




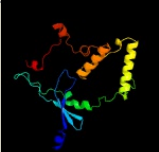



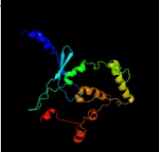

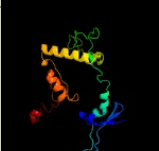

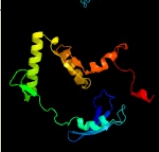

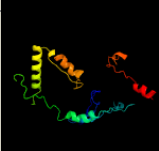








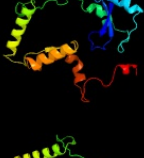
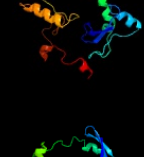



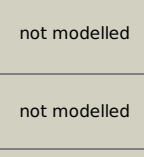


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1736c_(narX)_1962235_1964193
Date	Fri Aug 2 13:30:34 BST 2019
Unique Job ID	9cabb749944431cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y5ia2	 Alignment		100.0	60	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
2	c1y5ia_	 Alignment		100.0	60	PDB header: oxidoreductase Chain: A: PDB Molecule: respiratory nitrate reductase 1 alpha chain; PDBTitle: the crystal structure of the narghi mutant nari-k86a
3	c2ivfA_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: ethylbenzene dehydrogenase alpha-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
4	d1y5ic1	 Alignment		100.0	30	Fold: Heme-binding four-helical bundle Superfamily: Respiratory nitrate reductase 1 gamma chain Family: Respiratory nitrate reductase 1 gamma chain
5	c5ch7E_	 Alignment		100.0	45	PDB header: oxidoreductase Chain: E: PDB Molecule: dmsmo reductase family type ii enzyme, molybdopterin PDBTitle: crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
6	c1vlfO_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: Q: PDB Molecule: pyrogallol hydroxytransferase large subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
7	c2nyaF_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: F: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the periplasmic nitrate reductase2 (nap) from escherichia coli
8	d1vlfm2	 Alignment		100.0	30	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
9	c2v45A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
10	c6cz7C_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: arra; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3
11	d1logya2	 Alignment		100.0	21	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3

12	d2iv2x2	Alignment		100.0	23	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
13	d2jioa2	Alignment		100.0	27	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
14	c1ogyA	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
15	c2iv2X	Alignment		100.0	23	PDB header: oxidoreductase Chain: X: PDB Molecule: formate dehydrogenase h; PDBTitle: reinterpretation of reduced form of formate dehydrogenase h from e.2 coli
16	d1h0ha2	Alignment		100.0	21	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
17	d1tmoa2	Alignment		99.9	18	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
18	c1eu1A	Alignment		99.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethyl sulfoxide reductase; PDBTitle: the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
19	c1kqgA	Alignment		99.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase, nitrate-inducible, major subunit; PDBTitle: formate dehydrogenase n from e. coli
20	c1h0hA	Alignment		99.9	21	PDB header: electron transport Chain: A: PDB Molecule: formate dehydrogenase subunit alpha; PDBTitle: tungsten containing formate dehydrogenase from desulfovibrio gigas
21	c2vpyE	Alignment	not modelled	99.9	30	PDB header: oxidoreductase Chain: E: PDB Molecule: thiosulfate reductase; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
22	c2e7zA	Alignment	not modelled	99.9	20	PDB header: lyase Chain: A: PDB Molecule: acetylene hydratase ahy; PDBTitle: acetylene hydratase from pelobacter acetylenicus
23	c1tmoA	Alignment	not modelled	99.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: trimethylamine n-oxide reductase; PDBTitle: trimethylamine n-oxide reductase from shewanella massilia
24	c1h5nC	Alignment	not modelled	99.9	29	PDB header: oxidoreductase Chain: C: PDB Molecule: dmsO reductase; PDBTitle: dmsO reductase modified by the presence of dms and air
25	d1eu1a2	Alignment	not modelled	99.9	28	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
26	d1kqfa2	Alignment	not modelled	99.9	26	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
27	d1dmra2	Alignment	not modelled	99.9	29	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
28	c4aayE	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: E: PDB Molecule: aroa; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26 PDB header: oxidoreductase

29	c1g8jC_	Alignment	not modelled	99.9	18	Chain: C; PDB Molecule: arsenite oxidase; PDBTitle: crystal structure analysis of arsenite oxidase from <i>Alcaligenes faecalis</i>
30	c5lnk3_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: 3; PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
31	d1g8ka2	Alignment	not modelled	99.8	15	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
32	d2fug32	Alignment	not modelled	99.8	21	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
33	c6gcsA_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A; PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from <i>Yarrowia lipolytica</i>
34	c2fugC_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: C; PDB Molecule: nahd-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from <i>Thermus thermophilus</i>
35	c6btmB_	Alignment	not modelled	99.7	15	PDB header: membrane protein Chain: B; PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from <i>Flavobacterium johnsoniae</i> 2 (wild type)
36	d2o9xa1	Alignment	not modelled	99.6	26	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
37	c2o9xA_	Alignment	not modelled	99.5	25	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: reductase, assembly protein; PDBTitle: crystal structure of a putative redox enzyme maturation protein from <i>Archaeoglobus fulgidus</i>
38	c6f0kB_	Alignment	not modelled	99.5	16	PDB header: membrane protein Chain: B; PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
39	c5t5mB_	Alignment	not modelled	99.4	29	PDB header: oxidoreductase Chain: B; PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdb; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from <i>Methanothermobacter wolfeii</i> , trigonal form at 2.5 a.
40	d1s9ua_	Alignment	not modelled	98.4	16	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
41	d1n1ca_	Alignment	not modelled	98.3	15	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
42	d2idga1	Alignment	not modelled	93.2	11	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
43	c5oc0A_	Alignment	not modelled	70.5	15	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome b561; PDBTitle: structure of <i>E. coli</i> superoxide oxidase
44	d1kqfc_	Alignment	not modelled	68.1	15	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Formate dehydrogenase N, cytochrome (gamma) subunit
45	c2kluA_	Alignment	not modelled	64.7	21	PDB header: immune system, membrane protein Chain: A; PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
46	c5jydN_	Alignment	not modelled	62.3	41	PDB header: transcription, transferase/dna/rna Chain: N; PDB Molecule: transcription initiation factor iia subunit 1; PDBTitle: human core-pic in the initial transcribing state (no iis)
47	c5n0cB_	Alignment	not modelled	61.1	12	PDB header: toxin Chain: B; PDB Molecule: tetanus toxin; PDBTitle: crystal structure of the tetanus neurotoxin in complex with gm1a
48	c1h3oA_	Alignment	not modelled	61.0	23	PDB header: transcription/tpb-associated factors Chain: A; PDB Molecule: transcription initiation factor tfiid 135 kda subunit; PDBTitle: crystal structure of the human taf4-taf12 (tafi135-tafii20) complex
49	d1h3oa_	Alignment	not modelled	61.0	23	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
50	c3kdpH_	Alignment	not modelled	56.7	19	PDB header: hydrolase Chain: H; PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
51	c3kdpG_	Alignment	not modelled	56.7	19	PDB header: hydrolase Chain: G; PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
52	c2uuiA_	Alignment	not modelled	51.2	22	PDB header: lyase Chain: A; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
53	c2jo1A_	Alignment	not modelled	50.3	26	PDB header: hydrolase regulator Chain: A; PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
54	c5gasN_	Alignment	not modelled	50.3	15	PDB header: hydrolase Chain: N; PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: <i>Thermus thermophilus</i> v/a-atpase, conformation 2
						Fold: Transcription factor IIA (TFIIA), beta-barrel domain

55	d1yfc_	Alignment	not modelled	49.6	50	Superfamily: Transcription factor IIA (TFIIA), beta-barrel domain Family: Transcription factor IIA (TFIIA), beta-barrel domain
56	d1nvpc_	Alignment	not modelled	49.6	41	Fold: Transcription factor IIA (TFIIA), beta-barrel domain Superfamily: Transcription factor IIA (TFIIA), beta-barrel domain Family: Transcription factor IIA (TFIIA), beta-barrel domain
57	c1nvpC_	Alignment	not modelled	49.6	41	PDB header: transcription/dna Chain: C: PDB Molecule: transcription initiation factor iia beta chain; PDBTitle: human tfiia/tbp/dna complex
58	c2mkvA_	Alignment	not modelled	48.8	26	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
59	c2jp3A_	Alignment	not modelled	46.7	11	PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
60	c1nh2C_	Alignment	not modelled	46.6	41	PDB header: transcription/dna Chain: C: PDB Molecule: transcription initiation factor iia large chain; PDBTitle: crystal structure of a yeast tfiia/tbp/dna complex
61	d1nh2c_	Alignment	not modelled	46.6	41	Fold: Transcription factor IIA (TFIIA), beta-barrel domain Superfamily: Transcription factor IIA (TFIIA), beta-barrel domain Family: Transcription factor IIA (TFIIA), beta-barrel domain
62	c1rm1C_	Alignment	not modelled	45.8	41	PDB header: transcription/dna Chain: C: PDB Molecule: transcription initiation factor iia large chain; PDBTitle: structure of a yeast tfiia/tbp/tata-box dna complex
63	c3ffzA_	Alignment	not modelled	45.8	28	PDB header: hydrolase Chain: A: PDB Molecule: botulinum neurotoxin type e; PDBTitle: domain organization in clostridium botulinum neurotoxin2 type e is unique: its implication in faster translocation
64	c5ir6B_	Alignment	not modelled	45.4	11	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
65	c2bp7F_	Alignment	not modelled	44.4	36	PDB header: oxidoreductase Chain: F: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
66	c5yk7A_	Alignment	not modelled	42.9	32	PDB header: lipid transport Chain: A: PDB Molecule: maintenance of mitochondrial morphology protein 1; PDBTitle: crystal structure of mdm12-mmm1 complex
67	c1olsB_	Alignment	not modelled	38.6	32	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: roles of his291-alpha and his146-beta' in the reductive acylation2 reaction catalyzed by human branched-chain alpha-ketoacid3 dehydrogenase
68	d1z05a2	Alignment	not modelled	38.0	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
69	c5kteA_	Alignment	not modelled	37.1	14	PDB header: transport protein/immune system Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of deinococcus radiodurans mnth, an nramp-family2 transition metal transporter
70	c2kncA_	Alignment	not modelled	36.8	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
71	c3s2xB_	Alignment	not modelled	34.7	19	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa synthase subunit alpha; PDBTitle: structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
72	d2ozlb1	Alignment	not modelled	34.3	32	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
73	c3hfxA_	Alignment	not modelled	31.1	8	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
74	c6ithA_	Alignment	not modelled	29.9	26	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
75	d2r6gf1	Alignment	not modelled	29.7	16	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
76	d1qs0b1	Alignment	not modelled	28.8	33	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
77	c2kncB_	Alignment	not modelled	28.6	25	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
78	d1umdb1	Alignment	not modelled	27.2	42	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
79	c5h92A_	Alignment	not modelled	27.1	17	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: sulfite reductase [ferredoxin], chloroplastic; PDBTitle: crystal structure of the complex between maize sulfite reductase and2 ferredoxin in the form-3 crystal

80	d2cmda1	Alignment	not modelled	26.4	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
81	c3e4hA	Alignment	not modelled	26.2	47	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
82	d1prt1	Alignment	not modelled	25.6	27	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
83	c1fftG	Alignment	not modelled	24.7	13	PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
84	c2zxeG	Alignment	not modelled	23.9	25	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
85	c2k1aA	Alignment	not modelled	23.7	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment
86	d2hoca2	Alignment	not modelled	23.5	6	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
87	c4ainB	Alignment	not modelled	23.0	12	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
88	c5m4sA	Alignment	not modelled	23.0	41	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor iia subunit 2,transcription PDBTitle: transcription factor tfiia as a single chain protein
89	d2bfd1	Alignment	not modelled	22.8	32	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
90	c6hwhB	Alignment	not modelled	22.7	15	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
91	c1ni4D	Alignment	not modelled	22.5	28	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate dehydrogenase e1 component: beta PDBTitle: human pyruvate dehydrogenase
92	c2k1kA	Alignment	not modelled	21.8	31	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
93	c2k1IA	Alignment	not modelled	21.8	31	PDB header: signaling protein Chain: A: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
94	c2k1kB	Alignment	not modelled	21.8	31	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
95	c2k1IB	Alignment	not modelled	21.8	31	PDB header: signaling protein Chain: B: PDB Molecule: ephrin type-a receptor 1; PDBTitle: nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
96	d1w85b1	Alignment	not modelled	21.0	28	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase Pyr module
97	d1rka2	Alignment	not modelled	21.0	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
98	c2jwmA	Alignment	not modelled	20.6	37	PDB header: plant protein Chain: A: PDB Molecule: kalata-b7; PDBTitle: nmr spatial srcture of ternary complex kalata b7/mn2+/dpc2 micelle
99	c5xcoB	Alignment	not modelled	20.5	45	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: ace-arg-arg-arg-arg-cys-pro-leu-tyr-ile-ser-tyr-asn-pro- PDBTitle: crystal structure of human k-ras g12d mutant in complex with gdp and2 cyclic inhibitory peptide