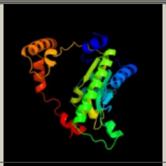
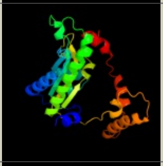
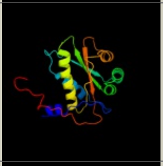
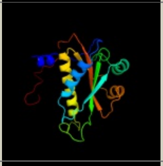
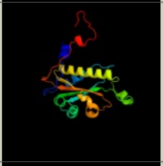
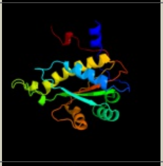
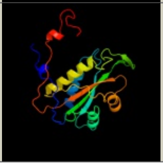
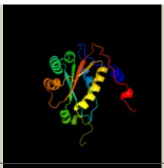
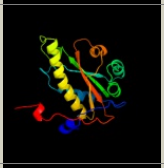
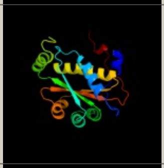
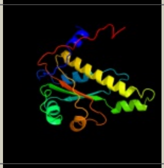
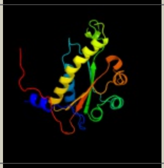
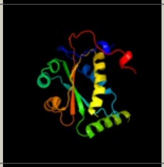
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P17117
Date	Thu Jan 5 11:36:00 GMT 2012
Unique Job ID	5806c420884b9571

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1f5va_	Alignment		100.0	100	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
2	d1zcha1	Alignment		100.0	38	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
3	d1bkja_	Alignment		100.0	52	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
4	c3n2sD_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadph-dependent nitro/flavin reductase; **PDBTitle:** structure of nfra1 nitroreductase from b. subtilis
5	c3eofB_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
6	c3kwkA_	Alignment		100.0	24	**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
7	c2islB_	Alignment		100.0	22	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**blub; **PDBTitle:** blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
8	c3m5kA_	Alignment		100.0	27	**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
9	c3e39A_	Alignment		100.0	25	**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
10	c3gagB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadh dehydrogenase, nadph nitroreductase; **PDBTitle:** crystal structure of a nitroreductase-like protein (smu.346) from2 streptococcus mutans at 1.70 a resolution
11	d2frea1	Alignment		100.0	18	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase

12	d1noxa_	Alignment		100.0	25	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
13	c3gbhC_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad(p)h-flavin oxidoreductase; **PDBTitle:** crystal structure of a putative nad(p)h:fmn oxidoreductase (se1966)2 from staphylococcus epidermidis atcc 12228 at 2.00 a resolution
14	d2b67a1	Alignment		100.0	19	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
15	d1vfra_	Alignment		100.0	15	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
16	c3bemA_	Alignment		100.0	17	**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
17	d2ifaa1	Alignment		100.0	13	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
18	c2hayD_	Alignment		100.0	18	**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
19	c3of4A_	Alignment		100.0	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
20	c3e10B_	Alignment		100.0	20	**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
21	c2wqfA_	Alignment	not modelled	100.0	17	**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
22	d1ywqa1	Alignment	not modelled	100.0	17	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
23	c3ge6B_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of a putative nitroreductase in complex with fmn2 (exig_2970) from exiguobacterium sibiricum 255-15 at 1.85 a3 resolution
24	c3gr3B_	Alignment	not modelled	100.0	24	**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
25	c3ge5A_	Alignment	not modelled	100.0	21	**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
26	c3g14B_	Alignment	not modelled	100.0	20	**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
27	d1ykia1	Alignment	not modelled	100.0	23	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
						Fold:FMN-dependent nitroreductase-like

28	d1kqba_	Alignment	not modelled	100.0	20	**Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
29	c3koqC_	Alignment	not modelled	100.0	22	**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
30	c2wzvB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nfnb protein; **PDBTitle:** crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
31	c2r01A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a putative fmn-dependent nitroreductase (ct0345)2 from chlorobium tepidum tls at 1.15 a resolution
32	c3eo8A_	Alignment	not modelled	100.0	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**blub-like flavoprotein; **PDBTitle:** crystal structure of blub-like flavoprotein (yp_001089088.1) from2 clostridium difficile 630 at 1.74 a resolution
33	c2i7hE_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitroreductase-like family protein; **PDBTitle:** crystal structure of the nitroreductase-like family protein from2 bacillus cereus
34	c3k6hB_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
35	c3pxvD_	Alignment	not modelled	100.0	24	**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
36	c2h0uA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-flavin oxidoreductase; **PDBTitle:** crystal structure of nad(p)h-flavin oxidoreductase from helicobacter2 pylori
37	c3ek3A_	Alignment	not modelled	100.0	20	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nitroreductase; **PDBTitle:** crystal structure of nitroreductase with bound fmn (yp_211706.1) from2 bacteroides fragilis nctc 9343 at 1.70 a resolution
38	c3gh8A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iodotyrosine dehalogenase 1; **PDBTitle:** crystal structure of mus musculus iodotyrosine deiodinase (iyd) bound2 to fmn and di-iodotyrosine (dit)
39	c3gfaB_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nitroreductase; **PDBTitle:** crystal structure of a putative nitroreductase in complex with fmn2 (cd3205) from clostridium difficile 630 at 1.35 a resolution
40	c3hj9A_	Alignment	not modelled	100.0	27	**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
41	c3bm2B_	Alignment	not modelled	100.0	20	**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
42	c3hoiA_	Alignment	not modelled	100.0	20	**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
43	c3eo7A_	Alignment	not modelled	100.0	23	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative nitroreductase; **PDBTitle:** crystal structure of a putative nitroreductase (ava_2154) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
44	d1vkwa_	Alignment	not modelled	99.9	18	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**Putative nitroreductase TM1586
45	c3k4iC_	Alignment	not modelled	54.3	23	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
46	d1vi4a_	Alignment	not modelled	38.9	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
47	c3c8oB_	Alignment	not modelled	36.0	15	**PDB header:**hydrolase regulator **Chain:** B: **PDB Molecule:**regulator of ribonuclease activity a; **PDBTitle:** the crystal structure of rraa from pao1
48	c2c5qE_	Alignment	not modelled	35.6	21	**PDB header:**structural genomics,unknown function **Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
49	d1nxja_	Alignment	not modelled	34.6	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
50	c1nxjA_	Alignment	not modelled	34.6	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable s-adenosylmethionine:2- **PDBTitle:** structure of rv3853 from mycobacterium tuberculosis
51	c2pcnA_	Alignment	not modelled	33.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:2-demethylmenaquinone **PDBTitle:** crystal structure of s-adenosylmethionine: 2-dimethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
52	d1q5xa_	Alignment	not modelled	33.1	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like

						Family: RraA-like
53	d1j3la_	Alignment	not modelled	32.1	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
54	d1cr6a1	Alignment	not modelled	29.6	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
55	d1oeyj_	Alignment	not modelled	29.1	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
56	d2paga1	Alignment	not modelled	18.1	20	**Fold:**SMI1/KNR4-like **Superfamily:**SMI1/KNR4-like **Family:**SMI1/KNR4-like
57	d2oc6a1	Alignment	not modelled	17.6	13	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
58	d1gz0a2	Alignment	not modelled	17.2	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
59	d1zd3a1	Alignment	not modelled	17.2	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**YihX-like
60	c3nojA_	Alignment	not modelled	16.4	3	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate **PDBTitle:** the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
61	d1ni8a_	Alignment	not modelled	16.2	10	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
62	c3gyxJ_	Alignment	not modelled	15.1	14	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
63	c3nr7A_	Alignment	not modelled	14.2	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein h-ns; **PDBTitle:** crystal structure of s. typhimurium h-ns 1-83
64	c3ed5A_	Alignment	not modelled	12.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**yfnb; **PDBTitle:** the crystal structure of yfnb from bacillus subtilis subsp. subtilis2 str. 168
65	d1e7la1	Alignment	not modelled	12.4	4	**Fold:**LEM/SAP HeH motif **Superfamily:**Recombination endonuclease VII, C-terminal and dimerization domains **Family:**Recombination endonuclease VII, C-terminal and dimerization domains
66	c2i6xA_	Alignment	not modelled	12.0	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, haloacid dehalogenase-like family; **PDBTitle:** the structure of a predicted had-like family hydrolase from2 porphyromonas gingivalis.
67	d2ovra1	Alignment	not modelled	11.9	11	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
68	d1gz0f2	Alignment	not modelled	11.6	19	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**RNA 2'-O ribose methyltransferase substrate binding domain
69	d1lr1a_	Alignment	not modelled	11.3	10	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
70	d1nexa1	Alignment	not modelled	11.0	13	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
71	c3p8bB_	Alignment	not modelled	11.0	16	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
72	d1ng6a_	Alignment	not modelled	10.0	24	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/YqeY domain
73	c1cr6A_	Alignment	not modelled	10.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
74	d2ogga1	Alignment	not modelled	9.9	15	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
75	d1fs2b1	Alignment	not modelled	9.9	14	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
76	d1i1qb_	Alignment	not modelled	9.9	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
77	d2a2pa1	Alignment	not modelled	9.6	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
						PDB header:transferase **Chain:** B: **PDB Molecule:**archaeosine trna-guanine

78	c1iq8B_	Alignment	not modelled	9.3	23	transglycosylase; **PDBTitle:** crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
79	d2fi1a1	Alignment	not modelled	9.2	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Phosphonoacetaldehyde hydrolase-like
80	d2i8da1	Alignment	not modelled	8.8	19	**Fold:**Secretion chaperone-like **Superfamily:**YdhG-like **Family:**YdhG-like
81	c1l9xA_	Alignment	not modelled	8.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
82	d1l9xa_	Alignment	not modelled	8.8	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
83	d1xuba2	Alignment	not modelled	8.6	16	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
84	c1d0rA_	Alignment	not modelled	8.5	12	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
85	d1itza2	Alignment	not modelled	8.1	10	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
86	d1i7qb_	Alignment	not modelled	7.7	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
87	d1f2va_	Alignment	not modelled	7.5	28	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH
88	d1ov9a_	Alignment	not modelled	7.4	17	**Fold:**H-NS histone-like proteins **Superfamily:**H-NS histone-like proteins **Family:**H-NS histone-like proteins
89	d2i5ha1	Alignment	not modelled	7.3	23	**Fold:**AF1531-like **Superfamily:**AF1531-like **Family:**AF1531-like
90	c2i5hA_	Alignment	not modelled	7.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1531; **PDBTitle:** crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
91	c2ds2B_	Alignment	not modelled	6.9	14	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**sweet protein mabinlin-2 chain b; **PDBTitle:** crystal structure of mabinlin ii
92	c2p1nD_	Alignment	not modelled	6.4	11	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
93	c1vcnA_	Alignment	not modelled	6.2	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
94	d1nlna_	Alignment	not modelled	6.2	25	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
95	c3dnjB_	Alignment	not modelled	6.1	12	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease adapter protein clps; **PDBTitle:** the structure of the caulobacter crescentus clps protease2 adaptor protein in complex with a n-end rule peptide
96	c3l5kA_	Alignment	not modelled	6.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase domain- **PDBTitle:** the crystal structure of human haloacid dehalogenase-like2 hydrolase domain containing 1a (hdhd1a)
97	c1jrjA_	Alignment	not modelled	5.9	12	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**exendin-4; **PDBTitle:** solution structure of exendin-4 in 30-vol% trifluoroethanol
98	d1ny8a_	Alignment	not modelled	5.8	11	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
99	d1ou0a_	Alignment	not modelled	5.7	22	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH