Phyre^2

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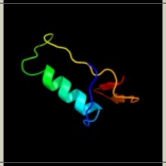
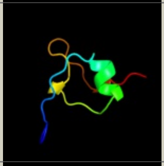
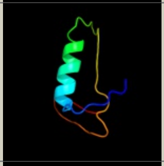
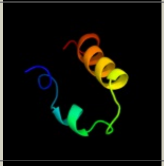
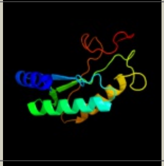
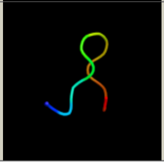
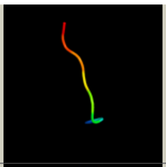
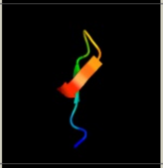
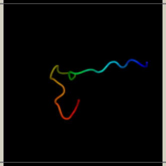
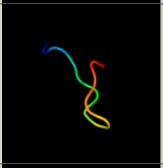
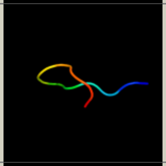
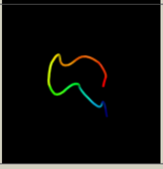
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mcnA_	Alignment		84.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-amino-4-hydroxy-6-hydroxymethyldihydropteridine **PDBTitle:** crystal structure of the 6-hyroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
2	d1f6ya_	Alignment		67.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
3	c2cg8B_	Alignment		58.3	38	**PDB header:**lyase/transferase **Chain:** B: **PDB Molecule:**dihydroneopterin aldolase 6-hydroxymethyl-7,8- **PDBTitle:** the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae
4	d3bofa1	Alignment		42.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
5	c3a1yG_	Alignment		40.5	27	**PDB header:**ribosomal protein **Chain:** G: **PDB Molecule:**acidic ribosomal protein p0; **PDBTitle:** the structure of protein complex
6	d1f9ya_	Alignment		39.5	20	**Fold:**Ferredoxin-like **Superfamily:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK **Family:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
7	c3k13A_	Alignment		37.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
8	c2bpbB_	Alignment		36.7	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
9	c2qx0A_	Alignment		36.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**7,8-dihydro-6-hydroxymethylpterin- **PDBTitle:** crystal structure of yersinia pestis hppk (ternary complex)
10	c2yciX_	Alignment		35.9	14	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
11	d1glua_	Alignment		35.0	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor

12	c1xyr6_	Alignment		31.5	33	**PDB header:**virus **Chain:** 6: **PDB Molecule:**genome polyprotein, coat protein vp3; **PDB Fragment:**residues 620-630 **PDBTitle:** poliovirus 135s cell entry intermediate
13	d1s6la1	Alignment		30.7	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
14	d1dszb_	Alignment		29.6	15	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
15	d1nm8a1	Alignment		26.8	19	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
16	d1ndba1	Alignment		26.5	19	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
17	d1lo1a_	Alignment		25.9	46	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
18	d1kb6b_	Alignment		25.5	45	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
19	c1r4iA_	Alignment		24.6	42	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**androgen receptor; **PDBTitle:** crystal structure of androgen receptor dna-binding domain2 bound to a direct repeat response element
20	d1r4ia_	Alignment		24.6	42	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
21	d1cbka_	Alignment	not modelled	22.7	18	**Fold:**Ferredoxin-like **Superfamily:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK **Family:**6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
22	c1no3A_	Alignment	not modelled	22.1	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lipoxygenase-3; **PDBTitle:** refined structure of soybean lipoxygenase-3 with 4-nitrocatechol at2 2.15 angstrom resolution
23	d3bnea1	Alignment	not modelled	22.0	33	**Fold:**Lipoxigenase **Superfamily:**Lipoxigenase **Family:**Plant lipoxigenases
24	d1hcqa_	Alignment	not modelled	21.9	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
25	c1u22A_	Alignment	not modelled	20.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydropteroyltriglutamate-- **PDBTitle:** a. thaliana cobalamine independent methionine synthase
26	d1hraa_	Alignment	not modelled	18.6	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
27	c2envA_	Alignment	not modelled	18.6	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peroxisome proliferator-activated receptor delta; **PDBTitle:** solution sturcture of the c4-type zinc finger domain from2 human peroxisome proliferator-activated receptor delta
28	d1phza1	Alignment	not modelled	18.5	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain

29	c1t7qA_	Alignment	not modelled	17.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine acetyltransferase; **PDBTitle:** crystal structure of the f565a mutant of murine carnitine2 acetyltransferase in complex with carnitine and coa
30	d1ynwa1	Alignment	not modelled	17.7	42	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
31	d1r4ra_	Alignment	not modelled	17.4	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
32	c2h4tB_	Alignment	not modelled	17.4	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carnitine o-palmitoyltransferase ii, **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase ii
33	d1u1ha2	Alignment	not modelled	16.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Cobalamin-independent methionine synthase
34	c1nj2A_	Alignment	not modelled	16.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
35	c2e9hA_	Alignment	not modelled	15.9	12	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
36	c1qfqB_	Alignment	not modelled	15.4	31	**PDB header:**transcription/rna **Chain:** B: **PDB Molecule:**36-mer n-terminal peptide of the n protein; **PDBTitle:** bacteriophage lambda n-protein-nutboxb-rna complex
37	d1nj1a2	Alignment	not modelled	15.2	30	**Fold:**IF3-like **Superfamily:**C-terminal domain of ProRS **Family:**C-terminal domain of ProRS
38	d1hc7a3	Alignment	not modelled	15.2	30	**Fold:**IF3-like **Superfamily:**C-terminal domain of ProRS **Family:**C-terminal domain of ProRS
39	c2y9zA_	Alignment	not modelled	15.1	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**imitation switch protein 1 (del_atpase); **PDBTitle:** chromatin remodeling factor isw1a(del_atpase) in dna complex
40	c2eblA_	Alignment	not modelled	14.5	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**coup transcription factor 1; **PDBTitle:** solution structure of the zinc finger, c4-type domain of2 human coup transcription factor 1
41	d1lata_	Alignment	not modelled	14.4	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
42	d1naqa_	Alignment	not modelled	14.4	11	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
43	c2fyoA_	Alignment	not modelled	14.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carnitine o-palmitoyltransferase ii, **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase 22 in space group p43212
44	d1rrha1	Alignment	not modelled	13.7	30	**Fold:**Lipoxigenase **Superfamily:**Lipoxigenase **Family:**Plant lipoxigenases
45	d1nzaa_	Alignment	not modelled	13.0	11	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
46	d1g2ra_	Alignment	not modelled	12.9	18	**Fold:**YlxR-like **Superfamily:**YlxR-like **Family:**YlxR-like
47	d1z5ye1	Alignment	not modelled	12.8	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
48	c1xk8A_	Alignment	not modelled	12.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**divalent cation tolerant protein cuta; **PDBTitle:** divalent cation tolerant protein cuta from homo sapiens2 o60888
49	d2zfha1	Alignment	not modelled	12.7	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
50	d1vjea_	Alignment	not modelled	12.4	16	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
51	c2x4jA_	Alignment	not modelled	11.6	67	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hypothetical protein orf137; **PDBTitle:** crystal structure of orf137 from pyrobaculum spherical2 virus
52	d1j6xa_	Alignment	not modelled	11.5	19	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
53	c2zfhA_	Alignment	not modelled	11.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cuta; **PDBTitle:** crystal structure of putative cuta1 from homo sapiens at 2.05a2 resolution
54	d1kr4a_	Alignment	not modelled	11.5	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
55	c2nuhA_	Alignment	not modelled	11.5	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**periplasmic divalent cation tolerance protein; **PDBTitle:** crystal structure of cuta from the phytopathgen bacterium

						xylella2 fastidiosa
56	c2p0gB_	Alignment	not modelled	11.4	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**selenoprotein w-related protein; **PDBTitle:** crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75
57	d1ukua_	Alignment	not modelled	11.2	8	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
58	c2dcuB_	Alignment	not modelled	11.1	12	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 beta subunit; **PDBTitle:** crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
59	c1neeA_	Alignment	not modelled	11.0	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
60	c3dexA_	Alignment	not modelled	10.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sav_2001; **PDBTitle:** crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
61	c2kpaA_	Alignment	not modelled	10.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arno(375-400); **PDBTitle:** specific motifs of the v-atpase a2-subunit isoform interact2 with catalytic and regulatory domains of arno
62	c2ojlB_	Alignment	not modelled	10.6	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
63	c3ialB_	Alignment	not modelled	10.5	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prolyl-trna synthetase; **PDBTitle:** giardia lamblia prolyl-trna synthetase in complex with prolyl-2 adenylate
64	d2hfva1	Alignment	not modelled	10.2	28	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**RPA1041-like
65	d1j98a_	Alignment	not modelled	10.1	21	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
66	c3bboY_	Alignment	not modelled	10.1	21	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**ribosomal protein l28; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
67	d1tx2a_	Alignment	not modelled	9.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
68	c1tx2A_	Alignment	not modelled	9.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
69	c3mwbA_	Alignment	not modelled	9.4	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
70	d2jz6a1	Alignment	not modelled	9.2	20	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
71	c3ahpA_	Alignment	not modelled	9.1	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cuta1; **PDBTitle:** crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
72	d1j6wa_	Alignment	not modelled	9.1	19	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
73	d1pbya1	Alignment	not modelled	9.0	5	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
74	c2hfvA_	Alignment	not modelled	8.7	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa1041; **PDBTitle:** solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
75	d2es7a1	Alignment	not modelled	8.4	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
76	d2nllb_	Alignment	not modelled	8.3	30	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
77	d2qamz1	Alignment	not modelled	8.3	16	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
78	d1dsza_	Alignment	not modelled	8.2	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
79	d1k5oa_	Alignment	not modelled	8.2	39	**Fold:**Myosin phosphatase inhibitor 17kDa protein, CPI-17 **Superfamily:**Myosin phosphatase inhibitor 17kDa protein, CPI-17 **Family:**Myosin phosphatase inhibitor 17kDa protein, CPI-17
80	d1vhfa_	Alignment	not modelled	8.1	16	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
						Fold: Myosin phosphatase inhibitor 17kDa protein, CPI-17

81	d1j2na_	Alignment	not modelled	7.8	36	**Superfamily:**Myosin phosphatase inhibitor 17kDa protein, CPI-17 **Family:**Myosin phosphatase inhibitor 17kDa protein, CPI-17
82	d1kb2a_	Alignment	not modelled	7.7	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
83	d1cita_	Alignment	not modelled	7.7	44	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
84	d1p1la_	Alignment	not modelled	7.6	8	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
85	c1a92B_	Alignment	not modelled	7.5	35	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
86	c3jyw8_	Alignment	not modelled	7.5	17	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**60s ribosomal protein lp0; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
87	d1xl7a1	Alignment	not modelled	7.2	35	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
88	c2xm5A_	Alignment	not modelled	6.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cloq; **PDBTitle:** structural and mechanistic analysis of the magnesium-2 independent aromatic prenyltransferase cloq from the3 clorobiocin biosynthetic pathway
89	c2zomC_	Alignment	not modelled	6.9	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**protein cuta, chloroplast, putative, expressed; **PDBTitle:** crystal structure of cuta1 from oryza sativa
90	d2qmwa2	Alignment	not modelled	6.8	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
91	c2kpbA_	Alignment	not modelled	6.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arno-p(375-400); **PDBTitle:** specific motifs of the v-atpase a2-subunit isoform interact2 with catalytic and regulatory domains of arno
92	d1jmxa1	Alignment	not modelled	6.8	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
93	d1ef4a_	Alignment	not modelled	6.7	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
94	c3swfA_	Alignment	not modelled	6.7	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
95	c1yx7A_	Alignment	not modelled	6.5	12	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calsensin; **PDBTitle:** nmr structure of calsensin, energy minimized average2 structure.
96	d2d8va1	Alignment	not modelled	6.4	38	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
97	d1yuza2	Alignment	not modelled	6.2	14	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
98	c1lj2B_	Alignment	not modelled	6.1	33	**PDB header:**viral protein/ translation **Chain:** B: **PDB Molecule:**nonstructural rna-binding protein 34; **PDBTitle:** recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
99	d1t1ua1	Alignment	not modelled	6.1	25	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase