

Supplementary Material for “The Unfolded State of the C-terminal Domain of the Ribosomal Protein L9 Contains Significant Secondary Structure in the Absence of Denaturant but is No More Compact than the Urea Unfolded State”

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Table-S1. Chemical shift assignments for the pH 2.0 unfolded state of CTL9 at 25 °C. Chemical shifts were referenced to DSS.

Table-S2. Chemical shift assignments for the pH 2.5, 7.6 M urea unfolded state of CTL9 at 25 °C. Chemical shifts were referenced to DSS.

Table-S3. ^{15}N R2 relaxation rates of the pH 2.0 and pH 2.5, 7.6 M urea unfolded states of CTL9 at 25 °C.

Figure-S1. SSP analysis of the pH 2.0 unfolded state of CTL9 calculated using only $^{13}\text{C}_\alpha$ and $^{13}\text{C}_\beta$ chemical shifts.

Figure-S2. AGADIR analysis of the primary sequence of CTL9 at pH 2.0, 298 °K.

Table-S1 CTL9 backbone and $^{13}\text{C}_\beta$ and $^1\text{H}_\beta$ assignments at pH 2.0

Residue	NH	N	CA	CB	CO	HA	HB	HB'
A58			51.92	19.18	173.49	4.10	1.56	--
A59	8.61	123.73	52.68	19.15	177.65	4.36	1.41	--
E60	8.46	120.28	55.99	28.73	176.06	4.36	2.05	--
E61	8.43	121.88	55.99	28.56	176.18	4.38	2.06	--
L62	8.28	123.78	55.73	42.53	177.65	4.31	1.64	--
A63	8.22	123.83	53.20	18.91	178.18	4.24	1.41	--
N64	8.30	117.35	53.70	38.62	175.76	4.62	2.83	--
A65	8.12	123.98	53.70	18.93	178.64	4.21	1.44	--
K66	8.13	119.44	57.50	32.62	177.35	4.18	1.82	--
K67	8.03	121.32	57.00	32.63	177.30	4.24	1.82	--
L68	8.08	122.32	55.99	42.27	177.94	4.29	1.63	--
K69	8.15	121.26	57.28	32.62	177.29	4.21	1.84	--
E70	8.17	120.22	56.75	28.57	176.65	4.27	2.08	--
Q71	8.30	121.01	56.74	29.08	176.51	4.29	2.09	--
L72	8.18	122.61	55.74	42.27	177.88	4.30	1.66	--
E73	8.19	120.48	56.23	28.57	176.12	4.34	2.07	--
K74	8.16	121.95	56.62	32.89	176.46	4.30	1.80	--
L75	8.17	123.20	55.35	42.53	177.53	4.43	1.64	--
T76	8.16	116.09	62.09	69.95	174.31	4.73	4.31	--
V77	8.15	123.11	62.33	32.89	176.01	4.23	2.08	--
T78	8.30	119.64	61.82	69.95	174.07	4.36	4.10	--
I79	8.29	125.96	58.53	38.72	174.45	--	--	--
P80	--	--	63.35	32.12	176.61	4.38	2.30	1.90
A81	8.32	124.48	52.54	19.17	177.94	4.28	1.39	--
K82	8.21	120.50	56.23	33.12	176.36	4.29	1.78	--
A83	8.26	125.38	52.69	19.18	178.29	4.30	1.39	--
G84	8.38	108.31	45.33		174.42	3.97	--	--
E85	8.24	119.73	55.98	28.71	176.82	4.40	2.17	2.01
G86	8.53	110.01	45.58		174.77	3.97	--	--
G87	8.25	108.62	45.32		174.25	3.96	--	--
R88	8.09	120.39	56.36	30.60	176.18	4.30	1.76	--
L89	8.22	122.93	55.23	42.28	177.12	4.30	1.51	--
F90	8.22	120.81	58.02	39.74	176.27	4.60	3.17	3.03
G91	8.30	110.33	45.24		174.07	3.94	--	--
S92	8.16	115.70	58.27	64.11	174.74	4.49	3.89	--
I93	8.25	122.54	61.58	38.72	176.70	4.29	1.93	--
T94	8.18	117.44	62.08	69.95	174.95	4.34	--	--
S95	8.31	117.95	59.28	63.71	175.19	4.42	3.92	--
K96	8.27	123.33	57.25	32.88	176.82	4.28	1.80	--
Q97	8.21	120.88	56.87	29.70	177.06	4.26	2.07	--
I98	8.12	122.24	62.33	38.47	176.83	4.05	1.87	--
A99	8.26	126.44	53.45	18.91	178.76	4.26	1.43	--
E100	8.27	119.09	56.85	28.57	177.09	4.29	2.09	--
S101	8.23	116.61	59.29	63.60	175.36	4.40	3.95	--
L102	8.17	123.55	56.39	42.14	178.35	4.28	1.69	1.60
Q103	8.13	119.81	56.76	28.83	176.65	4.23	2.08	--
A104	8.10	123.90	53.18	18.92	178.29	4.06	1.41	--

Q105	8.15	118.42	56.49	29.07	176.42	4.22	2.05	--
H106	8.38	118.49	55.58	28.82	175.07	4.70	3.35	3.21
G107	8.38	109.38	45.58		174.13	3.96	--	--
L108	8.04	121.77	55.48	42.53	177.59	4.34	1.61	--
K109	8.32	122.31	56.75	32.63	176.65	4.34	1.80	--
L110	8.17	123.22	55.47	42.53	177.18	4.33	1.60	--
D111	8.41	120.16	53.19	38.21	175.36	4.67	2.91	--
K112	8.26	122.21	57.00	32.88	176.83	4.25	1.80	--
R113	8.18	121.47	56.75	30.59	176.60	4.26	1.82	--
K114	8.22	122.36	57.01	32.89	177.06	4.24	1.80	--
I115	8.08	122.55	61.58	38.62	176.42	4.08	1.84	--
E116	8.33	124.00	55.99	28.56	176.59	4.37	2.06	--
L117	8.26	123.80	55.48	42.28	177.62	4.33	1.63	--
A118	8.29	124.30		19.18	178.35	4.24	1.41	--
D119	8.30	117.34	53.45	37.95	175.42	4.62	2.91	--
A120	8.06	124.27	53.19	18.92	178.09	4.30	1.41	--
I121	7.95	119.39	61.82	38.46	176.83	4.06	1.87	--
R122	8.18	124.50	56.50	30.60	176.24	4.29	1.80	--
A123	8.17	124.78	52.68	19.04	177.82	4.29	1.39	--
L124	8.10	121.14	55.48	42.53	178.06	4.29	1.65	1.54
G125	8.24	108.69	45.32		173.90	3.92	--	--
Y126	7.95	119.82	58.02	38.73	175.95	4.63	3.03	--
T127	8.03	115.91	61.57	69.95	173.66	4.32	4.14	--
N128	8.36	121.55	53.19	38.98	174.60	4.70	2.76	--
V129	8.04	122.19	60.06	32.64	174.36	--	2.02	--
P130	--	--	63.35	32.03	177.06	4.44	2.29	1.85
V131	8.17	120.98	62.58	32.88	176.18	4.04	2.03	--
K132	8.33	125.39	55.99	32.89	176.12	4.32	1.73	--
L133	8.21	123.71	55.22	42.54	176.83	4.28	1.58	1.44
H134	8.50	119.29			172.20	--	3.19	3.11
P135	--	--	63.35	32.11	176.82	4.44	2.29	1.92
E136	8.53	121.21	55.74	28.82	176.09	4.43	2.06	--
V137	8.29	122.32	62.34	32.87	176.30	4.20	2.09	--
T138	8.24	118.82	62.08	69.95	174.25	4.32	4.19	--
A139	8.36	127.04	52.68	19.17	177.77	4.39	1.42	--
T140	8.12	114.08	62.08	69.94	174.48	4.28	4.17	--
L141	8.18	125.11	55.36	42.53	177.12	4.37	1.61	--
K142	8.31	122.98	56.24	32.88	176.30	4.35	1.75	--
V143	8.00	120.99	62.33	32.88	175.83	4.08	2.00	--
H144	8.65	122.86	55.22	28.82	174.13	4.76	3.19	--
V145	8.28	122.98	62.33	32.89	176.10	4.18	2.06	--
T146	8.33	119.12	62.08	69.94	174.25	4.34	4.16	--
E147	8.41	123.41	55.62	28.82	175.65	4.42	2.11	2.00
Q148	8.45	122.53	55.99	29.58	175.77	4.36	2.05	
K149	8.49	123.97	55.73	32.63	178.41		1.76	

Table-S2 CTL9 backbone and $^{13}\text{C}_\beta$ and $^1\text{H}_\beta$ assignments at pH 2.5, in 7.6 M urea

Residue	NH	N	CA	CB	CO	HA	HB	HB'
A58			51.88	19.08	173.46	4.07	1.49	
A59	8.58	123.90	52.47	19.06	177.35	4.32	1.34	
E60	8.40	120.23	55.99	29.02	175.87	4.31	1.96	
E61	8.44	122.19	55.98	29.02	175.78			
L62								
A63			52.48	19.07	177.52	4.23	1.31	
N64	8.31	117.78	53.06	38.99	175.01	4.64	2.75	
A65	8.12	124.43	53.06	19.06	177.50	4.23	1.32	
K66	8.21	120.45	56.58	33.14	176.56	4.20	1.73	
K67	8.24	122.76	56.57	33.14	176.48			
L68			54.83	42.51	177.35	4.29	1.51	
K69	8.43	122.77	56.59	33.13	176.53	4.23	1.71	
E70	8.35	121.89	56.02	29.02	175.87	4.29	1.96	
Q71	8.49	122.32	55.98	29.61	175.76			
L72			55.42	42.22	177.59	4.26	1.55	
E73	8.25	120.53	55.42	29.58	175.95	4.27	1.93	
K74	8.38	123.30	56.00	33.14	176.14			
L75			54.82	42.51	177.37	4.41	1.54	
T76	8.27	116.53	61.87	70.06	174.27	4.32	4.12	
V77	8.19	122.81	61.86	33.13	175.96	4.18	2.00	
T78	8.26	119.04	61.86	70.06	174.04	4.33	4.05	
I79	8.26	125.23	58.35	39.00	174.31			
P80			63.03	31.96	176.44	4.32	2.21	1.83
A81	8.30	124.61	53.04	19.07	177.69	4.23	1.32	
K82	8.23	120.79	56.58	33.14	176.27			
A83	8.31	125.53	52.50	19.06	178.06	4.27	1.34	
G84	8.32	108.33	45.44		174.17	3.94		
E85	8.20	119.58	56.00	29.02	176.54	4.35	2.10	1.94
G86	8.45	109.90	45.45		174.43	3.94		
G87	8.20	108.47	45.43		173.93	3.93		
R88	8.14	120.53	56.27	30.80	176.03	4.25	1.66	
L89	8.25	123.37	54.82	42.52	176.93	4.26	1.42	
F90	8.31	121.17	57.76	39.60	176.15	4.59	3.02	
G91	8.30	110.31	45.43		173.80	3.92		
S92	8.17	115.67	58.34	64.20	174.60	4.48	3.79	
I93	8.27	122.58	61.27	38.85	176.41	4.23	1.83	
T94	8.17	117.51	61.84	70.06	174.60	4.25	4.23	
S95	8.26	118.16	58.43	64.18	174.60	4.39	3.82	
K96	8.31	123.42	56.57	33.13	176.43	4.24	1.71	
Q97	8.30	121.56	56.58	29.61	176.16	4.26	1.95	
I98	8.16	122.62	61.27	38.97	176.10	4.07	1.78	
A99	8.31	127.69	53.05	19.05	177.76	4.26	1.33	
E100	8.27	119.87	56.00	29.03	176.28	4.29	1.99	
S101	8.30	116.86	58.34	63.84	174.77			
L102								
Q103			55.99	30.81	175.77	4.28	1.72	
A104	8.26	125.74	52.47	19.07	177.44	4.20	1.43	

Q105	8.23	119.24	55.99	29.61	176.00	4.23	1.98	
H106	8.48	119.09	55.39	29.02	174.73	4.70	3.18	
G107	8.40	109.79	45.42		173.66	3.95		
L108	8.10	121.87	55.10	42.52	177.21	4.29	1.49	
K109	8.46	123.36	56.24	33.11	176.20			
L110			54.82	42.50	176.94	4.30	1.42	
D111	8.56	120.91	53.06	38.39	175.03	4.25	2.81	
K112	8.32	122.67	56.57	33.13	176.29	4.68	1.70	
R113	8.32	122.67	55.99	29.60	176.16	4.24	1.73	
K114	8.42	123.87	56.58	32.56	176.27	4.25	1.66	
I115	8.25	123.37	61.25	39.00	175.93	4.23	1.72	
E116	8.31	125.53	55.99	30.81	175.75			
L117								
A118			52.45	19.06	177.55	4.23	1.32	
D119	8.33	117.99	53.05	38.39	174.78			
A120			52.45	19.06	177.43	4.26	1.31	
I121	8.00	120.10	61.25	38.97	176.19	4.08	1.73	
R122	8.42	125.23	55.40	29.03	175.65	4.37	1.95	
A123	8.33	124.81	53.06	19.07	177.50	4.27	1.31	
L124	8.19	121.84	55.39	42.50	177.74	4.25	1.51	
G125	8.26	109.05	45.42		173.59	3.85		
Y126	8.02	119.92	57.75	39.00	175.94	4.60	2.93	
T127	8.09	115.73	61.83	70.06	173.74	4.28	4.09	
N128	8.38	121.59	53.06	38.99	174.59	4.68	2.71	
V129	8.02	121.46	60.01	32.38	174.23			
P130			63.02	31.96	176.66	4.39	2.19	1.77
V131	8.13	120.98	62.74	32.53	176.01	4.02	1.92	
K132	8.32	125.60	55.99	33.13	175.70			
L133			54.82	42.51	177.01	4.23	1.33	
H134	8.64	119.69	53.06	28.43	172.34			
P135			63.01	31.98	176.61	4.39	2.23	1.86
E136	8.53	121.46	55.99	29.03	175.92	4.39	1.96	
V137	8.27	122.07	62.44	33.11	176.20	4.16	1.92	
T138	8.22	118.41	61.53	70.06	174.18	4.30	4.16	
A139	8.28	126.75	52.49	19.43	177.57	4.37	1.34	
T140	8.10	113.99	61.85	70.06	174.40	4.16	4.14	
L141	8.20	125.15	54.84	42.52	177.00	4.27	1.50	
K142	8.39	123.43	55.99	33.12	176.28	4.31	1.68	
V143	8.09	121.30	62.42	33.12	175.79	4.05	1.93	
H144	8.67	123.03	54.85	29.03	174.11	4.73	3.13	
V145	8.31	123.19	62.43	33.13	175.98	4.18	2.00	
T146	8.31	118.92	61.84	69.80	174.27	4.27	4.25	
E147	8.38	123.30	55.99	29.01	176.16	4.35	1.95	
Q148	8.46	122.51	55.99	29.61	175.69	4.29	1.97	
K149	8.46	123.73	55.98	32.55	178.57			

Table-S3 ^{15}N R2 relaxation rates for the pH 2.0 and pH 2.5, 7.6 M urea unfolded states of CTL9 and calculated R2 rates using random coil model

Residue	R2 urea (sec^{-1})	R2 pH 2.0 (sec^{-1})	Model values (sec^{-1})
A58			1.6
A59	1.1 ± 0.1	0.93 ± 0.02	1.8
E60	1.9 ± 0.1	1.7 ± 0.02	1.9
E61		1.1 ± 0.02	2.0
L62		1.8 ± 0.03	2.2
A63		4.4 ± 0.04	2.3
N64	2.5 ± 0.03	1.9 ± 0.02	2.3
A65	2.1 ± 0.2	2.8 ± 0.02	2.4
K66	3.2 ± 0.03	2.6 ± 0.03	2.5
K67	3.5 ± 0.04	3.1 ± 0.03	2.5
L68		3.7 ± 0.04	2.6
K69	3.0 ± 0.03	3.1 ± 0.03	2.6
E70	4.0 ± 0.04	3.6 ± 0.04	2.7
Q71	3.7 ± 0.04	3.3 ± 0.03	2.7
L72		3.6 ± 0.04	2.8
E73	3.2 ± 0.03		2.8
K74		3.1 ± 0.04	2.8
L75		3.2 ± 0.03	2.8
T76	3.4 ± 0.02	2.6 ± 0.03	2.9
V77	3.2 ± 0.02	3.1 ± 0.02	2.9
T78	3.3 ± 0.01	3.6 ± 0.04	2.9
I79	4.1 ± 0.1	3.8 ± 0.03	2.9
P80			2.9
A81		2.0 ± 0.03	2.9
K82			2.9
A83		2.3 ± 0.03	2.9
G84	3.0 ± 0.04	2.7 ± 0.03	2.9
E85	3.0 ± 0.04	2.1 ± 0.03	3.0
G86	2.8 ± 0.1	1.6 ± 0.03	3.0
G87	2.5 ± 0.05	1.8 ± 0.02	3.0
R88	2.8 ± 0.03	1.5 ± 0.02	3.0
L89		2.2 ± 0.03	3.0
F90	2.5 ± 0.04	3.1 ± 0.02	3.0
G91	2.5 ± 0.05	2.2 ± 0.02	3.0
S92	2.4 ± 0.02	2.3 ± 0.02	3.0
I93	3.7 ± 0.04		3.0
T94	4.4 ± 0.05	3.0 ± 0.03	3.0
S95		4.2 ± 0.03	3.0
K96		3.8 ± 0.03	3.0
Q97	3.2 ± 0.05		3.0
I98	4.3 ± 0.06	4.4 ± 0.04	3.0
A99	4.4 ± 0.1	4.7 ± 0.04	3.0
E100	3.5 ± 0.02	4.7 ± 0.04	3.0
S101	4.3 ± 0.04	4.0 ± 0.03	3.0

L102		1.9 ± 0.03	3.0
Q103		3.5 ± 0.03	3.0
A104	3.4 ± 0.04		3.0
Q105	3.5 ± 0.03	2.6 ± 0.03	3.0
H106	3.4 ± 0.03	2.8 ± 0.03	3.0
G107	3.4 ± 0.1	3.7 ± 0.03	3.0
L108	4.2 ± 0.04	2.9 ± 0.03	3.0
K109	3.4 ± 0.03		3.0
L110			3.0
D111	3.4 ± 0.02	2.9 ± 0.03	3.0
K112		3.0 ± 0.03	3.0
R113		5.0 ± 0.05	3.0
K114	4.7 ± 0.03	3.0 ± 0.03	3.0
I115		4.2 ± 0.03	3.0
E116		4.9 ± 0.04	3.0
L117			3.0
A118		1.7 ± 0.02	3.0
D119	3.0 ± 0.02		3.0
A120		3.8 ± 0.03	3.0
I121	3.4 ± 0.03	3.5 ± 0.03	3.0
R122	4.3 ± 0.05	3.3 ± 0.03	3.0
A123		3.2 ± 0.03	2.9
L124	2.9 ± 0.05	3.2 ± 0.03	2.9
G125	3.6 ± 0.05	2.6 ± 0.03	2.9
Y126	3.8 ± 0.05	3.2 ± 0.04	2.9
T127	3.8 ± 0.05	2.0 ± 0.03	2.9
N128	3.9 ± 0.04	2.8 ± 0.03	2.9
V129	3.6 ± 0.03	2.3 ± 0.04	2.9
P130			2.9
V131	3.5 ± 0.03	2.9 ± 0.04	2.9
K132		3.1 ± 0.03	2.8
L133		3.2 ± 0.04	2.8
H134	4.2 ± 0.02	2.0 ± 0.03	2.8
P135			2.8
E136	3.3 ± 0.03	2.2 ± 0.03	2.7
V137	3.7 ± 0.1	3.1 ± 0.04	2.7
T138	3.8 ± 0.3	2.5 ± 0.03	2.6
A139	4.2 ± 0.1	2.3 ± 0.03	2.6
T140	3.6 ± 0.1	2.2 ± 0.02	2.5
L141		2.6 ± 0.03	2.5
K142		1.6 ± 0.02	2.4
V143	2.5 ± 0.03	2.0 ± 0.03	2.3
H144	3.3 ± 0.06	1.8 ± 0.04	2.3
V145	3.0 ± 0.05	1.5 ± 0.02	2.1
T146	3.3 ± 0.05	2.4 ± 0.03	2.0
E147		1.3 ± 0.02	1.9
Q148	1.7 ± 0.03	1.8 ± 0.02	1.8
K149	2.2 ± 0.05	1.4 ± 0.02	1.6

Figure-S1

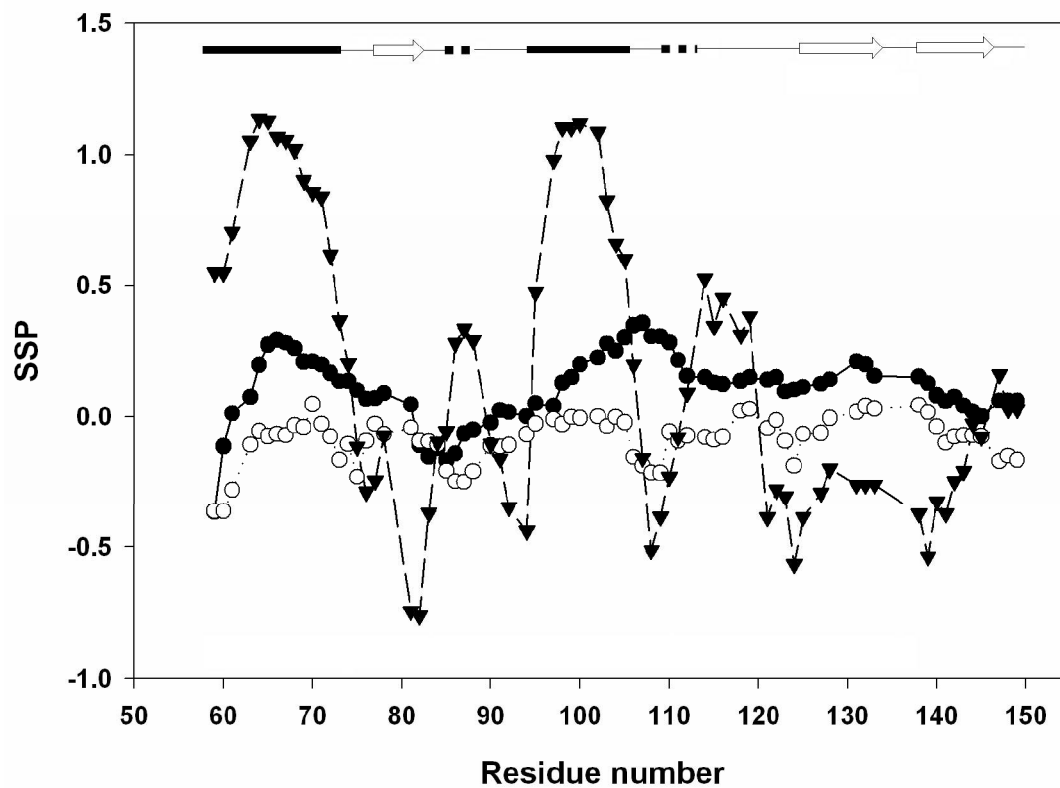


Figure-S2

