

## Supplementary Information for

# State-Targeting Stabilization of Adenosine A<sub>2A</sub> Receptor by Fusing a Custom-Made De Novo Designed $\alpha$ -Helical Protein

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## Supplementary Figures

### 1. SDS-PAGE results for FiX1 and FiX2

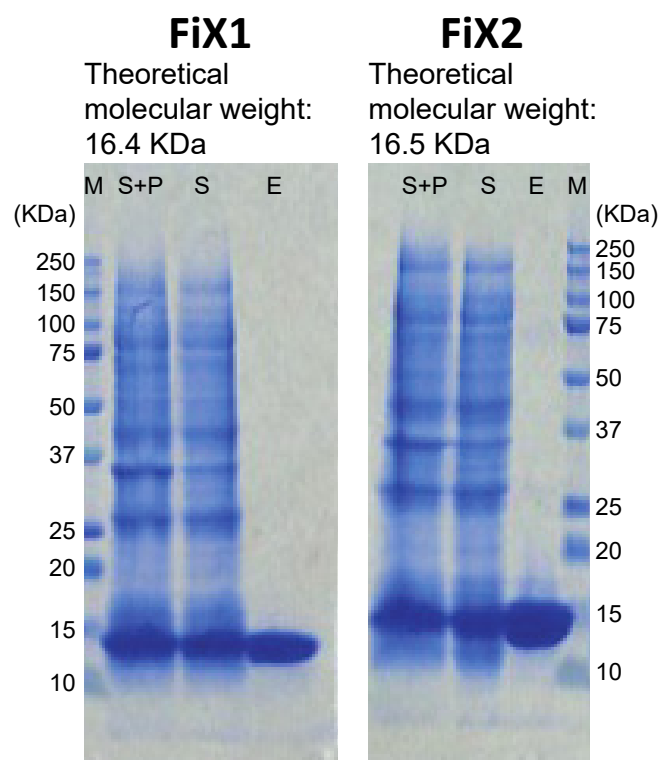
## Supplementary Tables

### 1. Sequence regions for A<sub>2A</sub>R and fusion partner proteins in A<sub>2A</sub>R chimeras

### 2. Amino acid sequences of FiX1 and FiX2

### 3. Amino acid sequences of A<sub>2A</sub>R fused with FiX1 and FiX2

### 4. Residues used for superposition between A<sub>2A</sub>R and *de novo* designed fusion partner proteins



**Figure S1 | SDS-PAGE results for FiX1 and FiX2**

M, S+P, S and E indicate marker, a mixture of supernatant (S) and pellet (P) after cell lysates; S, supernatant after centrifugation of cell lysates; and E, elution after Ni purification, respectively.

**Table S1 | Sequence regions for A<sub>2A</sub>R and fusion partner proteins in A<sub>2A</sub>R chimeras**

<b>Construct</b>	<b>Truncated regions in A<sub>2A</sub>R</b>	<b>Inserted regions in fusion partner proteins</b>
<b>A<sub>2A</sub>R-BRIL</b>	K209 - G218	A1 – L106
<b>A<sub>2A</sub>R-FiX1</b>	K209 - R220	R10 - E119
<b>A<sub>2A</sub>R-FiX2</b>	K209 - E219	R10 - E118

**Table S2 | Amino acid sequences of FiX1 and FiX2**

Computationally designed amino acid sequences are described in uppercase and residues added to allow expression and purification are described in lowercase.

<b>Construct</b>	<b>Sequence</b>
<b>FiX1</b>	mGEEEEERRRRLLELLKRIAELLERGDLEEALKLVKKLAKEQGRQEIIDYIEEVLRLRYQEGNREEARKLLE ELLRRLEKEGDTEFRELIRIILEFLELEERGDLEEAKKLARELKKQVDEQEKRGLGlehhhhhh
<b>FiX2</b>	mGEEEEERRRRLLELLERLRIARLLKRGDLEEALKLVKKLAKEQGEQEIIDFIEEVLRLRYQEGNREQARELLE RLLRNLEKRGNQDFRNLIIEILRILELEQRGNQEEIKKLAEEELRREVEERKRKRLGlehhhhhh

**Table S3 | Amino acid sequences of A<sub>2A</sub>R fused with FiX1 and FiX2**

Amino acid sequences of fusion partner proteins, FiX1 and FiX2, are highlighted by underlines. Glycine spacer + TEV protease recognition site + TagRFP + 8xHis-tag (lowercase) is added at the C-terminal of each designed protein.

Construct	Sequence
A <sub>2A</sub> R-FiX1	<p>MPIMGSSVYITVELAIAVLAILGNVLVCWAVWLNSNLQNVNTNYFVVSLSAAADIAVGVLAI PFAITISTG  FCAACHGCLFIACFVLVLTQSSIFSLLAIAIDRYIAIRIPLRYNGLVTGTRAKGIIAICWVLSFAIGLT  PMLGWNNGCQPKQKQHSQGCQGVACLFEDVVPNMVMVYFNFFACVLVPLLLMLGVYLRI FLAARRQ  <u>LRLELLKRIAELLERGDLEEALKLVKKLAKEQGRQEI IDYIEEVLRLYQEGNREEARKLLEELLRRLE</u>  <u>KEGDTEFRELIRIILEFLELEERGDLEEAKKLARELKKQVDEARSTLQKEVHAAKSLAII VGLFALCWL</u>  PLHI INCFTFFCPDCSHAPLWLMYLAIVLSHTNSVVPNPFYAYRIREFRQTFRKIIRSHVLRQQEPFKA  genlyfqgvskeelikenmhmklmegtvn nhhfktctsegegkpyegtqtmrikvveggplpfafdil  atsfmygsrtfinhtqgipdffkqs fpegftwervttiedggvltatqdt slqdgcliynvkirgvnfp  sngpvmqkktlgweantemlypadggleg rsdmalklvvgghlicnfkktysrskkpaknlkmpgvvyvd  hrlerikeadketyveqhevavarycdlpsklghklnhhhhhhhh</p>
A <sub>2A</sub> R-FiX2	<p>MPIMGSSVYITVELAIAVLAILGNVLVCWAVWLNSNLQNVNTNYFVVSLSAAADIAVGVLAI PFAITISTG  FCAACHGCLFIACFVLVLTQSSIFSLLAIAIDRYIAIRIPLRYNGLVTGTRAKGIIAICWVLSFAIGLT  PMLGWNNGCQPKQKQHSQGCQGVACLFEDVVPNMVMVYFNFFACVLVPLLLMLGVYLRI FLAARRQ  <u>LRLELLER IARLLKRGDLEEALKLVKKLAKEQGEQEI IDFIEEVLRLYQEGNREQARELLERLLRNLE</u>  <u>KRGNQDFRNLEIEILRILELEQRGNQEEIKKLAEELRREVERARSTLQKEVHAAKSLAII VGLFALCWL</u>  PLHI INCFTFFCPDCSHAPLWLMYLAIVLSHTNSVVPNPFYAYRIREFRQTFRKIIRSHVLRQQEPFKA  genlyfqgvskeelikenmhmklmegtvn nhhfktctsegegkpyegtqtmrikvveggplpfafdil  atsfmygsrtfinhtqgipdffkqs fpegftwervttiedggvltatqdt slqdgcliynvkirgvnfp  sngpvmqkktlgweantemlypadggleg rsdmalklvvgghlicnfkktysrskkpaknlkmpgvvyvd  hrlerikeadketyveqhevavarycdlpsklghklnhhhhhhhh</p>

**Table S4 | Residues used for superposition between A<sub>2A</sub>R and *de novo* designed fusion partner proteins**

	TM5 and TM6 in A <sub>2</sub> A <sub>R</sub>	N- and C-terminal regions in FiX1 and FiX2
<b>A<sub>2</sub>A<sub>R</sub> vs FiX1</b>	R206-L208 and A221-S223	R7-R9 and Q120-K122
<b>A<sub>2</sub>A<sub>R</sub> vs FiX2</b>	R206-L208 and R220-R222	R7-R9 and E119-K121