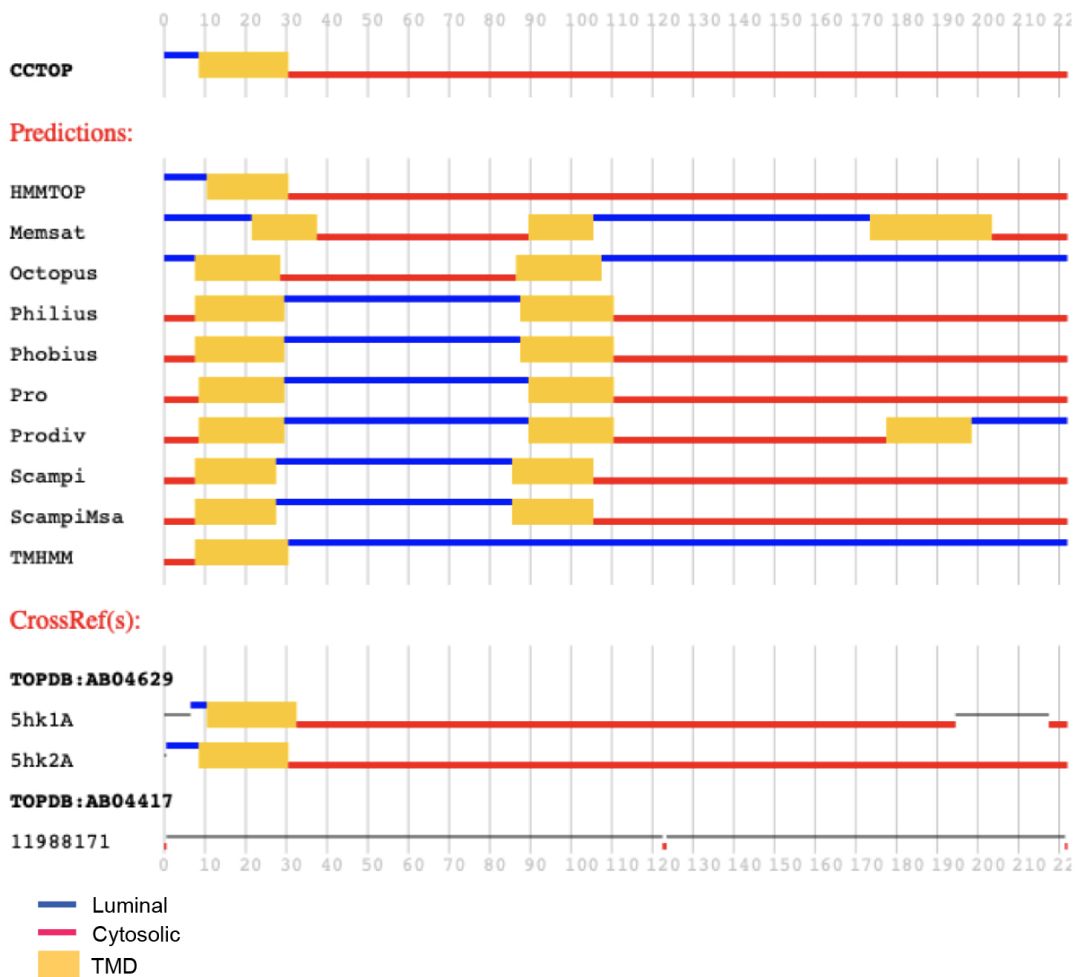# The Sigma-1 receptor is an ER-localized type II membrane protein

Neeraj Sharma, Chaitanya Patel, Marina Shenkman, Amit Kessel, Nir Ben-Tal and Gerardo Z. Lederkremer
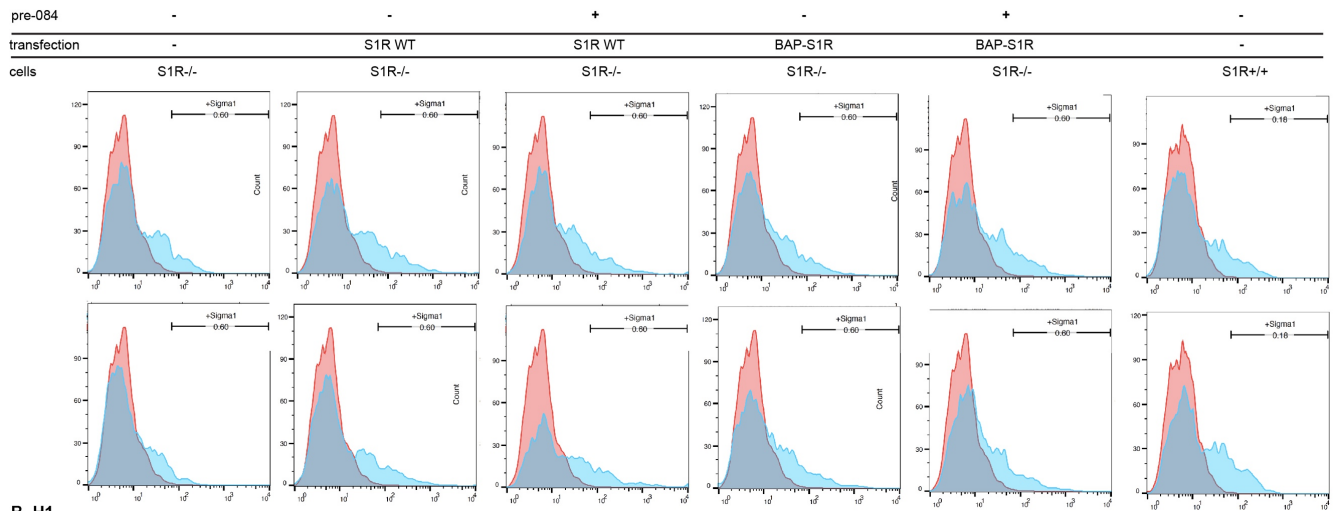
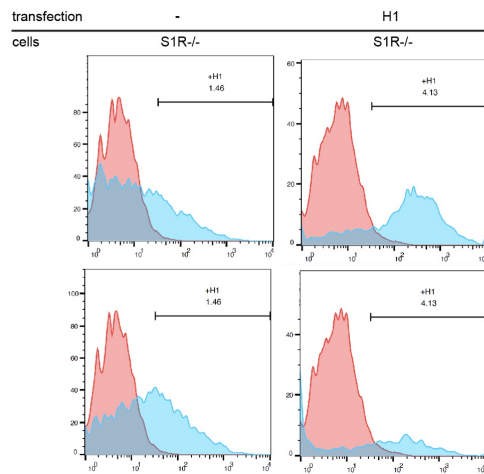## Supplementary Material

Supplementary figures

Suppl. Fig. 1. Bioinformatic predictions estimate conflicting topologies and number of transmembrane domains for the S1R. The CCTOP server predicts a type III membrane protein topology (top), based on a series of predictive methods yielding a variety of topologies.
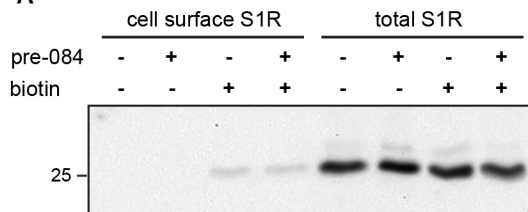
A. S1R

pre-084	-	-	+	-	+	-
transfection	-	S1R WT	S1R WT	BAP-S1R	BAP-S1R	-
cells	S1R-/-	S1R-/-	S1R-/-	S1R-/-	S1R-/-	S1R+/+

B. H1

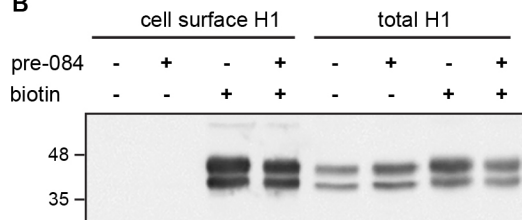| transfection	-	H1
cells	S1R-/-	S1R-/-

Suppl. Fig. 2. Raw FACS data of a representative experiment of 3 independent repeats corresponding to Fig. 7A. In addition, BAP-S1R was also analyzed showing a minor cell surface expression, similar to S1R WT.

A

	cell surface S1R	total S1R		
pre-084	- + - +	- + - +
biotin	- - + +	- - + +

25

B

	cell surface H1	total H1		
pre-084	- + - +	- + - +
biotin	- - + +	- - + +

48

35

Suppl. Fig. 3. Experiment similar to that shown in Fig. 8, with S1R-/- HEK293 cells expressing WT S1R (A) or H1 (B). In this case controls were added where incubation with biotin was omitted, showing no detectable signal.