Phyre2

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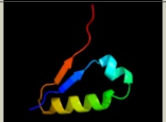
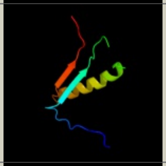
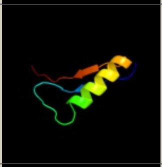
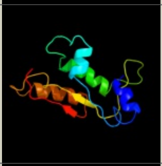
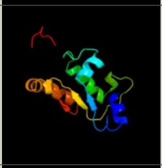
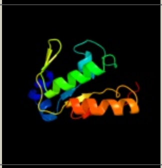
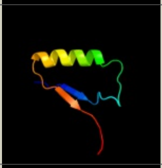
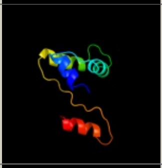
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nxua_	Alignment		100.0	95	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
2	c1vbiA_	Alignment		100.0	24	**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
3	d1xrha_	Alignment		100.0	22	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
4	c3i0pA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from entamoeba histolytica
5	c1z2iA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium
6	d1rfma_	Alignment		100.0	27	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
7	c1wtjB_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
8	c2g8yB_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
9	c1v9nA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of malate dehydrogenase from pyrococcus horikoshii ot3
10	c3uoeB_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from sinorhizobium meliloti
11	c3eefA_	Alignment		49.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-carbamoylsarcosine amidase related protein; **PDBTitle:** crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum

12	c2qiwA_	Alignment		48.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
13	c3irvA_	Alignment		46.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysteine hydrolase; **PDBTitle:** crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
14	c3kl2K_	Alignment		46.2	11	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase from streptomyces2 avermitilis
15	c2ze3A_	Alignment		42.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dfa0005; **PDBTitle:** crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
16	d1muma_	Alignment		41.7	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
17	c2hjpA_	Alignment		38.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
18	d1nbaa_	Alignment		37.7	20	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
19	d2ebfx2	Alignment		37.3	25	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
20	c3b8iF_	Alignment		37.3	14	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
21	c2b34C_	Alignment	not modelled	37.3	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
22	d1nf9a_	Alignment	not modelled	37.2	11	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
23	c3ih1A_	Alignment	not modelled	36.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
24	c3ot4F_	Alignment	not modelled	35.7	11	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative isochorismatase; **PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf
25	c3eooL_	Alignment	not modelled	31.8	13	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
26	c1e0mA_	Alignment	not modelled	28.8	21	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**wwprototype; **PDBTitle:** prototype ww domain
27	c1yiuA_	Alignment	not modelled	27.4	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy e3 ubiquitin protein ligase; **PDBTitle:** itch e3 ubiquitin ligase ww3 domain
28	c2ysbA_	Alignment	not modelled	25.9	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**salvador homolog 1 protein; **PDBTitle:** solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
29	d1wdjb_	Alignment	not modelled	25.4	10	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like

						Family: Hypothetical protein TT1808 (TTHA1514)
30	c3mcwA_	Alignment	not modelled	25.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
31	c3l4hA_	Alignment	not modelled	25.2	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hecw1; **PDBTitle:** helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
32	c3hb7G_	Alignment	not modelled	24.6	16	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**isochorismatase hydrolase; **PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
33	d1wdja_	Alignment	not modelled	23.9	10	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein TT1808 (TTHA1514)
34	c2px0D_	Alignment	not modelled	23.0	10	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
35	c2ysdA_	Alignment	not modelled	22.9	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz **PDBTitle:** solution structure of the first ww domain from the human2 membrane-associated guanylate kinase, ww and pdz domain-3 containing protein 1. magi-1
36	d1f8ab1	Alignment	not modelled	22.8	20	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
37	d1yaca_	Alignment	not modelled	22.4	15	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
38	c1wr7A_	Alignment	not modelled	22.2	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nedd4-2; **PDBTitle:** solution structure of the third ww domain of nedd4-2
39	c2fq1A_	Alignment	not modelled	21.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
40	d1sgma2	Alignment	not modelled	21.4	25	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
41	c2djyA_	Alignment	not modelled	21.4	21	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**smad ubiquitination regulatory factor 2; **PDBTitle:** solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
42	c3ot2A_	Alignment	not modelled	21.2	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
43	c3ot2B_	Alignment	not modelled	21.2	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
44	d1t57a_	Alignment	not modelled	20.9	16	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
45	c1wr4A_	Alignment	not modelled	20.7	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2
46	d1bdga1	Alignment	not modelled	20.5	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
47	c2lawA_	Alignment	not modelled	20.4	21	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**yorkie homolog; **PDBTitle:** structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
48	c3oqpA_	Alignment	not modelled	20.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
49	c1wmvA_	Alignment	not modelled	20.3	29	**PDB header:**oxidoreductase, apoptosis **Chain:** A: **PDB Molecule:**ww domain containing oxidoreductase; **PDBTitle:** solution structure of the second ww domain of wwox
50	c2uygF_	Alignment	not modelled	20.0	20	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallogaphic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
51	d1k9ra_	Alignment	not modelled	19.8	18	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
52	c2h0rD_	Alignment	not modelled	19.5	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
53	d2cfua2	Alignment	not modelled	19.5	14	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
54	d3bzra1	Alignment	not modelled	19.4	13	**Fold:**EscU C-terminal domain-like **Superfamily:**EscU C-terminal domain-like

						Family: EscU C-terminal domain-like
55	c3bzrA_	Alignment	not modelled	19.4	13	**PDB header:**membrane protein, protein transport **Chain:** A: **PDB Molecule:**escu; **PDBTitle:** crystal structure of escu c-terminal domain with n262d mutation, space2 group p 41 21 2
56	c3t7yB_	Alignment	not modelled	19.0	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
57	d3ci0k2	Alignment	not modelled	18.6	15	**Fold:**SAM domain-like **Superfamily:**GspK insert domain-like **Family:**GspK insert domain-like
58	d1tk7a1	Alignment	not modelled	18.3	14	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
59	c1ymzA_	Alignment	not modelled	18.1	36	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cc45; **PDBTitle:** cc45, an artificial ww domain designed using statistical2 coupling analysis
60	d1j2ra_	Alignment	not modelled	17.0	14	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
61	c2k29A_	Alignment	not modelled	16.5	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
62	d1i5hw_	Alignment	not modelled	16.5	20	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
63	d1f61a_	Alignment	not modelled	16.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
64	d3djba1	Alignment	not modelled	15.6	14	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
65	c3lqyA_	Alignment	not modelled	15.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase hydrolase; **PDBTitle:** crystal structure of putative isochorismatase hydrolase from2 oleispira antarctica
66	c2kxqA_	Alignment	not modelled	14.2	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase smurf2; **PDBTitle:** solution structure of smurf2 ww2 and ww3 bound to smad7 py motif2 containing peptide
67	d1mnta_	Alignment	not modelled	14.0	19	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
68	d1a4sa_	Alignment	not modelled	13.9	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
69	c2jlhA_	Alignment	not modelled	13.7	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
70	c3o93A_	Alignment	not modelled	13.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
71	c3hu5B_	Alignment	not modelled	13.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
72	c3oqpB_	Alignment	not modelled	12.9	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
73	c3ivlA_	Alignment	not modelled	12.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zinc protease; **PDBTitle:** the crystal structure of the inactive peptidase domain of a putative2 zinc protease from bordetella parapertussis to 2.2a
74	c2hg2A_	Alignment	not modelled	12.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
75	c3fpvC_	Alignment	not modelled	12.6	21	**PDB header:**heme binding protein **Chain:** C: **PDB Molecule:**extracellular haem-binding protein; **PDBTitle:** crystal structure of hbps
76	d1lvaa3	Alignment	not modelled	12.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
77	d1zk8a2	Alignment	not modelled	12.5	21	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
78	c3le4A_	Alignment	not modelled	12.1	22	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**microprocessor complex subunit dgcr8; **PDBTitle:** crystal structure of the dgcr8 dimerization domain
79	c2dmvA_	Alignment	not modelled	11.9	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**itchy homolog e3 ubiquitin protein ligase; **PDBTitle:** solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itch)
80	c2h6rG	Alignment	not modelled	11.8	18	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase;

80	c2h6rG_	Alignment	not modelled	11.8	18	**PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
81	c2dclB_	Alignment	not modelled	11.8	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503; **PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3
82	c3ju8B_	Alignment	not modelled	11.6	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
83	c2a67C_	Alignment	not modelled	11.4	14	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein
84	c2cfuA_	Alignment	not modelled	11.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sdsa1; **PDBTitle:** crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
85	c3k2wD_	Alignment	not modelled	11.3	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
86	d2jmfa1	Alignment	not modelled	11.3	21	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
87	d1o51a_	Alignment	not modelled	10.6	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
88	c2xetB_	Alignment	not modelled	10.5	5	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
89	c3e0kA_	Alignment	not modelled	10.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amino-acid acetyltransferase; **PDBTitle:** crystal structure of c-termianl domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
90	d2bfda1	Alignment	not modelled	10.5	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
91	c2vovA_	Alignment	not modelled	10.4	38	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**surface-associated protein; **PDBTitle:** an oxidized tryptophan facilitates copper-binding in2 methylococcus capsulatus secreted protein mope. the3 stucture of wild-type mope to 1.35aa
92	c3jz4C_	Alignment	not modelled	10.3	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
93	c3iwkB_	Alignment	not modelled	10.3	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
94	d1vp8a_	Alignment	not modelled	10.3	19	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
95	c1qzrA_	Alignment	not modelled	10.3	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase ii; **PDBTitle:** crystal structure of the atpase region of saccharomyces cerevisiae2 topoisomerase ii bound to icrf-187 (dexrazoxane)
96	c3hazA_	Alignment	not modelled	10.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
97	d1nnsa_	Alignment	not modelled	10.0	14	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
98	d2pw9a1	Alignment	not modelled	10.0	26	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**FdhD/NarQ
99	d1ig8a1	Alignment	not modelled	10.0	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase