

# Supplementary Materials

## Supplemental Figure 1

TM1		TM2				
61	LFASFYLLDFILALVGNLALWLFIRDHKSQTPANVFLM	LAVADLSCVLLVLP	TRLVYHF	120	Q13304	GPR17_HUMAN
25	WYSTLYSHISVUVCFPCNGFVLYVLIKTYHKS	SAFOVYMINLAWADLLCVCTLPLR	VVYV	84	Q9Y271	CLTR1_HUMAN
40	FFPIVYLLIFWFCVLCNGLSIYVFLQPYKRST	SVNVMFLNLAI	SDLLFISTLPPFRADYLL	99	Q9NS75	CLTR2_HUMAN
53	YLPNAVYLLVFTICFLCNSVAIWMFVFMHPW	SGISVYHFNALADFLYVLTLP	PALIFYYF	112	P47900	P2RY1_HUMAN
27	LPPLLYTVLFFVGLITNGLAMRIFF-QIRSKSN	FIIFLNTVISDLLMLT	FPFKILSDA	85	Q9H244	P2Y12_HUMAN
35	YLPVIYGLIFLVGFCNAVVISYIFKMPWKSST	IIMLNLA	CTDLLYLTSLPFLIHYYA	94	Q96P68	OXGR1_HUMAN
25	YLSIFGIEFVVVGVLCNTIVVYGYIFSLK	NWSSNIYLFNLSVSDLAFLCTLP	PLIRSYA	84	Q9BXA5	SUCR1_HUMAN
	* : : : : * : : : : * : : : : *					
TM3						
121	SCNHWPFGRIACRLTGFLFYLNMYASIIYFL	TCISADRFLAIVHPVKS	SLRRLRPLYA	180	Q13304	GPR17_HUMAN
85	HKGIWFLGDFLCLSTYALYVNLVYCSIFFHT	AMSFFCIAIVFPVQMINLVTQ	KARFVC	144	Q9Y271	CLTR1_HUMAN
100	RGSNWFCDLACRIMSYSLYVNMYSIIYFL	TVLSVVF	LAMVFPFLLHVTSIRSANILC	159	Q9NS75	CLTR2_HUMAN
113	NKTDWIFGDAMCKLQAFIFVNLVYCSIL	FLTCISAHRYSCVVYPLKSLCRL	KKKNAICIS	172	P47900	P2RY1_HUMAN
86	KLGTGPLRTFVQCQVTSVIFFTMYISIS	IFLGLITIDRYQKTRPFR	TSPKLLGAKILS	145	Q9H244	P2Y12_HUMAN
95	SGENWIFGDFMCKFIIFSFHFNLYSSIL	FLTCFSIF	YCVIIIPMSCFSIHKTRCAVAVAC	154	Q96P68	OXGR1_HUMAN
85	NG-NWICYGDVLCISNRYVLHANLYTSIL	FLTFISIDYLLIKYFPREHLLQ	KKEFALLIS	143	Q9BXA5	SUCR1_HUMAN
	* : : : * * * : : * : *					
TM4						
181	AFLWVVAVAMAPLLVSPQTQVQTMH-TVV	CLQLYREKAS----	HHALVSLAVAF	234	Q13304	GPR17_HUMAN
145	VGCIWIFVLITSSPFLMAR	PQRDEKN-NTRCFEPPQDNQTKNH	VLVLHYVSLFVGFILPFV	203	Q9Y271	CLTR1_HUMAN
160	GIWILIMASSIM-LDSCSEQNGS-VTSC	LELNLYK--IAKLQTMNYIALV	GCCLLPFF	215	Q9NS75	CLTR2_HUMAN
173	VLVWLVVVVAISPIIFYSCTGVREKNTI	TCYDITTSDEY-LRSYFIYSMCT	TVAMFCVPLV	231	P47900	P2RY1_HUMAN
146	VVITWAFMFLLSLPNMILNRPDRK	MVRRCSFLKSEFG-LVWHIVM	YIC-QVIFWINFL	203	Q9H244	P2Y12_HUMAN
155	AVVVWISLWAVIPMTFLITSTNRTN- RSACLDLTSSDE-LNTIKWYMLIL	TATTFCLPLV		212	Q96P68	OXGR1_HUMAN
144	LAIWVLTLELLPILPLINPVITDN- CTTCNDFASSGD-PNYNLIYSMCL	TLLGFLIPLF		201	Q9BXA5	SUCR1_HUMAN
	* : : * : *					
TM5		TM6				
235	TTVTCYLLIIRSLRQGLRVE---KR	RTKAVMIAIVLAI	FLVCFVFPVWNR	288	Q13304	GPR17_HUMAN
204	IIIVCYTHIILTLKRSMEK---NLS	SHRKAIGMIMVVTAAFLV	SFMPYHIQR	258	Q9Y271	CLTR1_HUMAN
216	TLSICYLLIIRVLLKVEVPESC-LRV	SHRKLTTIIITLIIFFLC	FLPLVYTLR	272	Q9NS75	CLTR2_HUMAN
232	LILGCYCLLIVRALIYKD--L-D-NSP	LRKRIYLVIIVLTVFAVSYL	FPVWMLMNL	287	P47900	P2RY1_HUMAN
204	IIIVCYTHIIRKELYSYVTRCVGKVP	RRKRVVVFIIIAVFFIC	FVFPFARIPYTL	261	Q9H244	P2Y12_HUMAN
213	IIVTLCYTHIIRHGL--Q-T-DSC	LKQKARRLTILLLLAFV	YVCFPLP	268	Q96P68	OXGR1_HUMAN
202	VMCFYFKIALFLKQNRQV-A-TAL	PLEKLNLVIMAVVIFSVL	FTFPVWNRVRIASR	259	Q9BXA5	SUCR1_HUMAN
	* * * * *	* : : * : *				
TM7						
289	--HYRSHGASCATQRILALANRITSCL	TSLNGALDPIN	YFFVAEKRHALCNLLCGKRLK	346	Q13304	GPR17_HUMAN
259	--FLHNETKPCDSVLRMQKSVVITLS	LAAASCCFDPLLYFFSGGNFR	KRLSTFRKHSLS	316	Q9Y271	CLTR1_HUMAN
273	--TWKV--CLCK--DLHKA	LVITLALAAANACFNPLLY	YFACENFDRKLSALRKC	323	Q9NS75	CLTR2_HUMAN
288	LDFQTP--AMCAFNDRVYATYQVT	GLASLNSCVDPILYFL	ACDTFRRLRSRATRKASRR	345	P47900	P2RY1_HUMAN
262	--SQTBDVFDCAENTLIFYVKE	STLWLTSLNA	CLDPFIYFPLCKSFRNSLISMLKCPNSA	319	Q9H244	P2Y12_HUMAN
269	LL--S--ISCSIEHQIHEAYIVS	PLAALNTFCMLLLYVVVSDNF	QQAVCSTVRCRVSG	323	Q96P68	OXGR1_HUMAN
260	LGSWRQ--YQCT-QVVINSFYIVTR	PLAFLNSVINPVVYFL	LCDFRDLMLMQLRHNFKS	316	Q9BXA5	SUCR1_HUMAN
	* : : * : *					

Fig. S1. Sequence alignment of hGPR17 with phylogenetically related P2Y, CysLT, and small carboxylic acid receptors. Sequences for human GPR17, CysLT<sub>1</sub> (CLTR1), CysLT<sub>2</sub> (CLTR2), P2Y<sub>1</sub>, P2Y<sub>12</sub>, 2-oxo-glutarate receptor 1 (OXGR1), and succinate receptor 1 (SUCR1) were aligned using Clustal W. Predicted transmembrane domains are

highlighted in yellow. Positively charged residues that likely form part of the orthosteric binding site for the aligned receptors are boxed in red.