SUPPORTING INFORMATION:

1H Chemical shifts of conotoxin pl14a

4	4.561	0.000	HA	1
6	3.295	0.000	HB2	1
7	3.062	0.000	HB3	1
21	7.329	0.001	QD	1
27	4.487	0.006	HA	2
29	2.293	0.006	HB2	2
30	1.869	0.002	HB3	2
35	1.994	0.006	QG	2
36	3.773	0.001	HD2	2
37	3.444	0.005	HD3	2
41	8.579	0.001	HN	3
43	4.608	0.004	HA	3
45	1.824	0.005	HB2	3
46	1.760	0.004	HB3	3
51	1.681	0.002	QG	3
55	3.185	0.000	QD	3
69	4.400	0.004	HA	4
73	2.402	0.006	QB	4
77	1.998	0.008	QG	4
78	3.986	0.002	HD2	4
79	3.654	0.002	HD3	4
83	8.652	0.001	HN	5
85	4.090	0.000	HA	5
87	1.861	0.000	HB2	5
88	1.725	0.001	HB3	5
93	1.640	0.001	QG	5
109	8.290	0.001	HN	6
111	4.083	0.002	HA	6
113	1.859	0.007	HB	6
114	0.722	0.003	QG2	6
120	1.135	0.002	HG12	6
123	0.759	0.001	QD1	6
130	7.960	0.001	HN	7
132	4.462	0.005	HA	7
134	3.099	0.005	HB2	7
135	2.840	0.004	HB3	7
140	8.161	0.003	HN	8
142	4.361	0.003	HA	8
144	2.878	0.008	HB2	8
145	2.827	0.004	HB3	8
149	7.720	0.001	HD21	8
154	7.660	0.000	HN	9
156	4.162	0.001	HA	9
160	1.730	0.003	QB	9
162	1.613	0.006	HG	9
163	0.890	0.004	QD1	9
164	0.846	0.000	QD2	9
176	8.384	0.002	HN	10
178	3.946	0.002	HA	10
179	1.217	0.004	QB	10
186	8.488	0.002	HN	11
188	4.557	0.004	HA	11
190	3.316	0.002	HB2	11
191	2.957	0.004	HB3	11
196	7.577	0.001	HN	12
198	4.198	0.003	HA	12

202	1.924	0.002	QB	12
206	1.734	0.001	QG	12
222	7.887	0.003	HN	13
224	4.418	0.004	HA	13
225	1.491	0.006	QB	13
232	7.787	0.001	HN	14
234	4.182	0.001	HA1	14
235	3.993	0.001	HA2	14
239	7.862	0.002	HN	15
241	4.633	0.001	HA	15
243	2.145	0.001	HB	15
244	0.901	0.006	QG2	15
250	1.441	0.004	HG12	15
251	1.173	0.001	HG13	15
253	0.957	0.004	QD1	15
260	8.632	0.002	HN	16
262	3.912	0.000	HA1	16
263	3.492	0.003	HA2	16
267	8.631	0.003	HN	17
269	4.326	0.003	HA	17
273	3.149	0.005	QB	17
284	7.690	0.002	HN	18
286	3.905	0.005	HA	18
288	1.523	0.005	HB2	18
289	1.395	0.005	HB3	18
294	0.927	0.000	QG	18
298	1.080	0.000	QD	18
302	2.880	0.000	QE	18
306	7.584	0.000	QZ	18
309	7.413	0.003	HN	19
311	4.553	0.002	HA	19
315	2.245	0.007	QB	19
328	6.726	0.001	QE	19
329	6.955	0.002	QD	19
334	4.191	0.002	HA	20
336	2.282	0.005	HB2	20
337	1.967	0.006	HB3	20
342	2.030	0.005	QG	20
343	3.636	0.003	HD2	20
344	3.426	0.006	HD3	20
348	6.754	0.002	HN	21
350	4.397	0.003	HA	21
352	3.261	0.122	HB2	21
353	3.173	0.122	HB3	21
367	7.152	0.001	QD	21
368	7.377	0.003	QE	21
371	7.741	0.003	HN	22
373	4.692	0.004	HA	22
375	2.947	0.005	HB2	22
376	2.845	0.009	HB3	22
381	8.143	0.003	HN	23
383	4.391	0.000	HA	23
387	3.254	0.002	QB	23
398	8.676	0.000	HN	24
400	4.672	0.004	HA	24
402	3.181	0.004	HB2	24
403	2.874	0.001	HB3	24
408	8.772	0.001	HN	25
410	4.241	0.000	HA	25
412	1.837	0.000	HB2	25
413	1.772	0.000	HB3	25
416	1.680	0.000	HG2	25
417	1.629	0.000	HG3	25
422	3.173	0.002	QD	25

Oligonucleotide Primers

3' RACE
1st amplification: Q_0 (*1*) and Primer 033 (derived from pl14a sequence …GIGHKYP…)
Primer 033: GGNATHGGNCAYAAATATC
2nd amplification: Q_1 (*1*) and Primer 031 (derived from pl14a sequence …HKYPFCHC..)
Primer 031: CAYAARTAYCCNTTYTGYCAYTG

5' RACE
1st amplification: SMART RACE universal primer and Primer 041 (derived from the 3'UTR) with the sequence: GCGTCATTGGAATGAGTATGCCGTC
2nd amplification: SMART RACE nested primer and Primer 042 (derived from the 3'UTR and upstream of Primer 041): CCGCGTCCCGTTTCCCTCTGCAATG

J-superfamily Screening Primers
Primer 041 (above) and Primer 045 (derived from the sequence obtained in the 5' RACE)
Primer 045: CCATGCCGTCTGTTCGGTCTGTG

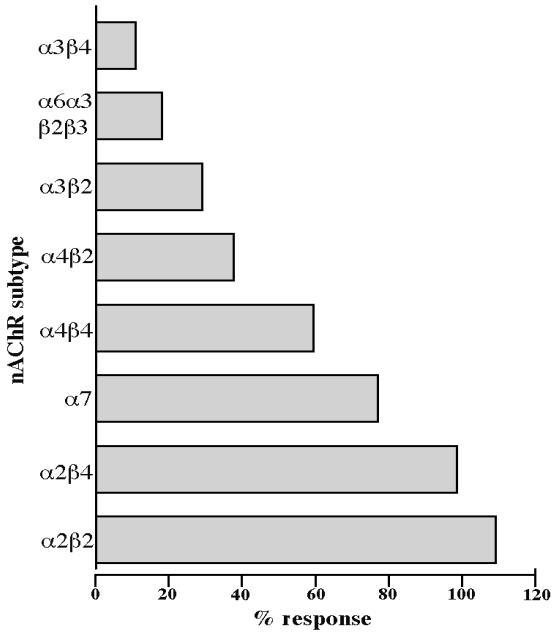

Figure 1. The effect of 10μM pl14a on the responses of neuronal nAChR subtypes expressed in oocytes compared to blank controls. The preparation of oocytes and the conditions used in the clamping experiments were as described in Materials and Methods.

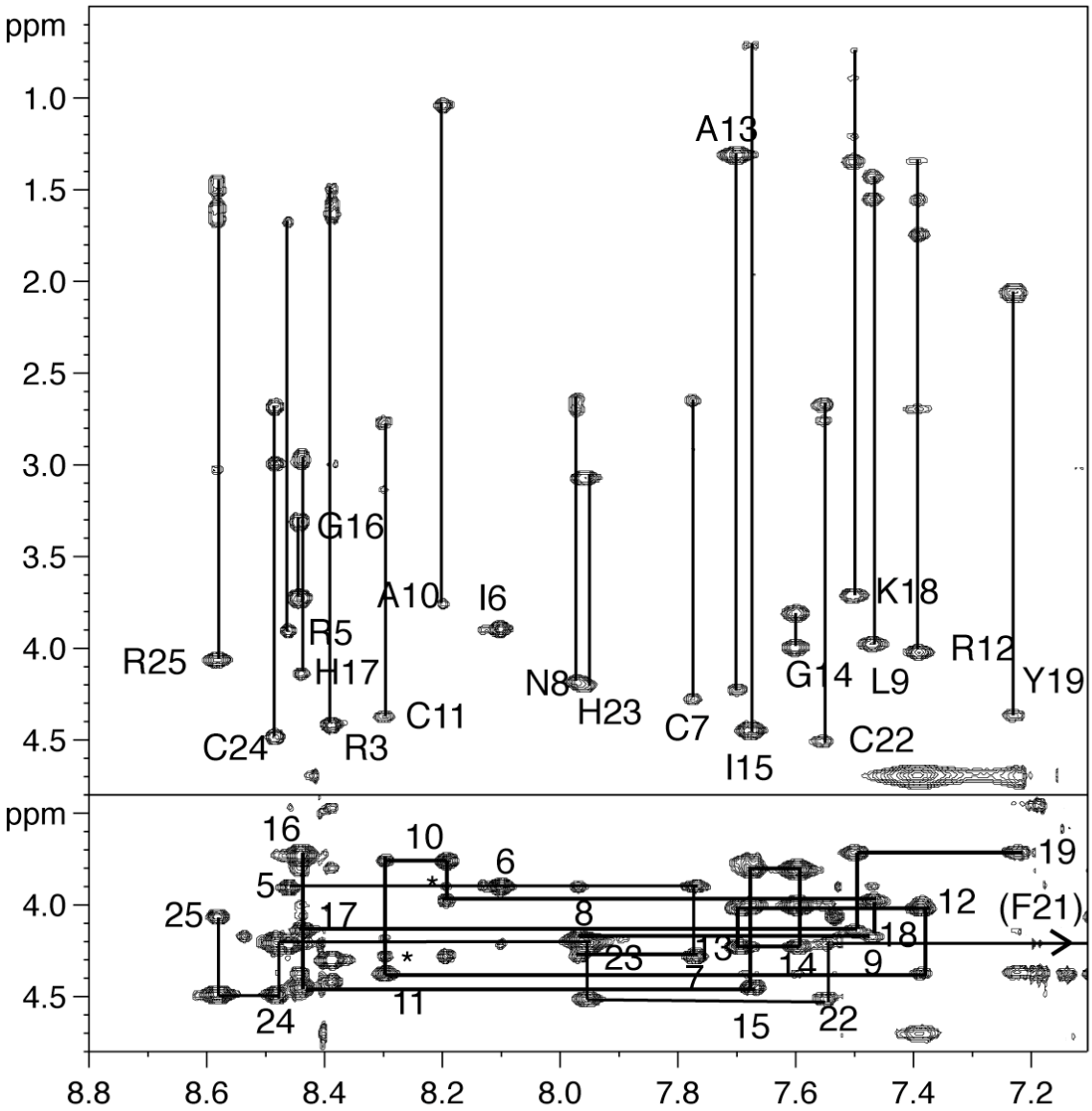

Figure 2. *NMR spectra of pl14a*. Regions of the TOCSY (top) and NOESY (bottom) spectra of pl14a recorded on a Bruker 600 MHz spectrometer at 290 K. The amino acids are labelled with their one letter code and residue number in the TOCSY spectrum and with the residue number alone in the NOESY spectra for clarity. Residue 21 is not shown in this expansion as it is shifted upfield to 6.7 ppm.

The structure calculations suggest the presence of an α-helix over residues 6-12 and 3_{10}-helix over residues 15-17 and 20-22. The asterisks highlight the i,i+4 NOEs between 6HA – 10 HN and 7HA- 11HN. dαN(i,i+4) NOEs help distinguish α and 3_{10} helices as they are present in the former but not the latter (Wuthrich, NMR of proteins and nucleic acids p 127).

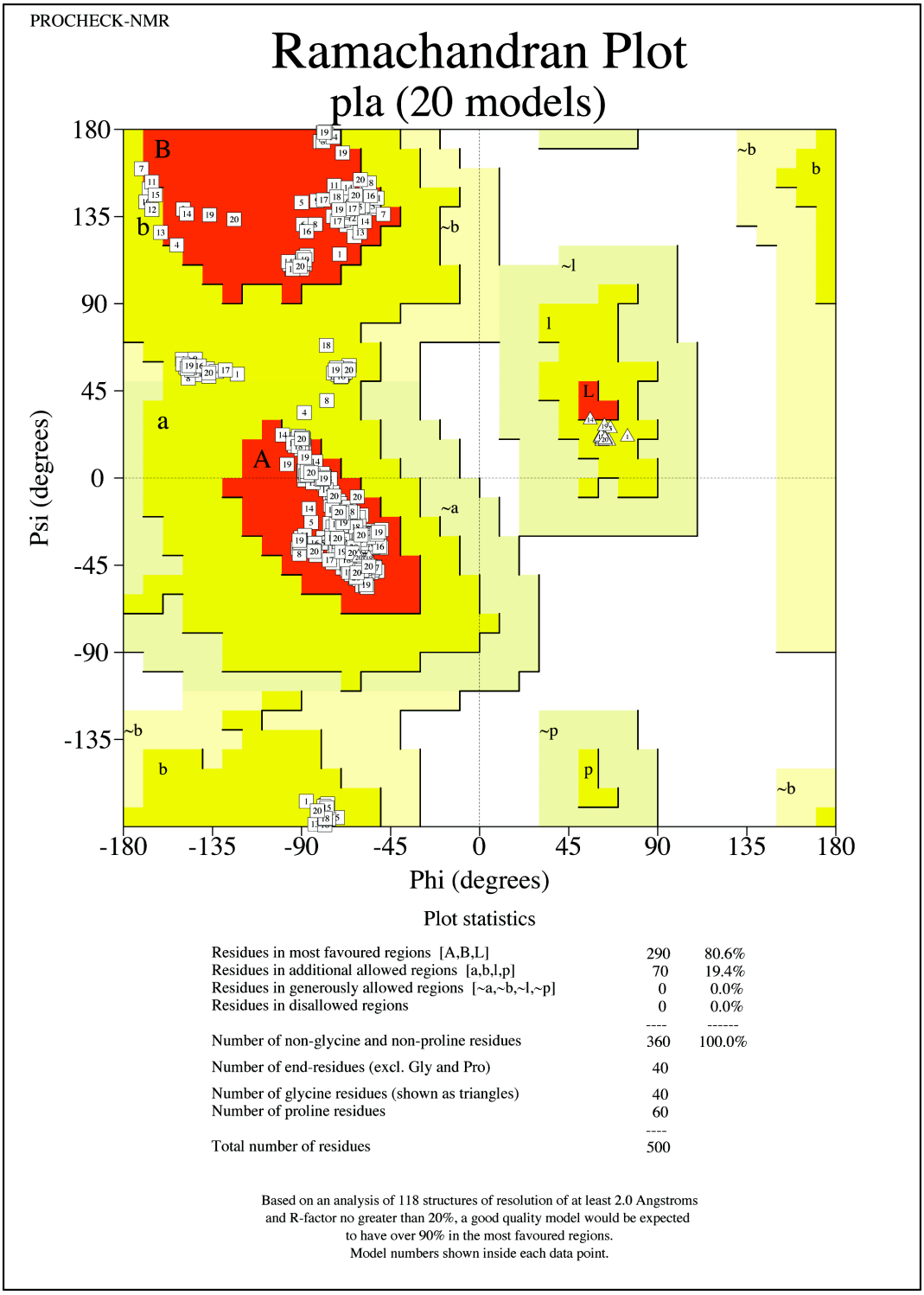

Figure 4. Ramachandran plot of the 20 lowest energy structures of pl14a

REFERENCE

(1) Frohman, M. A. (1990) RACE: rapid amplification of cDNA ends, in *PCR Protocols* (Innis, M. A., Ed.) pp 28-45, Academic Press, San Diego, CA.