Supplementary information file

Beyond retigabine: design, synthesis, and pharmacological characterization of a potent and chemically-stable neuronal Kv7 channel activator with anticonvulsant activity

Simona Musella,^{‡,#} Lidia Carotenuto,^{¶,#}, Nunzio Iraci,^{T,#} Giulia Baroli,[¶] Tania Ciaglia,[‡] Piera Nappi,[¶] Manuela Giovanna Basilicata^{‡,}, Emanuela Salviati[‡], Vincenzo Barrese,[¶] Vincenzo Vestuto,[‡] Giuseppe Pignataro,[¶] Giacomo Pepe,[‡] Eduardo Sommella,[‡] Veronica Di Sarno,[‡] Michele Manfra,[†] Pietro Campiglia,[‡] Isabel Gomez Monterrey,[¥] Alessia Bertamino,[‡] Maurizio Taglialatela,^{¶,*} Carmine Ostacolo, ^{¥,*} and Francesco Miceli[¶].

[‡] Department of Pharmacy, University of Salerno, Via G. Paolo II 132, 84084, Fisciano, Salerno, Italy

[¶] Department of Neuroscience, Reproductive Sciences and Dentistry, University Federico II of Naples, Via Pansini, 5, 80131, Naples, Italy

^T Department of Chemical, Biological, Pharmaceutical and Environmental Sciences (CHIBIOFARAM), University of Messina, Viale Ferdinando Stagno d'Alcontres 31, 98166, Messina, Italy

Department of Science, University of Basilicata, Via dell'Ateneo Lucano 10, 85100 Potenza, Italy

[¥] Department of Pharmacy, University Federico II of Naples, Via D. Montesano 49, 80131, Naples, Italy

*Corresponding authors (Maurizio Taglialatela: mtaglial@unina.it; Carmine Ostacolo: ostacolo@unina.it)

[#]Equal contribution

Table of content:

1.	NMR	spectra	and	HPLC	traces	of	synthesized
	compounds	5	•••••			••••••	S3-S86
2.	Table S1.Lighting	Photoinduced	degradation	of retigabine	(RET) and	its analogu	es under UV S87
	Figures S8	5- S92: HPLC t	races of selec	cted compound	s at 550 nm.	•••••	S88-S95
3.	Figure	S93:	Sequence	alignmen	it of	Kv7	channels
	•••••	•••••		•••••	•••••	•••••	

	Figure S94: Ligand interaction of Kv7.2 in complex with retigabine, 23a and
	24a
	TableS2.Distancesbetweenretigabine,23aand24aandselectedKv7.2
	residues
	Figure S95. Ligand interaction diagram of Kv7.2 in complex with
	42
	Table S3. Average distances between retigabine, 42 and selected Kv7.2 residues
4.	Figure S96. HPLC chormatograms of compound 60 solubilized in saline buffer at different
	time points
5.	Figure S97. Plasma concentration-time curves after a single-dose of Retigabine (3mg/Kg) or
	compound 60 (0,3 mg/Kg) injected i.p in rats S100
6.	Figure S99. Pharmacological characterization of CHO stably expressing Kv7.2+Kv7.3
	channels



Figure S1: ¹H NMR spectra of derivative 2



Figure S2: DEPT NMR spectra of derivative 2



Figure S3: HPLC trace of derivative 2



Figure S4:¹H NMR spectra of derivative 13



Figure S5: DEPT NMR spectra of derivative 13





Figure S7: ¹H NMR spectra of derivative 14



Figure S8:¹³C NMR spectra of derivative 14



Figure S9: HPLC trace of derivative 14



Figure S10: ¹H NMR spectra of derivative 15



Figure S11: DEPT NMR spectra of derivative 15



Figure S12: HPLC trace of derivative 15



Figure S13: ¹H NMR spectra of derivative 16



Figure S14: DEPT NMR spectra of derivative 16



Figure S15: HPLC trace of derivative 16



Figure S16: ¹H NMR spectra of derivative 17



Figure S17: DEPT NMR spectra of derivative 17



Figure S18: HPLC trace of derivative 17



Figure S19: ¹H NMR spectra of derivative 18



Figure S20: DEPT NMR spectra of derivative 18



Figure S21: HPLC trace of derivative 18



Figure S22: ¹H NMR spectra of derivative 19



Figure S23: DEPT NMR spectra of derivative 19



Figure S24: HPLC trace of derivative 19



Figure S25: ¹H NMR spectra of derivative 20



Figure S26: DEPT NMR spectra of derivative 20



S-29



Figure S28: ¹H NMR spectra of derivative 23



Figure S29: DEPT NMR spectra of derivative 23





Figure S31: ¹H NMR spectra of derivative 24

S-33



Figure S32: DEPT NMR spectra of derivative 24



Figure S33: HPLC trace of derivative 24



Figure S34: ¹H NMR spectra of derivative 25


Figure S35: DEPT NMR spectra of derivative 25





Figure S37: ¹H NMR spectra of derivative 26



Figure S38: DEPT NMR spectra of derivative 26



Figure S39: HPLC trace of derivative 26



Figure S30: ¹H NMR spectra of derivative 27



Figure S41: DEPT NMR spectra of derivative 27



S-44



Figure S43: ¹H NMR spectra of derivative 28



Figure S44: ¹³C NMR spectra of derivative 28



Figure S45: HPLC trace of derivative 28



Figure S46: ¹H NMR spectra of derivative 31



Figure S47: DEPT NMR spectra of derivative 31



Figure S48: HPLC trace of derivative 31



Figure S49: ¹H NMR spectra of derivative 41



Figure S50: DEPT NMR spectra of derivative 41



Figure S51: HPLC trace of derivative 41



Figure S52: ¹H NMR spectra of derivative 42



Figure S53: DEPT NMR spectra of derivative 42



Figure S54: HPLC trace of derivative 42



Figure S55: ¹H NMR trace of derivative **43**



Figure S56: DEPT NMR spectra of derivative 43



Figure S57: HPLC trace of derivative 43



Figure S58: ¹H NMR spectra of derivative 47



Figure S59: DEPT NMR spectra of derivative 47



Figure S60: HPLC trace of derivative 47



Figure S61: ¹H NMR spectra of derivative 51



Figure S62: DEPT NMR spectra of derivative 51



Figure S63: HPLC trace of derivative 51



Figure S64: ¹H NMR spectra of derivative 52



Figure S65: DEPT NMR spectra of derivative 52



Figure S66: HPLC trace of derivative 52



Figure S67:¹H NMR spectra of derivative 57



Figure S68: DEPT NMR spectra of derivative 57



Figure S69: HPLC trace of derivative 57



Figure S70: ¹H NMR spectra of derivative 59


Figure S71: DEPT NMR spectra of derivative 59



Figure S72: HPLC trace of derivative 59



Figure S73: ¹H NMR spectra of derivative 60



Figure S74: DEPT NMR spectra of derivative 60



Figure S75: HPLC trace of derivative 60



Figure S76: ¹H NMR spectra of derivative 67



Figure S77: DEPT NMR spectra of derivative 67



Figure S78: HPLC trace of derivative 67



Figure S79: ¹H NMR spectra of derivative 68



Figure S80: DEPT NMR spectra of derivative 68



Figure S81: HPLC trace of derivative 68



Figure S82:¹H NMR spectra of derivative 71



Figure S83: DEPT NMR spectra of derivative 71



Figure S84: HPLC trace of derivative 71

Compound	% Degradation (3h, UV)	Dimers Formation
RET	61.3±0.1	Yes
13	30.6 ± 2.2	Yes
14	73.2±0.4	Yes
17	79.8 ± 4.2	Yes
19	64.8 ± 0.9	Yes
23	97.7 ± 1.0	No
24	79.8 ± 4.2	No
41	19.5±4.7	Yes
43	98.4±0.2	Yes
52	74.9 ± 0.1	Yes
25	63.3±2.8	No
26	99.5±0.1	No
60	34.8 ± 1.8	No

Table S1. Photoinduced degradation of retigabine (RET) and its analogues under UV Lighting.Results are expressed as percentage of degradation \pm SD.



Figure S85: A) HPLC traces of retigabine at 550 nm together with picture of the clear sample vial at T_0 ; B) HPLC traces of retigabine at 550 nm 3h after exposition to light together with picture of the oxidized sample vial



Figure S86: HPLC traces of compound 18 at 550 nm 3h after exposition to light together with picture of the oxidized sample vial



Figure S87: HPLC traces of compound 19 at 550 nm 3h after exposition to light together with picture of the oxidized sample vial



Figure S88: HPLC traces of compound 25 at 550 nm 3h after exposition to light together with picture of the clear sample vial



Figure S89: HPLC traces of compound 52 at 550 nm 3h after exposition to light together with picture of the oxidized sample vial



Figure S90: HPLC traces of compound 17 at 550 nm 3h after exposition to light together with picture of the oxidized sample vial



Figure S91: HPLC traces of compound 26 at 550 nm 3h after exposition to light together with picture of the clear sample vial



Figure S92: HPLC traces of compound 60 at 550 nm 3h after exposition to light together with picture of the clear sample vial

	2	25 236 2	240 St	5
hKv7.2	ILRMIRMDRRGGTWKLLGS	VYAHSKELVTA <mark>W</mark> YI	G <mark>F</mark> LCLILASFLVYLAEK	GE 257
hKv7.4	ILRMVRMDRRGGTWKLLGS	VYAHSKELITA <mark>W</mark> YI	G <mark>F</mark> LVLIFASFLVYLAEKI	A 263
hKv7.5	ILRMVRMDRRGGTWKLLGS\	VYAHSKELITA <mark>W</mark> YI	G <mark>F</mark> LVLIFSSFLVYLVEKI	A 291
hKv7.3	ILRMLRMDRRGGTWKLLGSA	ICAHSKELITA <mark>W</mark> YI	G <mark>F</mark> LTLILSSFLVYLVEKI	VPEVDAQG 293
hKv7.1	ILRMLHVDRQGGTWRLLGS	VFIHRQELITT <mark>L</mark> YI	G <mark>F</mark> LGLIFSSYFVYLAEKI	AVN 289
				_
			304	
	Pore helix	Filter	304 303 302 30	05 312 S6
hKv7.2	Pore helix	Filter	304 303 302 30 NGR <mark>LLAATFTLIG<mark>VSFF</mark>A</mark>	05 312 S6 Alpagi <mark>l</mark> gsgfal 318
hKv7.2 hKv7.4	Pore helix	Filter TTTIGYGDKYPQTW TTTIGYGDKTPHTW	304 302 30 NGR <mark>LLAATFTLIGVSFF</mark> LGRVLAAGFALLG <mark>ISFF</mark>	05 312 S6 Alpagi <mark>l</mark> gsgfal 318 Alpagi <mark>l</mark> gsgfal 324
hKv7.2 hKv7.4 hKv7.5	Pore helix	Filter TTTIGYGDKYPQTW TTTIGYGDKTPHTW TTTIGYGDKTPLTW	304 302 30 NGRLLAATFTLIGVSFF LGRVLAAGFALLGISFF LGRLLSAGFALLGISFF	05 312 S6 ALPAGILGSGFAL 318 ALPAGILGSGFAL 324 ALPAGILGSGFAL 352
hKv7.2 hKv7.4 hKv7.5 hKv7.3	Pore helix	Filter LTTIGYGDKYPQTW LTTIGYGDKTPHTW LTTIGYGDKTPLTW LATIGYGDKTPKTW	304 303 NGRLLAATFTLIGVSFED LGRVLAAGFALLGISFF LGRLLSAGFALLGISFF EGRLIAATFSLIGVSFF	05 312 SG ALPAGILGSGFAL 318 ALPAGILGSGFAL 324 ALPAGILGSGFAL 352 ALPAGILGSGLAL 357

Figure S93. Sequence alignment of the S5, S6 and the S5-S6 intervening linker forming the pore domain of the indicated Kv subunits (www.ebi.ac.uk/Tools/psa/). Numbers above the sequences indicate the residues interacting with retigabine, **23a** and **24a**.





Figure S94. Ligand interaction diagram of 120ns-long MD simulations of Kv7.2 in complex with retigabine (A), **23a** (B) and **24a** (C). Only residues interacting with the ligand for at least 12ns out of 120ns of MD simulation time are shown. Hydrophobic residues are depicted in green, polar ones in cyan. H-bonds are represented by magenta arrows (dashed when side chain atoms are involved); green solid lines represent π - π interactions.

Compound	V225	F304	L312
Retigabine	6.59±0.59 Å	3.83±0.42 Å	4.52±0.38 Å
23a	4.21±0.49 Å	4.17±0.46 Å	3.85±0.32 Å
24a	4.78±0.35 Å	3.80±0.34 Å	3.88±0.24 Å

Table S2. Average distances between ligands retigabine, **23a** and **24a** and Kv7.2 residues V225, F304 and L312. Minimum distances between ligands and protein atoms are averaged over 120ns-long MD simulations and are reported together with their standard deviations. For the protein, side chain heavy atoms only have been considered, while for the ligands were considered only the heavy atoms at N1 (excluding amide moiety atoms).



Figure S95. Ligand interaction diagram of 120ns-long MD simulations of Kv7.2 in complex with **42**. Only residues interacting with the ligand for at least 12ns out of 120ns of MD simulation time are shown. Hydrophobic residues are depicted in green, polar ones in cyan. H-bonds are represented by magenta arrows (dashed when side chain atoms are involved); green solid lines represent π - π interactions.

Compound	F240	L272	F305
Retigabine	5.34±0.48 Å	6.57±0.63 Å	6.12±0.34 Å
42	5.13±0.45 Å	7.60±0.79 Å	6.96±0.58 Å

Table S3. Average distances between ligands retigabine and **42** and Kv7.2 residues F240, L272 and F305. Distances between ligands and protein atoms are averaged over 120ns-long MD simulations and are reported together with their standard deviations. Distances have been calculated between residues side chain atoms centroids and the centroid of each ligand terminal phenyl group.



Figure S96. HPLC chromatograms at different time points showing stability of compound 60 solubilized in saline buffer



Figure S97. Plasma concentration-time curves after a single-dose of Retigabine (3mg/Kg) or compound 60 (0,3 mg/Kg) injected i.p in rats. Values are represented as mean with \pm SD (n=3)



Figure S98. Pharmacological characterization of CHO cells expressing Kv7.2/Kv7.3 channels. (A) Representative current traces from CHO cells transiently- or stably-expressing Kv7.2/Kv7.3 channels. (B) Current density calculated at 0 mV from CHO cells transiently- (CTL) or stably-expressing Kv7.2/Kv7.3 (Clone 5) channels. (C) Current inhibition induced by application of 3 mM tetraethylammonium (TEA).