
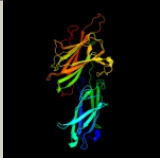


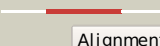






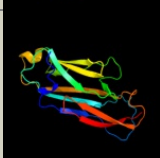



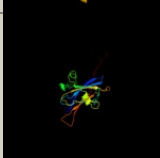



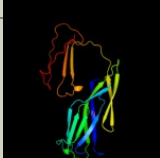

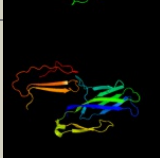
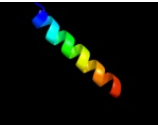






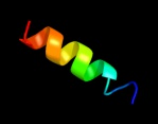



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P14738
Date	Tue Jul 17 17:05:09 BST 2012
Unique Job ID	03f4effed6783aa6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1n67A_	 Alignment		99.9	23	PDB header: cell adhesion Chain: A; PDB Molecule: clumping factor; PDBTitle: clumping factor a from staphylococcus aureus
2	c3at0A_	 Alignment		99.9	20	PDB header: cell adhesion/blood clotting Chain: A; PDB Molecule: clumping factor b; PDBTitle: structural and biochemical characterization of clfb:ligand2 interactions
3	c2vr3B_	 Alignment		99.9	23	PDB header: cell adhesion Chain: B; PDB Molecule: clumping factor a; PDBTitle: structural and biochemical characterization of fibrinogen2 binding to clfa from staphylococcus aureus
4	c1r19B_	 Alignment		99.8	19	PDB header: cell adhesion Chain: B; PDB Molecule: fibrinogen-binding protein sdrg; PDBTitle: crystal structure analysis of s.epidermidis adhesin sdrg2 binding to fibrinogen (apo structure)
5	c3irpX_	 Alignment		99.4	13	PDB header: cell adhesion Chain: X; PDB Molecule: uro-adherence factor a; PDBTitle: crystal structure of functional region of uafa from staphylococcus2 saprophyticus at 1.50 angstrom resolution
6	d1n67a1	 Alignment		99.4	33	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Fibrinogen-binding domain
7	d1r17a1	 Alignment		99.3	21	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Fibrinogen-binding domain
8	d1r17a2	 Alignment		99.1	21	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Fibrinogen-binding domain
9	d1n67a2	 Alignment		98.9	16	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Fibrinogen-binding domain
10	c2f6aA_	 Alignment		98.1	12	PDB header: cell adhesion/structural protein Chain: A; PDB Molecule: collagen adhesin; PDBTitle: collagen adhesin and collagen complex structure
11	c2z1pA_	 Alignment		96.9	13	PDB header: cell adhesion Chain: A; PDB Molecule: collagen adhesin protein; PDBTitle: the enterococcus faecalis msgramm ace binds its ligands by2 the collagen hug model

12	c2jp3A_	Alignment		81.4	45	PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
13	c2jo1A_	Alignment		77.7	23	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
14	c3kdpG_	Alignment		68.7	35	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
15	c3kdpH_	Alignment		68.7	35	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
16	c2zxeG_	Alignment		64.7	18	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
17	c2l2tA_	Alignment		61.2	30	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain
18	c3n23E_	Alignment		57.5	38	PDB header: hydrolase Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
19	c1m57H_	Alignment		52.0	17	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaerooides (eq(i-286) mutant)
20	c2k9yB_	Alignment		38.8	24	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
21	c2k9yA_	Alignment	not modelled	34.4	24	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
22	c2k1kB_	Alignment	not modelled	32.1	31	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
23	c2k1lA_	Alignment	not modelled	32.1	31	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
24	c2k1kA_	Alignment	not modelled	32.1	31	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
25	c2k1lB_	Alignment	not modelled	32.1	31	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
26	c1lijA_	Alignment	not modelled	28.5	22	PDB header: signaling protein Chain: A: PDB Molecule: erbb-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbb-2 membrane spanning2 segment
27	d3ehbb2	Alignment	not modelled	26.4	13	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
28	d3dtub2	Alignment	not modelled	25.9	17	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region

29	d1ffb2	Alignment	not modelled	25.6	8	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
30	d1d3va	Alignment	not modelled	24.5	13	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
31	c1qleB	Alignment	not modelled	24.4	12	PDB header: oxidoreductase/immune system Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
32	c1ar1B	Alignment	not modelled	24.4	12	PDB header: complex (oxidoreductase/antibody) Chain: B: PDB Molecule: cytochrome c oxidase; PDBTitle: structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
33	c3of4A	Alignment	not modelled	23.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a fmn/fad- and nad(p)h-dependent nitroreductase2 (nfnb, il2077) from idiomarina loihiensis l2tr at 1.90 a resolution
34	d2frea1	Alignment	not modelled	22.0	25	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
35	d1vkwa	Alignment	not modelled	21.3	25	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: Putative nitroreductase TM1586
36	c3g2eA	Alignment	not modelled	21.3	35	PDB header: oxidoreductase Chain: A: PDB Molecule: oorc subunit of 2-oxoglutarate:acceptor oxidoreductase; PDBTitle: structure of putative oorc subunit of 2-oxoglutarate:acceptor2 oxidoreductase from campylobacter jejuni
37	c2wqfA	Alignment	not modelled	21.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: copper induced nitroreductase d; PDBTitle: crystal structure of the nitroreductase cind from2 lactococcus lactis in complex with fmn
38	c2f5uA	Alignment	not modelled	21.0	21	PDB header: viral protein Chain: A: PDB Molecule: virion protein ul25; PDBTitle: structural characterization of the ul25 dna packaging2 protein from herpes simplex virus type 1
39	d2ifaa1	Alignment	not modelled	21.0	20	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
40	c2h0uA	Alignment	not modelled	19.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-p-h-flavin oxidoreductase; PDBTitle: crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
41	c2okrF	Alignment	not modelled	18.3	63	PDB header: transferase Chain: F: PDB Molecule: map kinase-activated protein kinase 2; PDBTitle: crystal structure of the p38a-mapkap kinase 2 heterodimer
42	c2okrC	Alignment	not modelled	18.3	63	PDB header: transferase Chain: C: PDB Molecule: map kinase-activated protein kinase 2; PDBTitle: crystal structure of the p38a-mapkap kinase 2 heterodimer
43	c3rkoF	Alignment	not modelled	17.6	9	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
44	c3m5kA	Alignment	not modelled	17.2	40	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh dehydrogenase/nad(p)h nitroreductase; PDBTitle: crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (bdi_1728) from parabacteroides distasonis atcc 85033 at 1.86 a resolution
45	d1bkja	Alignment	not modelled	17.0	38	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
46	c2hayD	Alignment	not modelled	16.8	30	PDB header: oxidoreductase Chain: D: PDB Molecule: putative nad(p)h-flavin oxidoreductase; PDBTitle: the crystal structure of the putative nad(p)h-flavin oxidoreductase2 from streptococcus pyogenes m1 gas
47	c3g14B	Alignment	not modelled	16.7	30	PDB header: oxidoreductase Chain: B: PDB Molecule: nitroreductase family protein; PDBTitle: crystal structure of nitroreductase family protein (yp_877874.1) from2 clostridium novyi nt at 1.75 a resolution
48	c3ge5A	Alignment	not modelled	16.4	30	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nad(p)h:fmn oxidoreductase; PDBTitle: crystal structure of a putative nad(p)h:fmn oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution
49	c3j0cG	Alignment	not modelled	16.0	24	PDB header: virus Chain: G: PDB Molecule: e1 envelope glycoprotein; PDBTitle: models of e1, e2 and cp of venezuelan equine encephalitis virus tc-832 strain restrained by a near atomic resolution cryo-em map
50	c2wzvB	Alignment	not modelled	14.9	25	PDB header: oxidoreductase Chain: B: PDB Molecule: nfnb protein; PDBTitle: crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
51	c3kwaA	Alignment	not modelled	14.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh dehydrogenase/nad(p)h nitroreductase; PDBTitle: crystal structure of putative nadh dehydrogenase/nad(p)h2 nitroreductase (np_809094.1) from bacteroides thetaiotaomicron vpi-3 5482 at 1.54 a resolution
						PDB header: flavoprotein Chain: A: PDB Molecule: nitroreductase:

52	c3ek3A_	Alignment	not modelled	13.9	20	PDBTitle: crystal structure of nitroreductase with bound fmn (yp_211706.1) from2 bacteroides fragilis nctc 9343 at 1.70 a resolution
53	d1kqba_	Alignment	not modelled	13.8	14	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
54	c3n2sD_	Alignment	not modelled	13.3	25	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh-dependent nitro/flavin reductase; PDBTitle: structure of nfra1 nitroreductase from b. subtilis
55	c1qcrD_	Alignment	not modelled	13.1	33	PDB header: PDB COMPND:
56	c3b9yA_	Alignment	not modelled	13.1	18	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
57	c3pxvD_	Alignment	not modelled	12.2	40	PDB header: oxidoreductase Chain: D: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a nitroreductase with bound fmn (dhaf_2018) from2 desulfitobacterium hafniense dcb-2 at 2.30 a resolution
58	d2csba2	Alignment	not modelled	12.1	60	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
59	c2w2hB_	Alignment	not modelled	12.1	21	PDB header: rna-binding protein Chain: B: PDB Molecule: cyclin-t1; PDBTitle: structural basis of transcription activation by the cyclin2 t1-tat-tar rna complex from eiaf
60	c2r01A_	Alignment	not modelled	12.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: nitroreductase family protein; PDBTitle: crystal structure of a putative fmn-dependent nitroreductase (ct0345)2 from chlorobium tepidum t1s at 1.15 a resolution
61	d1q90m_	Alignment	not modelled	12.0	50	Fold: Single transmembrane helix Superfamily: PetM subunit of the cytochrome b6f complex Family: PetM subunit of the cytochrome b6f complex
62	d1ppiw_	Alignment	not modelled	12.0	17	Fold: Single transmembrane helix Superfamily: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
63	d1f5va_	Alignment	not modelled	11.6	25	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
64	c2b9n6_	Alignment	not modelled	11.6	9	PDB header: ribosome Chain: 6: PDB Molecule: 50s ribosomal protein l33; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf2,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400.
65	d2zjr11	Alignment	not modelled	11.6	9	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L33p
66	c3e39A_	Alignment	not modelled	11.6	38	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nitroreductase; PDBTitle: crystal structure of a putative nitroreductase in complex with fmn2 (dde_0787) from desulfovibrio desulfuricans subsp. at 1.70 a3 resolution
67	c2l2oA_	Alignment	not modelled	11.5	33	PDB header: unknown function Chain: A: PDB Molecule: upf0727 protein c6orf115; PDBTitle: solution structure of human hspc280 protein
68	d2f93b1	Alignment	not modelled	11.4	40	Fold: Transmembrane helix hairpin Superfamily: Htr2 transmembrane domain-like Family: Htr2 transmembrane domain-like
69	c2f93B_	Alignment	not modelled	11.4	40	PDB header: membrane protein Chain: B: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: k intermediate structure of sensory rhodopsin ii/transducer complex in2 combination with the ground state structure
70	d1vfra_	Alignment	not modelled	11.3	43	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
71	d3cx5i1	Alignment	not modelled	11.3	11	Fold: Single transmembrane helix Superfamily: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: Subunit X (non-heme 7 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
72	c3gr3B_	Alignment	not modelled	11.2	38	PDB header: flavoprotein Chain: B: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a nitroreductase-like family protein (pnba,2 bh06130) from bartonella henselae str. houston-1 at 1.45 a resolution
73	c3ge6B_	Alignment	not modelled	11.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: nitroreductase; PDBTitle: crystal structure of a putative nitroreductase in complex with fmn2 (exig_2970) from exigobacterium sibiricum 255-15 at 1.85 a3 resolution
74	c2hg5D_	Alignment	not modelled	11.1	20	PDB header: membrane protein Chain: D: PDB Molecule: kcsa channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
75	c3bm2B_	Alignment	not modelled	11.1	10	PDB header: oxidoreductase Chain: B: PDB Molecule: protein ydja; PDBTitle: crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor
						PDB header: metal transport/membrane protein

76	c2bbjB_	Alignment	not modelled	11.0	11	Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
77	c1bhbA_	Alignment	not modelled	10.9	38	PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy
78	c1zrtD_	Alignment	not modelled	10.8	29	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
79	c2kjfA_	Alignment	not modelled	10.8	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: carnocyclin-a; PDBTitle: the solution structure of the circular bacteriocin2 carnocyclin a (ccla)
80	c3hj9A_	Alignment	not modelled	10.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of a putative nitroreductase (reut a1228) from2 ralstonia eutropha jmp134 at 2.00 a resolution
81	d1zcha1	Alignment	not modelled	10.7	25	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
82	c3eofB_	Alignment	not modelled	10.7	50	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
83	c2f95B_	Alignment	not modelled	10.6	40	PDB header: membrane protein Chain: B: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: m intermediate structure of sensory rhodopsin ii/transducer complex in2 combination with the ground state structure
84	c3koqC_	Alignment	not modelled	10.4	38	PDB header: oxidoreductase Chain: C: PDB Molecule: nitroreductase family protein; PDBTitle: crystal structure of a nitroreductase family protein (cd3355) from2 clostridium difficile 630 at 1.58 a resolution
85	c2ktrA_	Alignment	not modelled	10.2	29	PDB header: signaling protein, transport protein Chain: A: PDB Molecule: sequestosome-1; PDBTitle: nmr structure of p62 pb1 dimer determined based on pcs
86	c3bemA_	Alignment	not modelled	10.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nad(p)h nitroreductase ydfn; PDBTitle: crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
87	c3e10B_	Alignment	not modelled	10.0	50	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadh oxidase; PDBTitle: crystal structure of putative nadh oxidase (np_348178.1)2 from clostridium acetobutylicum at 1.40 a resolution
88	d1dd3a1	Alignment	not modelled	9.8	24	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
89	c1x3nA_	Alignment	not modelled	9.7	23	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
90	c3ol4B_	Alignment	not modelled	9.7	50	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
91	d1pbua_	Alignment	not modelled	9.7	25	Fold: Ferredoxin-like Superfamily: eEF1-gamma domain Family: eEF1-gamma domain
92	c2b2hA_	Alignment	not modelled	9.7	5	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: ammonium transporter amt-1 from a. fulgidus (as)
93	c2j5dA_	Alignment	not modelled	9.6	23	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: nmr structure of bni3 transmembrane domain in lipid2 bicelles
94	c2i7hE_	Alignment	not modelled	9.6	25	PDB header: oxidoreductase Chain: E: PDB Molecule: nitroreductase-like family protein; PDBTitle: crystal structure of the nitroreductase-like family protein from2 bacillus cereus
95	d1h2sb_	Alignment	not modelled	9.5	40	Fold: Transmembrane helix hairpin Superfamily: Htr2 transmembrane domain-like Family: Htr2 transmembrane domain-like
96	c1h2sB_	Alignment	not modelled	9.5	40	PDB header: membrane protein Chain: B: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: molecular basis of transmembrane signalling by sensory2 rhodopsin ii-transducer complex
97	d1mgta2	Alignment	not modelled	9.4	25	Fold: Ribonuclease H-like motif Superfamily: Methylated DNA-protein cysteine methyltransferase domain Family: Methylated DNA-protein cysteine methyltransferase domain
98	c3iddA_	Alignment	not modelled	9.3	4	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
99	c3hoiA_	Alignment	not modelled	9.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nitroreductase bf3017; PDBTitle: crystal structure of fmn-dependent nitroreductase bf3017 from2 bacteroides fragilis nctc 9343 (yp_212631.1) from bacteroides3 fragilis nctc 9343 at 1.55 a resolution