Phyre2

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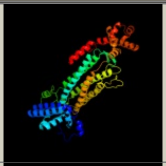
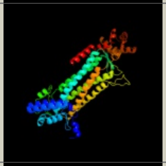
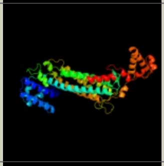
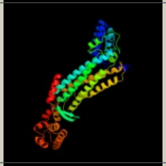
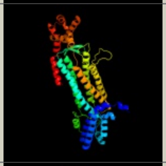
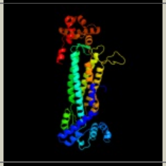
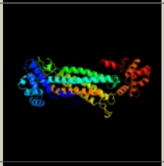
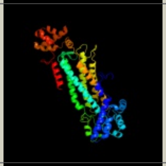
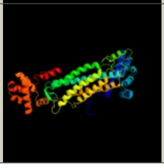
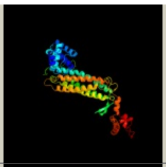
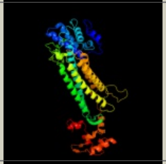
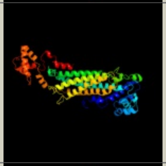
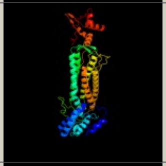
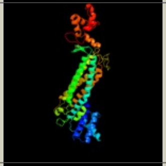
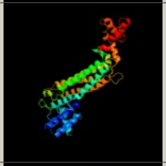
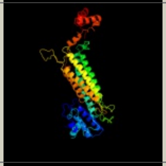
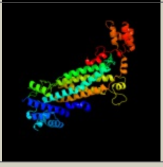
Description	P11447
Date	Thu Jan 5 11:32:38 GMT 2012
Unique Job ID	3aaa938b36751f11

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tj7a_	Alignment		100.0	100	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
2	d1i0aa_	Alignment		100.0	41	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
3	d1tjva_	Alignment		100.0	44	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
4	d1k62a_	Alignment		100.0	44	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
5	c2e9fC_	Alignment		100.0	50	**PDB header:**lyase **Chain:** C: **PDB Molecule:**argininosuccinate lyase; **PDBTitle:** crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
6	d1hy0a_	Alignment		100.0	43	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
7	c2pfmA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
8	d1c3ca_	Alignment		100.0	18	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
9	d1q5na_	Alignment		100.0	19	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
10	d1re5a_	Alignment		100.0	23	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
11	c3c8tA_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fumarate lyase; **PDBTitle:** crystal structure of fumarate lyase from mesorhizobium sp. bnc1

12	d1fuoa_	Alignment		100.0	20	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
13	d1j3ua_	Alignment		100.0	20	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
14	c2vd6B_	Alignment		100.0	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** human adenylosuccinate lyase in complex with its substrate2 n6-(1,2-dicarboxyethyl)-amp, and its products amp and3 fumarate.
15	d1yfma_	Alignment		100.0	20	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
16	c1yfmA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fumarase; **PDBTitle:** recombinant yeast fumarase
17	d1vdka_	Alignment		100.0	20	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
18	c3no9C_	Alignment		100.0	19	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fumarate hydratase class ii; **PDBTitle:** crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
19	d1jswa_	Alignment		100.0	19	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
20	c2qgaC_	Alignment		100.0	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** plasmodium vivax adenylosuccinate lyase pv003765 with amp bound
21	c3ocfB_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fumarate lyase:delta crystallin; **PDBTitle:** crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form
22	d1dofa_	Alignment	not modelled	100.0	19	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
23	c3bhgA_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of adenylosuccinate lyase from legionella2 pneumophila
24	d1jswc_	Alignment	not modelled	100.0	19	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
25	c2ptsA_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** crystal structure of wild type escherichia coli adenylosuccinate lyase
26	c1yisA_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylosuccinate lyase; **PDBTitle:** structural genomics of caenorhabditis elegans: adenylosuccinate lyase
27	c3e04C_	Alignment	not modelled	100.0	19	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fumarate hydratase; **PDBTitle:** crystal structure of human fumarate hydratase
28	c3gtdB_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fumarate hydratase class ii; **PDBTitle:** 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
						PDB header:isomerase

29	c2fenA_	Alignment	not modelled	100.0	17	**Chain:** A: **PDB Molecule:**3-carboxy-cis,cis-muconate lactonizing enzyme; **PDBTitle:** 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2
30	d1f1oa_	Alignment	not modelled	100.0	19	**Fold:**L-aspartase-like **Superfamily:**L-aspartase-like **Family:**L-aspartase/fumarase
31	c3r6yG_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** G: **PDB Molecule:**aspartase; **PDBTitle:** crystal structure of chymotrypsin-treated aspartase from bacillus sp.2 ym55-1
32	c2rcyB_	Alignment	not modelled	61.8	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline carboxylate reductase; **PDBTitle:** crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
33	c1x5bA_	Alignment	not modelled	50.7	29	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2; **PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
34	d2ahra1	Alignment	not modelled	38.0	28	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
35	d2di4a1	Alignment	not modelled	33.6	18	**Fold:**FtsH protease domain-like **Superfamily:**FtsH protease domain-like **Family:**FtsH protease domain-like
36	d1yqga1	Alignment	not modelled	32.1	25	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
37	c2ctoA_	Alignment	not modelled	30.2	58	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**novel protein; **PDBTitle:** solution structure of the hmg box like domain from human2 hypothetical protein flj14904
38	c2xgvA_	Alignment	not modelled	27.8	28	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**psiv capsid n-terminal domain; **PDBTitle:** structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
39	d1u5ta1	Alignment	not modelled	22.9	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
40	c1p74B_	Alignment	not modelled	19.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
41	d1nvta2	Alignment	not modelled	19.0	14	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
42	c3fbtB_	Alignment	not modelled	18.7	13	**PDB header:**oxidoreductase, lyase **Chain:** B: **PDB Molecule:**chorismate mutase and shikimate 5-dehydrogenase **PDBTitle:** crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum
43	d1vi2a2	Alignment	not modelled	16.5	15	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
44	c3bbnC_	Alignment	not modelled	16.1	63	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**ribosomal protein s3; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
45	c2vs0B_	Alignment	not modelled	15.6	10	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
46	d1npya2	Alignment	not modelled	15.1	21	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
47	c3pgjB_	Alignment	not modelled	14.9	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
48	c2ev9B_	Alignment	not modelled	14.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
49	c2zmeA_	Alignment	not modelled	14.4	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
50	d1phza2	Alignment	not modelled	14.4	22	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
51	d1g3pa2	Alignment	not modelled	14.3	33	**Fold:**N-terminal domains of the minor coat protein g3p **Superfamily:**N-terminal domains of the minor coat protein g3p **Family:**N-terminal domains of the minor coat protein g3p
52	c1nvtA_	Alignment	not modelled	14.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5'-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
53	d2ga1a1	Alignment	not modelled	13.8	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like

54	c3o8qB_	Alignment	not modelled	13.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
55	c3tozA_	Alignment	not modelled	13.5	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
56	c2nloA_	Alignment	not modelled	13.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
57	c2hk8B_	Alignment	not modelled	12.9	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
58	c2ag8A_	Alignment	not modelled	12.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
59	d1mlwa_	Alignment	not modelled	12.3	17	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
60	c1u5tA_	Alignment	not modelled	12.1	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
61	c3e2tA_	Alignment	not modelled	11.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tryptophan 5-hydroxylase 1; **PDBTitle:** the catalytic domain of chicken tryptophan hydroxylase 12 with bound tryptophan
62	d1dlja1	Alignment	not modelled	11.4	20	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
63	c1wjvA_	Alignment	not modelled	11.2	56	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cell growth regulating nucleolar protein lyar; **PDBTitle:** solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar
64	d1j8ua_	Alignment	not modelled	11.2	22	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
65	c3gt0A_	Alignment	not modelled	11.1	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
66	d2qalc1	Alignment	not modelled	11.0	38	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
67	c3pwzA_	Alignment	not modelled	10.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3; **PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida
68	c2eggA_	Alignment	not modelled	10.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
69	d1p77a2	Alignment	not modelled	10.8	15	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
70	d1k6ya1	Alignment	not modelled	10.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**N-terminal Zn binding domain of HIV integrase **Family:**N-terminal Zn binding domain of HIV integrase
71	c1nytC_	Alignment	not modelled	10.7	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** shikimate dehydrogenase aroe complexed with nadp+
72	c3cuqA_	Alignment	not modelled	10.5	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
73	d1e0ea_	Alignment	not modelled	10.5	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**N-terminal Zn binding domain of HIV integrase **Family:**N-terminal Zn binding domain of HIV integrase
74	d2qy9a1	Alignment	not modelled	10.5	21	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
75	c3u62A_	Alignment	not modelled	10.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from thermotoga maritima
76	c1npyA_	Alignment	not modelled	10.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like **PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607
77	c3ke2A_	Alignment	not modelled	10.3	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1; **PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution

78	d1q3ma_	Alignment	not modelled	10.0	33	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
79	d1nyta2	Alignment	not modelled	9.9	15	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Shikimate dehydrogenase-like
80	d1wjfa_	Alignment	not modelled	9.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**N-terminal Zn binding domain of HIV integrase **Family:**N-terminal Zn binding domain of HIV integrase
81	c2o8kA_	Alignment	not modelled	9.4	23	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
82	c3hfrA_	Alignment	not modelled	9.0	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes
83	d1vkma_	Alignment	not modelled	9.0	15	**Fold:**Indigoidine synthase A-like **Superfamily:**Indigoidine synthase A-like **Family:**Indigoidine synthase A-like
84	d1ltza_	Alignment	not modelled	9.0	25	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
85	c3c24A_	Alignment	not modelled	9.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
86	c2jfqA_	Alignment	not modelled	8.8	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
87	d2voua2	Alignment	not modelled	8.8	12	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**PHBH-like
88	c1dipA_	Alignment	not modelled	8.8	22	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
89	c3m1eA_	Alignment	not modelled	8.7	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of benm_dbd
90	c2gzmB_	Alignment	not modelled	8.2	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
91	c1vi2B_	Alignment	not modelled	8.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
92	c3lq9B_	Alignment	not modelled	7.7	20	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**dna-damage-inducible transcript 4 protein; **PDBTitle:** crystal strucure of human redd1, a hypoxia-induced regulator2 of mtor
93	d1sxjb1	Alignment	not modelled	7.6	14	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
94	d1v5pa_	Alignment	not modelled	7.5	50	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
95	c3eq5G_	Alignment	not modelled	7.3	29	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**ski-like protein; **PDBTitle:** crystal structure of fragment 137 to 238 of the human ski-like protein
96	d1q8ha_	Alignment	not modelled	7.3	29	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
97	c1q8hA_	Alignment	not modelled	7.3	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**osteocalcin; **PDBTitle:** crystal structure of porcine osteocalcin
98	c2p9xB_	Alignment	not modelled	7.3	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph0832; **PDBTitle:** crystal structure of ph0832 from pyrococcus horikoshii ot3
99	c2v27A_	Alignment	not modelled	7.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenylalanine hydroxylase; **PDBTitle:** structure of the cold active phenylalanine hydroxylase from2 colwellia psychrerythraea 34h