Supplemental Information

Identification of positive allosteric modulators VU0155094 (ML397) and VU0422288 (ML396) reveals new insights into the biology of metabotropic glutamate receptor 7

Nidhi Jalan-Sakrikar**, Julie R. Field**, Rebecca Klar*, Margrith E. Mattmann*, Karen J. Gregory*, Rocio Zamorano*, Darren W. Engers*, Sean R. Bollinger*, C. David Weaver*, Emily L. Days*, L. Michelle Lewis*, Thomas J. Utley*, Miguel Hurtado*, Delphine Rigault^, Francine Acher^, Adam G. Walker*, Bruce J. Melancon*, Michael R. Wood**, Craig W. Lindsley**, P. Jeffrey Conn*, Zixiu Xiang*, Corey R. Hopkins*, and Colleen M. Niswender*

[#]Department of Pharmacology and Vanderbilt Center for Neuroscience Drug Discovery, Vanderbilt University

[%]Department of Pharmacology and Vanderbilt Institute of Chemical Biology, Vanderbilt University

\$Department of Chemistry, Vanderbilt University

&Drug Discovery Biology, Monash Institute of Pharmaceutical Sciences, Parkville, VIC, Australia

^Université Paris Descartes, Paris, France

Vanderbilt is a Specialized Chemistry Center in the Molecular Libraries Probe Centers Networks

Corresponding author:
Colleen M. Niswender, Ph.D.
12478C MRB IV
Vanderbilt Center for Neuroscience Drug Discovery
Department of Pharmacology
Vanderbilt University Medical Center
Nashville, TN 37212
615-343-4303 (phone)
615-383-3088 (fax)
Colleen.niswender@vanderbilt.edu

^{*}These authors contributed equally to this work

All NMR spectra were recorded on a 400 MHz FT-NMR DRX-400 FT-NMR spectrometer or 500 MHz Bruker DRX-500 FT-NMR spectrometer. ¹H chemical shifts are reported in δ values in ppm downfield with the deuterated solvent as the internal standard. Data are reported as follows: chemical shift, multiplicity (s = singlet, d = doublet, t = triplet, q = quartet, br = broad, m = multiplet), integration, coupling constant (Hz). High resolution mass spectra were recorded on a Waters Q-TOF API-US plus Acquity system with electrospray ionization. Reversed-phase LCMS analysis was performed using an Agilent 1200 system comprising a binary pump with degasser, high-performance autosampler, thermostatted column compartment, diode-array detector (DAD) and a C18 column. Flow from the column was split to a 6130 SQ mass spectrometer and Polymer Labs ELSD. The MS detector was configured with an electrospray ionization source. Data acquisition was performed with Agilent Chemstation and Analytical Studio Reviewer software. Samples were separated on a ThermoFisher Accucore C18 column (2.6 um, 2.1 x 30 mm) at 1.5 mL/min, with column and solvent temperatures maintained at 45 C. The gradient conditions were 7% to 95% acetonitrile in water (0.1% TFA) over 1.1 minutes. Low-resolution mass spectra were acquired by scanning from 135 to 700 AMU in 0.25 seconds with a step size of 0.1 AMU and peak width of 0.03 minutes. Drying gas flow was 11 liters per minute at a temperature of 350 C and a nebulizer pressure of 40 psi. The capillary needle voltage was 3000 V, and the fragmentor voltage was 100V. Preparative purification was performed on a custom HP1100 purification system (reference 16) with collection triggered by mass detection. Solvents for extraction, washing and chromatography were HPLC grade. All reagents were purchased from Aldrich Chemical Co. and were used without purification.

Methyl 4-(3-(2-((4-acetamidophenyl)thio)acetyl)-2,5-dimethyl-1H-pyrrol-1-yl)benzoate (1), ML397. Probe compound ML397 (VU0155094) is commercially available compound and was purchased from ChemDiv and had the following characterization. LCMS: $R_T = 2.481$ min, >99% @ 254 nm, >99% @ 215 nm; m/z [M + H]⁺ = 437. ¹H NMR (400 MHz, CDCl3, δ ppm): 8.18 (dd; J = 6.8, 2 Hz, 2 H), 7.42 (d; J = 8.8 Hz, 2 H), 7.38 (d; J = 8.8 Hz; 2 H), 7.34-7.29 (m; 6 H), 6.33 (s; 1 H), 4.03 (s; 2H), 3.97 (s, 3 H), 2.30 (s; 3 H), 2.16 (s; 3 H), 1.99 (s; 3 H). HRMS calculated for $C_{24}H_{24}N_2O_4S$ [M + H]⁺ m/z: 437.1535, measured: 437.1539.

Representative procedure A:

3-chloro-4-((5-chloropyridin-2-yl)oxy)aniline (18). To a microwave vial (20 mL) was added 4-amino-2-chlorophenol (1) (1.0 g, 6.97 mmol, 1.0 eq), 5-chloro-2-fluoropyridine (2) (0.7 mL, 6.97 mmol, 1.0 eq), K_2CO_3 (1.44 g, 10.45 mmol, 1.5 eq) and DMF (10 mL). The rxn mixture was subjected to microwave irradiation at 150°C for 45 min. The rxn was added to EtOAc:water (1:1, 1000 mL) and the organic layer was separated. The water layer was re-extracted with EtOAc (3 x 50 ml) and the combined organic layers were washed with water (2 x 50 mL), brine (50 mL), dried (MgSO4), filtered and concentrated. The residue was purified on a Biotage Isolera One (Zip 80 column, 50-100% EtOAc:hexanes) to afford 3-chloro-4-((5-chloropyridin-2-yl)oxy)aniline (3)(1.36g, 76% yield). LCMS: RT = 0.796 min, >98% @ 215 and 254 nM, m/z = 254.8 [M + H]+.

N-(3-chloro-4-((5-chloropyridin-2-yl)oxy)phenyl)picolinamide (24). To a solution of 3-chloro-4-((5-chloropyridin-2-yl)oxy)aniline (1.36g, 5.35 mmol, 1.0 eq) and Hunig's Base (2.05 mL, 11.78 mmol, 2.2 eq) in DMF (30 mL) at 0°C was added picolinoyl chloride hydrochloride (1.05g, 5.89 mmol, 1.1 eq). After 15 min, the ice bath was removed. After 12 h at rt, the rxn was added to EtOAc:H₂O (1:1, 500 mL). The separated organic layer was washed with NaHCO₃ (aq) (50 mL), H₂O (3 x 50 mL), Brine (50 mL) and dried (MgSO₄). The mixture was filtered and the solvent removed under vacuo. The residue was purified by recrystalization (EtOH) to afford N-(3-chloro-4-((5-chloropyridin-2-yl)oxy)phenyl)picolinamide (5) (1.17 g, 59% yield). LCMS: R_T = 1.214 min, >98% @ 215 and 254 nM, m/z = 359.6 [M + H]⁺; ¹H NMR (400 MHz, , d-DMSO): δ 10.93 (br s, 1H), 8.77 (d, J = 4.0 Hz, 1H), 8.23 (d, J = 2.4 Hz, 1H), 8.20-8.18 (m, 2H), 8.09 (ddd, J = 7.6, 7.6, 1.6 Hz, 1H), 7.99 (dd, J = 8.8, 2.7 Hz, 1H), 7.92 (dd, J = 8.8 Hz, 1H); HRMS, calc'd for C₁₇H₁₂N₃O₂Cl₂ [M + H]⁺, 360.0307; found 360.0304.

Representative Procedure B:

N-(3-chloro-4-((5-chloropyridin-2-yl)oxy)phenyl)-2-methylthiazole-4-carboxamide

(VU0468764, 4j). To a solution of 2-methylthiazole-4-carboxylic acid (56 mg, 0.39 mmol, 1 eq), DIEA (0.20 mL, 1.2 mmol, 3 eq) and HATU (149 mg, 0.39 mmol, 1 eq) in DMF (2 mL) was added 3-chloro-4-((5-chloropyridin-2-yl)oxy)aniline (100 mg, 0.39 mmol, 1.0 eq) at rt. The rxn was heated to 35°C. After 48 h, the rxn was filtered and purified by Gilson HPLC (acetonitrile:water w/0.1% TFA). The fractions were collected and added to EtOAc: NaHCO3 (aq). The organic layer was washed with water, Brine and dried (MgSO4), filtered and concentrated to afford N-(3-chloro-4-((5-chloropyridin-2-yl)oxy)phenyl)-2-methylthiazole-4-carboxamide (7)(120 mg, 81% yield). LCMS: $R_T = 1.178$ min, >98% @ 215 and 254 nm, m/z = 380.0 [M + H]⁺. ¹H NMR (400 MHz, DMSO- d_6): δ 10.49 (s, 1 H), 8.32 (s, 1 H), 8.18 (d, J = 2.2 Hz, 1 H), 8.15 (d, J = 2.5 Hz, 1 H), 7.99 (dd, J = 8.8, 2.7 Hz, 1 H), 7.85 (dd, J = 8.8, 2.4 Hz, 1 H), 7.32 (d, J = 8.8 Hz, 1 H), 7.19 (d, J = 9.2 Hz, 1 H), 2.79 (s, 3 H). HRMS, calc'd for $C_{16}H_{12}N_3O_2SCI_2$ [M + H]⁺, 380.0027; found 380.0029

All compounds were prepared following the general procedure outlined above in library format and isolated/purified via HPLC. Purity of all final compounds was determined by HPLC analysis. Purity and characterization information is provided in the table below.

			VU#/ SID/	LCMS
Cmpd	\mathbf{R}_1	R	CID	LUMS
20	Cl		VU0419699-1	LCMS: [M + H] ⁺ = 326.06, >98% @215nm and ELSD
21	Cl	z Iz *	VU0453733-1	LCMS: R_T =0.673 min, $[M + H]^+$ = 326.0; >98% @ 215 and 254 nm
22*	Cl	*_0_N	VU0419700-1	LCMS: [M + H] ⁺ = 327.06, >98% @215nm and ELSD
23*	Cl	* O N CF3	VU0419939-1	LCMS: [M + H] ⁺ = 394.0, >98% @215nm and ELSD
24	Cl	*_O_N_CI	VU0422288-1	See above
25	F	* O N CF3	VU0419937-1	LCMS: [M + H] ⁺ = 378.1, >98% @215nm and ELSD
26	F	* O N CI	VU0419938-1	LCMS: [M + H] ⁺ = 344.0, >98% @215nm and ELSD
27	F	* 0 N	VU0422289-1	LCMS: Rt = 0.993 min, [M + H] ⁺ = 311.1; >98% @ 220 and 254 nm

$$\bigcap_{R} \bigcap_{H} \bigcap_{Cl} \bigcap_{Cl} \bigcap_{Cl}$$

Cmpd	R	VU#/ SID/ CID	LCMS
28	N*	VU0468753-1	LCMS: [M + H] ⁺ = 395, >99% at 215 and 254 nm
29	*	VU0468334-1	LCMS: [M + H] ⁺ = 361, >95% at 215 nm and 99% at 254 nm
30	*	VU0468749-1	LCMS: $[M + H]^+ = 361, >99\%$ at 215 and 254 nm
31	CI_N*	VU0468751-1	LCMS: [M + H] ⁺ = 396, >99% at 215 and 254 nm
32	***************************************	VU0468767-1	LCMS: [M + H] ⁺ = 375, >99% at 215 and 254 nm
33	-N**	VU0468747-1	LCMS: $R_T = 1.092 \text{ min}$, >98% @ 215 and 254 nm, $m/z = 363.0 \text{ [M + H]}^+$. ^1H NMR (400 MHz, DMSO- d_6): δ 10.33 (s, 1 H), 8.18 (d, $J = 2.2 \text{ Hz}$, 1 H), 8.12 (d, $J = 2.5 \text{ Hz}$, 1 H), 7.99 (dd, $J = 8.8$, 2.7 Hz, 1 H), 7.87 (d, $J = 2.2 \text{ Hz}$, 1 H), 7.82 (dd, $J = 8.8$, 2.4 Hz, 1 H), 7.30 (d, $J = 8.8 \text{ Hz}$, 1 H), 7.18 (d, $J = 8.3 \text{ Hz}$, 1 H), 6.78 (d, $J = 2.3 \text{ Hz}$, 1 H), 3.98 (s, 3 H); HRMS, calc'd for $C_{16}H_{13}N_4O_2Cl_2 \text{ [M + H]}^+$, 363.0416; found 363.0419
34	HN *	VU0468748-1	LCMS: $[M + H]^+ = 350$, >99% at 215 and 254 nm
35	*	VU0468762-1	LCMS: $[M + H]^+ = 364$, >99% at 215 and 254 nm
36	**	VU0468763-1	LCMS: [M + H] ⁺ = 351, >99% at 215 and 254 nm
37	N*	VU0468764-1	See above
38	(T)	VU0468765-1	LCMS: $R_T = 1.175 \text{ min}$, >98% @ 215 and 254 nm, $m/z = 364.9 \text{ [M + H]}^+$. ^1H NMR (400 MHz, DMSO- d_6): δ 10.41 (s, 1 H), 8.18 (dd, $J = 2.7$, 0.6 Hz, 1 H), 8.04-8.02 (m, 2 H), 8.00 (dd, $J = 8.8$, 2.7 Hz, 1 H), 7.90 (dd, $J = 5.0$, 1.1 Hz, 1 H), 7.71 (dd, $J = 8.8$, 2.5 Hz, 1 H), 7.34 (d, $J = 8.8$, 1 H), 7.25 (dd, $J = 5.0$, 3.8 Hz, 1 H), 7.19 (dd, $J = 8.8$, 0.5 Hz, 1 H); HRMS, cale'd for $C_{16}H_{11}N_2O_2SCl_2 \text{ [M + H]}^+$, 364.9918; found 364.9919
39	*	VU0468766-1	LCMS: [M + H] ⁺ = 380, >92% at 215 nm; >99% at 254 nm
40	Ů,	VU0468758-1	LCMS: $R_T = 1.189 \text{ min}$, >98% @ 215 and 254 nm, $m/z = 367.0 \text{ [M + H]}^+$. ^1H NMR (400 MHz, DMSO- d_6): δ 9.80 (s, 1 H), 8.16 (d, $J = 2.3 \text{ Hz}$, 1 H), 8.01 (d, $J = 2.4 \text{ Hz}$, 1 H), 7.98 (dd, $J = 8.8$, 2.7 Hz, 1 H), 7.68 (dd, $J = 8.9$, 2.5 Hz, 1 H), 7.27 (d, $J = 8.8 \text{ Hz}$, 1 H), 7.17 (d, $J = 8.8 \text{ Hz}$, 1 H), 4.06-4.03 (m, 1 H), 3.95 (dd, $J = 11$, 2.6 Hz, 1 H), 3.56-3.50 (m, 1 H), 1.95-1.84 (m, 2 H), 1.56-1.45 (m, 4 H). HRMS, calc'd for $C_{17}H_{17}N_2O_3Cl_2 \text{ [M + H]}^+$, 367.0616; found 367.0616
41		VU0468151-1	LCMS: $R_T = 1.191 \text{ min}$, >98% @ 215 and 254 nm, $m/z = 359.0 \text{ [M + H]}^+$. ^1H NMR (400 MHz, DMSO- d_6): δ 10.45 (s, 1 H), 8.18 (d, $J = 2.3 \text{ Hz}$, 1 H), 8.09 (d, $J = 2.5 \text{ Hz}$, 1 H), 8.01-7.98 (m, 1 H), 7.97 (dd, $J = 9.1$, 1.6 Hz, 2 H), 7.77 (dd, $J = 8.9$, 2.5 Hz, 1 H), 7.63 (dddd, $J = 7.3$, 7.3, 1.4, 1.4 Hz, 1 H), 7.58-7.55 (m, 2 H), 7.34 (d, $J = 8.8 \text{ Hz}$, 1 H), 7.19 (d, $J = 8.8 \text{ Hz}$, 1 H); HRMS, calc'd for $C_{15}H_{13}N_2O_2C1_2 \text{ [M + H]}^+$, 359.0354; found 359.0355

Supplemental Table 1. The group III mGlu PAMs VU0155094 and VU0422288 affect the affinity of orthosteric agonists. Using calcium assays with chimeric G proteins, the data from Figures S3, S4, and S5 were fit using Equation 2. In the first round of data fitting, it was assumed that there was no effect on orthosteric agonist affinity (i.e., α =1) and the E_m value was shared across datasets. Data were assessed statistically using a one-way ANOVA with a Tukey's post-test to compare all columns. Revised data analysis accounting for affinity modulation (α shared) is shown in Supplemental Tables 2 and 3 and Tables 5 and 6. Data are comprised of three individual experiments performed in duplicate (Mean \pm SD values shown).

	mGlu₄			mGlu ₇			mGlu ₈		
DMSO	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022
pΚ _A	5.93±0.30	7.35±0.45	6.88±0.28 ^a	3.21±0.12 ^b	3.97±0.15 ^c	5.02±0.29 ^d	6.01±0.11	7.19±0.06 ^e	4.97±0.13 [†]
K _A (μΜ)	1.2	0.04	0.13	623	106	9.6	0.98	0.06	10.7
VU0155094	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022
pΚ _A	5.80±0.73	6.94±0.22	6.39±0.06 ^a	3.88±0.06 ^b	3.82±0.12	4.13±0.17 ^d	6.29±0.84	6.49±0.04 ^e	4.21±0.19 ^f
K _A (μΜ)	1.60	0.12	0.41	133	151	73.7	0.52	0.33	62.3
VU0422288	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022
pΚ _A	5.62±0.10	6.75±0.17	6.34±0.00 ^a	3.04±0.07 ^b	3.64±0.12 ^c	4.67±0.10	5.84±0.08	6.67±0.08 ^e	4.30±0.17 [†]
Κ _Α (μΜ)	2.4	0.18	0.46	910	231	21.2	1.4	0.21	49.6

All p values<0.05

- (a) pK_A for mGlu₄/LSP4-2022 in absence of modulator versus either mGlu₄/LSP4-2022/VU0155094 or mGlu₄/LSP4-2022/VU0422288
- (b) pK_A for mGlu₇/glutamate in absence of modulator versus mGlu₇/glutamate/VU0155094 and mGlu₇/glutamate/VU0155094 versus mGlu₇/glutamate/VU0422288
- (c) pK_A significantly different for mGlu₇/L-AP4 in absence of modulator versus mGlu₇/L-AP4/VU0422288
- (d) pK_A for mGlu₇/LSP4-2022 in absence of modulator versus mGlu₇/LSP4-2022/VU0155094
- (e) pK_A significantly different from each other in all conditions, mGlu₈/L-AP4 in absence of modulator, mGlu₈/L-AP4/VU0155094, and mGlu₈/L-AP4/VU0422288
- (f) pK_A for mGlu₈/LSP4-2022 in absence of modulator versus mGlu₈/LSP4-2022/VU0155094 or mGlu₈/LSP4-2022/VU0422288

Supplemental Table 2. Revised curve fitting reveals differential interactions of VU0155094 and VU042288 with distinct group III mGlus. Using calcium assays with chimeric G proteins, the data from Figures S3, S4, and S5 were fit using Equation 2. A was shared across datasets and the system maximum (E_m) was constrained to the maximum level of potentiation observed for any agonist/potentiator pair (all above 100% of agonist E_{max} , average max value across three experiments shown). Data were assessed statistically using a one-way ANOVA with a Tukey's post-test to compare all columns. Data are comprised of three individual experiments performed in duplicate (Mean \pm SD values shown).

		mGlu₄		mGlu ₇			mGlu ₈		
DMSO	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022
pΚ _A	5.96±0.29	7.37±0.44 ^a	6.90±0.26 ^b	3.26±0.21	4.04±0.23	5.11±0.44	6.01±0.11	7.19±0.06 ^d	4.97±0.13 ^e
K _A (μM)	1.1	0.04	0.13	549	77	7.8	0.98	0.06	10.7
Log <i>T</i> _A	-0.01±0.01	0.02±0.01 ^f	0.03±0.02	-0.06±0.05	0.15±0.08	0.47±0.26	0.35±0.09	0.32±0.06 ^g	0.28±0.02 ^h
T _A	0.98	1.05	1.06	0.88	1.42	2.95	2.24	2.07	1.93
n	4.8±2.0	4.8±2.0	4.8±2.0	2.9±1.1	2.9±1.1	2.9±1.1	3.5±0.6	3.5±0.6	3.5±0.6
basal	8.1±0.9	8.1±0.9	8.1±0.9	1.8±1.5	1.8±1.5	1.8±1.5	2.5±0.2	2.5±0.2	2.5±0.2
Em#	196	196	196	377.2	377.2	377.2	102.3	102.3	102.3
VU0155094	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022
pΚ _A	6.10±0.26	6.90±0.30	6.49±0.07	3.23±0.13	4.49±0.20°	5.05±0.50	6.09±0.33	7.02±0.13 ^d	4.83±0.11 ^e
K _A (µM)	0.79	0.13	0.33	593	32.2	9.0	0.82	0.10	13.9
Log TA	-0.01±0.01	0.05±0.02	0.06±0.02	-0.09±0.04	0.06±0.04	0.52±0.31	0.33±0.18	0.40±0.06	0.34±0.07 ^h
T _A	0.99	1.12	1.15	0.81	1.16	3.28	2.12	2.50	2.19
n	6.2±1.8	2.0±0.2	2.2±0.03	2.3±0.4	6.7±3.1	2.9±1.2	4.6±2.5	2.9±0.4	3.0±0.3
basal	6.9±1.8	7.1±0.7	7.6±0.6	0.4±2.3	3.3±2.4	3.8±0.8	3.3±0.4	2.4±0.3	2.3±0.5
Em#	196	196	196	377.2	377.2	377.2	102.3	102.3	102.3
VU0422288	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022
pΚ _A	5.58±0.11	6.62±0.20 ^a	6.27±0.11 ^b	3.23±0.13	3.93±0.14°	4.82±0.40	5.84±0.14	6.71±0.04 ^d	4.53±0.07 ^e
K _A (μM)	2.6	0.24	0.54	910	119	15.1	1.5	0.20	29.6
Log TA	-0.01±0.02	0.08±0.03 [†]	0.08±0.03	-0.05±0.04	0.18±0.10	0.64±0.30	0.44±0.08	0.59±0.15 ^g	0.53±0.07 ^h
<i>T</i> A	0.98	1.20	1.21	0.88	1.52	4.34	2.76	3.86	3.39
n	2.3±0.08	1.3±0.05	1.6±0.2	2.6±0.6	2.4±0.7	2.1±0.4	2.7±0.5	2.1±0.5	2.1±0.06
basal	7.1±1.8	7.2±0.9	7.8±0.4	1.3±2.4	0.3±1.8	3.6±1.4	2.4±0.5	1.9±0.2	1.8±0.4
Em#	196	196	196	377.2	377.2	377.2	102.3	102.3	102.3

[#] E_m value constrained to the maximal level of potentiation observed for that subtype between any combination of ligands in a given experiment; the mean is reported.
All p values<0.05

- (a) pK_A for mGlu₄/L-AP4 in absence of modulator versus mGlu₄/L-AP4/VU0422288
- (b) pK_A for mGlu₄/LSP4-2022 in absence of modulator versus mGlu₄/LSP4-2022/VU0422288
- (c) pK_A for mGlu₇/L-AP4/VU0155094 versus mGlu₇/L-AP4/VU0422288
- (d) pK_A for mGlu₈/L-AP4 in absence of modulator versus mGlu₈/L-AP4/VU0422288 and mGlu₈/L-AP4/VU0155094 versus mGlu₈/L-AP4/VU0422288
- (e) pK_A for mGlu₈/LSP4-2022 in absence of modulator versus mGlu₈/LSP4-2022/VU0422288 and mGlu₈/LSP4-2022/VU0155094 versus mGlu₈/LSP4-2022/VU0422288
- (f) Log τ_A for mGlu₄/L-AP4 in the absence of modulator versus mGlu₄/L-AP4/VU0422288

- (g) Log $\tau_{\rm A}$ for mGlu₈/L-AP4 in the absence of modulator versus mGlu₈/L-AP4/VU0422288
- (h) Log τ_A for mGlu₈/LSP4-2022 in the absence of modulator versus mGlu₈/LSP4-2022/VU0155094 or mGlu₈/LSP4-2022/VU0422288

Supplemental Table 3. Summary of agonist affinity and efficacy estimates across each group III mGlu subtype. To directly fit the data represented in Figure S3, we used Equation 2. The system maximum (E_m) was constrained to the maximum level of potentiation observed for any agonist/potentiator pair (all above 100% of agonist E_{max}) for calcium assays and to a value just above the largest agonist max value for GIRK assays. For statistical analyses, $Log \tau_A$ and pK_A values were compared between agonists at one receptor, then separately between each agonist at the three receptors and then $Log \tau_A$ and pK_A values were compared between assays (for example, mGlu₄ calcium versus mGlu₄ GIRK). All statistical tests were one way ANOVA with a Tukey post-test to compare columns with the exception of between-assay comparisons, which were performed via a student's t-test. Data are comprised of three individual experiments performed in duplicate (Mean \pm SD values shown).

	mGlu₄				mGlu ₇		mGlu ₈		
Calcium	Glu	L-AP4	LSP4-2022	Glu	L-AP4	LSP4- 2022	Glu	L-AP4	LSP4- 2022
pEC ₅₀	5.40±0.12	6.82±0.24	6.34±0.06	3.08±0.03	3.93±0.15	5.34±0.02	6.11±0.04	7.23±0.17	4.96±0.08
EC ₅₀ (μM)	4.0	0.15	0.45	840	119	4.5	0.77	0.06	10.9
Log <i>T</i> _A	-0.01±0.01 ^{ach}	0.02±0.01 ^{di}	0.03±0.02 ^{ae}	-0.06±0.05 ^{bc}	0.15±0.08 ^d	0.47±0.26 ^{be}	0.35±0.09 ^c	0.32±0.06 ^d	0.28±0.02
τ _A	0.98	1.05	1.06	0.88	1.42	2.95	2.24	2.07	1.93
pΚ _A	5.96±0.29 ^j	7.37±0.44	6.90±0.26	3.26±0.21	4.04±0.23	5.11±0.44	6.01±0.11 ^k	7.19±0.06 ^l	4.97±0.13
K _A (μM)	1.1	0.04	0.13	549	92.3	7.8	0.98	0.06	10.7
Log (т/K _A)	5.95±0.30	7.39±0.43	6.93±0.24	3.20±0.25	4.19±0.20	5.58±0.19	6.36±0.03	7.51±0.12	5.26±0.11
Fold ΔpK _A vs. Glu	1	26	8.8	1	6.0	70	1	15	0.09
ΔLog(τ/K _A) vs. Glu	0	1.44±0.14	0.98±0.12	0	0.99±0.14	2.37±0.09	0	1.15±0.14	-1.10±0.10
n	4.8±2.0	4.8±2.0	4.8±2.0	2.9±1.1	2.9±1.1	2.9±1.1	3.5±0.6	3.5±0.6	3.5±0.6
basal	8.1±0.9	8.1±0.9	8.1±0.9	1.8±1.5	1.8±1.5	1.8±1.5	2.5±0.2	2.5±0.2	2.5±0.2
Em	196	196	196	377.2	377.2	377.2	102.3	102.3	102.3
		mGlu₄		mGlu ₇			mGlu ₈		
GIRK	Glu	L-AP4	LSP4-2022	Glu	L-AP4	LSP4-2022	Glu	L-AP4	LSP4- 2022
pEC ₅₀	5.10±0.07	7.06±0.11	7.01±0.12	3.59±0.33	3.86±0.04	5.28±0.06	5.20±0.01	7.14±0.11	5.20±0.07
EC ₅₀ (μM)	7.9	0.09	0.10	260	138	5.3	6.3	0.07	6.3
Log <i>T</i> _A	0.11±0.03 ^{gh}	0.12±0.06 ¹	0.14±0.11	0.01±0.02 ^{fg}	0.31±0.07 [†]	0.40±0.09 [†]	0.36±0.11 ^g	0.14±0.44	0.35±0.33
T _A	1.28	1.31	1.38	1.03	2.06	2.54	2.28	1.38	2.24
pΚ _A	5.39±0.16 ^J	7.36±0.24	7.25±0.32	3.69±0.41	3.77±0.08	5.05±0.09	4.88±0.03 ^k	6.78±0.10 ¹	4.69±0.30
K _A (μM)	4.1	0.04	0.06	205	170	8.9	13.3	0.17	20.2
Fold ΔpK _A vs. Glu	1	93	72	1	1.2	23	1	80	0.66
Log (t/K _A)	5.50±0.13	7.48±0.18	7.38±0.22	3.70±0.39	4.09±0.02	5.46±0.01	5.23±0.14	6.92±0.36	5.05±0.16
ΔLog(τ/K _A) vs. Glu	0	1.98±0.08	1.89±0.09	0	1.55±2.20	1.75±0.38	0	3.40±3.20	-0.19±0.06
n	3.9±1.2	3.9±1.2	3.9±1.2	2.7±0.4	2.7±0.4	2.7±0.4	1.3±0.05	1.3±0.05	1.3±0.05
basal	1.9±0.2	1.9±0.2	1.9±0.2	4.7±1.1	4.7±1.1	4.7±1.1	1.2±0.5	1.2±0.5	1.2±0.5
Em	140	140	140	220	220	220	140	140	140

All noted p values < 0.05

- (a) Log τ_A between all receptors for L-AP4/calcium
- (b) Log τ_A between mGlu₈/glutamate/calcium versus mGlu₄/glutamate and mGlu₇/glutamate
- (c) Log τ_A between mGlu₄/LSP4-2022/calcium versus mGlu₇/LSP4-2022/calcium
- (d) Log τ_A between mGlu₄/glutamate/calcium and mGlu₄/LSP4-2022/calcium
- (e) Log τ_A between mGlu₇/glutamate/calcium versus mGlu₇/LSP4-2022/calcium
- (f) Log τ_A between mGlu₇/glutamate, GIRK assay versus mGlu₇/L-AP4 and mGlu₇/LSP4-2022, GIRK assay
- (g) Log τ_A between mGlu₈/glutamate, GIRK assay versus mGlu₄/glutamate and mGlu₇/glutamate, GIRK assay
- (h) Log r_A between mGlu₄/glutamate, calcium assay versus mGlu₄/glutamate, GIRK assay
- (i) Log τ_A between mGlu₄/L-AP4, calcium assay versus mGlu₄/L-AP4, GIRK assay
- (j) pK_A between mGlu₄/glutamate, calcium assay versus mGlu₄/glutamate, GIRK assay
- (k) pK_A between mGlu₈/glutamate, calcium assay versus mGlu₈/glutamate, GIRK assay
- (I) pK_A between mGlu₈/L-AP4 calcium assay versus mGlu₈/L-AP4, GIRK assay

Supplemental Figures

Supplemental Figure 1. Selectivity profiling of VU0155094 reveals that VU0155094 is a pan group III mGlu PAM. Glutamate was used as the agonist for all receptors except mGlu₇ where L-AP4 was used; *N*=1 experiment performed in duplicate. FS=fold shift of the agonist-concentration-response curve. Ago-PAM=agonist+PAM activity observed.

Supplemental Figure 2. Selectivity profiling of VU0422288 reveals that VU0422288 is a pan group III mGlu PAM. Glutamate was used as the agonist for all receptors except mGlu₇ where L-AP4 was used; *N*=1 experiment performed in duplicate. FS=fold shift of the agonist-concentration-response curve. Ago-PAM=agonist+PAM activity observed.

Supplemental Figure 3. Agonist concentration-response curves for mGlu₄, mGlu₇, and mGlu₈ compared across assays. (A-C) Increasing concentrations of each agonist were applied to cells expressing mGlu₄ and G_{qi5} , mGlu₇ and $G_{\alpha15}$, and mGlu₈ and $G_{\alpha15}$ and calcium responses were measured. (D-F) Increasing concentrations of each agonist were applied to cells expressing mGlu₄ and GIRK1/2 subunits, mGlu₇ and GIRK1/2, and mGlu₈ and GIRK 1/2 and thallium flux responses were measured. Data represent three-four independent experiments performed in quadruplicate.

Supplemental Figure 4. VU0155094 exhibits efficacy as a PAM for mGlu₄, mGlu₇, and mGlu₈ as assessed by calcium mobilization. Increasing concentrations of VU0155094 were applied prior to a full agonist concentration-response curve and the shift of the agonist response was measured in the calcium mobilization assay. These data were used to calculate results found in Table 5 and Supplemental Tables 1 and 2. Data are representative of three individual experiments performed in duplicate.

Supplemental Figure 5. VU0422288 exhibits efficacy as a PAM for mGlu₄, mGlu₇, and mGlu₈ as assessed by calcium mobilization. Increasing concentrations of VU0422288 were applied prior to a full agonist concentration-response curve and the shift of the agonist response was measured in the calcium mobilization assay. These data were used to calculate results found in Table 6 and Supplemental Tables 1 and 2. Data are representative of three individual experiments performed in duplicate.

Supplemental Figure 6. VU0422288 exhibits efficacy as a PAM for mGlu₄, mGlu₇, and mGlu₈ as assessed by thallium flux through GIRK channels. Increasing concentrations of VU0422288 were applied prior to a full agonist concentration-response curve and the shift of the agonist response was measured in the thallium flux. These data were used to calculate results found in Table 6. Data are representative of three individual experiments performed in duplicate.

Supplemental Figure 7. Orthosteric agonists show distinctions in interactions with mGlu₄, mGlu₇, and mGlu₈ that are assay dependent. A. Efficacy/affinity values (Log τ_A/K_A) were calculated for glutamate, L-AP4, and LSP4-2022 at mGlu₄, mGlu₇, and mGlu₈ and plotted for the GIRK and calcium pathways. There was a strong correlation noted between assays across all three receptors (linear regression fit, r²=0.88). B, C, D. Bias plots for mGlu₄, mGlu₇ and mGlu₈ reveal that distinct agonists show bias for different receptors. Curves were generated by performing a nonlinear regression across a 150 point range to compare responses between two pathways at equivalent agonist concentrations. Bias factors (ΔΔLog τ/K_A) were calculated using glutamate as the reference agonist and calcium as the reference pathway. These plots correspond to bias factors for L-AP4 at mGlu₄, mGlu₇ and mGlu₈ of 0.54±0.09, -0.60±0.23, 0.65±0.19 (Mean±S.E.M), respectively. For LSP4-2022 bias factors were 0.91±0.08, -0.62±0.23, 1.02±0.12 (Mean±S.E.M), respectively at mGlu₄, mGlu₇ and mGlu₈.

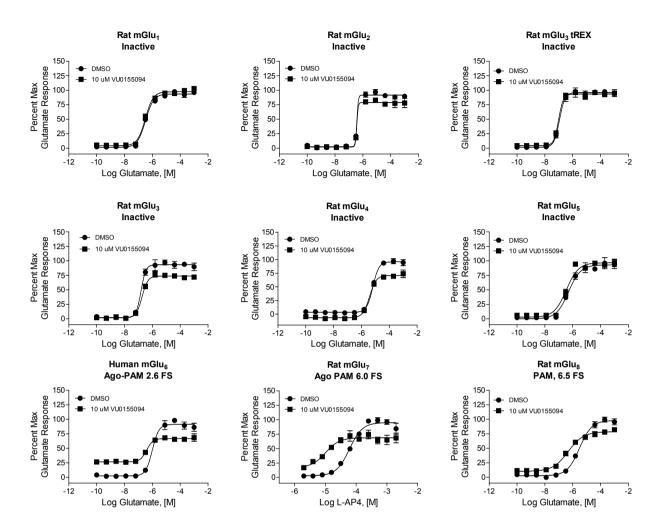


Figure S1.

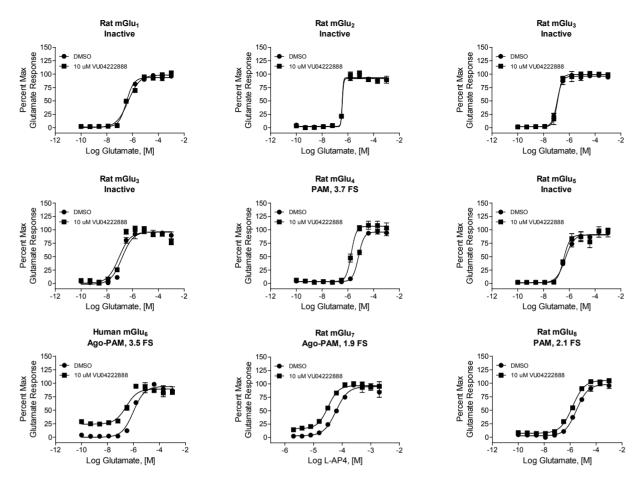


Figure S2.

Calcium Α В С mGlu₇ $mGlu_4$ $mGlu_8$ Percent Max Glutamate Response Percent Max Glutamate Response Percent Max Glutamate Response Glutamate Glutamate Glutamate 400 -O- L-AP4 -**O**- LSP4-2022 -O- L-AP4 -O- L-AP4 LSP4-2022 -O- LSP4-2022 300 200 100--8 -6 Log Agonist, [M] -8 -6 Log Agonist, [M] -12 -10 -8 -6 Log Agonist, [M] -12 -10 -12 -10 **GIRK** D Ε F mGlu₄ mGlu₇ mGlu₈ Percent Max Glutamate Response Percent Max Glutamate Response -0-1001 Glutamate Glutamate Glutamate Percent Max Glutamate Response -O- L-AP4 -O- L-AP4 -O- L-AP4 -O- LSP4-2022 -O- LSP4-2022 -O- LSP4-2022 -50| -12

-8 -6 Log Agonist, [M]

-10

-8 -6 Log Agonist, [M]

-10

Figure S3.

-12

-10

-8 -6 Log Agonist, [M]

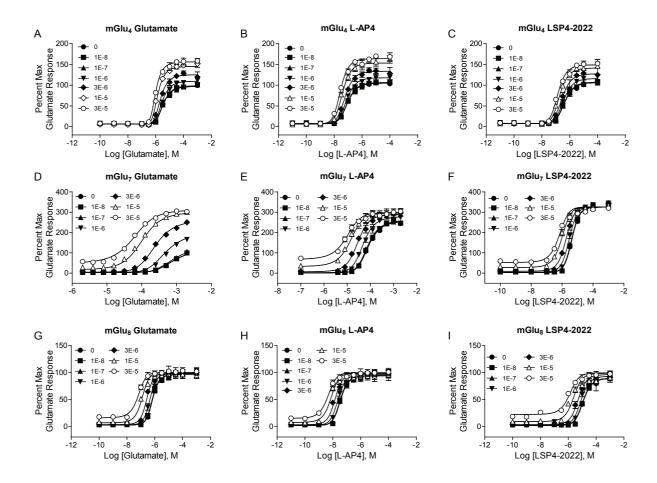


Figure S4.

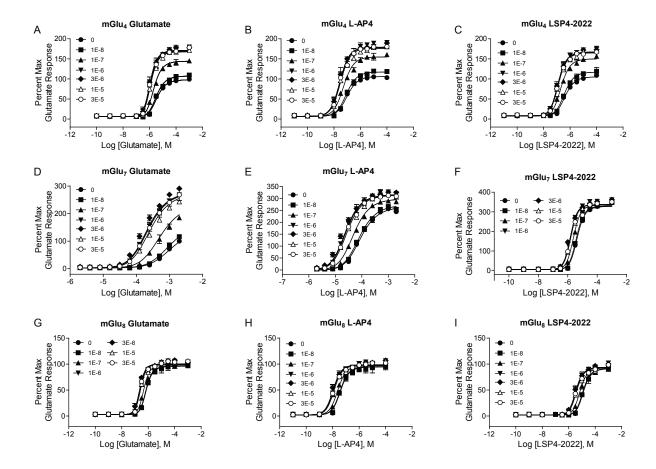


Figure S5.

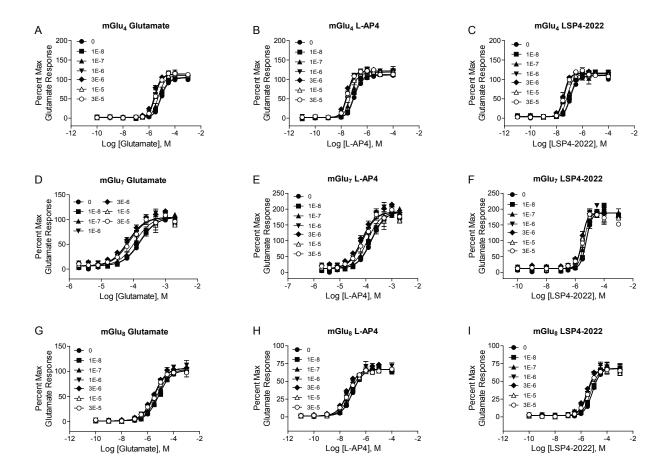


Figure S6.

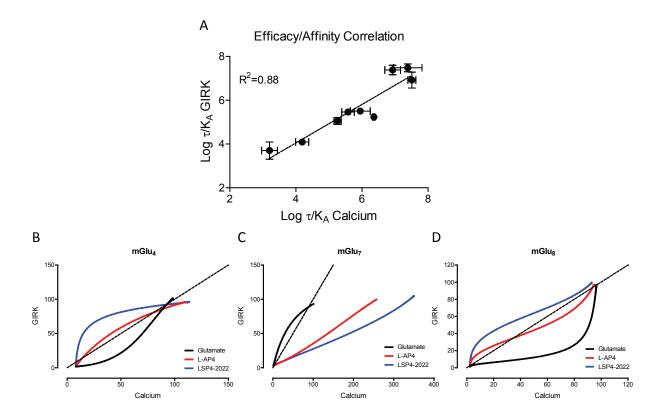


Figure S7.