

The human adenosine A_{2A} receptor co-isolates with anionic phospholipids in SMALPs from *Pichia pastoris* plasma membrane.

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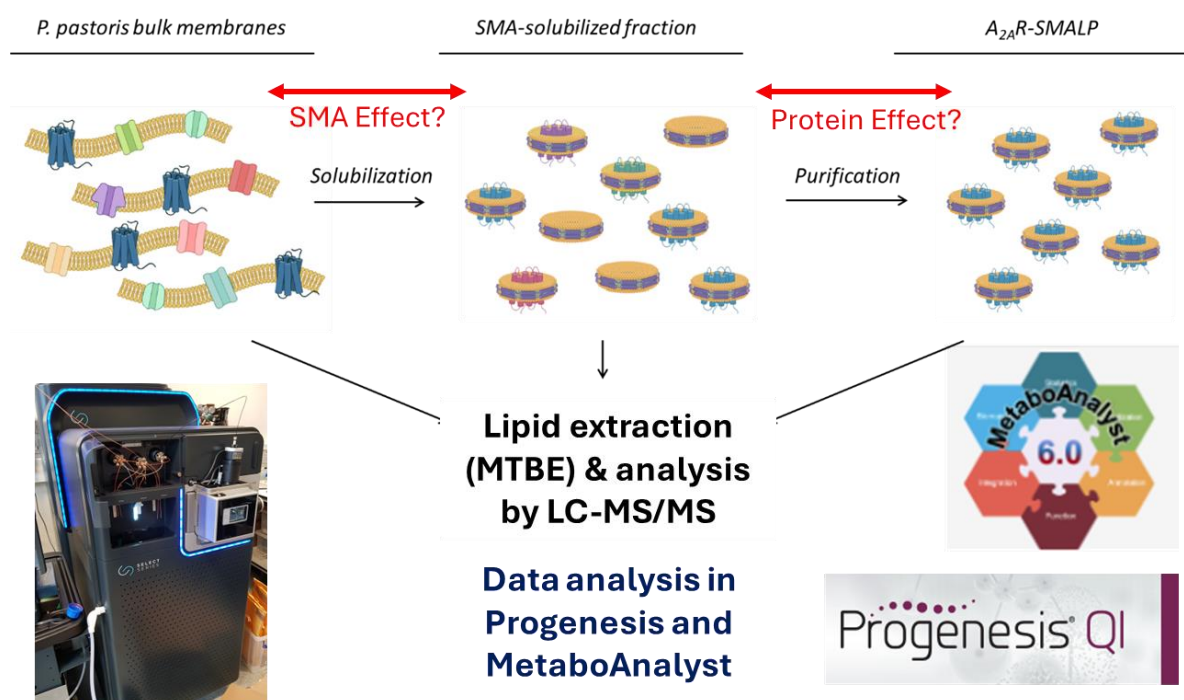
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Experimental Design Graphic



Materials and methods

The experimental details for the work are described in full in the published article in BBA-Biomembranes with additional detail in the Supplementary methods. *P. pastoris* SMD1163 cells were transformed with the pPICZB-hA2AR (A316) plasmid to overexpress the human C-terminal truncated human Adenosine A_{2A} Receptor (A_{2A}R). A large batch of cell membranes was prepared and divided into 3 aliquots for solubilization of the membranes by SMA2000 and subsequent isolation of the SMALPs containing the A_{2A}R using the his-tag. QCs were prepared by combining




LIST OF FILES

MASS SPECTROMETRY DATA




Positive Ion Analysis

LC-MSMS data were acquired using an ACQUITY UPLC I-Class PLUS System (Waters) coupled to a SELECT SERIES Cyclic ion mobility (cIM) mass spectrometry system (Waters) with data-independent acquisition (DIA) and a single pass of the cyclic IMS. The data format is Waters .raw files. The data are in Zipped folders, one for each sample set, except for the positive Membrane data, which is zipped in 2 folders: 1&2 and 3&4.




Pos Membrane data (n=3)

-  20230706_Mem1_pos
-  20230706_Mem2_pos
-  20230706_Mem3_pos

Pos SMA data (n=3)

-  20230706_SMA1_pos
-  20230706_SMA2_pos
-  20230706_SMA3_pos



Pos A2AR data (n=3)

-  20230706_A2AR1_pos
-  20230706_A2AR2_pos
-  20230706_A2AR3_pos



Pos QC data (n=4)

Done in 2 separate zip folders as it was too large to upload as one.

20230706_pooledQC_pos_1&2

-  20230706_pooledQC_pos_1
-  20230706_pooledQC_pos_2



20230706_pooledQC_pos_3&4

-  20230706_pooledQC_pos_3
-  20230706_pooledQC_pos_4




Negative Ion Analysis

LC-MSMS data were acquired using an ACQUITY UPLC I-Class PLUS System (Waters) coupled to a SELECT SERIES Cyclic ion mobility (cIM) mass spectrometry system (Waters) with data-dependent acquisition (DDA) without ion mobility. The data format is Waters .raw files. The data are in Zipped folders, one for each sample set.




Neg Membrane data (n=2)

-  20230706_Mem2_neg_DDA
-  20230706_Mem3_neg_DDA





Neg SMA data (n=3)

-  20230706_SMA1_neg_DDA
-  20230706_SMA2_neg_DDA
-  20230706_SMA3_neg_DDA

Neg A2AR data (n=3)

-  20230706_A2AR1_neg_DDA
-  20230706_A2AR2_neg_DDA
-  20230706_A2AR3_neg_DDA

Neg QC data (n=4)

-  20230706_pooledQC_neg_DDA_1 File folder
-  20230706_pooledQC_neg_DDA_2 File folder
-  20230706_pooledQC_neg_DDA_3 File folder
-  20230706_pooledQC_neg_DDA_4 File folder