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Supporting Information

Impact of Hydrostatic Pressure on an Intrinsically Disordered Protein: A High-Pressure NMR Study of α-Synuclein

Julien Roche, Jinfa Ying, Alexander S. Maltsev, and Ad Bax*[a]

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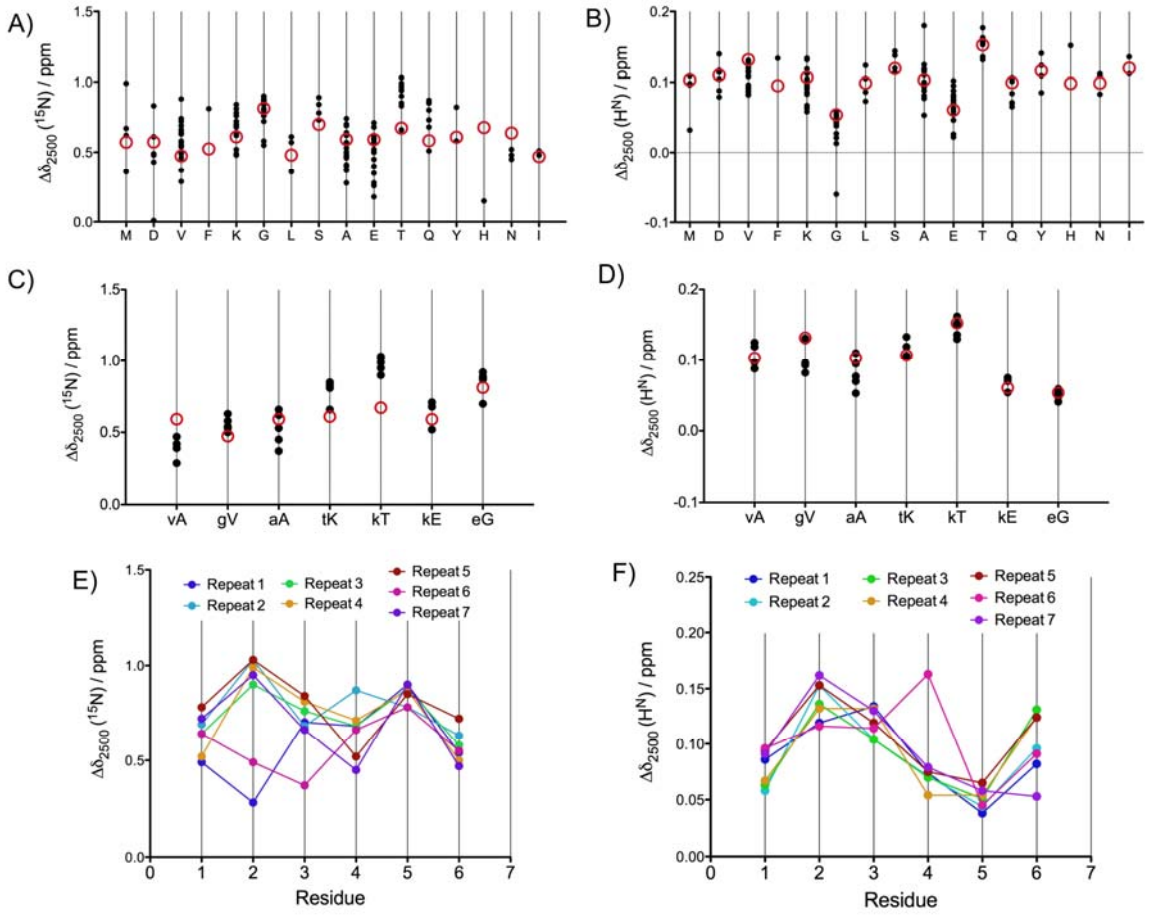

Figure S1: The chemical shift differences between 2500 and 1 bar ($\Delta\delta_{2500}$) measured for the ^{15}N (A) and $^{1}H^{N}$ (B) nucleus are reported for each type of amino acid in α-synuclein sequence (black dot) and compared with the predicted chemical shift differences for model tetrapeptides (open red symbol) (31). The chemical shift differences $\Delta\delta_{2500}$ for ^{15}N (C) and H^{N} (D) are presented for a series of amino acid (upper case) with identical preceding residues (lower case) and compared with the $\Delta\delta_{2500}$ values predicted for model tetrapeptides (open red symbol) (31). The chemical shift differences $\Delta\delta_{2500}$ for ^{15}N (E) and H^{N} (F) are reported for the 7 hexamer motifs found in the N-terminal and NAC regions of α-synuclein, with repeat 1: KAKEGV (blue), repeat 2: KTKQGV (cyan), repeat 3: KTKEGV (green), repeat 4: KTKEGV (yellow), repeat 5: KTKEQV (red), repeat 6: AVVTGV (pink) and repeat 7: KTVEGA (purple). Uncertainties in the $\Delta\delta(^{1}H)$ values are ca 0.001 ppm; uncertainties in the $\Delta\delta(^{15}N)$ values are ca. 0.01 ppm.

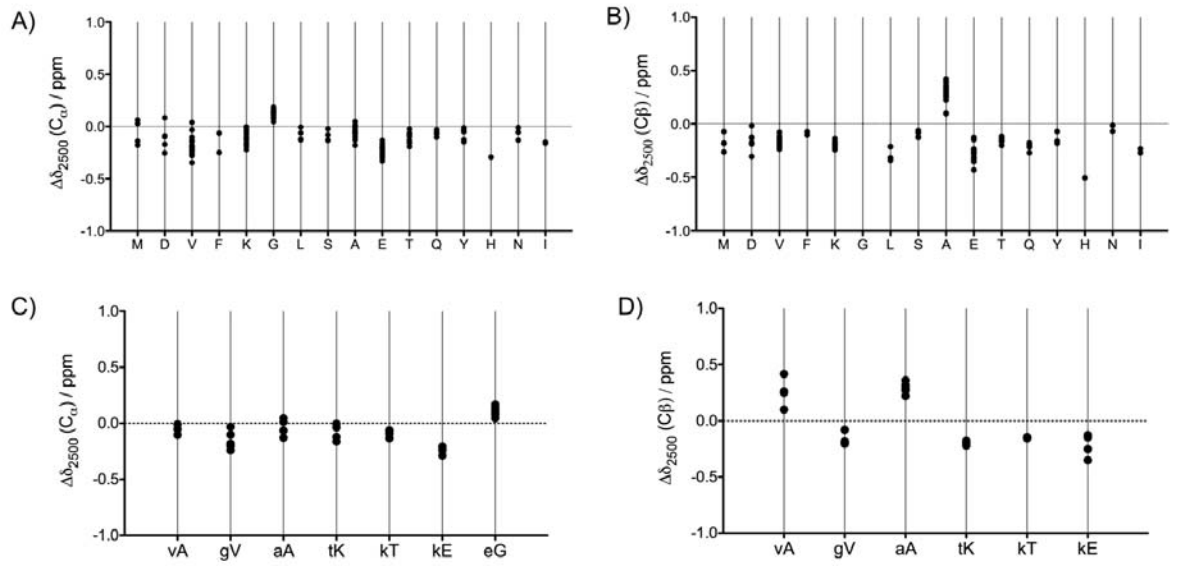

Figure S2: The chemical shift differences measured between 2500 and 1 bar ($\Delta\delta_{2500}$) for Cα (A) and Cβ (B) are reported for each type of amino acid in a-synuclein sequence. The $\Delta\delta_{2500}$ values for Cα (C) and Cβ (D) are presented for a series of amino acid (upper case) with identical preceding residues (lower case). Uncertainties in the $\Delta\delta(^{13}C)$ values are ~0.01 ppm.

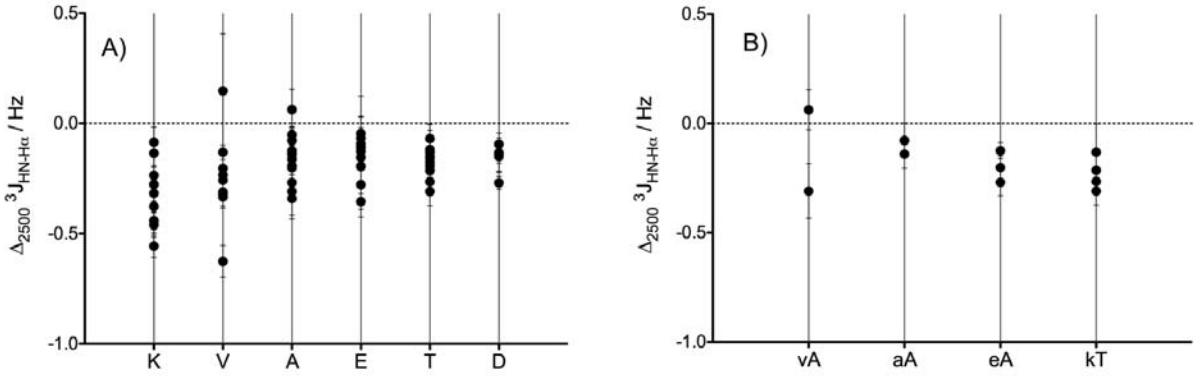

Figure S3: A) The $^{3}J_{HN\text{-}H\alpha}$ coupling differences between 2500 and 1 bar are reported for the most statistically relevant type of amino acid in α-synuclein sequence. B) The difference in the $^{3}J_{HN\text{-}H\alpha}$ couplings are presented for a series of amino acid (upper case) with identical preceding residues (lower case). $^{3}J_{HN\text{-}H\alpha}$ values at 1 and 2500 bar and their uncertainties are listed in Table S3.

Table S1: ^{15}N amide chemical shifts measured from ^{15}N TROSY-HSQC experiments at 500 MHz (the average precision on the ^{15}N chemical shift measurements is ± 0.01 ppm). The sample conditions are: $^{15}N/^{13}C$-enriched N-acetylated α-synuclein (0.4 mM) in 20 mM sodium phosphate pH 6.0. All the experiments were recorded at 288 K.

	1 bar	500 bar	625 bar	1000 bar	1250 bar	1500 bar	1875 bar	2200 bar	2500 bar
M1	125.85	125.99	126.03	126.12	126.19	126.25	126.34	126.41	126.47
D2	120.87	121.08	121.13	121.27	121.35	121.43	121.54	121.63	121.70
V3	119.43	119.64	119.68	119.81	119.87	119.94	120.02	120.09	120.13
F4	122.47	122.73	122.79	123.00	123.04	123.12	123.17	123.24	123.29
M5	120.87	121.23	121.29	121.46	121.56	121.64	121.75	121.83	121.88
K6	121.83	122.08	122.13	122.27	122.34	122.41	122.50	122.57	122.62
G7	109.33	109.56	109.61	109.75	109.84	109.91	110.02	110.10	110.16
L8	121.47	121.62	121.66	121.76	121.82	121.88	121.96	122.03	122.08
S9	116.46	116.71	116.76	116.91	116.99	117.07	117.17	117.24	117.30
K10	123.56	123.73	123.78	123.83	123.88	123.94	123.99	124.02	124.04
A11	125.19	125.34	125.37	125.42	125.41	125.40	125.38	125.40	125.39
K12	120.81	121.02	121.06	121.18	121.25	121.30	121.38	121.44	121.49
E13	122.02	122.31	122.35	122.48	122.56	122.60	122.68	122.77	122.70
G14	110.04	110.28	110.34	110.49	110.56	110.66	110.75	110.85	110.94
V15	120.17	120.30	120.33	120.41	120.46	120.51	120.59	120.65	120.70
V16	125.17	125.32	125.34	125.39	125.41	125.42	125.43	125.43	125.46
A17	128.43	128.56	128.59	128.63	128.64	128.59	128.61	128.63	128.66
A18	123.68	123.82	123.85	123.91	123.94	123.97	124.01	124.03	124.05
A19	123.02	123.22	123.26	123.36	123.42	123.46	123.52	123.53	123.56
E20	120.11	120.31	120.35	120.44	120.49	120.54	120.60	120.64	120.67
K21	122.25	122.49	122.55	122.67	122.74	122.80	122.87	122.92	122.95
T22	115.19	115.49	115.56	115.73	115.83	115.93	116.05	116.14	116.21
K23	123.74	123.97	124.02	124.14	124.21	124.27	124.35	124.41	124.45
Q24	121.70	122.25	122.31	122.38	122.45	122.46	122.48	122.54	122.57
G25	110.56	110.78	110.82	110.96	111.04	111.10	111.20	111.27	111.32
V26	119.77	119.91	119.95	120.04	120.11	120.17	120.25	120.33	120.39
A27	127.41	127.57	127.60	127.67	127.71	127.74	127.78	127.80	127.80
E28	120.58	120.75	120.79	120.89	120.95	120.99	121.06	121.10	121.14
A29	125.26	125.41	125.42	125.52	125.57	125.62	125.67	125.71	125.72
A30	123.02	123.21	123.25	123.35	123.40	123.44	123.50	123.53	123.55
G31	107.79	108.00	108.05	108.18	108.26	108.34	108.45	108.53	108.60
K32	120.71	120.88	120.92	121.02	121.08	121.14	121.21	121.26	121.30
T33	115.58	115.83	115.89	116.05	116.14	116.23	116.34	116.41	116.47
K34	123.85	124.04	124.10	124.26	124.35	124.42	124.52	124.60	124.67
E35	122.08	122.36	122.40	122.51	122.57	122.63	122.68	122.70	122.76
G36	110.01	110.25	110.31	110.47	110.55	110.65	110.77	110.84	110.86
V37	119.55	119.68	119.72	119.83	119.90	119.95	120.04	120.09	120.14
L38	125.84	126.03	126.08	126.18	126.25	126.30	126.37	126.42	126.46
Y39	122.44	122.70	122.76	122.91	122.99	123.06	123.16	123.22	123.28
V40	123.26	123.53	123.58	123.72	123.79	123.86	123.93	123.98	124.00
G41	112.13	112.28	112.31	112.41	112.46	112.52	112.60	112.66	112.70
S42	115.60	115.80	115.86	115.94	116.01	116.09	116.18	116.27	116.33
K43	123.47	123.62	123.65	123.74	123.79	123.83	123.90	123.95	123.99
T44	115.46	115.76	115.82	116.01	116.09	116.18	116.29	116.39	116.45
K45	123.83	124.06	124.10	124.22	124.30	124.38	124.46	124.50	124.66
E46	121.84	122.20	122.22	122.30	122.36	122.42	122.49	122.52	122.55
G47	109.97	110.20	110.26	110.41	110.50	110.58	110.70	110.80	110.84
V48	119.83	119.97	120.00	120.08	120.13	120.18	120.24	120.29	120.34
V49	124.93	125.08	125.11	125.19	125.22	125.26	125.31	125.32	125.35
H50	123.73	123.76	123.75	123.78	123.80	123.82	123.85	123.86	123.88
G51	110.57	110.79	110.83	110.95	111.02	111.10	111.19	111.26	111.30
V52	119.55	119.69	119.72	119.81	119.87	119.93	120.00	120.04	120.09
A53	128.25	128.41	128.45	128.54	128.59	128.63	128.69	128.74	128.77
T54	114.85	115.14	115.20	115.36	115.45	115.54	115.65	115.73	115.79
V55	123.07	123.24	123.29	123.37	123.42	123.47	123.52	123.56	123.59
A56	128.13	128.29	128.31	128.40	128.46	128.48	128.54	128.55	128.57
E57	120.91	121.10	121.14	121.25	121.33	121.37	121.43	121.48	121.53
K58	122.81	123.06	123.11	123.24	123.32	123.39	123.48	123.54	123.59

T59	115.89	116.21	116.28	116.46	116.56	116.65	116.77	116.85	116.92
K60	123.66	123.91	123.96	124.13	124.20	124.28	124.37	124.44	124.51
E61	122.11	122.29	122.35	122.44	122.47	122.49	122.58	122.70	122.63
Q62	121.76	122.27	122.31	122.41	122.47	122.51	122.53	122.54	122.61
V63	121.90	122.15	122.19	122.30	122.38	122.44	122.52	122.57	122.61
T64	118.07	118.34	118.40	118.55	118.63	118.71	118.80	118.87	118.92
N65	121.84	121.99	122.03	122.12	122.17	122.23	122.30	122.35	122.38
V66	120.74	120.84	120.86	120.90	120.92	120.91	120.96	120.98	120.99
G67	112.66	112.79	112.82	112.91	112.97	113.02	113.09	113.15	113.20
G68	108.84	109.04	109.09	109.22	109.31	109.39	109.51	109.60	109.68
A69	123.79	123.94	123.97	124.07	124.13	124.21	124.30	124.37	124.43
V70	120.50	120.66	120.69	120.78	120.83	120.89	120.92	120.96	120.99
V71	125.41	125.55	125.58	125.66	125.69	125.72	125.75	125.77	125.78
T72	118.65	118.85	118.90	119.01	119.08	119.14	119.21	119.27	119.31
G73	111.36	111.55	111.60	111.73	111.81	111.88	111.99	112.07	112.15
V74	119.54	119.67	119.71	119.80	119.85	119.90	119.96	120.02	120.07
T75	118.92	119.18	119.24	119.38	119.46	119.54	119.63	119.70	119.75
A76	127.41	127.63	127.67	127.80	127.88	127.95	128.03	128.10	128.15
V77	120.06	120.24	120.28	120.38	120.43	120.48	120.54	120.59	120.62
A78	128.16	128.32	128.35	128.43	128.49	128.51	128.57	128.58	128.59
Q79	120.34	120.54	120.59	120.71	120.78	120.84	120.92	120.99	121.03
K80	123.28	123.50	123.55	123.67	123.74	123.81	123.89	123.95	123.99
T81	116.92	117.20	117.27	117.43	117.53	117.61	117.72	117.80	117.87
V82	123.00	123.22	123.27	123.38	123.45	123.51	123.58	123.63	123.66
E83	125.33	125.49	125.52	125.60	125.65	125.69	125.73	125.76	125.78
G84	110.73	110.95	111.01	111.16	111.25	111.33	111.45	111.55	111.63
A85	123.99	124.10	124.13	124.21	124.25	124.30	124.37	124.42	124.46
G86	108.19	108.41	108.46	108.60	108.69	108.77	108.89	108.98	109.06
S87	115.70	115.89	115.93	116.05	116.13	116.21	116.32	116.41	116.48
I88	122.78	122.92	122.95	123.09	123.12	123.18	123.23	123.30	123.40
A89	128.09	128.28	128.32	128.42	128.47	128.51	128.57	128.60	128.63
A90	123.37	123.56	123.60	123.71	123.77	123.83	123.90	123.95	123.99
A91	123.44	123.65	123.69	123.81	123.87	123.93	124.01	124.06	124.10
T92	112.61	112.89	112.96	113.12	113.21	113.30	113.42	113.51	113.58
G93	110.70	110.90	110.95	111.08	111.16	111.24	111.34	111.43	111.50
F94	120.34	120.51	120.53	120.66	120.72	120.78	120.89	120.97	121.03
V95	123.71	123.98	124.04	124.19	124.29	124.36	124.46	124.54	124.59
K96	126.46	126.64	126.68	126.79	126.85	126.91	126.98	127.03	127.07
K97	123.84	123.99	124.05	124.12	124.16	124.19	124.24	124.27	124.30
D98	121.26	121.42	121.46	121.54	121.60	121.62	121.68	121.69	121.75
Q99	120.20	120.35	120.37	120.49	120.55	120.59	120.64	120.69	120.72
L100	122.87	123.03	123.07	123.17	123.23	123.28	123.34	123.39	123.44
G101	109.80	110.00	110.04	110.17	110.25	110.32	110.42	110.51	110.58
K102	120.77	120.93	120.97	121.07	121.13	121.19	121.26	121.33	121.38
N103	120.05	120.18	120.21	120.28	120.32	120.36	120.41	120.45	120.49
E104	121.38	121.47	121.49	121.54	121.58	121.60	121.64	121.64	121.69
G106	110.25	110.45	110.49	110.60	110.69	110.71	110.85	110.94	110.96
A107	124.96	125.08	125.11	125.19	125.24	125.28	125.35	125.40	125.44
Q109	121.21	121.40	121.44	121.56	121.64	121.70	121.80	121.87	121.93
E110	122.55	122.70	122.73	122.81	122.87	122.91	122.96	123.00	123.03
G111	110.28	110.51	110.56	110.70	110.79	110.87	110.99	111.09	111.17
I112	120.18	120.31	120.33	120.42	120.48	120.52	120.58	120.62	120.66
L113	127.09	127.23	127.25	127.32	127.36	127.38	127.41	127.43	127.45
E114	122.24	122.45	122.48	122.56	122.63	122.64	122.71	122.71	122.86
D115	121.45	121.62	121.64	121.73	121.77	121.79	121.82	121.85	121.89
M116	122.05	122.16	122.20	122.29	122.34	122.35	122.38	122.40	122.43
V118	120.84	121.03	121.07	121.17	121.25	121.32	121.40	121.47	121.53
D119	126.02	126.08	126.08	126.09	126.10	126.09	126.07	126.05	126.03
D121	119.40	119.57	119.60	119.70	119.77	119.82	119.89	119.94	120.00
N122	119.20	119.33	119.36	119.44	119.49	119.53	119.59	119.63	119.67
E123	121.68	121.74	121.74	121.79	121.85	121.85	121.89	121.91	121.94
A124	124.53	124.74	124.78	124.90	124.97	125.03	125.11	125.17	125.23
Y125	119.97	120.16	120.19	120.29	120.36	120.40	120.46	120.51	120.56
E126	123.74	123.89	123.92	123.98	124.06	124.05	124.08	124.11	124.14
M127	123.91	124.05	124.10	124.21	124.30	124.36	124.42	124.46	124.62

S129	116.77	117.01	117.05	117.20	117.30	117.38	117.49	117.58	117.66
E130	123.24	123.30	123.31	123.34	123.37	123.37	123.39	123.40	123.42
E131	121.76	121.98	122.01	122.08	122.14	122.18	122.25	122.29	122.33
G132	109.98	110.19	110.25	110.38	110.47	110.55	110.66	110.74	110.82
Y133	120.33	120.49	120.52	120.63	120.70	120.74	120.81	120.86	120.90
Q134	122.78	122.92	122.95	123.02	123.08	123.13	123.20	123.24	123.29
D135	121.75	121.90	121.92	122.01	122.07	122.11	122.17	122.21	122.25
Y136	120.66	120.82	120.86	120.96	121.01	121.07	121.15	121.22	121.24
E137	125.35	125.46	125.48	125.54	125.59	125.61	125.65	125.68	125.71
E139	121.60	121.73	121.76	121.84	121.89	121.94	122.00	122.05	122.09
A140	130.96	131.12	131.15	131.25	131.31	131.36	131.43	131.48	131.52

Table S2: H^N chemical shifts measured from ^{15}N TROSY-HSQC experiments at 500 MHz (the average precision on the H^N chemical shift measurements is ± 0.001 ppm). The sample conditions are: ^{15}N, ^{13}C enriched N-acetylated α-synuclein (0.4 mM) in 20 mM sodium phosphate pH 6.0. All the experiments were recorded at 288 K.

	1 bar	500 bar	625 bar	1000 bar	1250 bar	1500 bar	1875 bar	2200 bar	2500 bar
M1	8.457	8.463	8.465	8.470	8.474	8.477	8.482	8.486	8.489
D2	8.533	8.549	8.554	8.567	8.576	8.583	8.595	8.604	8.612
V3	7.913	7.951	7.959	7.981	7.995	8.007	8.024	8.036	8.042
F4	8.196	8.236	8.245	8.273	8.283	8.296	8.307	8.322	8.328
M5	8.223	8.243	8.248	8.264	8.275	8.284	8.298	8.309	8.318
K6	8.213	8.245	8.253	8.272	8.284	8.294	8.308	8.318	8.327
G7	8.344	8.362	8.365	8.374	8.380	8.383	8.387	8.389	8.391
L8	7.999	8.027	8.032	8.046	8.054	8.059	8.066	8.070	8.072
S9	8.295	8.336	8.345	8.370	8.383	8.396	8.412	8.425	8.433
K10	8.353	8.376	8.379	8.402	8.410	8.412	8.425	8.429	8.435
A11	8.302	8.335	8.343	8.366	8.379	8.383	8.395	8.401	8.399
K12	8.338	8.369	8.377	8.400	8.413	8.414	8.426	8.433	8.431
E13	8.468	8.496	8.499	8.509	8.512	8.520	8.530	8.536	8.542
G14	8.488	8.492	8.494	8.506	8.514	8.519	8.523	8.525	8.526
V15	7.998	8.032	8.040	8.055	8.063	8.070	8.077	8.081	8.083
V16	8.309	8.343	8.354	8.372	8.379	8.393	8.402	8.409	8.419
A17	8.462	8.494	8.501	8.518	8.529	8.530	8.542	8.553	8.562
A18	8.334	8.361	8.368	8.386	8.396	8.402	8.408	8.419	8.425
A19	8.265	8.303	8.309	8.326	8.335	8.342	8.345	8.342	8.343
E20	8.354	8.374	8.380	8.382	8.379	8.382	8.381	8.379	8.375
K21	8.357	8.384	8.390	8.402	8.407	8.412	8.416	8.416	8.415
T22	8.147	8.190	8.200	8.227	8.242	8.257	8.275	8.289	8.298
K23	8.360	8.401	8.409	8.430	8.440	8.449	8.459	8.465	8.468
Q24	8.445	8.473	8.476	8.483	8.493	8.499	8.513	8.519	8.516
G25	8.510	8.523	8.527	8.536	8.540	8.541	8.547	8.547	8.550
V26	8.037	8.066	8.073	8.089	8.099	8.107	8.118	8.126	8.132
A27	8.448	8.476	8.482	8.499	8.508	8.516	8.525	8.532	8.536
E28	8.424	8.444	8.448	8.461	8.468	8.475	8.483	8.488	8.493
A29	8.288	8.320	8.330	8.353	8.363	8.368	8.378	8.384	8.392
A30	8.254	8.287	8.296	8.299	8.305	8.311	8.325	8.329	8.324
G31	8.336	8.348	8.351	8.356	8.358	8.360	8.360	8.360	8.358
K32	8.133	8.155	8.160	8.171	8.176	8.181	8.187	8.192	8.194
T33	8.253	8.294	8.301	8.322	8.337	8.349	8.366	8.379	8.390
K34	8.495	8.528	8.535	8.551	8.560	8.570	8.582	8.591	8.599
E35	8.482	8.508	8.511	8.520	8.522	8.530	8.542	8.548	8.552
G36	8.463	8.475	8.479	8.489	8.494	8.498	8.505	8.506	8.510
V37	7.926	7.957	7.966	7.989	8.002	8.016	8.034	8.046	8.054
L38	8.302	8.337	8.344	8.366	8.378	8.390	8.405	8.417	8.426
Y39	8.292	8.333	8.342	8.367	8.382	8.395	8.411	8.422	8.431
V40	8.108	8.133	8.139	8.157	8.169	8.179	8.194	8.206	8.216
G41	8.070	8.055	8.052	8.043	8.037	8.032	8.023	8.016	8.010
S42	8.272	8.303	8.310	8.333	8.344	8.356	8.371	8.383	8.391
K43	8.513	8.534	8.538	8.551	8.557	8.563	8.569	8.573	8.582

T44	8.197	8.230	8.238	8.253	8.269	8.282	8.299	8.311	8.324
K45	8.453	8.480	8.487	8.504	8.519	8.528	8.538	8.540	8.556
E46	8.489	8.498	8.502	8.512	8.523	8.526	8.534	8.539	8.543
G47	8.450	8.456	8.464	8.469	8.479	8.481	8.491	8.488	8.497
V48	7.940	7.978	7.986	8.008	8.020	8.032	8.046	8.056	8.064
V49	8.318	8.349	8.356	8.376	8.387	8.396	8.414	8.426	8.438
H50	8.673	8.723	8.735	8.762	8.775	8.789	8.805	8.816	8.823
G51	8.500	8.516	8.519	8.528	8.531	8.533	8.535	8.538	8.538
V52	8.107	8.138	8.143	8.160	8.170	8.178	8.193	8.197	8.203
A53	8.520	8.546	8.553	8.569	8.579	8.588	8.599	8.608	8.615
T54	8.246	8.292	8.303	8.330	8.346	8.362	8.382	8.397	8.410
V55	8.294	8.315	8.319	8.335	8.349	8.352	8.378	8.386	8.397
A56	8.439	8.470	8.479	8.498	8.510	8.527	8.539	8.550	8.563
E57	8.392	8.421	8.426	8.443	8.453	8.459	8.469	8.470	8.483
K58	8.453	8.483	8.490	8.507	8.516	8.525	8.535	8.542	8.547
T59	8.227	8.271	8.281	8.307	8.322	8.337	8.355	8.369	8.379
K60	8.407	8.444	8.452	8.477	8.484	8.495	8.508	8.520	8.531
E61	8.456	8.480	8.484	8.492	8.506	8.511	8.521	8.531	8.531
Q62	8.438	8.460	8.464	8.475	8.481	8.492	8.494	8.502	8.503
V63	8.300	8.330	8.337	8.361	8.377	8.391	8.406	8.416	8.424
T64	8.319	8.365	8.375	8.402	8.418	8.433	8.451	8.466	8.477
N65	8.539	8.570	8.578	8.597	8.607	8.618	8.631	8.641	8.648
V66	8.258	8.291	8.299	8.318	8.327	8.330	8.349	8.355	8.367
G67	8.577	8.583	8.585	8.588	8.589	8.590	8.590	8.590	8.590
G68	8.253	8.268	8.271	8.280	8.285	8.290	8.295	8.299	8.302
A69	8.182	8.209	8.213	8.231	8.242	8.252	8.264	8.273	8.280
V70	8.237	8.269	8.277	8.297	8.306	8.325	8.334	8.345	8.350
V71	8.410	8.444	8.452	8.472	8.483	8.494	8.506	8.516	8.523
T72	8.325	8.371	8.382	8.409	8.426	8.441	8.461	8.476	8.489
G73	8.457	8.470	8.473	8.481	8.486	8.490	8.496	8.500	8.503
V74	8.102	8.129	8.136	8.151	8.164	8.170	8.181	8.188	8.191
T75	8.315	8.359	8.369	8.396	8.412	8.426	8.445	8.460	8.472
A76	8.388	8.421	8.429	8.449	8.461	8.471	8.485	8.495	8.503
V77	8.159	8.199	8.208	8.231	8.244	8.256	8.271	8.282	8.292
A78	8.428	8.462	8.472	8.490	8.501	8.517	8.524	8.537	8.547
Q79	8.408	8.441	8.448	8.467	8.478	8.487	8.498	8.506	8.511
K80	8.456	8.485	8.491	8.508	8.517	8.526	8.537	8.546	8.551
T81	8.309	8.355	8.366	8.393	8.410	8.425	8.444	8.459	8.471
V82	8.320	8.362	8.370	8.393	8.406	8.418	8.433	8.444	8.453
E83	8.595	8.619	8.624	8.638	8.647	8.654	8.663	8.670	8.675
G84	8.537	8.556	8.560	8.571	8.577	8.582	8.588	8.593	8.596
A85	8.282	8.300	8.304	8.313	8.319	8.323	8.329	8.332	8.335
G86	8.515	8.524	8.526	8.531	8.534	8.537	8.539	8.541	8.542
S87	8.172	8.205	8.213	8.236	8.248	8.262	8.275	8.286	8.290
I88	8.216	8.249	8.263	8.288	8.289	8.304	8.315	8.329	8.336
A89	8.368	8.402	8.409	8.430	8.442	8.453	8.467	8.478	8.486
A90	8.229	8.263	8.271	8.290	8.301	8.312	8.324	8.333	8.340
A91	8.311	8.337	8.342	8.357	8.365	8.372	8.379	8.383	8.384
T92	8.110	8.160	8.171	8.201	8.220	8.236	8.257	8.273	8.286
G93	8.325	8.342	8.346	8.356	8.362	8.366	8.372	8.376	8.378
F94	8.105	8.133	8.137	8.157	8.164	8.174	8.189	8.199	8.207
V95	8.080	8.112	8.119	8.139	8.152	8.163	8.179	8.191	8.201
K96	8.420	8.447	8.453	8.469	8.479	8.487	8.499	8.507	8.514
K97	8.507	8.525	8.530	8.547	8.557	8.564	8.576	8.584	8.591
D98	8.432	8.456	8.462	8.477	8.485	8.506	8.511	8.516	8.518
Q99	8.367	8.385	8.387	8.405	8.415	8.422	8.430	8.434	8.437
L100	8.320	8.349	8.355	8.371	8.380	8.386	8.395	8.401	8.406
G101	8.494	8.509	8.512	8.521	8.526	8.529	8.534	8.538	8.540
K102	8.234	8.258	8.263	8.278	8.287	8.295	8.305	8.312	8.319
N103	8.646	8.668	8.673	8.687	8.697	8.704	8.714	8.722	8.728
E104	8.506	8.514	8.516	8.519	8.520	8.515	8.519	8.523	8.525
G106	8.451	8.468	8.472	8.482	8.486	8.492	8.498	8.499	8.502
A107	8.132	8.160	8.166	8.183	8.192	8.200	8.211	8.219	8.225
Q109	8.605	8.634	8.640	8.657	8.668	8.677	8.689	8.698	8.706
E110	8.545	8.570	8.576	8.591	8.601	8.608	8.618	8.626	8.633
G111	8.504	8.517	8.520	8.528	8.533	8.536	8.540	8.544	8.545

I112	8.014	8.041	8.049	8.070	8.084	8.090	8.107	8.118	8.126
L113	8.429	8.460	8.467	8.485	8.496	8.505	8.517	8.526	8.534
E114	8.448	8.470	8.475	8.491	8.499	8.506	8.514	8.515	8.530
D115	8.382	8.414	8.421	8.438	8.458	8.466	8.482	8.492	8.499
M116	8.280	8.320	8.327	8.347	8.350	8.356	8.366	8.372	8.377
V118	8.321	8.362	8.369	8.392	8.405	8.423	8.442	8.461	8.473
D119	8.543	8.583	8.592	8.616	8.631	8.644	8.661	8.674	8.684
D121	8.407	8.435	8.441	8.459	8.470	8.479	8.493	8.503	8.512
N122	8.155	8.190	8.197	8.217	8.229	8.238	8.252	8.261	8.269
E123	8.386	8.405	8.410	8.424	8.427	8.434	8.440	8.445	8.450
A124	8.244	8.273	8.279	8.297	8.307	8.317	8.329	8.339	8.346
Y125	8.056	8.094	8.101	8.123	8.135	8.146	8.160	8.170	8.179
E126	8.166	8.198	8.204	8.218	8.234	8.238	8.249	8.259	8.269
M127	8.446	8.471	8.479	8.496	8.510	8.518	8.527	8.528	8.547
S129	8.507	8.547	8.555	8.580	8.596	8.608	8.625	8.639	8.651
E130	8.600	8.614	8.616	8.625	8.631	8.634	8.639	8.643	8.648
E131	8.489	8.488	8.498	8.513	8.522	8.528	8.536	8.542	8.548
G132	8.430	8.440	8.454	8.456	8.465	8.466	8.474	8.474	8.480
Y133	8.096	8.123	8.129	8.145	8.156	8.162	8.169	8.174	8.179
Q134	8.229	8.263	8.275	8.286	8.299	8.311	8.326	8.339	8.350
D135	8.265	8.295	8.302	8.321	8.334	8.344	8.358	8.370	8.378
Y136	8.079	8.110	8.117	8.137	8.148	8.160	8.174	8.184	8.189
E137	8.272	8.299	8.304	8.320	8.331	8.337	8.347	8.355	8.361
E139	8.538	8.558	8.563	8.576	8.585	8.592	8.602	8.610	8.617
A140	8.022	8.070	8.081	8.112	8.130	8.147	8.169	8.187	8.201

Table S3 $^{13}C^{\alpha}$, $^{13}C^{\beta}$ and $^{13}C'$ chemical shifts measured from HNCACB and HNCO experiments at 500 MHz (the average precision on the ^{13}C chemical shift measurements is ± 0.01 ppm). The sample conditions are: ^{15}N, ^{13}C enriched N-acetylated α-synuclein (0.4 mM) in 20 mM sodium phosphate pH 6.0. All experiments were recorded at 288 K.

	$^{13}C^{\alpha}$ 1 bar	$^{13}C^{\alpha}$ 2500 bar	$^{13}C^{\beta}$ 1 bar	$^{13}C^{\beta}$ 2500 bar	$^{13}C'$ 1 bar	$^{13}C'$ 2500 bar
M1	55.91	55.77	32.90	32.83	176.59	176.62
D2	54.56	54.39	40.82	40.80	176.73	176.59
V3	63.28	62.93	32.33	32.21	176.56	176.56
F4	58.54	58.29	39.19	39.09	176.36	176.34
M5	55.79	55.62	32.44	32.26	176.51	176.48
K6	57.15	56.96	32.76	32.54	177.38	177.47
G7	45.47	45.61			174.35	174.46
L8	55.30	55.18	42.47	42.26	177.72	177.83
S9	58.51	58.43	63.73	63.61	174.66	174.74
K10	56.31	56.29	32.97	32.77	176.50	176.74
A11	52.72	52.67	19.12	19.37	177.95	178.10
K12	56.49	56.44	32.95	32.76	176.67	176.60
E13	56.86	56.63	30.22	29.97	177.05	177.16
G14	45.28	45.43			174.05	174.30
V15	62.62	62.59	32.72	32.52	176.50	176.74
V16	62.48	62.52	32.71	32.48	176.02	176.30
A17	52.56	52.50	19.13	19.55	177.70	177.99
A18	52.71	52.76	19.11	19.33	177.93	178.08
A19	52.75	52.76	19.09	19.36	178.21	178.32
E20	56.83	56.66	30.20	29.94	176.96	176.95
K21	56.76	56.66	32.87	32.68	177.17	177.33
T22	62.30	62.23	69.80	69.65	174.71	174.79
K23	56.67	56.67	32.91	32.70	176.69	176.75
Q24	56.20	56.32	29.49	29.32	176.59	176.83
G25	45.36	45.50			174.25	174.45
V26	62.59	62.49	32.74	32.53	176.38	176.51
A27	52.82	52.81	19.01	19.26	178.14	178.28
E28	56.85	56.71	30.17	29.92	176.67	176.68
A29	52.72	52.67	19.06	19.45	177.75	177.83

A30	52.83	52.73	19.06	19.38	178.47	178.53
G31	45.37	45.50			174.21	174.31
K32	56.25	56.08	33.20	33.07	177.00	177.12
T33	61.90	61.83	70.00	69.84	174.67	174.71
K34	56.50	56.47	32.95	32.73	176.50	176.61
E35	56.81	56.57	30.21	30.06	176.94	176.98
G36	45.32	45.46			174.01	174.15
V37	62.34	62.16	32.75	32.56	175.90	176.05
L38	54.99	54.93	42.50	42.16	176.64	176.78
Y39	57.88	57.87	38.87	38.69	175.58	175.68
V40	62.20	61.94	32.82	32.65	176.15	176.14
G41	45.19	45.30			173.95	174.09
S42	58.37	58.24	63.91	63.83	174.78	174.82
K43	56.45	56.32	33.01	32.85	176.87	176.97
T44	61.90	61.81	69.90	69.75	174.60	174.61
K45	56.58	56.46	32.94	32.75	176.54	176.43
E46	56.86	56.58	30.20	29.85	176.93	176.98
G47	45.26	45.35			173.87	174.02
V48	62.27	62.07	32.80	32.62	176.06	176.24
V49	62.24	62.11	32.75	32.52	175.91	176.03
H50	55.46	55.17	29.68	29.17	175.00	174.90
G51	45.17	45.36			173.73	173.88
V52	62.01	61.81	32.97	32.89	175.91	175.96
A53	52.43	52.38	19.30	19.59	177.82	177.97
T54	61.83	61.74	69.97	69.84	174.55	174.59
V55	62.31	62.10	32.86	32.72	175.86	175.93
A56	52.54	52.44	19.21	19.31	177.78	177.89
E57	56.62	56.42	30.38	30.14	176.72	176.68
K58	56.54	56.38	33.00	32.82	176.99	177.06
T59	62.16	62.03	69.81	69.66	174.66	174.66
K60	56.67	56.51	32.95	32.77	176.70	176.74
E61	56.74	56.54	30.16	30.03	176.43	176.84
Q62	55.79	55.72	29.50	29.32	175.97	176.01
V63	62.41	62.17	32.81	32.67	176.35	176.42
T64	61.77	61.70	69.91	69.74	174.05	174.13
N65	53.12	53.11	38.90	38.88	175.25	175.31
V66	62.68	62.40	32.51	32.38	176.86	176.90
G67	45.35	45.50			174.67	174.81
G68	45.04	45.15			173.73	173.89
A69	52.31	52.22	19.36	19.70	177.64	177.80
V70	62.41	62.19	32.73	32.57	176.33	176.39
V71	62.17	62.03	32.80	32.60	176.28	176.37
T72	61.85	61.69	69.92	69.79	174.91	174.97
G73	45.26	45.43			174.02	174.16
V74	62.34	62.10	32.85	32.66	176.55	176.64
T75	61.93	61.90	69.80	69.59	174.08	174.15
A76	52.45	52.43	19.30	19.61	177.55	177.67
V77	62.23	62.02	32.83	32.68	176.01	176.07
A78	52.49	52.48	19.15	19.41	177.62	177.75
Q79	55.70	55.64	29.62	29.45	175.93	175.98
K80	56.37	56.27	33.16	32.96	176.68	176.81
T81	61.90	61.83	69.93	69.77	174.44	174.53
V82	62.30	62.04	32.82	32.67	176.15	176.18
E83	56.80	56.58	30.22	29.95	177.02	177.08
G84	45.29	45.46			174.15	174.22
A85	52.90	52.72	19.19	19.57	178.49	178.51
G86	45.31	45.40			174.30	174.42
S87	58.36	58.23	63.89	63.82	174.71	174.80
I88	61.32	61.16	38.68	38.41	176.26	176.37
A89	52.61	52.56	19.08	19.36	177.55	177.69
A90	52.49	52.42	19.18	19.47	177.72	177.74
A91	52.63	52.50	19.13	19.49	178.12	178.21
T92	62.00	61.80	69.88	69.76	175.14	175.21
G93	45.19	45.33			173.61	173.77
F94	57.80	57.73	39.73	39.66	175.47	175.59

V95	62.00	61.81	33.14	32.91	175.39	175.43
K96	56.37	56.37	33.02	32.78	176.45	176.55
K97	56.48	56.37	33.19	32.97	176.35	176.47
D98	54.42	54.32	41.02	40.90	176.21	176.16
Q99	55.85	55.73	29.41	29.22	176.01	176.05
L100	55.40	55.27	42.22	42.01	177.98	178.04
G101	45.31	45.45			174.07	174.19
K102	56.21	56.14	33.18	32.94	176.44	176.60
N103	53.35	53.29	38.77	38.75	175.32	175.31
E104	56.70	56.40	30.18	29.91	177.02	177.04
G106	45.04	45.15			173.43	173.56
A107	50.50	50.52	18.18	18.50	177.04	177.10
Q109	55.71	55.68	29.64	29.43	175.97	176.01
E110	56.62	56.37	30.41	30.13	176.82	176.84
G111	45.27	45.35			173.74	173.94
I112	60.92	60.77	38.66	38.43	176.23	176.33
L113	55.00	54.99	42.35	42.04	177.13	177.18
D115	54.21	54.12	41.05	40.87	175.85	175.88
M116	53.19	53.22	32.48	32.22	175.74	175.71
V118	61.94	61.75	33.06	32.94	176.70	176.83
D119	52.09	52.17	41.05	40.75	175.75	175.80
D121	54.50	54.25	40.84	40.71	176.91	176.89
N122	53.47	53.34	39.29	39.22	176.13	176.02
E123	56.75	56.48	29.97	29.64	175.36	175.37
A124	52.36	52.30	19.13	19.47	176.02	176.05
Y125	57.72	57.67	39.04	38.88	177.19	177.32
E126	55.61	55.42	30.63	30.20	175.33	175.44
M127	53.30	53.37	32.35	32.17	175.42	175.43
S129	58.25	58.22	63.91	63.78	176.87	177.01
E130	56.46	56.19	30.20	29.96	174.79	174.79
E131	56.84	56.64	30.16	29.89	176.55	176.52
G132	45.16	45.21			176.92	176.93
Y133	58.13	57.98	38.78	38.71	173.81	173.96
Q134	55.40	55.30	29.87	29.65	175.72	175.80
D135	54.15	54.06	41.07	40.89	174.83	174.99
Y136	57.59	57.56	39.12	38.96	175.47	175.46
E137	53.52	53.36	30.05	29.74	175.07	175.12
E139	56.53	56.21	30.26	29.92	176.85	176.89
A140	53.80	53.81	20.20	20.29		

Table S4. $^{3}J_{HN\text{-}H\alpha}$ couplings recorded at 2500 bar, 288 K. The atmospheric $^{3}J(H^{N}\text{-}H\alpha)$ values are reproduced from (27). The sample conditions are: ^{15}N enriched N-acetylated α-synuclein (0.3 mM) in 20 mM sodium phosphate pH 6.0.

	1 bar	1 bar error	2500 bar	2500 bar error
M1	6.50	0.02	6.27	0.02
D2	6.63	0.04	6.49	0.02
M5	6.69	0.06	6.63	0.04
K6	6.07	0.05	5.98	0.04
L8	6.87	0.05	6.67	0.04
S9	6.52	0.04	6.25	0.02
V15	7.47	0.06	6.84	0.04
E20	6.19	0.02	6.00	0.08
K21	6.51	0.03	6.24	0.08
T22	6.99	0.04	6.73	0.05
K23	6.60	0.04	6.22	0.11
V26	7.11	0.05	6.80	0.05
A27	5.55	0.02	5.62	0.09
E28	6.09	0.01	5.90	0.06
T33	7.20	0.05	7.00	0.01
E35	6.34	0.04	6.18	0.18
L38	7.10	0.06	6.77	0.05

Y39	7.47	0.04	6.94	0.04
V40	8.03	0.06	8.18	0.25
S42	6.60	0.04	6.54	0.01
K43	7.01	0.09	6.77	0.08
T44	7.24	0.07	7.03	0.05
K45	6.70	0.02	6.39	0.05
V48	7.59	0.02	7.26	0.03
H50	7.75	0.10	7.50	0.04
A53	5.79	0.02	5.67	0.11
T54	7.56	0.03	7.38	0.05
A56	5.55	0.03	5.21	0.07
K58	6.60	0.05	6.46	0.05
T59	6.99	0.03	6.86	0.13
V63	7.70	0.04	7.49	0.08
T64	7.86	0.05	7.71	0.14
N65	7.57	0.04	7.30	0.03
A69	5.86	0.02	5.73	0.04
V71	8.15	0.02	7.82	0.02
T72	7.69	0.02	7.57	0.03
T75	7.60	0.03	7.44	0.07
A76	5.89	0.02	5.70	0.07
V77	7.43	0.03	7.17	0.04
A78	5.62	0.01	5.31	0.13
Q79	6.78	0.03	6.51	0.03
K80	6.71	0.02	6.43	0.04
T81	7.54	0.03	7.23	0.06
V82	7.72	0.01	7.49	0.02
E83	6.22	0.02	6.11	0.03
A85	5.61	0.02	5.66	0.03
S87	6.84	0.02	6.65	0.02
A89	5.55	0.02	5.39	0.07
A90	5.61	0.02	5.53	0.08
A91	5.76	0.02	5.62	0.06
T92	7.50	0.02	7.43	0.03
F94	6.93	0.03	6.55	0.04
V95	8.03	0.03	7.90	0.02
K96	6.51	0.03	6.06	0.03
Q99	7.20	0.04	7.06	0.03
L100	6.83	0.01	6.74	0.01
K102	6.84	0.02	6.64	0.02
N103	7.19	0.05	7.10	0.03
E104	6.78	0.02	6.75	0.01
A107	5.90	0.02	5.78	0.03
Q109	6.93	0.02	6.69	0.02
E110	6.55	0.02	6.45	0.03
I112	7.76	0.02	7.42	0.03
L113	7.19	0.04	6.92	0.03
E114	6.76	0.01	6.48	0.15
D115	6.87	0.02	6.72	0.06
M116	7.29	0.05	7.09	0.01
D119	6.77	0.02	6.50	0.02
D121	7.16	0.07	7.03	0.06
N122	7.32	0.03	7.25	0.02
E123	6.49	0.06	6.45	0.05
A124	6.26	0.04	6.06	0.04
Y125	7.10	0.06	6.76	0.05
E126	7.57	0.16	7.46	0.17
S129	6.64	0.02	6.37	0.06
E130	6.84	0.02	6.77	0.04
Y133	6.72	0.05	6.53	0.00
D135	6.94	0.03	6.85	0.01
E139	6.64	0.04	6.51	0.04
A140	6.63	0.04	6.36	0.04

Table S5. ^{15}N $R_{1\rho}$ relaxation rates measured at 1 bar and 2500 bar, at 600 MHz ^{1}H frequency, for non-acetylated α-synuclein, using a 1.3 kHz ^{15}N RF field, with the ^{15}N carrier positioned at 120 ppm Sample conditions: ^{15}N-enriched α-synuclein (0.5 mM) in 20 mM sodium phosphate pH 6.0. All the experiments were performed at 288 K, and the raw $R_{1\rho}$ values are reported, not corrected for resonance offset.

	$R_{1\rho}$ (s^{-1}) 1 bar	1 bar error	$R_{1\rho}$ (s^{-1}) 2500 bar	2500 bar error
V3	2.74	0.03	2.13	0.02
F4	3.33	0.05	2.69	0.03
M5	3.54	0.06	2.96	0.04
K6	3.66	0.07	3.36	0.09
G7	3.01	0.05	3.15	0.04
L8	3.45	0.05	3.02	0.04
S9	3.25	0.05	3.25	0.05
A11	3.46	0.05	3.42	0.04
K12	3.36	0.06	3.39	0.06
E13	4.04	0.19	3.71	0.04
G14	3.48	0.04	3.40	0.04
A17	3.54	0.05	3.95	0.05
A18	3.53	0.04	3.87	0.05
E20	3.68	0.05	4.01	0.05
K21	3.89	0.07	4.16	0.08
T22	3.72	0.05	3.99	0.05
K23	3.73	0.09	3.91	0.07
V26	3.50	0.04	3.81	0.04
E28	3.33	0.04	3.59	0.04
A29	3.52	0.05	3.40	0.04
K32	3.31	0.05	3.66	0.05
T33	3.30	0.04	3.58	0.05
E35	3.57	0.04	3.82	0.08
V37	3.67	0.05	3.81	0.05
L38	3.85	0.06	3.99	0.06
Y39	4.06	0.06	4.36	0.07
V40	3.97	0.07	4.12	0.07
G41	3.53	0.06	3.71	0.06
S42	3.56	0.06	3.65	0.05
K43	3.58	0.08	3.69	0.06
T44	3.48	0.05	3.50	0.04
K45	3.58	0.06	3.64	0.05
V48	3.21	0.04	3.35	0.04
V49	3.31	0.02	3.65	0.05
H50	3.43	0.08	3.53	0.06
G51	3.09	0.05	3.24	0.03
A53	2.90	0.03	3.07	0.03
T54	2.90	0.04	3.12	0.04
V55	3.62	0.05	3.45	0.04
A56	3.32	0.04	3.79	0.03
E57	3.34	0.04	3.73	0.03
K58	3.54	0.06	3.69	0.06
T59	3.50	0.05	3.71	0.05
K60	3.53	0.04	3.52	0.06
E61	3.43	0.04	3.59	0.02
V63	3.07	0.04	3.26	0.04
T64	3.06	0.04	3.25	0.04
N65	2.88	0.04	3.03	0.04
V66	2.41	0.02	2.45	0.02
G67	2.37	0.03	2.51	0.02
G68	1.97	0.02	2.10	0.02
A69	2.16	0.02	2.30	0.02
V71	2.44	0.03	2.61	0.03
T72	2.62	0.03	2.79	0.03
G73	2.36	0.03	2.50	0.03
V74	2.80	0.02	2.99	0.02
T75	2.76	0.03	2.98	0.03
V77	2.66	0.03	2.88	0.03

A78	2.66	0.03	2.89	0.03
Q79	2.78	0.03	2.97	0.03
K80	2.93	0.04	3.09	0.04
T81	2.87	0.03	3.08	0.03
V82	2.83	0.03	3.01	0.03
E83	2.72	0.03	2.95	0.03
G84	2.34	0.03	2.49	0.03
A85	2.42	0.02	2.59	0.02
G86	2.04	0.03	2.13	0.02
S87	2.33	0.02	2.49	0.02
I88	2.47	0.02	2.90	0.02
A89	2.57	0.02	2.81	0.02
A90	2.51	0.02	2.73	0.02
A91	2.50	0.02	2.72	0.02
T92	2.53	0.03	2.76	0.03
G93	2.57	0.03	2.78	0.03
F94	3.03	0.04	3.26	0.03
V95	3.07	0.04	3.41	0.04
K96	3.19	0.04	3.48	0.05
K97	3.47	0.03	3.77	0.05
Q99	3.26	0.04	3.51	0.04
L100	3.19	0.04	3.30	0.03
G101	2.66	0.03	2.87	0.03
K102	3.00	0.04	3.19	0.04
N103	2.94	0.04	3.11	0.03
E104	2.90	0.03	3.32	0.03
G106	2.42	0.03	2.70	0.02
A107	2.76	0.02	2.94	0.02
Q109	2.85	0.03	3.09	0.03
E110	2.97	0.03	3.20	0.03
G111	2.62	0.03	2.82	0.03
I112	3.26	0.03	3.36	0.04
L113	3.18	0.04	3.44	0.05
E114	3.30	0.04	3.56	0.04
D115	3.38	0.04	3.64	0.05
M116	3.57	0.05	3.79	0.05
D119	3.86	0.06	4.06	0.06
D121	4.38	0.07	4.41	0.07
N122	4.06	0.06	4.16	0.06
E123	3.78	0.05	3.91	0.05
A124	3.74	0.05	3.87	0.05
Y125	3.66	0.05	3.85	0.05
E126	3.85	0.07	4.02	0.07
S129	3.44	0.05	3.62	0.04
E130	3.35	0.04	3.45	0.04
E131	3.49	0.03	3.63	0.02
Y133	3.08	0.04	3.28	0.03
D135	2.96	0.04	3.12	0.03
Y136	2.78	0.03	2.93	0.03
E137	2.62	0.03	2.74	0.03
E139	2.07	0.02	2.18	0.02
A140	1.28	0.01	1.33	0.01