

Pyrrolone Derivatives as Intracellular Allosteric Modulators for Chemokine Receptors: Selective and Dual-Targeting Inhibitors of CC Chemokine Receptors 1 and 2

Natalia V. Ortiz Zacarías, Jacobus P. D. van Veldhoven, Laura Portner, Eric van Spronsen, Salviana Ullo, Margo Veenhuizen, Wijnand J. C. van der Velden, Annelien J. M. Zweemer, Roy M. Kreekel, Kenny Oenema, Eelke B. Lenselink, Laura H. Heitman, Adriaan P. IJzerman

Table of contents:

- Figure S1. Equilibrium and Kinetic characterization of [³H]-CCR2-RA-[R] in U2OS-CCR1 and U2OS-CCR2.
- Figure S2. Sequence alignment of key residues in hCCR1 and hCCR2b.
- Figure S3. Characterization of selected compounds as inverse agonists using a [³⁵S]GTP γ S binding assay.
- Figure S4. ¹H NMR spectrum of compound **43**
- Table S1. Characterization of [³H]CCR2-RA-[R] in U2OS-CCR1 and U2OS-CCR2.
- Table S2. Inhibition of [³⁵S]GTP γ S binding assay by compounds **37**, **39**, **41** and **43** in U2OS-CCR1, in absence of CCL3.

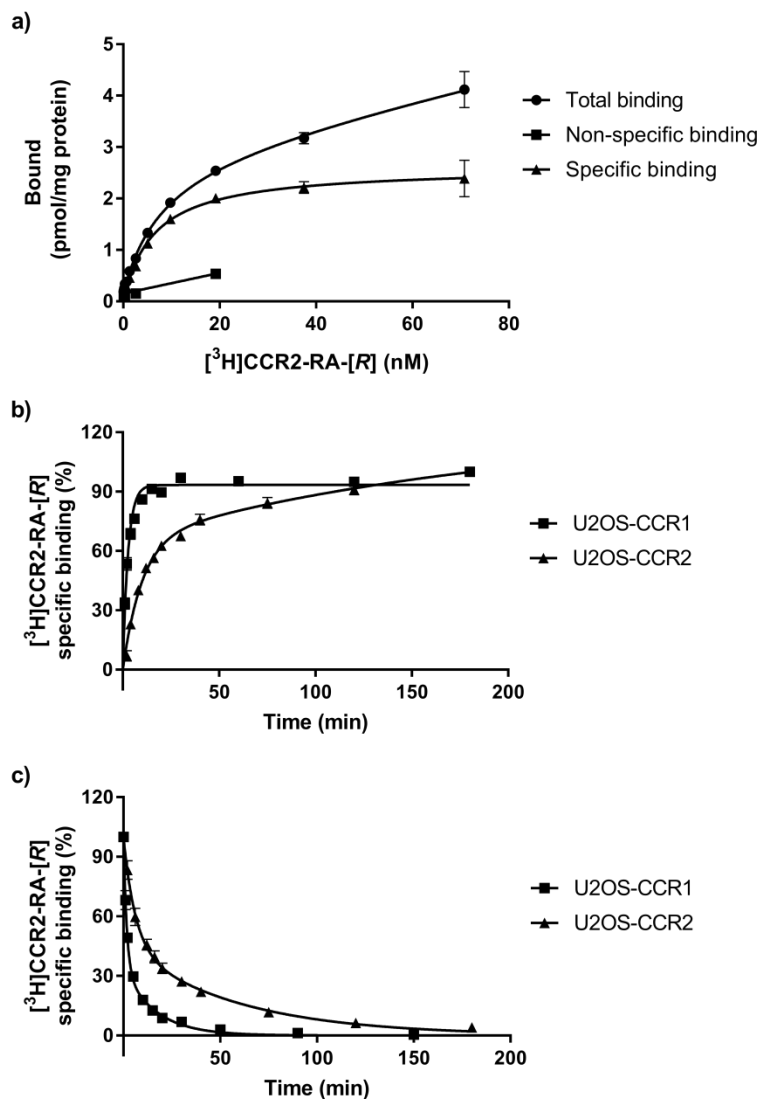


Figure S1. (a) Saturation binding of 0.05 – 70 nM $[^3\text{H}]\text{-CCR2-RA-[R]}$ to U2OS-CCR2 at 25°C, in absence (total binding) or presence (non-specific binding) of 10 μM JNJ-27141491. (b) Association kinetics of 6 nM $[^3\text{H}]\text{-CCR2-RA-[R]}$ to U2OS-CCR1 (■) and U2OS-CCR2 (▲) at 25°C. In both CCR1 and CCR2, data were best fitted using a two-phase association function. (c) Dissociation kinetics of 6 nM $[^3\text{H}]\text{-CCR2-RA-[R]}$ from U2OS-CCR1 (■) and U2OS-CCR2 (▲) at 25°C. In both CCR1 and CCR2, data were best fitted using a two-phase exponential decay function. For all experiments data shown are mean \pm SEM of at least three experiments performed in duplicate. See Supplementary Table 1 for pK_D , B_{max} , and rate constants.

	TM1			TM2			TM3			TM6						TM7		H8				
B&W Number	1x53	1x56	1x57	2x39	2x40	2x43	3x46	3x50	3x53	6x30	6x32	6x33	6x34	6x36	6x37	6x40	7x53	7x56	8x47	8x48	8x49	8x50
hCCR2b	V	I	L	T	D	L	L	R	A	R	R	A	V	V	I	I	Y	V	G	E	K	F
hCCR1	V	V	L	T	S	L	L	R	A	K	K	A	V	L	I	I	Y	V	G	E	R	F

Figure S2. Sequence conservation of the key residues involved in the intracellular binding of CCR2-RA-[R] in CCR2,¹ as obtained by sequence alignment of human CCR1 and human CCR2b using the “Structure-based alignment” tool and the “Similarity search” tool of the GPCR database (GPCRdb, <http://www.gpcrdb.org>).² The residues are numbered according to the structure-based Ballesteros-Weinstein system,² which corresponds to the system used by the GPCRdb. Different amino acids in both CCR1 and CCR2 are highlighted.

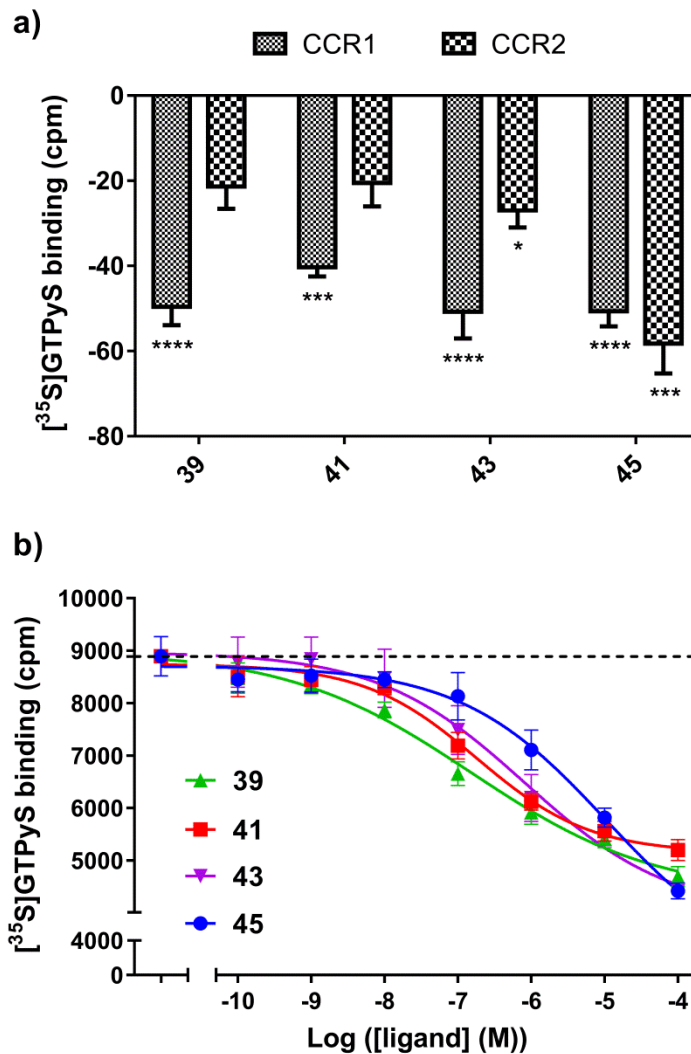


Figure S3. Compounds behave as inverse agonists in CCR1. (a) Maximal inhibition of CCL2 or CCL3-induced $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding achieved by the highest concentration tested of compounds **39**, **41**, **43** and **45** in U2OS-CCR1 (100 μM) and U2OS-CCR2 (**45** at 100 μM , **39**, **41**, **43** at 10 μM). One-way ANOVA with Dunnett's post-hoc test was performed to compare the maximal inhibition against basal $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding in CCR1 or CCR2. Significant differences are displayed as *, $p < 0.05$; ***, $p < 0.001$; and ****, $p < 0.0001$. (b) Inhibition of basal $[^{35}\text{S}]\text{GTP}\gamma\text{S}$ binding in absence of agonist CCL3 by compounds **39**, **41**, **43** and **45** in U2OS-CCR1. The level of basal activity in U2OS-CCR1 is indicated by a dashed line. Data shown are mean \pm SEM of at least three experiments performed in duplicate.

Table S1. Characterization of [³H]CCR2-RA-[R] in U2OS-CCR1 and U2OS-CCR2.^a

	U2OS-CCR1	U2OS-CCR2
p<i>K_D</i> (<i>K_D</i>, nM)	7.87 ± 0.03 (13.5) ^b	8.20 ± 0.05 (6.3) ^c
<i>B_{max}</i> (pmol/mg)	6.13 ± 0.24 ^b	2.63 ± 0.28 ^c
<i>k_{obs,fast}</i> (min⁻¹)^d	0.69 ± 0.08	0.12 ± 0.01*
<i>k_{obs,slow}</i> (min⁻¹)^d	0.11 ± 0.007	0.01 ± 0.001**
%fast	62 ± 2	55 ± 3
<i>k_{off,fast}</i> (min⁻¹)^e	0.62 ± 0.08	0.18 ± 0.02*
<i>k_{off,slow}</i> (min⁻¹)^e	0.06 ± 0.003	0.02 ± 0.002***
%fast	66 ± 2	54 ± 4

^aValues are means ± SEM of at least three independent experiments performed in duplicate. Unpaired *t*-test analysis with Welch's correction was performed to analyze differences in kinetic rates between receptors, with differences noted as *, *p* < 0.05; **, *p* < 0.01; ***, *p* < 0.001.

^bValues obtained from homologous displacement of 3, 6 and 12 nM [³H]-CCR2-RA-[R] from U2OS-CCR1 at 25°C. ^cValues obtained from saturation binding of 0.05 – 70 nM [³H]-CCR2-RA-[R] to U2OS-CCR2 at 25°C. ^dObserved association and ^edissociation rate constants of [³H]-CCR2-RA-[R] in U2OS-CCR1 or -CCR2 at 25°C.

Table S2. Inhibition of basal [³⁵S]GTPγS binding, i.e. in the absence of agonist CCL3, by compounds **37**, **39**, **41** and **43** in U2OS-CCR1.

Compound	pIC₅₀ ± SEM (IC₅₀, μM)^a	Hill slope^a
39	6.78 ± 0.04 (0.17)**	-0.4 ± 0.06*
41	6.70 ± 0.08 (0.21)**	-0.6 ± 0.05
43	6.13 ± 0.15 (0.85)	-0.4 ± 0.07*
45	5.17 ± 0.01 (6.73)	-0.5 ± 0.07*

^aAll values are means ± SEM of at least three independent experiments performed in duplicate. Unpaired *t*-test analysis with Welch's correction was performed to analyze differences in their inhibitory potencies and pseudo-Hill slopes as antagonists and inverse agonists in CCR1, with differences noted as *, *p* < 0.05; and **, *p* < 0.01.

REFERENCES

1. Zheng, Y.; Qin, L.; Ortiz Zacarías, N. V.; de Vries, H.; Han, G. W.; Gustavsson, M.; Dabros, M.; Zhao, C.; Cherney, R. J.; Carter, P.; Stamos, D.; Abagyan, R.; Cherezov, V.; Stevens, R. C.; IJzerman, A. P.; Heitman, L. H.; Tebben, A.; Kufareva, I.; Handel, T. M. Structure of CC chemokine receptor 2 with orthosteric and allosteric antagonists. *Nature* **2016**, 540, 458-461.
2. Isberg, V.; de Graaf, C.; Bortolato, A.; Cherezov, V.; Katritch, V.; Marshall, F. H.; Mordalski, S.; Pin, J.-P.; Stevens, R. C.; Vriend, G.; Gloriam, D. E. Generic GPCR residue numbers – aligning topology maps while minding the gaps. *Trends in Pharmacological Sciences* **2015**, 36, 22-31.