule: lp1413 - sccmec type iv-encoded dna binding protein; PDBTitle: sccmec type iv lp1413 - nucleic acids binding protein
42	c2v7sA_	Alignment	not modelled	6.9	25	PDB header: unknown function Chain: A: PDB Molecule: probable conserved lipoprotein lppa; PDBTitle: crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
43	d1ewqa2	Alignment	not modelled	6.7	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
44	c2ns2B_	Alignment	not modelled	6.7	54	PDB header: cell cycle Chain: B: PDB Molecule: spindlin-1; PDBTitle: crystal structure of spindlin1
45	c4lqxB_	Alignment	not modelled	6.6	42	PDB header: oxidoreductase Chain: B: PDB Molecule: tena/thi-4 domain-containing protein; PDBTitle: crystal structure of a tena/thi-4 domain-containing protein (sso2700)2 from sulfobolus solfataricus p2 at 2.34 a resolution
46	c1t3ba_	Alignment	not modelled	6.5	27	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from haemophilus influenzae
47	d1fcda2	Alignment	not modelled	6.5	43	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
48	c5ki9A_	Alignment	not modelled	6.4	43	PDB header: antimicrobial protein Chain: A: PDB Molecule: beta-defensin 104; PDBTitle: crystal structure of human beta-defensin 4 (hbd4)
49	d2akza1	Alignment	not modelled	6.4	23	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
50	c3fgrB_	Alignment	not modelled	6.4	32	PDB header: hydrolase Chain: B: PDB Molecule: putative phospholipase b-like 2 40 kda form; PDBTitle: two chain form of the 66.3 kda protein at 1.8 angstrom
51	d1qs0a_	Alignment	not modelled	6.3	35	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
52	c2ykqC_	Alignment	not modelled	6.3	18	PDB header: rna binding protein Chain: C: PDB Molecule: line-1 orf1p; PDBTitle: structure of the human line-1 orf1p trimer
53	d2vbua1	Alignment	not modelled	6.2	43	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: CTP-dependent riboflavin kinase-like
54	c3fbcC_	Alignment	not modelled	6.2	67	PDB header: transcription Chain: C: PDB Molecule: mediator of rna polymerase ii transcription subunit 7; PDBTitle: structure of the mediator submodule med7n/31
55	c1jzdA_	Alignment	not modelled	6.2	27	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex

56	d1ovma3	Alignment	not modelled	6.1	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
57	d1jicb1	Alignment	not modelled	6.1	17	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
58	d1eysc_	Alignment	not modelled	6.1	24	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)
59	c1eysC_	Alignment	not modelled	6.1	24	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
60	c6hhkB_	Alignment	not modelled	6.1	19	PDB header: viral protein Chain: B: PDB Molecule: gp105; PDBTitle: structure of gp105 of listeria bacteriophage a511
61	c3hi2C_	Alignment	not modelled	6.1	71	PDB header: dna binding protein/toxin Chain: C: PDB Molecule: hth-type transcriptional regulator mqsA(ygit); PDBTitle: structure of the n-terminal domain of the e. coli antitoxin mqsA2 (ygit/b3021) in complex with the e. coli toxin mqsR (ygiu/b3022)
62	c1vw4G_	Alignment	not modelled	6.0	50	PDB header: ribosome Chain: G: PDB Molecule: 54s ribosomal protein l50, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
63	c2ns2A_	Alignment	not modelled	5.8	54	PDB header: cell cycle Chain: A: PDB Molecule: spindlin-1; PDBTitle: crystal structure of spindlin1
64	d1of5b_	Alignment	not modelled	5.8	26	Fold: Cystatin-like Superfamily: NTF2-like Family: NTF2-like
65	c2wuIB_	Alignment	not modelled	5.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: glutaredoxin related protein 5; PDBTitle: crystal structure of the human glutaredoxin 5 with bound glutathione2 in an fes cluster
66	c3e9uA_	Alignment	not modelled	5.6	47	PDB header: membrane protein Chain: A: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of calx cbd2 domain
67	d2ozla1	Alignment	not modelled	5.6	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
68	c1jegB_	Alignment	not modelled	5.5	47	PDB header: transferase/hydrolase Chain: B: PDB Molecule: hematopoietic cell protein-tyrosine phosphatase PDBTitle: solution structure of the sh3 domain from c-terminal src2 kinase complexed with a peptide from the tyrosine3 phosphatase pep
69	c4ar0A_	Alignment	not modelled	5.5	24	PDB header: transport Chain: A: PDB Molecule: type iv pilus biogenesis and competence protein pilq; PDBTitle: n0 domain of neisseria meningitidis pilus assembly protein pilq
70	c6epcN_	Alignment	not modelled	5.4	28	PDB header: hydrolase Chain: N: PDB Molecule: 26s proteasome non-atpase regulatory subunit 1; PDBTitle: ground state 26s proteasome (gs2)
71	c5odwC_	Alignment	not modelled	5.4	37	PDB header: protein transport Chain: C: PDB Molecule: pyocin-s2; PDBTitle: structure of the fpva1-pyocin s2 complex
72	c1qo8A_	Alignment	not modelled	5.4	29	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
73	d1zpda3	Alignment	not modelled	5.4	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
74	c5cxmC_	Alignment	not modelled	5.4	32	PDB header: metal binding protein Chain: C: PDB Molecule: cytochrome b6/f complex iron-sulfur subunit; PDBTitle: crystal structure of the cyanobacterial plasma membrane rieske protein2 petc3 from synechocystis pcc 6803
75	c3bwrC_	Alignment	not modelled	5.3	28	PDB header: viral protein Chain: C: PDB Molecule: capsid protein vp1; PDBTitle: sv40 vp1 pentamer in complex with gm1 oligosaccharide
76	d2b4ya1	Alignment	not modelled	5.3	38	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
77	d1hc1a3	Alignment	not modelled	5.3	35	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arthropod hemocyanin, C-terminal domain
78	c4aqzA_	Alignment	not modelled	5.3	19	PDB header: transport protein Chain: A: PDB Molecule: type iv pilus biogenesis and competence protein pilq; PDBTitle: b2 domain of neisseria meningitidis pilus assembly protein pilq
79	d1q6za3	Alignment	not modelled	5.3	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
80	c3siiA_	Alignment	not modelled	5.3	19	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: poly(adp-ribose) glycohydrolase; PDBTitle: the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from

						thermomonospora curvata
81	c3u50C_	Alignment	not modelled	5.2	15	PDB header: dna binding protein Chain: C: PDB Molecule: telomerase-associated protein 82; PDBTitle: crystal structure of the tetrahymena telomerase processivity factor2 teb1 ob-c
82	c6gn5A_	Alignment	not modelled	5.2	30	PDB header: lipid transport Chain: A: PDB Molecule: gram domain-containing protein 1c; PDBTitle: crystal structure of human gramd1c start domain
83	c2lkwA_	Alignment	not modelled	5.2	58	PDB header: viral protein Chain: A: PDB Molecule: membrane fusion protein p15; PDBTitle: a myristoylated polyproline type ii helix functions as a novel fusion2 peptide during cell-cell membrane fusion induced by the baboon3 reovirus p15 fast protein
84	c4pogC_	Alignment	not modelled	5.2	30	PDB header: replication, dna binding protein/dna Chain: C: PDB Molecule: cell division control protein 21; PDBTitle: mcm-ssdna co-crystal structure
85	d1rg6a_	Alignment	not modelled	5.2	32	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
86	d1c8da_	Alignment	not modelled	5.1	36	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Parvoviridae-like VP
87	c3j2wH_	Alignment	not modelled	5.1	60	PDB header: virus Chain: H: PDB Molecule: glycoprotein e1; PDBTitle: electron cryo-microscopy of chikungunya virus
88	c3j2wE_	Alignment	not modelled	5.1	60	PDB header: virus Chain: E: PDB Molecule: glycoprotein e1; PDBTitle: electron cryo-microscopy of chikungunya virus
89	c1yi1A_	Alignment	not modelled	5.1	27	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
90	c6gqfC_	Alignment	not modelled	5.0	50	PDB header: lipid transport Chain: C: PDB Molecule: gram domain-containing protein 1a; PDBTitle: the structure of mouse astera (gramd1a) with 25-hydroxy cholesterol
91	d1wika_	Alignment	not modelled	5.0	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fcyA_	 Alignment		98.9	11	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
2	dlasua_	 Alignment		98.1	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
3	c1c0mA_	 Alignment		97.9	18	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
4	dlcxqa_	 Alignment		97.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	dlc0ma2	 Alignment		97.7	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
6	dlbcoa2	 Alignment		97.6	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
7	c5ejkG_	 Alignment		97.6	22	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
8	dlhyva_	 Alignment		97.2	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
9	c1bcoA_	 Alignment		97.2	13	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
10	c5cz1B_	 Alignment		97.0	14	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
11	c3jcaE_	 Alignment		97.0	14	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome

12	c3nf9A_	Alignment		96.9	17	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
13	d1exqa_	Alignment		96.9	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
14	c6gh5M_	Alignment		96.7	17	PDB header: transcription Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
15	c5u1cA_	Alignment		96.5	16	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
16	c3f9kV_	Alignment		96.3	12	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
17	c1ex4A_	Alignment		96.1	22	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
18	c5u1cD_	Alignment		96.1	15	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
19	c3hpgC_	Alignment		96.0	12	PDB header: transferase Chain: C: PDB Molecule: integrase; PDBTitle: visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
20	c4mq3A_	Alignment		95.7	19	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
21	c5ui5I_	Alignment	not modelled	95.5	18	PDB header: transcription/dna Chain: I: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: crystal structure of aquifex aeolicus sigman bound to promoter dna
22	c5byhM_	Alignment	not modelled	95.5	20	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
23	c2ahqA_	Alignment	not modelled	95.2	20	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
24	d1c6va_	Alignment	not modelled	94.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
25	c1u78A_	Alignment	not modelled	94.7	15	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
26	c5m0rF_	Alignment	not modelled	94.4	14	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
27	c3kksB_	Alignment	not modelled	94.3	14	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
28	c1k6yB_	Alignment	not modelled	94.3	15	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
29	c3dlrA_	Alignment	not modelled	94.3	18	PDB header: transferase Chain: A: PDB Molecule: integrase;

29	c5u1rA	Alignment	not modelled	94.3	18	PDBTitle: crystal structure of the catalytic core domain from pfv2 integrase PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: structure of -24 dna binding domain of sigma 54 from e.coli
30	c2mt3A	Alignment	not modelled	93.9	18	PDB header: transcription/dna Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
31	c2o8kA	Alignment	not modelled	93.8	21	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
32	c5nwtM	Alignment	not modelled	93.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
33	d2p5ka1	Alignment	not modelled	76.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
34	d1b4aa1	Alignment	not modelled	74.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
35	d1f9na1	Alignment	not modelled	74.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
36	c3l2tB	Alignment	not modelled	70.9	12	PDB header: recombination/dna Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
37	c5unkA	Alignment	not modelled	69.4	21	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the red subdomain of the sleeping beauty transposase
38	c4czdD	Alignment	not modelled	68.3	18	PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
39	d1aoya	Alignment	not modelled	60.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
40	c1b4aA	Alignment	not modelled	59.3	19	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
41	c3ereD	Alignment	not modelled	55.9	22	PDB header: dna binding protein/dna Chain: D: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
42	c5chhA	Alignment	not modelled	54.1	23	PDB header: transcription Chain: A: PDB Molecule: arac family transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
43	c4mtdA	Alignment	not modelled	51.2	17	PDB header: dna binding protein/dna Chain: A: PDB Molecule: zinc uptake regulation protein; PDBTitle: zinc uptake regulator complexed with zinc and dna
44	d1pdnc	Alignment	not modelled	49.8	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
45	c4i7hA	Alignment	not modelled	48.1	22	PDB header: transcription Chain: A: PDB Molecule: peroxide stress sensing regulator; PDBTitle: structural basis for peroxide sensing and gene regulation by perr from2 streptococcus pyogenes
46	d1stza1	Alignment	not modelled	46.4	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
47	d2ezia	Alignment	not modelled	45.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
48	c3eyyA	Alignment	not modelled	42.2	18	PDB header: transport Chain: A: PDB Molecule: putative iron uptake regulatory protein; PDBTitle: structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
49	c2w57A	Alignment	not modelled	41.8	20	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
50	d2ezha	Alignment	not modelled	40.9	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
51	c6paxA	Alignment	not modelled	39.4	20	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
52	c5l87A	Alignment	not modelled	37.3	19	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
53	c5n19B	Alignment	not modelled	36.8	16	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator (fur family); PDBTitle: crystal structure of a peroxide stress regulator from leptospira2 interrogans
54	c6b4cH	Alignment	not modelled	36.3	18	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens

55	c3oouA	Alignment	not modelled	35.7	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2118 protein; PDBTitle: the structure of a protein with unkown function from listeria innocua
56	c5xtdb	Alignment	not modelled	35.7	13	PDB header: oxidoreductase/electron transport Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: cryo-em structure of human respiratory complex i
57	c6q5uN	Alignment	not modelled	34.4	32	PDB header: virus Chain: N: PDB Molecule: infectivity protein (p16); PDBTitle: high resolution electron cryo-microscopy structure of the2 bacteriophage pr772
58	c3uoeB	Alignment	not modelled	34.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from sinorhizobium melliloti
59	c1w8xP	Alignment	not modelled	33.9	32	PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1
60	d1t56a2	Alignment	not modelled	33.5	6	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
61	c2fe3B	Alignment	not modelled	32.7	21	PDB header: dna binding protein Chain: B: PDB Molecule: peroxide operon regulator; PDBTitle: the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
62	c4go1A	Alignment	not modelled	32.2	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
63	c3i0pA	Alignment	not modelled	31.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from entamoeba histolytica
64	c2ky5A	Alignment	not modelled	30.6	19	PDB header: cell adhesion Chain: A: PDB Molecule: platelet endothelial cell adhesion molecule; PDBTitle: solution structure of the pecam-1 cytoplasmic tail with dpc
65	c2fu4B	Alignment	not modelled	29.3	20	PDB header: dna binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
66	c1zauA	Alignment	not modelled	29.0	17	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: adenylation domain of nad+ dependent dna ligase from m.tuberculosis
67	c5fd6A	Alignment	not modelled	28.7	20	PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: zinc-bound manganese uptake regulator
68	c1vbiA	Alignment	not modelled	26.9	7	PDB header: oxidoreductase Chain: A: PDB Molecule: type 2 malate/lactate dehydrogenase; PDBTitle: crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
69	c3v4gA	Alignment	not modelled	26.4	27	PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
70	c4iyvB	Alignment	not modelled	25.9	20	PDB header: hydrolase Chain: B: PDB Molecule: caspase-6; PDBTitle: crystal structure of full-length caspase-6 zymogen
71	c4razB	Alignment	not modelled	25.7	18	PDB header: metal binding protein Chain: B: PDB Molecule: dna-binding transcriptional dual regulator of siderophore PDBTitle: crystal structure of magnetospirillum gryphiswaldense msr-1 holo-fur
72	d1mzba	Alignment	not modelled	25.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like
73	d1a9xa1	Alignment	not modelled	25.6	14	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
74	c2g8yB	Alignment	not modelled	25.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
75	c1v9pB	Alignment	not modelled	24.7	13	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
76	c3qyxD	Alignment	not modelled	24.6	25	PDB header: transcription/dna Chain: D: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
77	c6dk4A	Alignment	not modelled	24.3	14	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni peroxide stress regulator
78	d1xrha	Alignment	not modelled	24.2	17	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
79	c4ifuA	Alignment	not modelled	22.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
						Fold: DNA/RNA-binding 3-helical bundle

80	d2cfxa1	Alignment	not modelled	22.5	19	Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
81	d1b04a	Alignment	not modelled	22.4	20	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD ⁺ -dependent DNA ligase
82	d2qrd1	Alignment	not modelled	22.4	13	Fold: TBP-like Superfamily: KA1-like Family: Ssp2 C-terminal domain-like
83	c6daqA	Alignment	not modelled	22.1	24	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
84	c1v9nA	Alignment	not modelled	21.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structure of malate dehydrogenase from pyrococcus horikoshii ot3
85	c2q0aA	Alignment	not modelled	21.1	9	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
86	c1j1eC	Alignment	not modelled	20.8	19	PDB header: contractile protein Chain: C: PDB Molecule: troponin i; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
87	c5buzC	Alignment	not modelled	20.3	47	PDB header: transport protein Chain: C: PDB Molecule: snap receptor-like protein; PDBTitle: crystal structure of a complex between the snare vam3 and the hops2 vps33-vps16 subcomplex from chaetomium thermophilum
88	c1z2iA	Alignment	not modelled	20.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
89	d1id3b	Alignment	not modelled	19.9	16	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
90	c4czdA	Alignment	not modelled	19.8	18	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
91	d1nxua	Alignment	not modelled	19.4	12	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
92	c6daoB	Alignment	not modelled	19.0	7	PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
93	c2xigA	Alignment	not modelled	18.4	16	PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
94	c1g2hA	Alignment	not modelled	18.2	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
95	d1g2ha	Alignment	not modelled	18.2	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
96	c4etsB	Alignment	not modelled	17.8	9	PDB header: metal binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni ferric uptake regulator
97	d2cg4a1	Alignment	not modelled	17.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
98	d1v9pa3	Alignment	not modelled	17.4	13	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD ⁺ -dependent DNA ligase
99	d1rkt2	Alignment	not modelled	17.1	10	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain