Phyre^2

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Description	RVBD0599c_(-)_697567_697803
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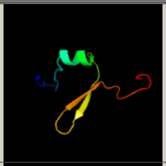
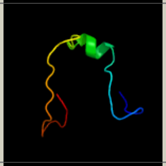
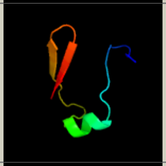
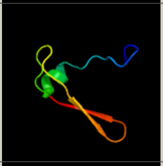
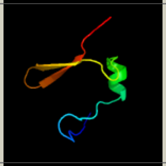
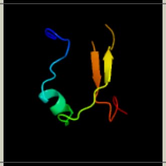
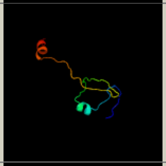
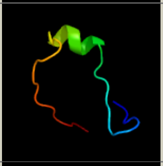
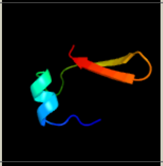
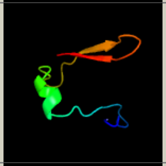
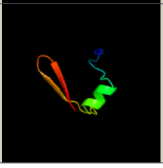
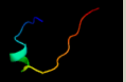
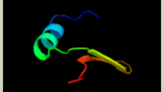
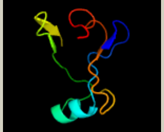
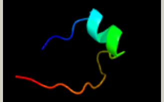
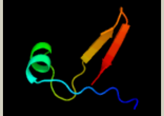
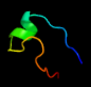
Unique Job ID	91259dbdeb09fd23

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w1tB_	Alignment		98.7	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
2	c2l66B_	Alignment		98.3	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family; **PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
3	d1yfba1	Alignment		98.2	33	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
4	d2fy9a1	Alignment		98.2	36	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
5	c2mrnB_	Alignment		98.0	24	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**antitoxin maze; **PDBTitle:** structure of truncated ecmaze
6	c2ro5B_	Alignment		97.9	28	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** rdc-refined solution structure of the n-terminal dna recognition2 domain of the bacillus subtilis transition-state regulator spovt
7	d1ub4c_	Alignment		97.6	23	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
8	c2glwA_	Alignment		97.6	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii
9	d1mvfd_	Alignment		97.2	27	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
10	c1n0fF_	Alignment		94.5	23	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**protein mraz; **PDBTitle:** crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
11	d1n0ea_	Alignment		93.8	23	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Hypothetical protein MraZ

12	c3o27B_	Alignment		91.8	29	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of c68 from the hybrid virus-plasmid pssvx
13	d2vbua1	Alignment		89.6	36	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
14	c3zvkG_	Alignment		84.5	26	**PDB header:**antitoxin/toxin/dna **Chain:** G: **PDB Molecule:**antitoxin of toxin-antitoxin system vapb; **PDBTitle:** crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
15	c5l6lD_	Alignment		78.5	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**vapb family protein; **PDBTitle:** structure of caulobacter crescentus vapbc1 bound to operator dna
16	c2c45F_	Alignment		78.0	23	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** native precursor of pyruvoyl dependent aspartate decarboxylase
17	d2d9ra1	Alignment		76.3	29	**Fold:**Double-split beta-barrel **Superfamily:**AF2212/PG0164-like **Family:**PG0164-like
18	c5udfB_	Alignment		76.0	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**lipoprotein-releasing system transmembrane protein lole; **PDBTitle:** structure of the n-terminal domain of lipoprotein-releasing system2 transmembrane protein lole from acinetobacter baumannii
19	c1pt1B_	Alignment		73.8	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
20	d1cz5a1	Alignment		70.7	28	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
21	c1zc1A_	Alignment	not modelled	70.5	44	**PDB header:**protein turnover **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation protein 1; **PDBTitle:** ufd1 exhibits the aaa-atpase fold with two distinct2 ubiquitin interaction sites
22	c1cz5A_	Alignment	not modelled	70.5	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vcp-like atpase; **PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
23	c2pjhB_	Alignment	not modelled	70.3	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex
24	d1ylea1	Alignment	not modelled	68.9	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**AstA-like
25	d1ppya_	Alignment	not modelled	67.5	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
26	c6nklD_	Alignment	not modelled	64.3	31	**PDB header:**antitoxin **Chain:** D: **PDB Molecule:**antitoxin vapb1; **PDBTitle:** 2.2 a resolution structure of vapbc-1 from nontypeable haemophilus2 influenzae
27	c2yujA_	Alignment	not modelled	56.1	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin fusion degradation 1-like; **PDBTitle:** solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
28	c5l6mA_	Alignment	not modelled	51.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vapb family protein; **PDBTitle:** structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
						PDB header:lyase

29	c1uheA_	Alignment	not modelled	51.3	26	**Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain; **PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex
30	c3ougA_	Alignment	not modelled	50.4	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
31	d2jioa1	Alignment	not modelled	47.8	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
32	c3plxB_	Alignment	not modelled	45.9	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
33	c1vc3B_	Alignment	not modelled	45.7	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-aspartate-alpha-decarboxylase heavy chain; **PDBTitle:** crystal structure of l-aspartate-alpha-decarboxylase
34	c2oqkA_	Alignment	not modelled	44.8	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
35	d1g8ka1	Alignment	not modelled	44.6	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
36	c2kl0A_	Alignment	not modelled	44.2	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
37	c5naaB_	Alignment	not modelled	43.9	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**lipoprotein-releasing system transmembrane protein lolc; **PDBTitle:** lipoprotein-releasing system transmembrane protein lolc
38	c1h9mB_	Alignment	not modelled	41.1	28	**PDB header:**binding protein **Chain:** B: **PDB Molecule:**molybdenum-binding-protein; **PDBTitle:** two crystal structures of the cytoplasmic molybdate-binding protein2 modg suggest a novel cooperative binding mechanism and provide3 insights into ligand-binding specificity. peg-grown form with4 molybdate bound
39	c4trtB_	Alignment	not modelled	41.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit beta; **PDBTitle:** deinococcus radiodurans dna polymerase iii subunit beta
40	c2k4vA_	Alignment	not modelled	40.6	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1076; **PDBTitle:** solution structure of uncharacterized protein pa1076 from pseudomonas2 aeruginosa. northeast structural genomics consortium (nesg) target3 pat3, ontario center for structural proteomics target pa1076 .
41	c1zeqX_	Alignment	not modelled	40.4	20	**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
42	d1vpka1	Alignment	not modelled	39.9	22	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
43	d2iv2x1	Alignment	not modelled	37.9	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
44	c4zsiA_	Alignment	not modelled	37.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor dasr; **PDBTitle:** crystal structure of the effector-binding domain of dasr (dasr-ebd) in2 complex with glucosamine-6-phosphate
45	c3tndF_	Alignment	not modelled	36.6	32	**PDB header:**translation, toxin **Chain:** F: **PDB Molecule:**antitoxin vapb; **PDBTitle:** crystal structure of shigella flexneri vapbc toxin-antitoxin complex
46	c3wwvA_	Alignment	not modelled	35.6	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**stomatin operon partner protein; **PDBTitle:** c-terminal domain of stomatin operon partner protein 1510-c from2 pyrococcus horikoshii
47	d1ogya1	Alignment	not modelled	34.9	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
48	d1h0ha1	Alignment	not modelled	34.8	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
49	c4bpp0_	Alignment	not modelled	34.7	8	**PDB header:**ribosome **Chain:** 0: **PDB Molecule:**translation initiation factor eif-1a family protein; **PDBTitle:** the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 4
50	d2eifa2	Alignment	not modelled	34.0	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
51	d1kqfa1	Alignment	not modelled	32.7	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
52	d1zq1a1	Alignment	not modelled	31.6	15	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
53	d1h9ma2	Alignment	not modelled	31.3	28	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain

54	c1uebB_	Alignment	not modelled	31.0	15	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**elongation factor p; **PDBTitle:** crystal structure of translation elongation factor p from2 thermus thermophilus hb8
55	c3m7aA_	Alignment	not modelled	30.8	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of saro_0823 (yp_496102.1) a protein of unknown2 function from novosphingobium aromaticivorans dsm 12444 at 1.22 a3 resolution
56	d2fa1a1	Alignment	not modelled	30.5	18	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
57	d1h9ma1	Alignment	not modelled	30.4	19	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
58	d2ra5a1	Alignment	not modelled	30.4	18	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
59	c2ra5A_	Alignment	not modelled	30.4	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator2 from streptomyces coelicolor
60	c3pjyB_	Alignment	not modelled	30.3	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**hypothetical signal peptide protein; **PDBTitle:** crystal structure of a putative transcription regulator (r01717) from2 sinorhizobium meliloti 1021 at 1.55 a resolution
61	c4cjdA_	Alignment	not modelled	29.4	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**nada; **PDBTitle:** crystal structure of neisseria meningitidis trimeric2 autotransporter and vaccine antigen nada
62	c5t5iL_	Alignment	not modelled	29.4	16	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase subunit fwdd; **PDBTitle:** tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
63	d1fr3a_	Alignment	not modelled	29.3	23	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
64	d1vlfm1	Alignment	not modelled	28.4	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
65	d3d31a1	Alignment	not modelled	28.4	15	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
66	c6c00A_	Alignment	not modelled	28.3	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** solution structure of translation initiation factor 1 from clostridium2 difficile
67	d1eu1a1	Alignment	not modelled	28.3	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
68	c2ki8A_	Alignment	not modelled	28.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase, **PDBTitle:** solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
69	c1qw1A_	Alignment	not modelled	27.1	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** solution structure of the c-terminal domain of dtxr2 residues 110-226
70	d2exda1	Alignment	not modelled	26.9	23	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
71	c4ql5A_	Alignment	not modelled	26.4	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor if-1 from2 streptococcus pneumoniae tigr4
72	c5lxyH_	Alignment	not modelled	26.3	38	**PDB header:**rna binding protein **Chain:** H: **PDB Molecule:**zinc finger cchc domain-containing protein 8; **PDBTitle:** structure of the minimal rbm7 - zcchc8 complex
73	c3ll7A_	Alignment	not modelled	26.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase pg_1098 from2 porphyromonas gingivalis w83
74	d1hr0w_	Alignment	not modelled	25.8	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
75	c2k5hA_	Alignment	not modelled	25.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
76	d1tmoa1	Alignment	not modelled	25.6	16	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
77	c5ccbA_	Alignment	not modelled	25.6	30	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna (adenine(58)-n(1))-methyltransferase catalytic subunit **PDBTitle:** crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
78	d3cnva1	Alignment	not modelled	25.3	27	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain

79	d1qw1a1	Alignment	not modelled	25.3	20	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
80	c1ybyB_	Alignment	not modelled	25.0	9	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation elongation factor p; **PDBTitle:** conserved hypothetical protein cth-95 from clostridium thermocellum
81	d1jt8a_	Alignment	not modelled	24.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
82	c3p16A_	Alignment	not modelled	24.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii subunit beta; **PDBTitle:** crystal structure of dna polymerase iii sliding clamp
83	c3i4oA_	Alignment	not modelled	24.7	10	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
84	c3nnqA_	Alignment	not modelled	24.5	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**n-terminal domain of moloney murine leukemia virus **PDBTitle:** crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
85	d2pkha1	Alignment	not modelled	24.3	18	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
86	d2p19a1	Alignment	not modelled	23.7	24	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
87	d3bwga2	Alignment	not modelled	23.3	9	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
88	c3treA_	Alignment	not modelled	23.3	5	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor p; **PDBTitle:** structure of a translation elongation factor p (efp) from coxiella2 burnetii
89	d1h9ra1	Alignment	not modelled	23.2	21	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
90	d1y5ia1	Alignment	not modelled	22.9	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
91	d1d7qa_	Alignment	not modelled	22.8	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
92	d2cu3a1	Alignment	not modelled	22.8	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
93	d1guta_	Alignment	not modelled	22.0	14	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
94	d1dgsa2	Alignment	not modelled	21.9	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
95	c1bkbA_	Alignment	not modelled	21.8	31	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 5a; **PDBTitle:** initiation factor 5a from archebacterium pyrobaculum2 aerophilum
96	d2ogga1	Alignment	not modelled	21.5	12	**Fold:**Chorismate lyase-like **Superfamily:**Chorismate lyase-like **Family:**UTRA domain
97	d1dmra1	Alignment	not modelled	21.4	14	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
98	d1zud21	Alignment	not modelled	21.3	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
99	d1qvpa_	Alignment	not modelled	21.1	30	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
100	d1tygb_	Alignment	not modelled	20.6	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS