Phyre^2

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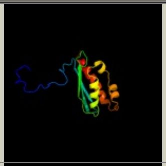
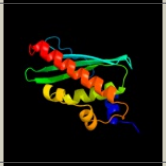
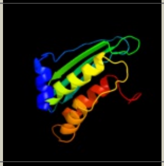
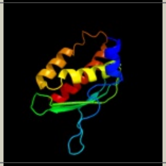
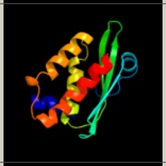
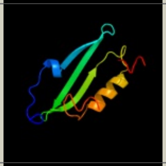
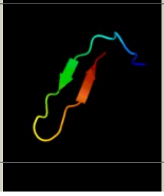
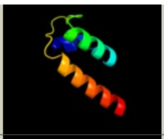
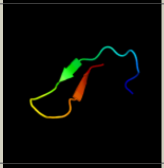
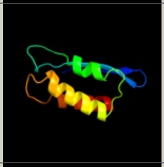
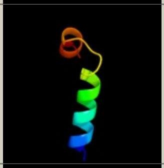
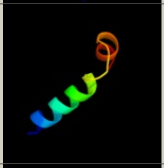
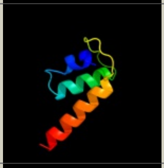
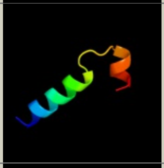
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r9pa_	Alignment		100.0	86	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
2	c2z7eB_	Alignment		100.0	53	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
3	d1wfza_	Alignment		100.0	74	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
4	d1xjsa_	Alignment		100.0	31	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
5	d1su0b_	Alignment		100.0	38	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
6	c2qq4A_	Alignment		100.0	32	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster biosynthesis protein iscu; **PDBTitle:** crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (ttha1736) from thermus thermophilus hb8
7	d1mzga_	Alignment		96.2	13	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
8	d1ni7a_	Alignment		94.9	21	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
9	c1wloA_	Alignment		91.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sufe protein; **PDBTitle:** solution structure of the hypothetical protein from thermus2 thermophilus hb8
10	c2e5aA_	Alignment		75.5	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoyltransferase 1; **PDBTitle:** crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
11	d1u0la1	Alignment		67.4	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like

12	c2zkrr_	Alignment		56.0	15	**PDB header:**ribosomal protein/rna **Chain:** R: **PDB Molecule:**rna expansion segment es39 part i; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
13	d1t9ha1	Alignment		54.1	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	d1v97a4	Alignment		52.3	8	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
15	d1ffvc1	Alignment		50.5	13	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
16	d1fs1b1	Alignment		49.6	24	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
17	d1fs2b1	Alignment		42.2	24	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
18	c3jywN_	Alignment		38.3	18	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l17(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
19	d1nexa1	Alignment		37.8	24	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
20	c2kelB_	Alignment		35.7	44	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
21	d1i4ja_	Alignment	not modelled	34.8	23	**Fold:**Ribosomal protein L22 **Superfamily:**Ribosomal protein L22 **Family:**Ribosomal protein L22
22	d1n62c1	Alignment	not modelled	33.6	15	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
23	c3cxoA_	Alignment	not modelled	33.3	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative galactonate dehydratase; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from2 salmonella typhimurium complexed with mg and 3-deoxy-l-3 rhamnonate
24	c4a17Q_	Alignment	not modelled	33.2	16	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**rpl17; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
25	c3iz5V_	Alignment	not modelled	33.0	18	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**60s ribosomal protein l17 (l22p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
26	c2ftcM_	Alignment	not modelled	31.8	16	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**mitochondrial ribosomal protein l22 isoform a; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
27	d2ovra1	Alignment	not modelled	31.7	24	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
28	c1x2gB_	Alignment	not modelled	28.7	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lipoate-protein ligase a; **PDBTitle:** crystal structure of lipate-protein ligase a from2

						escherichia coli
29	d1vqza1	Alignment	not modelled	28.0	17	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
30	d1t3qc1	Alignment	not modelled	27.9	17	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
31	d1x2ga1	Alignment	not modelled	27.6	26	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
32	d2zjrp1	Alignment	not modelled	25.9	23	**Fold:**Ribosomal protein L22 **Superfamily:**Ribosomal protein L22 **Family:**Ribosomal protein L22
33	d2p92a1	Alignment	not modelled	24.0	25	**Fold:**eIF1-like **Superfamily:**TM1457-like **Family:**TM1457-like
34	c3bboU_	Alignment	not modelled	23.6	23	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**ribosomal protein l22; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
35	d1jroa3	Alignment	not modelled	21.5	13	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
36	c2p1nD_	Alignment	not modelled	18.2	20	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
37	d2axoa1	Alignment	not modelled	18.1	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Atu2684-like
38	c3hrdC_	Alignment	not modelled	18.1	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
39	d1vqor1	Alignment	not modelled	15.8	24	**Fold:**Ribosomal protein L22 **Superfamily:**Ribosomal protein L22 **Family:**Ribosomal protein L22
40	d1io2a_	Alignment	not modelled	14.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
41	c1nexC_	Alignment	not modelled	14.7	24	**PDB header:**ligase, cell cycle **Chain:** C: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
42	c2yv5A_	Alignment	not modelled	14.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
43	c1t9hA_	Alignment	not modelled	14.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** the crystal structure of yloq, a circularly permuted gtpase.
44	c2axoA_	Alignment	not modelled	13.8	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu2684; **PDBTitle:** x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
45	c3h5fB_	Alignment	not modelled	13.0	27	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
46	c3h5fA_	Alignment	not modelled	13.0	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
47	c3h5gA_	Alignment	not modelled	13.0	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
48	c3h5gC_	Alignment	not modelled	13.0	27	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
49	c3h5fC_	Alignment	not modelled	13.0	27	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l16l-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
50	c3h5gB_	Alignment	not modelled	13.0	27	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l16d-pen; **PDBTitle:** switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
51	c2l55A_	Alignment	not modelled	12.7	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
52	d1rvka2	Alignment	not modelled	12.5	9	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
53	c1zeqX_	Alignment	not modelled	12.2	15	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
54	c1vqzA_	Alignment	not modelled	12.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a

						(sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
55	c2ovqA_	Alignment	not modelled	11.1	24	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
56	c2p0iA_	Alignment	not modelled	10.8	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-rhamnonate dehydratase; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from gibberella zeae
57	c2jnvA_	Alignment	not modelled	10.0	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
58	c1u0lB_	Alignment	not modelled	10.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
59	d1iloa_	Alignment	not modelled	9.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
60	d2if6a1	Alignment	not modelled	8.8	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**YiiX-like
61	c3nyeA_	Alignment	not modelled	8.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-arginine dehydrogenase; **PDBTitle:** crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine
62	c3iz5w_	Alignment	not modelled	8.0	35	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
63	c2fgxA_	Alignment	not modelled	7.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
64	d1r8ja1	Alignment	not modelled	7.6	29	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
65	c2k8sA_	Alignment	not modelled	7.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution nmr structure of dimeric thioredoxin-like protein2 ne0084 from nitrosomonas europea: northeast structural3 genomics target net6
66	d1ofcx1	Alignment	not modelled	7.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
67	d1lj8a3	Alignment	not modelled	7.3	23	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Mannitol 2-dehydrogenase
68	c2oz3F_	Alignment	not modelled	7.2	13	**PDB header:**lyase **Chain:** F: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of l-rhamnonate dehydratase from azotobacter2 vinelandii
69	c3ic4A_	Alignment	not modelled	7.2	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin (grx-1); **PDBTitle:** the crystal structure of the glutaredoxin(grx-1) from archaeoglobus2 fulgidus
70	c3f4yF_	Alignment	not modelled	7.0	41	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**mutant peptide derived from hiv gp41 chr domain; **PDBTitle:** hiv gp41 six-helix bundle containing a mutant chr alpha-2 peptide sequence
71	d1egoa_	Alignment	not modelled	7.0	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
72	d1yeya2	Alignment	not modelled	6.9	15	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
73	d1v2za_	Alignment	not modelled	6.8	14	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
74	d1rm6b1	Alignment	not modelled	6.8	14	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
75	d1sv1a_	Alignment	not modelled	6.7	14	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
76	d1r5qa_	Alignment	not modelled	6.5	7	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
77	c2x6pA_	Alignment	not modelled	6.4	29	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l19c; **PDBTitle:** crystal structure of coil ser l19c
78	c2x6pC_	Alignment	not modelled	6.4	29	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l19c; **PDBTitle:** crystal structure of coil ser l19c
79	c2x6pB_	Alignment	not modelled	6.4	29	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l19c; **PDBTitle:** crystal structure of coil ser l19c
						Fold: Rubredoxin-like

80	d2cona1	Alignment	not modelled	6.4	30	**Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
81	d1nm3a1	Alignment	not modelled	6.2	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
82	c1cosB_	Alignment	not modelled	6.1	29	**PDB header:**alpha-helical bundle **Chain:** B: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
83	c1cosA_	Alignment	not modelled	6.1	29	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
84	c1cosC_	Alignment	not modelled	6.1	29	**PDB header:**alpha-helical bundle **Chain:** C: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
85	c1ffuF_	Alignment	not modelled	6.1	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cutm, flavoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
86	d2jnya1	Alignment	not modelled	6.0	10	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
87	d1yq9h1	Alignment	not modelled	6.0	28	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
88	c2wpnB_	Alignment	not modelled	5.9	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic [nifese] hydrogenase, large subunit, **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
89	c3pdgA_	Alignment	not modelled	5.8	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
90	d1ryph_	Alignment	not modelled	5.6	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
91	d2gl5a2	Alignment	not modelled	5.5	13	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
92	c2kpiA_	Alignment	not modelled	5.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
93	d1u07a_	Alignment	not modelled	5.4	17	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
94	d1iyxa2	Alignment	not modelled	5.2	20	**Fold:**Enolase N-terminal domain-like **Superfamily:**Enolase N-terminal domain-like **Family:**Enolase N-terminal domain-like
95	c3b9jJ_	Alignment	not modelled	5.2	7	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
96	c3etrM_	Alignment	not modelled	5.2	7	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of xanthine oxidase in complex with2 lumazine
97	d1rypi_	Alignment	not modelled	5.2	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
98	c3hrdF_	Alignment	not modelled	5.2	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
99	d1e3db_	Alignment	not modelled	5.1	31	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit