

SUPPLEMENTARY INFORMATION

THE SH3 DOMAIN IS REQUIRED FOR JAM-A BINDING TO THE THIRD PDZ DOMAIN OF ZO-1*

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*Running title: Structure of the ZO-1 PDZ3-SH3-GUK domains

FIGURE LEGENDS

SUPPLEMENTARY FIGURE S1. *PSG asymmetric unit.* PSG crystallized in the P3₂ space group and contains 4 molecules in the asymmetric unit. Two of the four molecules are missing the GUK domain that could not be modeled. Molecules are represented as a ribbon diagram and colored by chain.

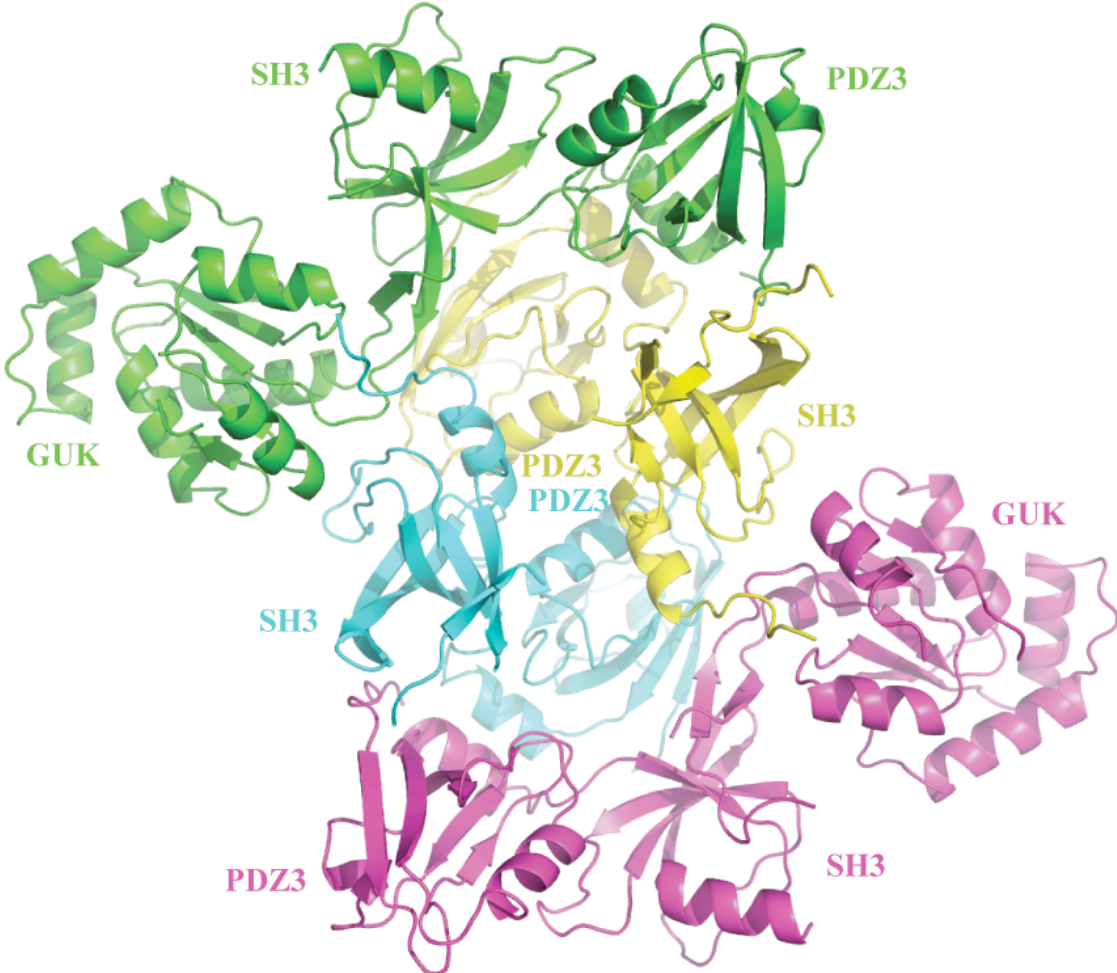
SUPPLEMENTARY FIGURE S2. *Electrostatic surface potential of the PSG core module.* The GUK domain presents a patch of basic residues (blue color) while the PDZ3 domain exhibits a negatively charged surface (red color) on the same face of the protein.

SUPPLEMENTARY FIGURE S3. *Sequence alignment of mammalian JAM proteins.* Sequences of mammalian JAM proteins have been aligned using Clustal W. Sequences corresponding to the 12mer cytoplasmic tail of JAM are boxed in grey. The highly conserved Phe -8 is highlighted in blue and Phe -2 and Ser -3 in red.

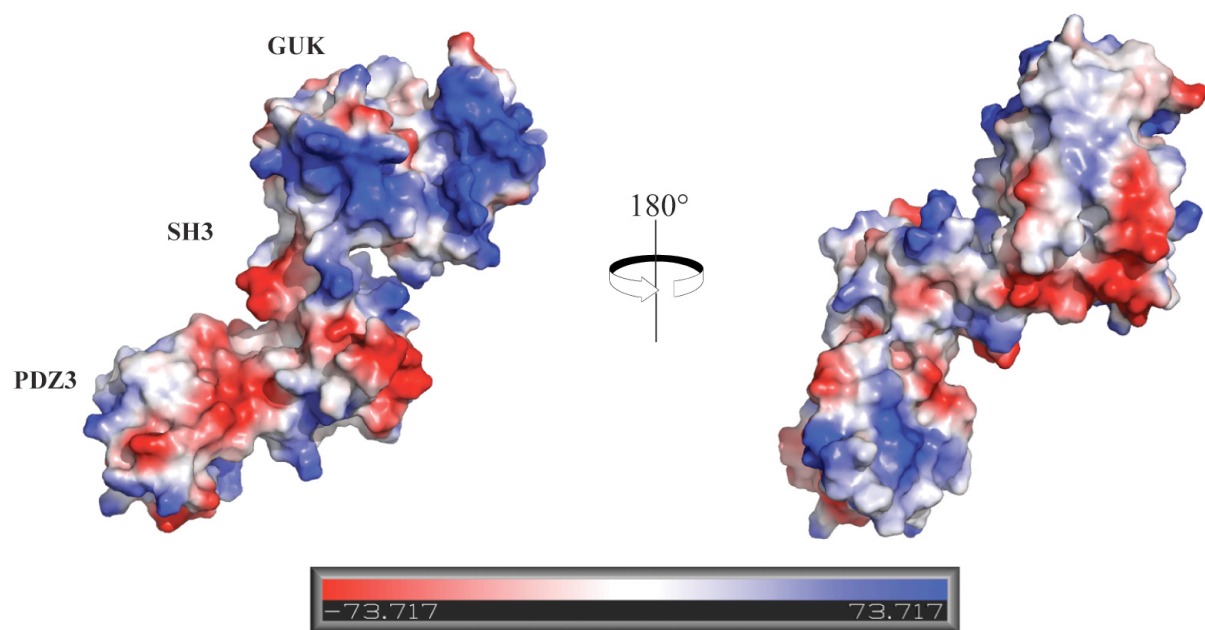
SUPPLEMENTARY FIGURE S4. *NMR characterization of JAM-A_P6 binding to PSG.* (A) 1D NMR spectrum of JAM-A_P6. (B) WaterLOGSY of JAM-A_P6. (C) WaterLOGSY of JAM-A_P6 in the presence of PSG. (D) WaterLOGSY of JAM-A_P6 in the presence of PDZ3. Experimental conditions were 300 μ M JAM-A_P6 and +/- 10 μ M PSG or PDZ3 in 100 mM PO₄/pH 7.2 at 25°C. Resonances corresponding to the sidechain of Phe2 are boxed in grey.

SUPPLEMENTARY FIGURE S5. *Titration of PSG with (A) JAM-A_P6 and (B) JAM-A_P12.* The intensity corresponds that to the phenylalanine signal at 7.2 ppm.

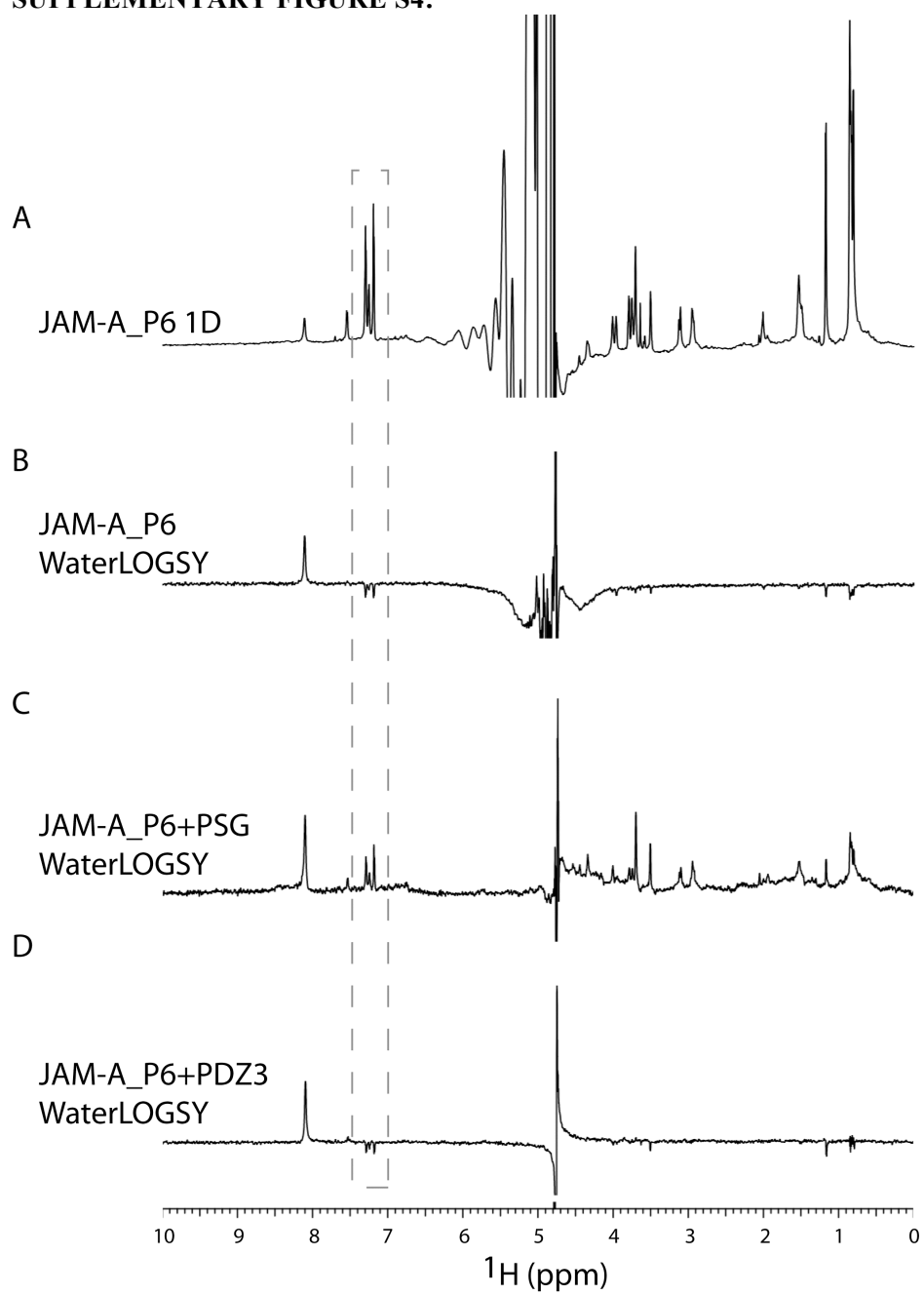
SUPPLEMENTARY FIGURE S1



SUPPLEMENTARY FIGURE S2

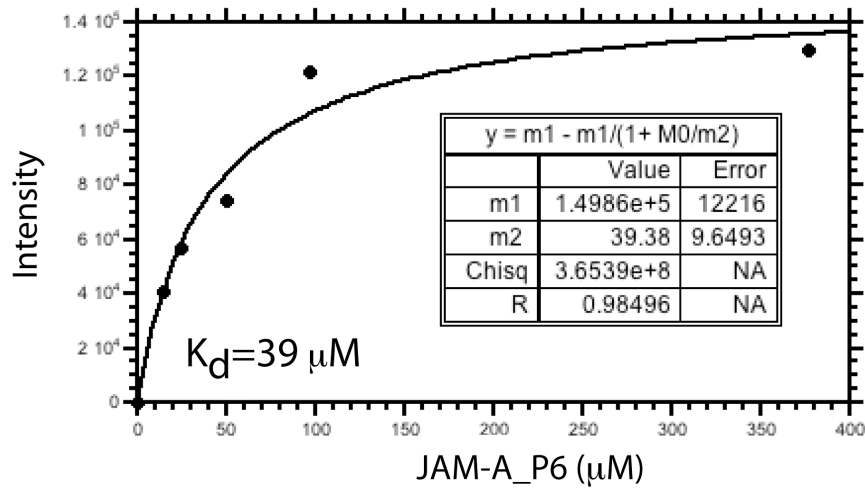


SUPPLEMENTARY FIGURE S4:



SUPPLEMENTARY FIGURE S5

A



B

