Phyre^2

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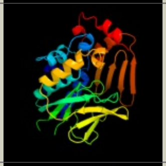
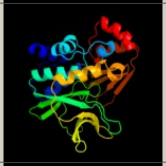
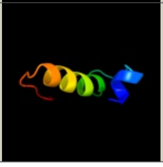
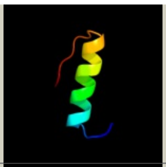
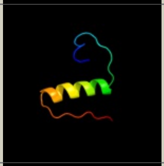
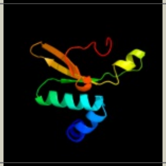
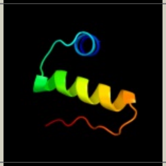
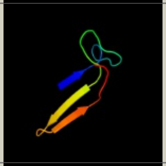
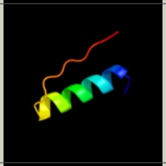
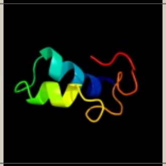
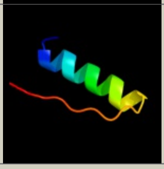
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e2ta_	Alignment		100.0	74	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
2	d1w5ra1	Alignment		100.0	36	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
3	d1w4ta1	Alignment		100.0	31	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
4	c2vfbA_	Alignment		100.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylamine n-acetyltransferase; **PDBTitle:** the structure of mycobacterium marinum arylamine n-2 acetyltransferase
5	d2bsza1	Alignment		100.0	37	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
6	c3d9wA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure analysis of nocardia farcinica arylamine2 n-acetyltransferase
7	c3lnbA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase family protein; **PDBTitle:** crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
8	c2pfrB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arylamine n-acetyltransferase 2; **PDBTitle:** human n-acetyltransferase 2
9	c3kd4A_	Alignment		97.6	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative protease; **PDBTitle:** crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
10	c3isrB_	Alignment		96.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transglutaminase-like enzymes, putative cysteine protease; **PDBTitle:** the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
11	c3eswA_	Alignment		77.1	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.

12	d1x3za1	Alignment		75.3	35	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
13	d2q3za4	Alignment		71.9	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
14	d2f4ma1	Alignment		69.9	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
15	c2qshA_	Alignment		68.9	24	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna repair protein rad4; **PDBTitle:** crystal structure of rad4-rad23 bound to a mismatch dna
16	c1zkpD_	Alignment		55.7	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ba1088; **PDBTitle:** 1.5a resolution crystal structure of a metallo beta lactamase family2 protein, the elac homolgue of bacillus anthracis, a putative3 ribonuclease
17	d1g0da4	Alignment		52.8	35	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
18	c3zwfA_	Alignment		50.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc phosphodiesterase elac protein 1; **PDBTitle:** crystal structure of human trnase z, short form (elac1).
19	d1gxha_	Alignment		48.1	13	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
20	d1ex0a4	Alignment		44.5	38	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
21	c1wv9B_	Alignment	not modelled	43.7	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**rhodanese homolog tt1651; **PDBTitle:** crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
22	d1icaa_	Alignment	not modelled	43.4	60	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Insect defensins
23	c3iacA_	Alignment	not modelled	38.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucuronate isomerase; **PDBTitle:** 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
24	c2nz3A_	Alignment	not modelled	35.6	50	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**defensin, mutant def-acaa; **PDBTitle:** nmr structure of def-acaa, a mutant of anopheles defensin2 def-aaa
25	d1zkpa1	Alignment	not modelled	34.4	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**YhfI-like
26	c2e3eA_	Alignment	not modelled	33.7	70	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**defensin, mutant def-bbb; **PDBTitle:** nmr structure of def-bbb, a mutant of anopheles defensin2 def-aaa
27	d1af7a1	Alignment	not modelled	33.1	15	**Fold:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Superfamily:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Family:**Chemotaxis receptor methyltransferase CheR, N-terminal domain
28	c3g1pA_	Alignment	not modelled	32.3	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein phnp; **PDBTitle:** crystals structure of phnp from e.coli k-12

29	c2lm1A_	Alignment	not modelled	29.9	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**lysine-specific demethylase lid; **PDBTitle:** solution nmr structure of lysine-specific demethylase lid from2 drosophila melanogaster, northeast structural genomics consortium3 target fr824d
30	c3nvaB_	Alignment	not modelled	29.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
31	d2vlqa1	Alignment	not modelled	27.5	10	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
32	c3chgB_	Alignment	not modelled	25.8	29	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**glycine betaine-binding protein; **PDBTitle:** the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
33	c4a19F_	Alignment	not modelled	25.8	23	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl14; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
34	d1s1ma2	Alignment	not modelled	25.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
35	d1kkxa_	Alignment	not modelled	24.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
36	c3g5jA_	Alignment	not modelled	24.2	37	**PDB header:**nucleotide binding protein **Chain:** A: **PDB Molecule:**putative atp/gtp binding protein; **PDBTitle:** crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
37	c2jo7A_	Alignment	not modelled	24.1	17	**PDB header:**surface active protein **Chain:** A: **PDB Molecule:**glycosylphosphatidylinositol-anchored merozoite **PDBTitle:** solution structure of the adhesion protein bd37 from2 babesia divergens
38	d1vjja4	Alignment	not modelled	23.4	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
39	c3h11A_	Alignment	not modelled	23.1	24	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**casp8 and fadd-like apoptosis regulator; **PDBTitle:** zymogen caspase-8:c-flipl protease domain complex
40	d1vcoa2	Alignment	not modelled	22.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
41	c3ce7A_	Alignment	not modelled	22.4	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**specific mitochodrial acyl carrier protein; **PDBTitle:** crystal structure of toxoplasma specific mitochodrial acyl2 carrier protein, 59.m03510
42	c3iz5N_	Alignment	not modelled	22.3	19	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
43	c2vgpD_	Alignment	not modelled	20.8	8	**PDB header:**transferase **Chain:** D: **PDB Molecule:**inner centromere protein a; **PDBTitle:** crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor
44	d2jq4a1	Alignment	not modelled	20.7	18	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
45	c2jq4A_	Alignment	not modelled	20.7	18	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein atu2571; **PDBTitle:** complete resonance assignments and solution structure2 calculation of atc2521 (nesg id: att6) from agrobacterium3 tumefaciens
46	d1pbya1	Alignment	not modelled	20.5	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
47	c3p45I_	Alignment	not modelled	20.1	29	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**caspase-6; **PDBTitle:** crystal structure of apo-caspase-6 at physiological ph
48	d1jmxa1	Alignment	not modelled	20.0	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
49	c1slmA_	Alignment	not modelled	20.0	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**stromelysin-1; **PDBTitle:** crystal structure of fibroblast stromelysin-1: the c-truncated human2 proenzyme
50	c1l9mB_	Alignment	not modelled	20.0	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein-glutamine glutamyltransferase e3; **PDBTitle:** three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
51	c3sirD_	Alignment	not modelled	19.5	33	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice
52	c3rnvA_	Alignment	not modelled	19.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helper component proteinase; **PDBTitle:** structure of the autocatalytic cysteine protease domain of potyvirus2 helper-component proteinase
53	c1cjyB_	Alignment	not modelled	19.3	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (cytosolic phospholipase a2);

						PDBTitle: human cytosolic phospholipase a2
54	d1yt8a4	Alignment	not modelled	19.2	25	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
55	d1ayia_	Alignment	not modelled	19.0	18	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
56	c2l9fA_	Alignment	not modelled	18.9	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cale8; **PDBTitle:** nmr solution structure of meacp
57	c2yqeA_	Alignment	not modelled	18.8	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**jumonji/arid domain-containing protein 1d; **PDBTitle:** solution structure of the arid domain of jarid1d protein
58	c3lmoA_	Alignment	not modelled	18.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**specialized acyl carrier protein; **PDBTitle:** crystal structure of specialized acyl carrier protein2 (rpa2022) from rhodopseudomonas palustris, northeast3 structural genomics consortium target rpr324
59	c3aj3A_	Alignment	not modelled	18.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**4-pyridoxolactonase; **PDBTitle:** crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
60	c3rbnB_	Alignment	not modelled	18.2	19	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** crystal structure of mutl protein homolog 1 isoform 1 [homo sapiens]
61	c3nhvE_	Alignment	not modelled	18.2	21	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**bh2092 protein; **PDBTitle:** crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
62	c1g0dA_	Alignment	not modelled	17.8	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** crystal structure of red sea bream transglutaminase
63	c2ql5A_	Alignment	not modelled	17.2	31	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of caspase-7 with inhibitor ac-dmqd-cho
64	d1rhsa1	Alignment	not modelled	17.2	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
65	c2dnwA_	Alignment	not modelled	16.8	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
66	c2kciA_	Alignment	not modelled	16.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acyl carrier protein; **PDBTitle:** solution nmr structure of gmet_2339 from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr141
67	c3izcN_	Alignment	not modelled	16.7	27	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
68	c1boiA_	Alignment	not modelled	16.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** n-terminally truncated rhodanese
69	d3ci0k2	Alignment	not modelled	16.2	28	**Fold:**SAM domain-like **Superfamily:**GspK insert domain-like **Family:**GspK insert domain-like
70	c2r2dC_	Alignment	not modelled	15.3	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**zn-dependent hydrolases; **PDBTitle:** structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
71	d1ig6a_	Alignment	not modelled	15.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
72	c1i3oC_	Alignment	not modelled	14.8	25	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**caspase 3; **PDBTitle:** crystal structure of the complex of xiap-bir2 and caspase 3
73	c3eshB_	Alignment	not modelled	14.6	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein similar to metal-dependent hydrolase; **PDBTitle:** crystal structure of a probable metal-dependent hydrolase2 from staphylococcus aureus. northeast structural genomics3 target zr314
74	c1i51A_	Alignment	not modelled	14.4	29	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-7 subunit p20; **PDBTitle:** crystal structure of caspase-7 complexed with xiap
75	c2eg4B_	Alignment	not modelled	14.3	45	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase
76	d1wlza1	Alignment	not modelled	14.3	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
77	c1wlzD_	Alignment	not modelled	14.3	11	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cap-binding protein complex interacting protein **PDBTitle:** crystal structure of djbp fragment which was obtained by2 limited proteolysis
						PDB header:hydrolase/ligase/hydrolase

78	c3sipC_	Alignment	not modelled	14.2	40	**Chain:** C: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice and diap1-bir1 complex
79	c2ad5B_	Alignment	not modelled	14.2	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
80	c1kv3F_	Alignment	not modelled	13.9	38	**PDB header:**transferase **Chain:** F: **PDB Molecule:**protein-glutamine gamma-glutamyltransferase; **PDBTitle:** human tissue transglutaminase in gdp bound form
81	c3ht4B_	Alignment	not modelled	13.8	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aluminum resistance protein; **PDBTitle:** crystal structure of the q81a77_baccr protein from bacillus2 cereus. northeast structural genomics consortium target3 bcr213
82	c2cgqA_	Alignment	not modelled	13.6	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**acyl carrier protein acpa; **PDBTitle:** a putative acyl carrier protein(rv0033) from mycobacterium2 tuberculosis
83	c2no8A_	Alignment	not modelled	13.2	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**colicin-e2 immunity protein; **PDBTitle:** nmr structure analysis of the colicin immuntiy protein im2
84	c1zfuA_	Alignment	not modelled	12.8	45	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plectasin; **PDBTitle:** plectasin:a peptide antibiotic with therapeutic potential2 from a saprophytic fungus
85	c2d7cD_	Alignment	not modelled	12.7	33	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**rab11 family-interacting protein 3; **PDBTitle:** crystal structure of human rab11 in complex with fip3 rab-2 binding domain
86	c1pyoA_	Alignment	not modelled	12.4	27	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**caspase-2; **PDBTitle:** crystal structure of human caspase-2 in complex with acetyl-leu-asp-2 glu-ser-asp-cho
87	c3e4cB_	Alignment	not modelled	12.3	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** procaspase-1 zymogen domain crystal strucutre
88	d1p9ea_	Alignment	not modelled	12.3	22	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
89	c1p9eA_	Alignment	not modelled	12.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
90	d1r9la_	Alignment	not modelled	12.2	29	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
91	c3bwwA_	Alignment	not modelled	12.1	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein of unknown function duf692/cog3220; **PDBTitle:** crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution
92	d1r3na1	Alignment	not modelled	11.9	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
93	c3on5B_	Alignment	not modelled	11.9	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bh1974 protein; **PDBTitle:** crystal structure of a xanthine dehydrogenase (bh1974) from bacillus2 halodurans at 2.80 a resolution
94	c3edqC_	Alignment	not modelled	11.5	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**caspase-3; **PDBTitle:** crystal structure of caspase-3 with inhibitor ac-ldesd-cho
95	d1h99a1	Alignment	not modelled	11.5	13	**Fold:**PTS-regulatory domain, PRD **Superfamily:**PTS-regulatory domain, PRD **Family:**PTS-regulatory domain, PRD
96	c2fq2A_	Alignment	not modelled	11.4	11	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of minor conformation of holo-acyl2 carrier protein from malaria parasite plasmodium falciparum
97	d1nw9b_	Alignment	not modelled	11.4	24	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
98	d1qxna_	Alignment	not modelled	11.4	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
99	c1qdul_	Alignment	not modelled	11.3	19	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**caspase-8 alpha-chain; **PDBTitle:** crystal structure of the complex of caspase-8 with the tripeptide2 ketone inhibitor zevd-dcbmk