

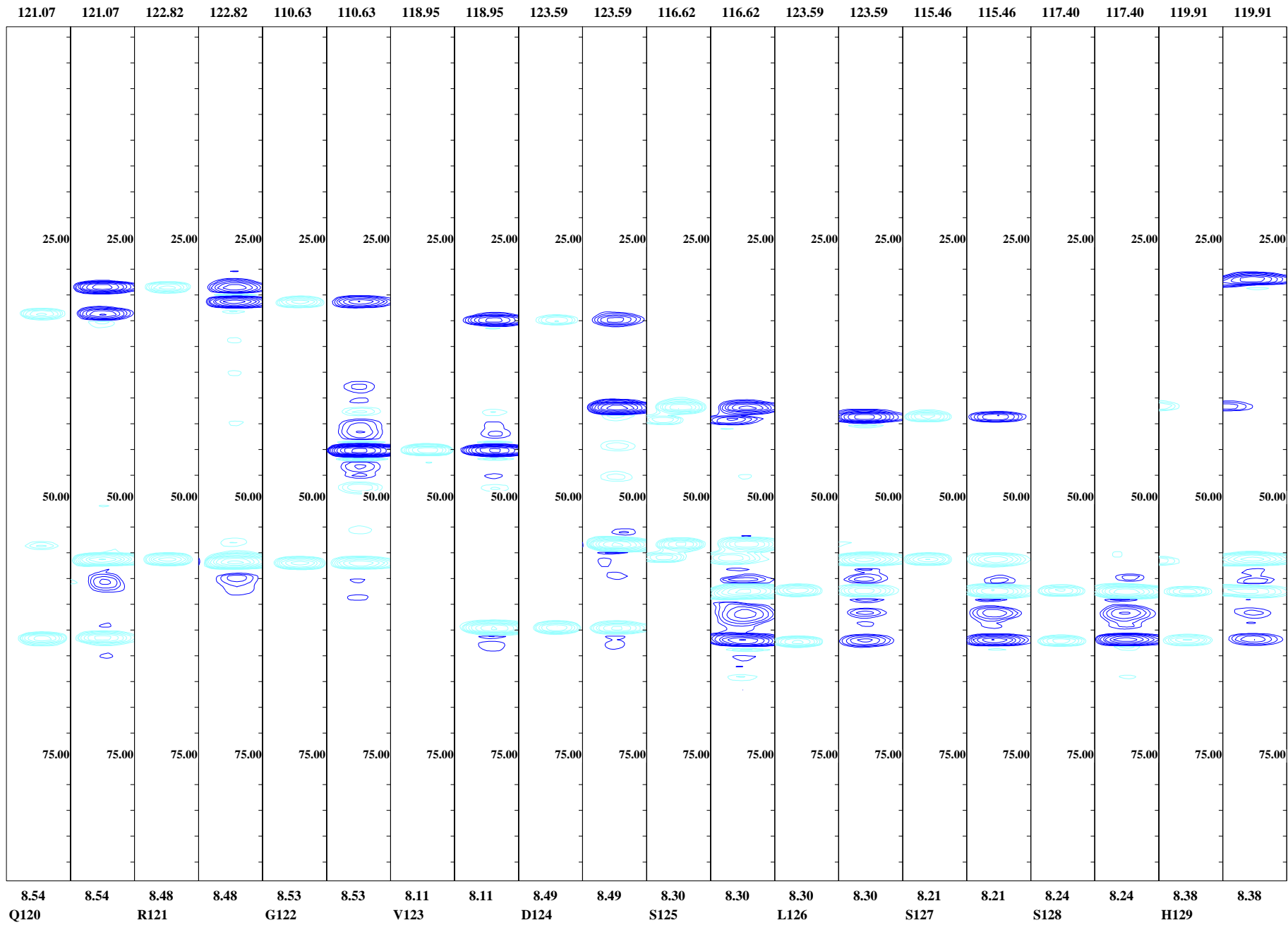
APPENDIX B

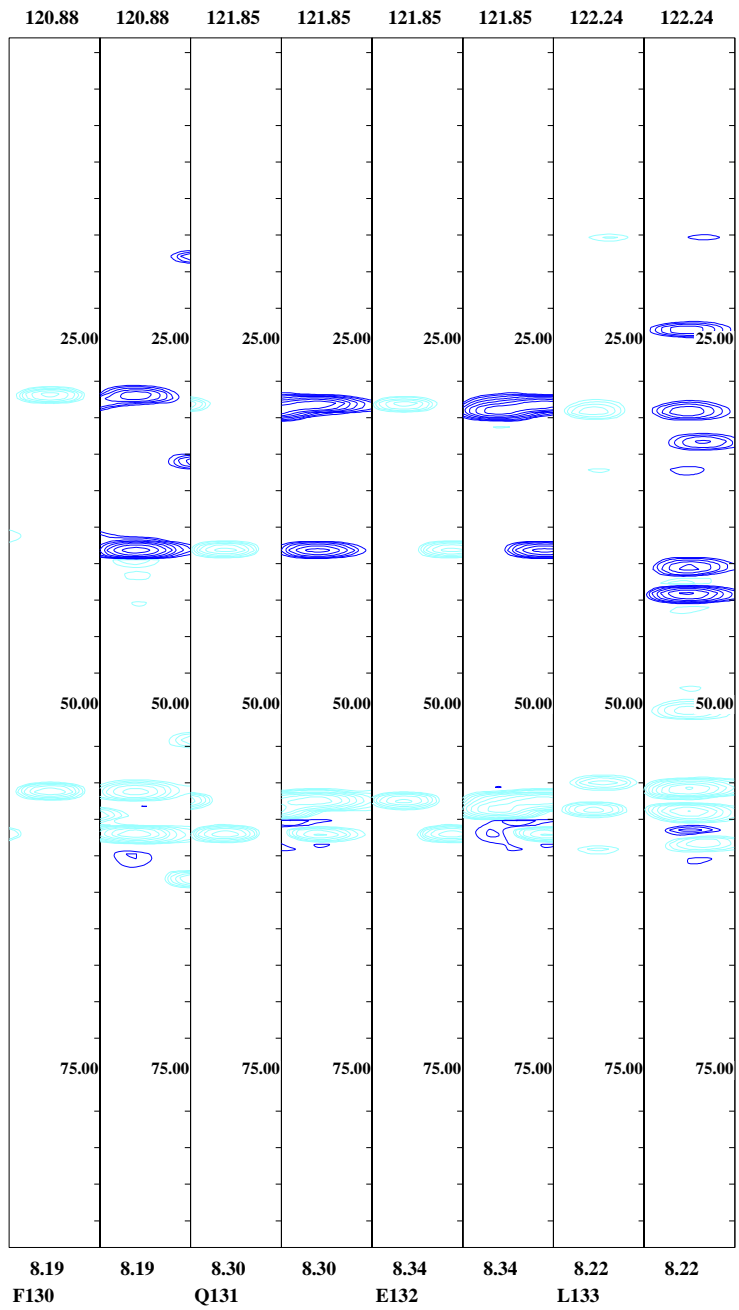
Supplementary NMR data

Sequential assignment by triple resonance experiments

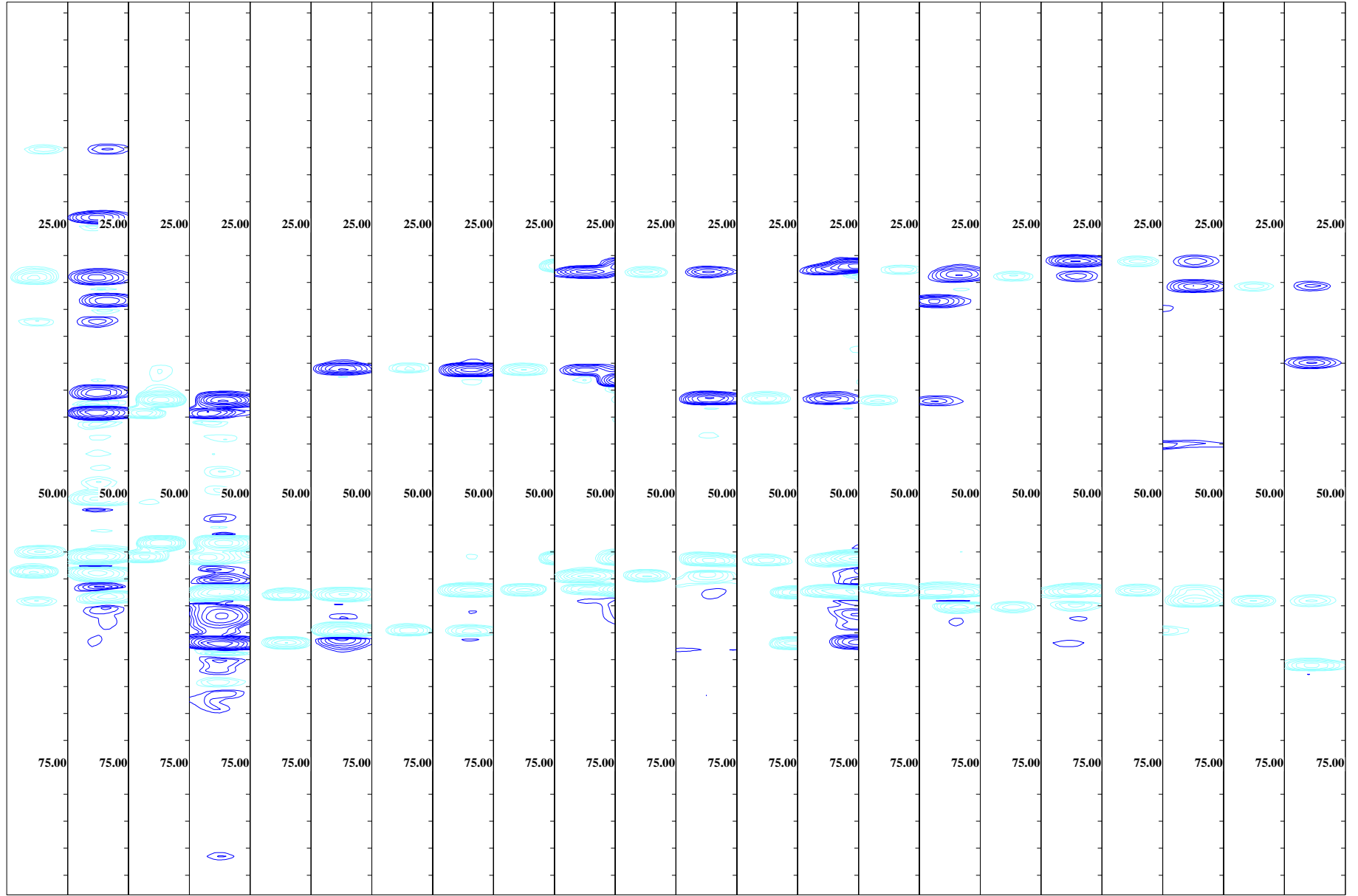
The sequential assignment of the Z α domain (residues 119 – 200) was verified by using triple resonance NMR experiments [18]. 2D strips were extracted from 3D CBCA(CO)NH and CBCANH spectra using the NMR analysis program Aurelia (Bruker). For each residue of Z α (except for the four prolines and the first two N-terminal residues) a pair of strips is shown aligned in sequential order (fig. 60).

fig. 60 **Sequential backbone assignment of Z α by using 3D CBCA(CO)NH and CBCANH triple resonance spectra (see following 9 pages).** The backbone ^{15}N chemical shift is listed above and the H_N chemical shift is listed below each strip. A ^{13}C chemical shift axis is represented at the long axis of a strip. The left strip of each pair originates from the CBCA(CO)NH spectrum showing the $\text{C}\alpha$ and $\text{C}\beta$ shifts of the residue one residue ahead in the primary sequence (i-1) in light gray color. The right strip of a pair originating from the CBCANH spectrum, shows the $\text{C}\alpha$ and $\text{C}\beta$ shifts of that very residue (i) in light gray and black color, respectively. In addition, it shows the $\text{C}\alpha$ and $\text{C}\beta$ shifts of the residue one residue ahead in sequence (i-1) with less intensity in light gray and black color, respectively. In conjunction with the information from the ^{15}N NOESY-HSQC sequential assignment approach, this data allowed unambiguous sequential assignment even for the poorly dispersed N-terminal residues of Z α .

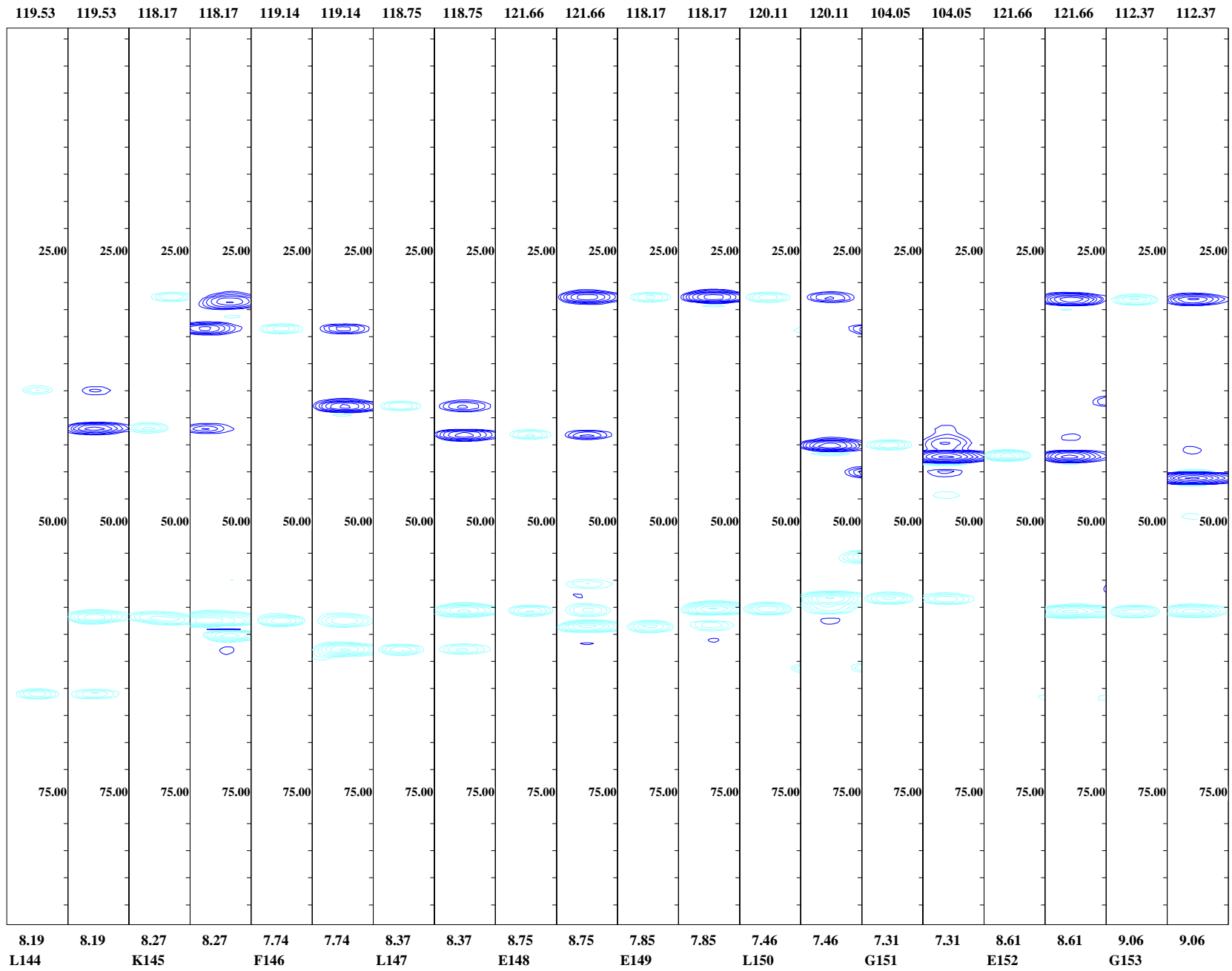


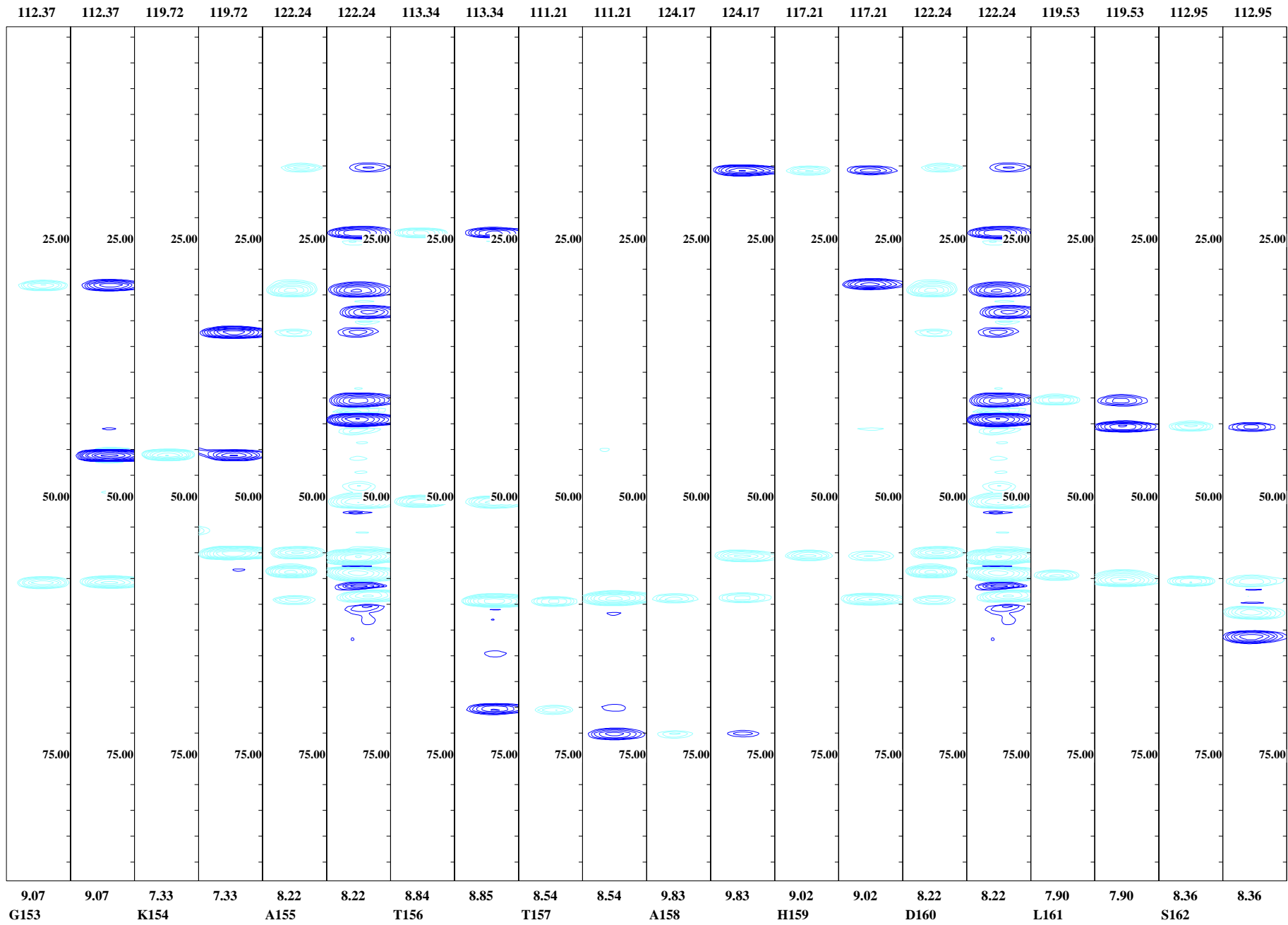


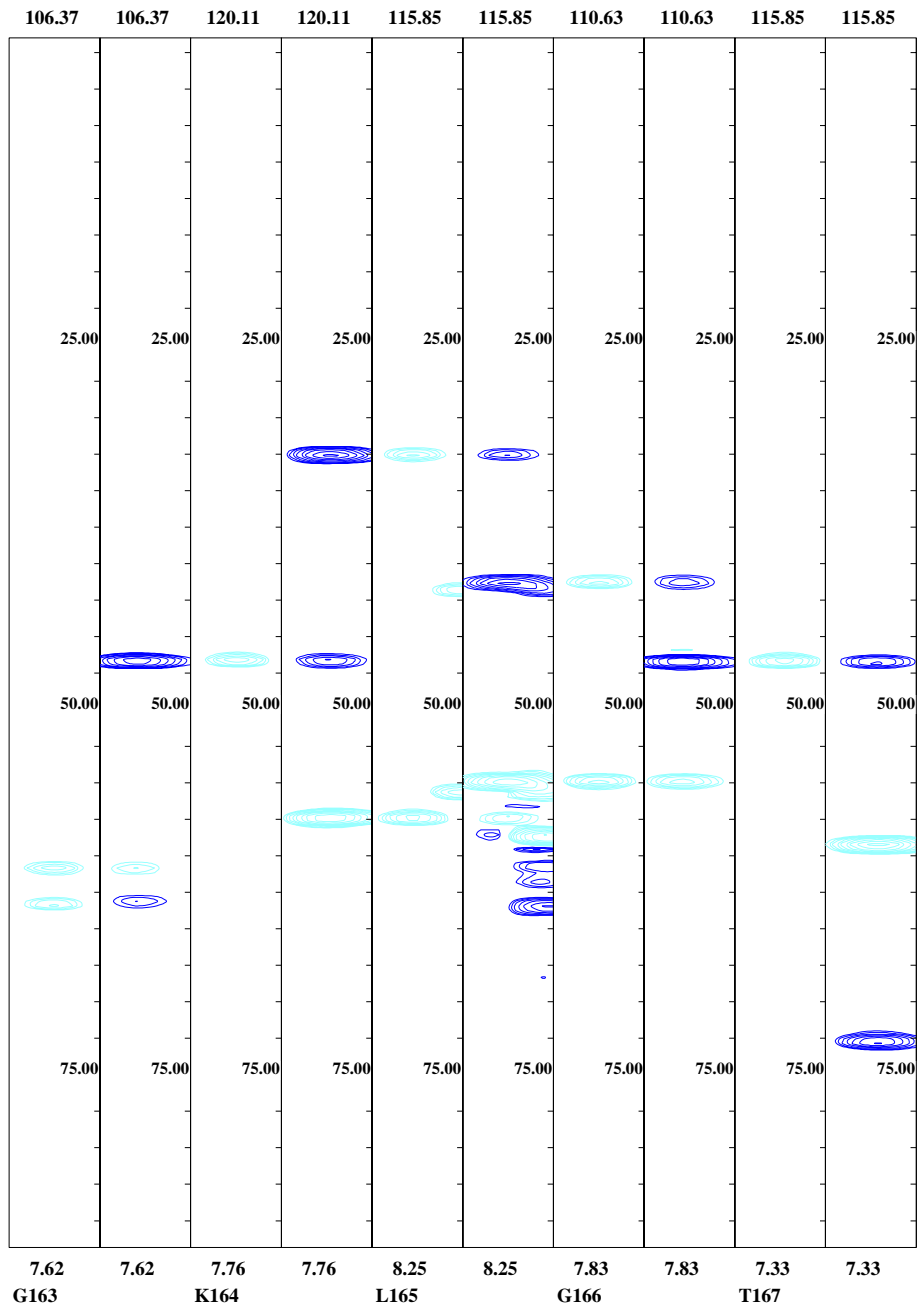
122.24 122.24 116.62 116.62 120.88 120.88 122.04 122.04 120.88 120.88 120.69 120.69 119.91 119.91 118.17 118.17 116.43 116.43 118.95 118.95 120.30 120.30



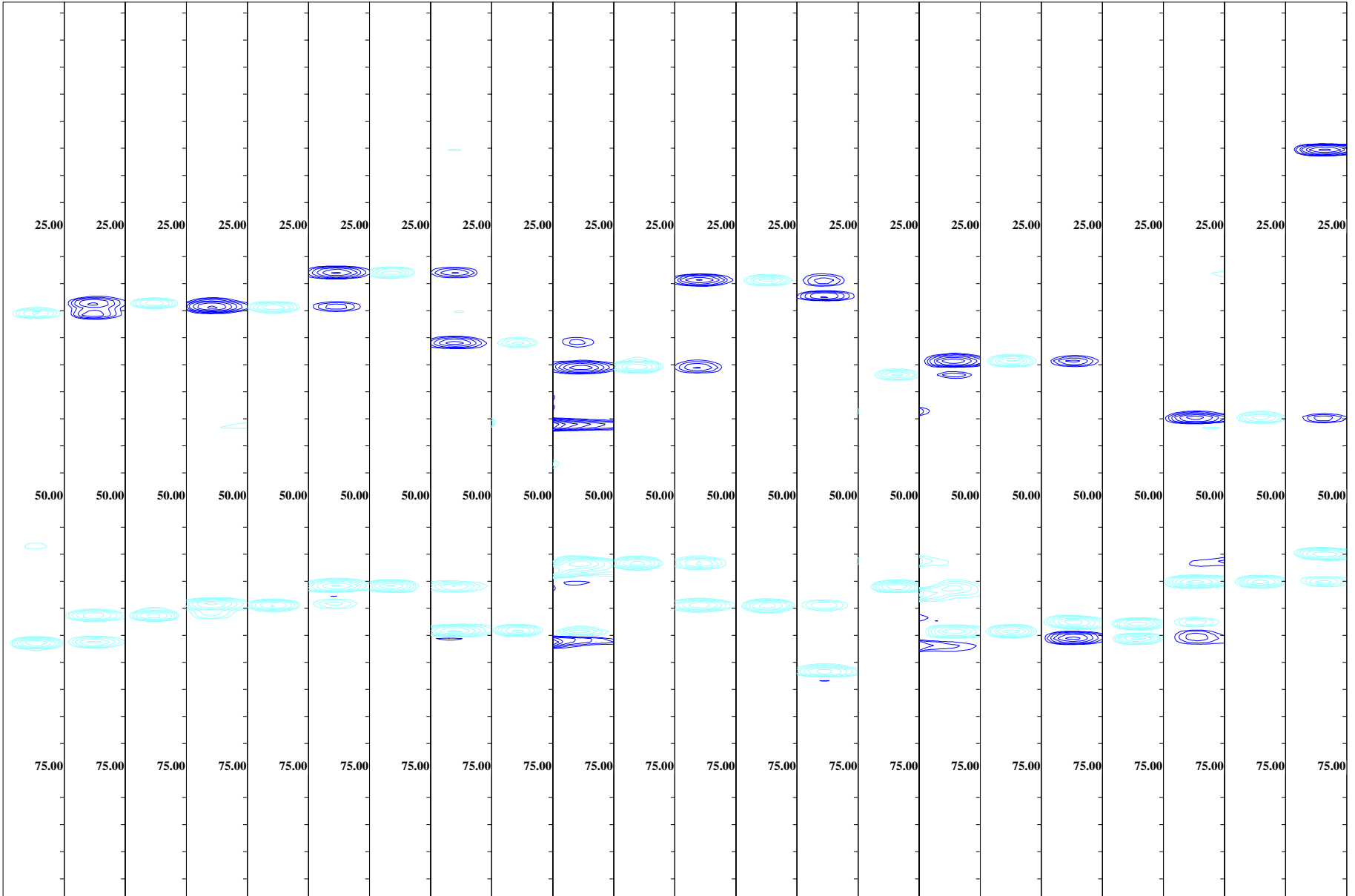
8.22 8.22 8.30 8.30 7.88 7.88 8.02 8.02 8.25 8.25 8.38 8.38 8.42 8.42 8.27 8.27 8.04 8.04 8.01 8.01 7.97 7.97
L133 S134 I135 Y136 Q137 D138 Q139 E140 Q141 R142 I143





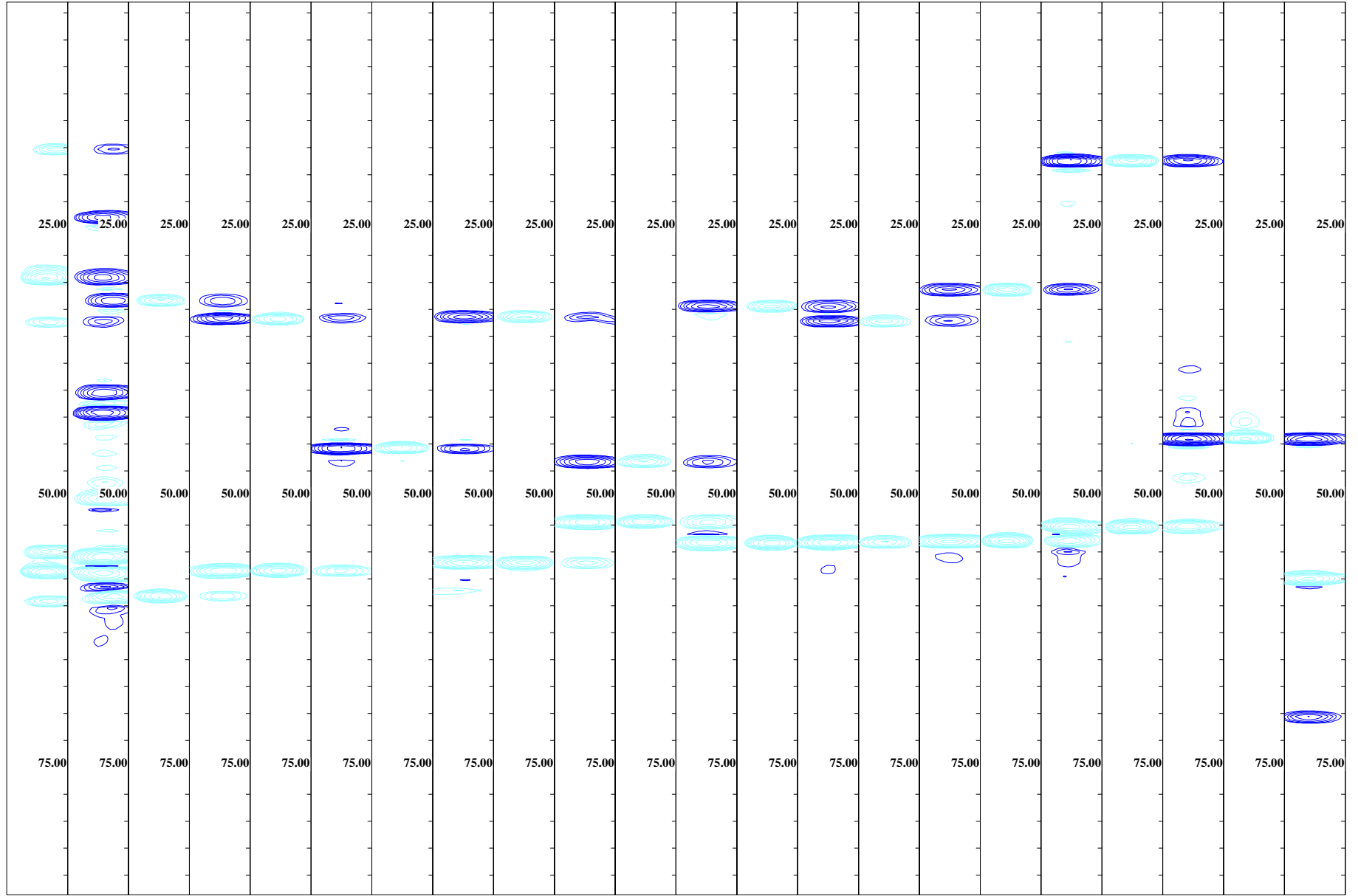


126.30 126.30 117.40 117.40 118.75 118.75 119.53 119.53 117.21 117.21 118.95 118.95 120.30 120.30 115.46 115.46 116.24 116.24 121.07 121.07 123.78 123.78

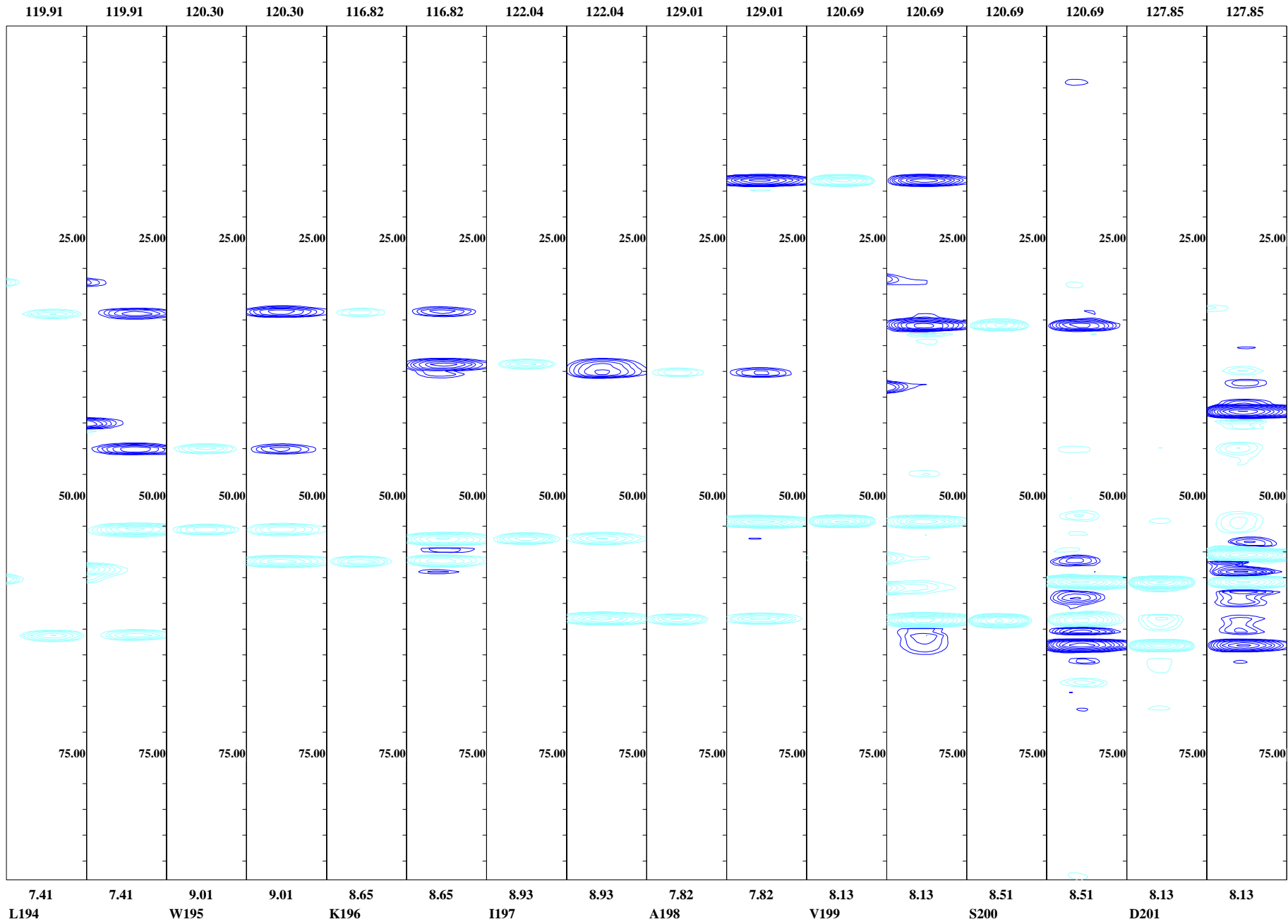


8.97 8.97 8.89 8.89 7.07 7.07 7.74 7.74 8.65 8.65 7.34 7.34 7.58 7.58 8.14 8.14 7.77 7.77 8.67 8.67 8.85 8.85
K169 K170 E171 I172 N173 R174 V175 Y177 S178 L179 A180

122.24 122.24 115.85 115.85 107.53 107.53 115.66 115.66 114.11 114.11 119.33 119.33 124.56 124.56 128.04 128.04 125.33 125.33 107.72 107.72 113.92 113.92



8.23 8.23 7.60 7.60 8.02 8.02 8.02 8.02 6.93 6.93 9.31 9.31 8.36 8.36 9.12 9.12 8.33 8.33 7.79 7.79 8.30 8.30
K181 K182 G183 K184 L185 Q186 K187 E188 A189 G190 T191



Chemical shift assignment list of Z α

The chemical shift table of the Z α domain (residues 119 - 200) from human ADAR1 contains the complete ^1H , ^{15}N and ^{13}C resonance assignment (table 13 and table 14). Residues are numbered according to the sequence of human ADAR1. The serine at the N-terminus and the aspartic acid at the C-terminus are vector-encoded. All chemical shifts are in ppm which were referenced to external DSS. ^{15}N and ^{13}C shifts were indirectly calibrated to the ^1H chemical shift of DSS by using magnetogyric ratios [22]. Atoms are named following the recommendations given in [22] except for methylene ^1H atoms which are numbered '1' and '2' rather than '2' and '3'.

The ^1H and backbone ^{15}N chemical shifts are shown in table 13, and the ^{13}C and side chain ^{15}N chemical shifts (N ϵ , N δ) are shown in table 14. The stereo-specific assignment is arbitrary because the solution of Z α was calculated by floating stereo-specific assignment. If geminal ^1H resonances are degenerate the common chemical shift is given in the first column ($\beta 1$, $\gamma 1$, $\delta 1$ or $\epsilon 1$). The C $\gamma 2$ and C $\delta 2$ resonances of valine and leucine residues are presented in the C δ and C ϵ column, respectively.

table 13 The ^1H chemical shifts of Z α .

residue	H _N	N	H α 1	H β 1	H β 2	H γ 1	H γ 2	H δ 1	H δ 2	H ϵ 1	H ϵ 2	
	S	8.714	117.3	4.846	3.881							
119	P			4.485	1.932	2.333	2.057		3.747	3.880		
120	Q	8.524	121.1	4.331	1.999	2.111	2.407			7.558	6.909	
121	R	8.460	122.8	4.379	1.799	1.902	1.669		3.225		7.255	
122	G	8.517	110.6	4.031	H α 2: 3.983							
123	V	8.091	119.0	4.147	2.125		0.941	0.964				
124	D	8.479	123.6	4.670	2.705	2.759						
125	S	8.290	116.5	4.398	3.880	3.936						
126	L	8.302	123.6	4.363	1.637	1.743	1.672		0.882	0.942		
127	S	8.213	115.5	4.409	3.909							
128	S	8.233	117.5	4.400	3.855							
129	H	8.378	120.0	4.694	3.135	3.250				7.152	8.259	
130	F	8.191	120.9	4.546	3.095	3.152	H ζ : 7.345		7.277		7.383	
131	Q	8.305	121.8	4.243	1.994	2.081	2.319				7.527	6.891
132	E	8.346	121.8	4.217	2.093	2.018	2.326					
133	L	8.211	122.3	4.360	1.613	1.696	1.67		0.88	0.944		
134	S	8.311	116.5	4.385	3.877	3.930						
135	I	7.860	120.9	4.084	1.805		1.061	1.181	0.796	H γ 2: 0.786		
136	Y	8.002	121.9	4.553	2.941	3.171			7.115		6.806	
137	Q	8.250	120.8	4.191	2.108		2.426				6.865	7.552
138	D	8.373	120.6	4.496	2.792							
139	Q	8.419	120.0	4.054	2.035	2.141	2.405	2.453			6.806	7.385

residue	H _N	N	H α 1	H β 1	H β 2	H γ 1	H γ 2	H δ 1	H δ 2	He1	He2	
140	E	8.265	118.2	3.712	1.973	2.266	2.080	2.407				
141	Q	8.034	116.5	3.987	2.174		2.544	2.474			6.891	7.578
142	R	8.005	118.9	3.994	1.874		1.588		3.189		7.377	
143	I	7.979	120.3	3.568	1.828		1.695	0.855	0.699	H γ 2: 0.656		
144	L	8.192	119.6	3.940	1.775	1.598	1.788		0.848			
145	K	8.286	118.3	4.069	1.912		1.522	1.437	1.706		2.98	
146	F	7.748	119.2	4.158	3.145	3.226	H ζ : 7.282		7.118		7.283	
147	L	8.382	118.7	4.078	2.031	1.552	2.031	1.931		1.025	0.822	
148	E	8.742	121.5	3.949	2.132	2.291	2.293	2.552				
149	E	7.847	118.1	4.026	2.022		2.285	2.542				
150	L	7.473	120.1	3.998	1.563	1.782	1.721		0.777	0.886		
151	G	7.330	104.1	4.381	H α 2: 3.751							
152	E	8.609	121.5	4.108	2.033		2.316	2.371				
153	G	9.053	112.3	4.090	H α 2: 3.849							
154	K	7.341	119.8	4.464	1.78		1.245	1.412	1.689		3.044	
155	A	8.211	122.3	5.218	1.328							
156	T	8.845	113.4	5.081	4.100		1.238					
157	T	8.540	111.2	5.223	4.902		1.408					
158	A	9.836	124.2	3.940	1.479							
159	H	9.017	117.2	4.174	3.494	3.225				7.367	8.528	
160	D	8.211	122.3	4.328	2.758	2.910						
161	L	7.912	119.5	3.554	1.104	1.901	0.605		0.53	1.688		
162	S	8.364	113.0	4.134	3.878	3.923						
163	G	7.633	106.3	3.961	H α 2: 3.839							
164	K	7.758	120.1	4.180	1.624	1.637	1.477		1.709		3.056	
165	L	8.246	115.9	4.326	1.570		1.429		0.558	0.644		
166	G	7.847	110.5	3.931								
167	T	7.326	115.9	4.761	3.494		1.226					
168	P			4.365	1.896	2.575	2.150	2.045	3.641	4.002		
169	K	8.959	126.4	3.692	1.906		1.411	1.464	1.783		3.048	3.107
170	K	8.886	117.5	4.180	1.776	1.942	1.416	1.544	1.753		3.040	
171	E	7.085	118.8	4.260	2.004		2.234					
172	I	7.750	119.5	3.517	2.084		1.334	1.042	0.549	H γ 2:0.767		
173	N	8.654	117.2	4.336	2.709				7.442	6.831		
174	R	7.352	118.8	4.051	1.981	2.040	1.615	1.802	3.200	3.277	7.544	
175	V	7.587	120.2	3.725	1.999		0.854	0.966				
176	L	8.559	121.4	3.403	0.972	-0.939	1.313		-0.025	-0.385		
177	Y	8.128	115.6	4.236	3.160	3.091			7.449		6.969	
178	S	7.776	116.2	4.340	4.196	4.106						
179	L	8.660	121.1	4.053	1.2	2.152	1.868		0.795	0.875		
180	A	8.844	123.7	4.630	1.765							
181	K	8.211	122.3	4.199	2.116		1.646	1.565	1.788		3.053	

residue	H _N	N	H α 1	H β 1	H β 2	H γ 1	H γ 2	H δ 1	H δ 2	He1	He2	
182	K	7.599	115.8	4.398	1.883	2.153	1.780	1.590	1.619	1.771	2.963	
183	G	8.027	107.5	4.242	H α 2: 3.964							
184	K	8.023	115.7	4.490	1.784	1.951	1.478		1.7		3.033	
185	L	6.940	114.2	5.227	1.467	1.797	0.841		0.859	0.848		
186	Q	9.313	119.4	4.641	1.881		2.223	2.169			7.627	6.937
187	K	8.355	124.7	4.199	1.092	0.658	0.448	-0.079	1.236	1.355	2.766	2.71
188	E	9.123	128.1	4.447	1.709	1.946	2.071					
189	A	8.325	125.3	4.085	1.355							
190	G	7.789	107.7	4.063	H α 2: 3.842							
191	T	8.293	113.9	4.621	4.1		1.169					
192	P			5.216	2.358	2.598	1.933	2.165	3.553	3.629		
193	P			4.150	1.473	2.029	2.248	2.182	3.808	3.950		
194	L	7.401	120.0	4.850	1.273	1.441	1.566		0.763	0.823		
195	W	9.014	120.3	5.225	2.787	2.928	H δ 1: 7.14 He1: 9.895 He3: 7.176 H ζ 2: 7.152 H ζ 3: 6.631 H η 2: 6.253 Ne1: 128.3					
196	K	8.662	116.8	5.086	1.823		1.402	1.207	1.545		2.826	2.764
197	I	8.936	122.1	4.166	1.857		1.614	1.296	0.965	H γ 2: 1.041		
198	A	7.839	129.1	4.329	1.176							
199	V	8.115	120.6	4.238	2.117		0.978	0.992				
200	S	8.502	120.5	4.544	3.894							
	D	8.127	127.8	4.451	2.709							

table 14 The ^{13}C chemical shifts of $Z\alpha$.

residue		$\text{C}\alpha$	$\text{C}\beta$	$\text{C}\gamma$	$\text{C}\delta$	$\text{C}\epsilon$	$\text{N}\epsilon$, $\text{N}\delta 2$, $\text{C}\gamma 2$
	S	56.66	63.23				
119	P	63.39	32.06	27.37	50.78		
120	Q	55.78	29.48	33.79			$\text{N}\epsilon 2$ 112.8
121	R	56.12	30.88	27.01	43.18		$\text{N}\epsilon$ 84.9
122	G	45.28					
123	V	62.46	32.69	20.24	21.07		
124	D	54.38	41.14				
125	S	58.93	63.58				
126	L	55.79	41.97	26.97	23.12	24.74	
127	S	58.78	63.58				
128	S	58.88	63.56				
129	H	55.75	28.66		119.8	137.8	
130	F	58.63	39.26		131.6	131.6	$\text{C}\zeta$ 131.6
131	Q	56.38	29.29	33.60			$\text{N}\epsilon 2$ 112.3
132	E	56.97	29.81	36.11			
133	L	55.57	42.28	27.07	23.12	24.74	
134	S	59.08	63.51				
135	I	62.48	38.22	27.14	13.18		$\text{C}\gamma 2$ 17.27
136	Y	58.66	38.31		133.2	118.2	
137	Q	57.37	29.24	34.04			$\text{N}\epsilon 2$ 112.0
138	D	55.86	40.95				
139	Q	58.67	29.01	33.74			$\text{N}\epsilon 2$ 110.8
140	E	60.25	29.64	37.42			
141	Q	58.73	28.25	34.08			$\text{N}\epsilon 2$ 112.2
142	R	59.65	30.56	27.89	43.50		$\text{N}\epsilon$ 85.0
143	I	65.57	37.65	30.61	13.81		$\text{C}\gamma 2$ 17.28
144	L	58.59	41.17	27.02	23.62	24.94	
145	K	58.89	31.93	24.87	28.67	41.89	
146	F	61.55	39.17		132.0	131.0	$\text{C}\zeta$ 129.7
147	L	57.95	41.78	28.15	24.24	27.11	
148	E	59.38	29.14	35.6			
149	E	57.75	29.10	36.4			
150	L	56.81	42.75	26.16	23.48	24.96	
151	G	43.76					
152	E	57.99	29.29	35.88			
153	G	45.73					
154	K	55.18	33.84	24.83	28.19	42.49	
155	A	50.25	24.17				
156	T	59.75	70.25	19.09			
157	T	59.58	72.62	21.93			
158	A	55.46	18.19				
159	H	59.63	29.18		120.1	136.3	

residue	C α	C β	C γ	C δ	C ϵ	N ϵ , N δ 2, C γ 2
160	D	57.34	40.36			
161	L	57.74	42.93	26.69	24.53	26.69
162	S	60.93	63.23			
163	G	46.80				
164	K	57.50	32.77	24.89	28.32	41.89
165	L	55.09	41.52	27.82	25.75	23.14
166	G	46.85				
167	T	59.36	72.82	20.82		
168	P	63.29	32.98	27.82	51.76	
169	K	60.84	32.11	25.57	28.95	41.50
170	K	59.84	32.40	24.88	29.31	41.61
171	E	58.05	29.21	35.67		
172	I	62.18	35.69	27.23	10.21	C γ 2 17.97
173	N	56.05	37.95			N δ 2 109.8
174	R	59.87	29.89	27.09	43.40	N ϵ 83.9
175	V	65.88	31.38	23.14	22.61	
176	L	58.11	38.64	25.0	21.79	24.15
177	Y	62.24	37.35		133.4	117.7
178	S	61.34	62.86			
179	L	57.67	42.58	27.18	26.13	23.89
180	A	55.12	17.90			
181	K	59.24	31.88	25.04	29.03	41.84
182	K	56.84	33.54	26.05	29.80	41.69
183	G	45.56				
184	K	56.13	33.41	24.95	28.15	42.16
185	L	52.44	46.78	28.61	23.90	24.84
186	Q	54.23	32.43	33.90		N ϵ 2 112.5
187	K	54.24	33.81	23.85	29.13	41.50
188	E	54.12	30.89	34.80		
189	A	52.81	18.99			
190	G	44.69				
191	T	57.62	70.38	20.56		
192	P	62.82	33.63	24.80	49.90	
193	P	63.22	32.14	27.52	50.61	
194	L	52.93	45.18	27.24	24.13	25.31
195	W	C α : 56.05 C β : 31.91 C δ 1: 126.4 C ϵ 3: 119.0 C ζ 2: 114.3 C ζ 3: 121.5 C η 2: 123.5				
196	K	53.87	37.04	23.13	29.56	41.79
197	I	61.60	37.67	28.42	12.41	C γ 2 17.58
198	A	52.22	19.24			
199	V	61.69	33.22	20.31	21.32	
200	S	58.05	64.14			
	D	55.43	41.57			

HNH α coupling constants of Z α

The HNH α coupling constants (table 15), J(HNHA), of human Z α (residues 119-200) were determined from a 3D ^{15}N -edited HNHA spectrum ($\xi=14\text{ms}$) by the method of Vuister and Bax using integrated diagonal and cross peaks [19]. Apparent coupling constants were multiplied by a factor of 1.11 to correct for H α spin flips [19]. J(HNHA) values smaller than 6 Hz are diagnostic of α -helical secondary structure, while J(HNHA) values larger than 8 Hz are diagnostic of extended chain conformation (β -strand) [22]. The secondary structure information derived from these coupling constants is in good agreement with the high resolution NMR structure of Z α (column „Secondary Structure derived from high resolution NMR structure“). The coupling constants were converted into dihedral phi angles applying the Karplus equation parameterized for proteins [194]. Allowing a tolerance of 30°, no dihedral angle restraint showed violations greater than 2° during structure calculation by dynamic simulated annealing. The coupling constants measured for glycines were not used for structure calculation because no stereo-specific assignment was available for the pair of H α atoms. Empty boxes indicate that the peak volumes could not be determined due to spectral overlap.

table 15 HNH α coupling constants in human Z α

#	residue	J(HNHA) in Hz (± 1)	Secondary structure derived from high resolution NMR structure
119	P	-	
120	Q		
121	R		
122	G		
123	V	6.6	
124	D		
125	S		
126	L	7.5	
127	S	6.4	
128	S	5.9	
129	H	5.0	
130	F	4.9	
131	Q	6.1	
132	E	6.6	
133	L		
134	S		
135	I	6.0	
136	Y	6.9	$\alpha 1$
137	Q	4.7	$\alpha 1$
138	D		$\alpha 1$
139	Q		$\alpha 1$
140	E		$\alpha 1$

141	Q	3.4	α 1
142	R	4.0	α 1
143	I	3.8	α 1
144	L	4.4	α 1
145	K		α 1
146	F		α 1
147	L	3.3	α 1
148	E	3.0	α 1
149	E	5.5	α 1
150	L	4.8	α 1
151	G	8.5; 3.4	
152	E	3.4	
153	G	5.6; 5.6	
154	K	6.7	
155	A		β 1
156	T	9.2	β 1
157	T		β 1
158	A		α 2
159	H	< 3	α 2
160	D		α 2
161	L	3.2	α 2
162	S	3.1	α 2
163	G	5.4; 5.4	α 2
164	K		α 2
165	L	6.9	α 2
166	G		
167	T	8.1	
168	P	-	
169	K	< 3	α 3
170	K	< 3	α 3
171	E	7.5	α 3
172	I		α 3
173	N	2.5	α 3
174	R	3.1	α 3
175	V	5.3	α 3
176	L		α 3
177	Y	< 3	α 3
178	S	4.5	α 3
179	L	3.6	α 3
180	A	3.8	α 3
181	K		α 3
182	K	7.1	α 3
183	G	7.3; 5.7	

184	K		
185	L		$\beta 2$
186	Q	10.0	$\beta 2$
187	K		$\beta 2$
188	E	10.0	$\beta 2$
189	A		
190	G		
191	T	9.7	
192	P	-	
193	P	-	
194	L	8.0	$\beta 3$
195	W	9.2	$\beta 3$
196	K		$\beta 3$
197	I	4.4	$\beta 3$
198	A	6.3	
199	V	8.5	
200	S	9.7	