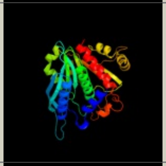
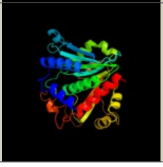
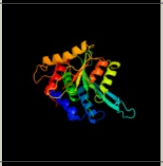
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P10423
Date	Thu Jan 5 11:32:15 GMT 2012
Unique Job ID	c49636104dfda361

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2afwa1	Alignment		100.0	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Glutaminyl-peptide cyclotransferase-like
2	c3pb6X_	Alignment		100.0	20	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glutaminyl-peptide cyclotransferase-like protein; **PDBTitle:** crystal structure of the catalytic domain of human golgi-resident2 glutaminyl cyclase at ph 6.5
3	d1tkja1	Alignment		100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
4	c3tc8A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** crystal structure of a hypothetical zn-dependent exopeptidase2 (bdi_3547) from parabacteroides distasonis atcc 8503 at 1.06 a3 resolution
5	d1rtqa_	Alignment		100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
6	c2ootA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
7	c3rbuA_	Alignment		100.0	24	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa
8	c1cx8F_	Alignment		100.0	20	**PDB header:**metal transport **Chain:** F: **PDB Molecule:**transferrin receptor protein; **PDBTitle:** crytal structure of the ectodomain of human transferrin receptor
9	c3iibA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m28; **PDBTitle:** crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution
10	d1de4c3	Alignment		100.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
11	d3bi1a3	Alignment		100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like

12	c2ek8A_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** aminopeptidase from aneurinibacillus sp. strain am-1
13	c3guxA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zn-dependent exopeptidase; **PDBTitle:** crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
14	d1vhoa2	Alignment		100.0	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
15	c3k9tA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase (np_348812.1) from clostridium2 acetobutylicum at 2.37 a resolution
16	d1xfoa2	Alignment		100.0	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
17	d1yloa2	Alignment		100.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
18	d1vhea2	Alignment		100.0	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
19	d1cg2a1	Alignment		99.9	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
20	d2fvga2	Alignment		99.9	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
21	d1z2la1	Alignment	not modelled	99.9	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
22	d1vixa1	Alignment	not modelled	99.9	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
23	d1fnoa4	Alignment	not modelled	99.9	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
24	d1r3na1	Alignment	not modelled	99.9	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
25	c3t6mA_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of the catalytic domain of dape protein from2 v.cholerea in the zn bound form
26	d1lfwa1	Alignment	not modelled	99.8	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
27	c2zogA_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic non-specific dipeptidase; **PDBTitle:** crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
28	d1xmba1	Alignment	not modelled	99.7	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
29	c1vhoA_	Alignment	not modelled	99.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endoglucanase;

						PDBTitle: crystal structure of a putative peptidase/endoglucanase
30	c2pokB_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae
31	c1q7lA_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
32	c3gb0A_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of aminopeptidase pept (np_980509.1) from bacillus2 cereus atcc 10987 at 2.04 a resolution
33	c2v8gD_	Alignment	not modelled	99.6	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-alanine synthase; **PDBTitle:** crystal structure of beta-alanine synthase from2 saccharomyces kluyveri in complex with the product beta-3 alanine
34	c2qyvB_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-his dipeptidase; **PDBTitle:** crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution
35	c3dljB_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-ala-his dipeptidase; **PDBTitle:** crystal structure of human carnosine dipeptidase 1
36	c3rzaA_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidase; **PDBTitle:** crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
37	c3kl9F_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**glutamyl aminopeptidase; **PDBTitle:** crystal structure of pepa from streptococcus pneumoniae
38	d1ysja1	Alignment	not modelled	99.6	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
39	c1cg2D_	Alignment	not modelled	99.5	18	**PDB header:**metallocarboxypeptidase **Chain:** D: **PDB Molecule:**carboxypeptidase g2; **PDBTitle:** carboxypeptidase g2
40	c3khzA_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative dipeptidase sacol1801; **PDBTitle:** crystal structure of r350a mutant of staphylococcus aureus2 metallopeptidase (sapep/dape) in the apo-form
41	c3pfoB_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
42	c2greC_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deblocking aminopeptidase; **PDBTitle:** crystal structure of deblocking aminopeptidase from bacillus cereus
43	c3pfeA_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a m20a metallo peptidase (dape, lpg0809) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 1.503 a resolution
44	c1vgyB_	Alignment	not modelled	99.5	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of succinyl diaminopimelate desuccinylase
45	c2q43A_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**iaa-amino acid hydrolase ilr1-like 2; **PDBTitle:** ensemble refinement of the protein crystal structure of iaa-aminoacid2 hydrolase from arabidopsis thaliana gene at5g56660
46	c3mruB_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacyl-histidine dipeptidase; **PDBTitle:** crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
47	c3n5fB_	Alignment	not modelled	99.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-carbamoyl-l-amino acid hydrolase; **PDBTitle:** crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
48	d2grea2	Alignment	not modelled	99.4	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
49	c1vixA_	Alignment	not modelled	99.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of a putative peptidase t
50	c2imoA_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoate amidohydrolase; **PDBTitle:** crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
51	c1lfwA_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pepv; **PDBTitle:** crystal structure of pepv
52	c1ysjB_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein yxep; **PDBTitle:** crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
53	c1vheA_	Alignment	not modelled	99.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**aminopeptidase/glucanase homolog; **PDBTitle:** crystal structure of a aminopeptidase/glucanase homolog
54	c3ct9B_	Alignment	not modelled	99.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative zinc peptidase (np_812461.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.31

						a resolution
55	c1y0yA_	Alignment	not modelled	99.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**frv operon protein frvx; **PDBTitle:** crystal structure of tetrahedral aminopeptidase from p. horikoshii in2 complex with amastatin
56	c3tx8A_	Alignment	not modelled	99.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a succinyl-diaminopimelate desuccinylase (arge)2 from corynebacterium glutamicum atcc 13032 at 2.97 a resolution
57	c1yloA_	Alignment	not modelled	99.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sf2450; **PDBTitle:** crystal structure of protein of unknown function (possible2 aminopeptidase) s2589 from shigella flexneri 2a str. 2457t
58	c2pe3A_	Alignment	not modelled	99.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**354aa long hypothetical operon protein frv; **PDBTitle:** crystal structure of frv operon protein frvx (ph1821)from pyrococcus2 horikoshii ot3
59	c3ic1A_	Alignment	not modelled	99.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
60	c3cpxC_	Alignment	not modelled	99.2	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**aminopeptidase, m42 family; **PDBTitle:** crystal structure of putative m42 glutamyl aminopeptidase2 (yp_676701.1) from cytophaga hutchinsonii atcc 33406 at 2.39 a3 resolution
61	c2rb7A_	Alignment	not modelled	99.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of co-catalytic metallopeptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution
62	d1y0ya2	Alignment	not modelled	99.1	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
63	c3ifeA_	Alignment	not modelled	99.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
64	c3l6sA_	Alignment	not modelled	99.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartyl aminopeptidase; **PDBTitle:** crystal structure of human aspartyl aminopeptidase (dnpep),2 in complex with aspartic acid hydroxamate
65	c2fvgA_	Alignment	not modelled	99.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
66	c3ramC_	Alignment	not modelled	99.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hmra protein; **PDBTitle:** crystal structure of hmra
67	d1vgya1	Alignment	not modelled	99.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
68	c3isxA_	Alignment	not modelled	99.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1050) from thermotoga2 maritima at 1.40 a resolution
69	c2cf4A_	Alignment	not modelled	98.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein ph0519; **PDBTitle:** pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
70	c2ijzF_	Alignment	not modelled	98.9	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**probable m18-family aminopeptidase 2; **PDBTitle:** crystal structure of aminopeptidase
71	c2glfB_	Alignment	not modelled	98.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
72	c1y7eA_	Alignment	not modelled	98.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
73	c2f7vA_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aectylcitrulline deacetylase; **PDBTitle:** structure of acetylcitrulline deacetylase complexed with2 one co
74	d1y7ea2	Alignment	not modelled	98.4	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
75	c3io1B_	Alignment	not modelled	98.3	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
76	c2gljR_	Alignment	not modelled	96.8	16	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:** **PDBTitle:** crystal structure of aminopeptidase i from clostridium2 acetobutylicum
77	c1q7lB_	Alignment	not modelled	63.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
78	d1tvca2	Alignment	not modelled	47.1	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
						Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain

79	d1krha2	Alignment	not modelled	41.7	16	**Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
80	d1gvha3	Alignment	not modelled	31.2	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
81	d1qfja2	Alignment	not modelled	19.9	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
82	c1ulqD_	Alignment	not modelled	19.5	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of tt0182 from thermus thermophilus hb8
83	c3ij3A_	Alignment	not modelled	18.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** 1.8 angstrom resolution crystal structure of cytosol aminopeptidase2 from coxiella burnetii
84	c2vosA_	Alignment	not modelled	13.1	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase protein folc; **PDBTitle:** mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
85	d1dpea_	Alignment	not modelled	11.3	21	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
86	c3tpaA_	Alignment	not modelled	11.3	16	**PDB header:**heme binding protein **Chain:** A: **PDB Molecule:**heme-binding protein a; **PDBTitle:** structure of hbpa2 from haemophilus parasuis
87	c1krhA_	Alignment	not modelled	9.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
88	d1ep3b2	Alignment	not modelled	9.6	25	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
89	d2piaa2	Alignment	not modelled	9.0	22	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
90	c3rqtA_	Alignment	not modelled	9.0	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** 1.5 angstrom crystal structure of the complex of ligand binding2 component of abc-type import system from staphylococcus aureus with3 nickel and two histidines
91	c2grvC_	Alignment	not modelled	8.8	14	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**lpqw; **PDBTitle:** crystal structure of lpqw
92	d1j0aa_	Alignment	not modelled	8.1	17	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
93	c1a8pA_	Alignment	not modelled	7.8	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph\:ferredoxin oxidoreductase; **PDBTitle:** ferredoxin reductase from azotobacter vinelandii
94	d1a8pa2	Alignment	not modelled	7.3	11	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
95	c3b64A_	Alignment	not modelled	7.2	13	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
96	c3m8uA_	Alignment	not modelled	7.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**heme-binding protein a; **PDBTitle:** crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
97	c3t66A_	Alignment	not modelled	6.5	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
98	d1nh2a1	Alignment	not modelled	6.3	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
99	d1xoca1	Alignment	not modelled	6.1	13	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like