

Crystal structure of multifunctional G β 5–RGS9: an R7-family RGS protein complex

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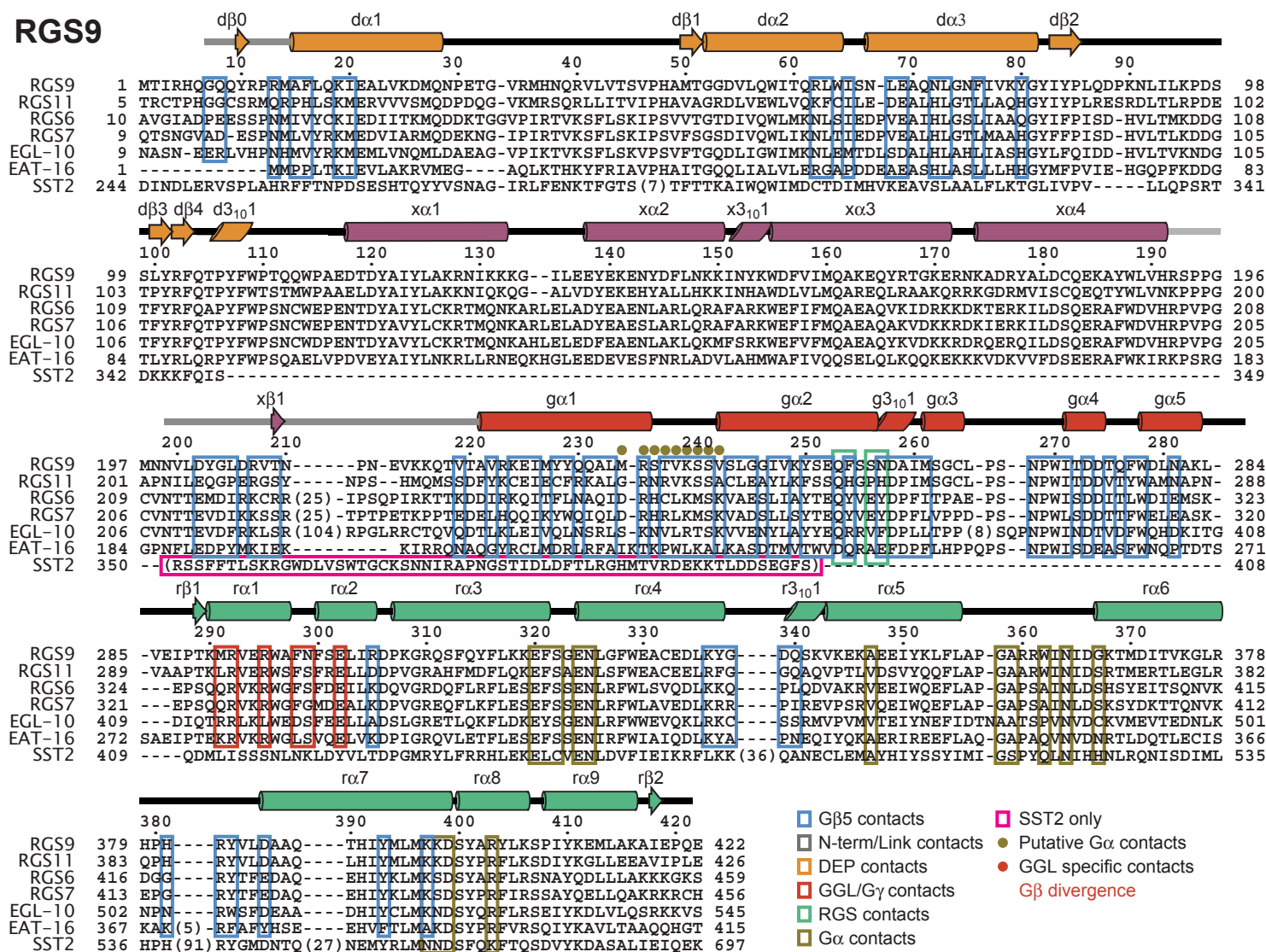
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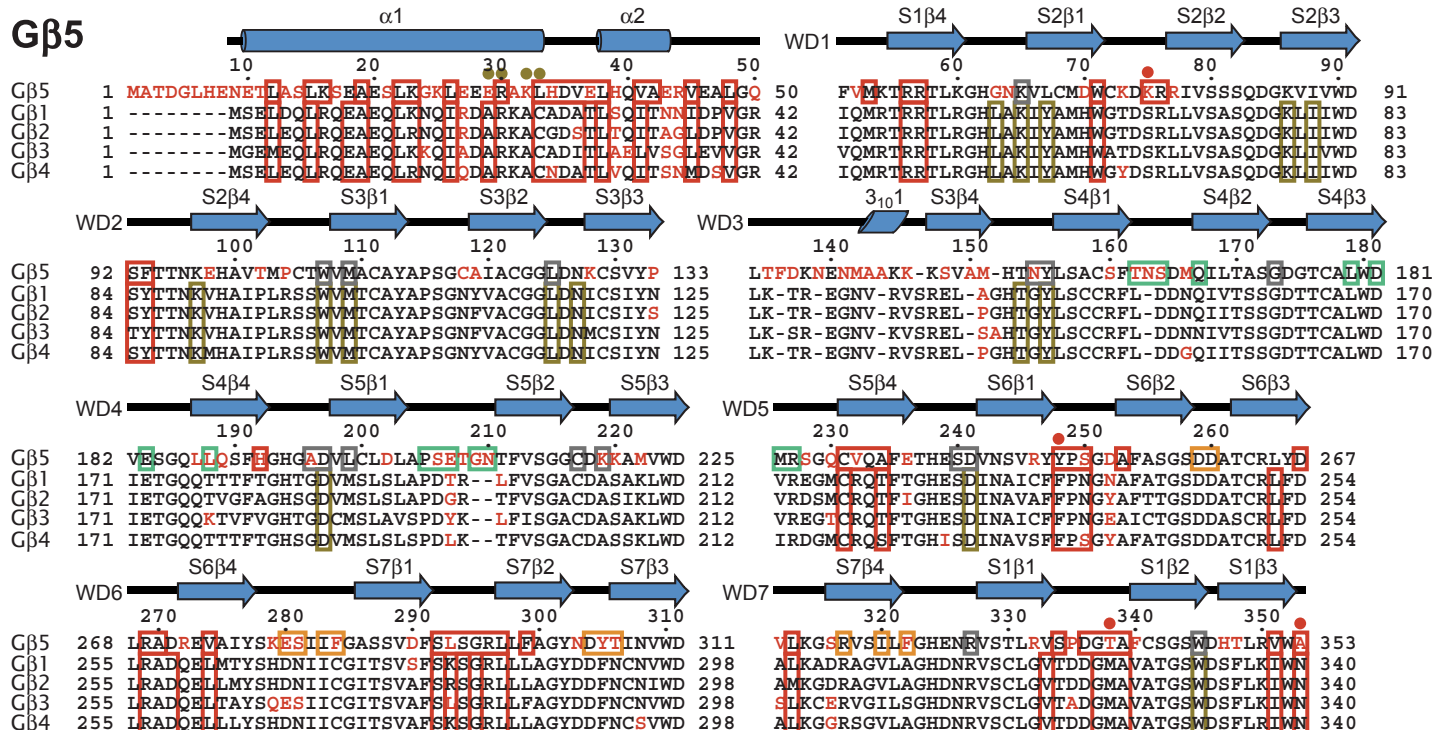
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Supplementary Figure 1

RGS9



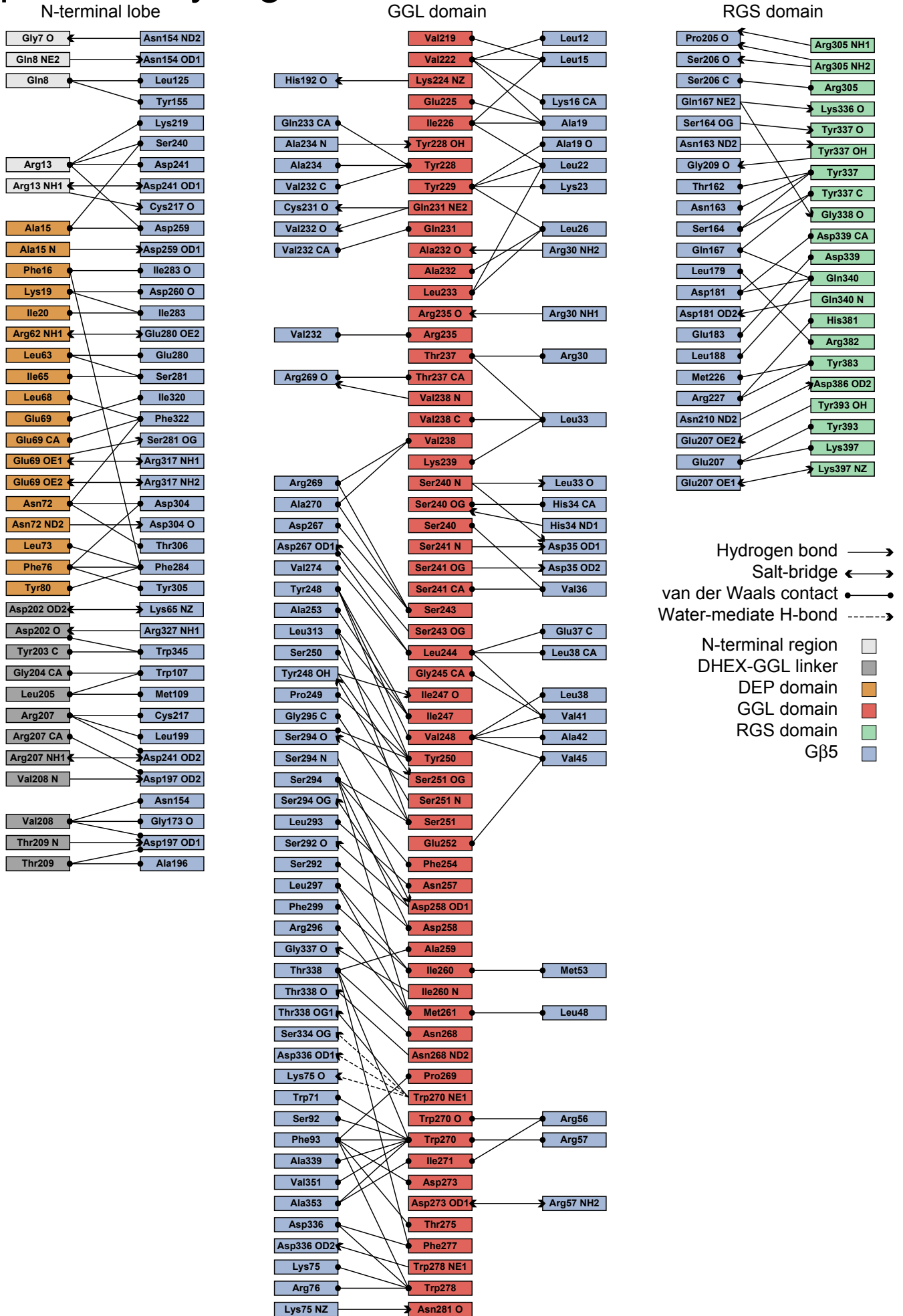
Gβ5



Supplementary Figure 1 R7-RGS and G β secondary-structure and sequence alignments. Secondary-structure elements from the G β 5–RGS9 complex are indicated above sequence alignments as cylinders (α -helices) and arrows (β -strands) and are colored as in **Figure 1**. Residue numbers above sequences are for mouse RGS9 and mouse G β 5. Intra- and intermolecular contacts of RGS9 as discussed above or in ref. 1 (G α contacts) are boxed and colored according to the inset legend. An SST2 segment with no homology to R7-RGS proteins is boxed with magenta. Residues boxed on the G β 5 sequence represent contacts with RGS9. Residues boxed on G β 1-4 sequences are G β subunit consensus contacts with G α and G γ subunits²⁻⁴. Sequentially and/or functionally divergent G β residues are indicated as red text. Additional contacts or modifications as discussed in the text are indicated and described in the figure. GenBank accession numbers for the proteins from top to bottom are BAE23565, NP_001074538, Q9Z2H2, AAH51133, P49809, NP_740905, P11972, NP_619733, P62874, P62880, Q61011 and P29387.

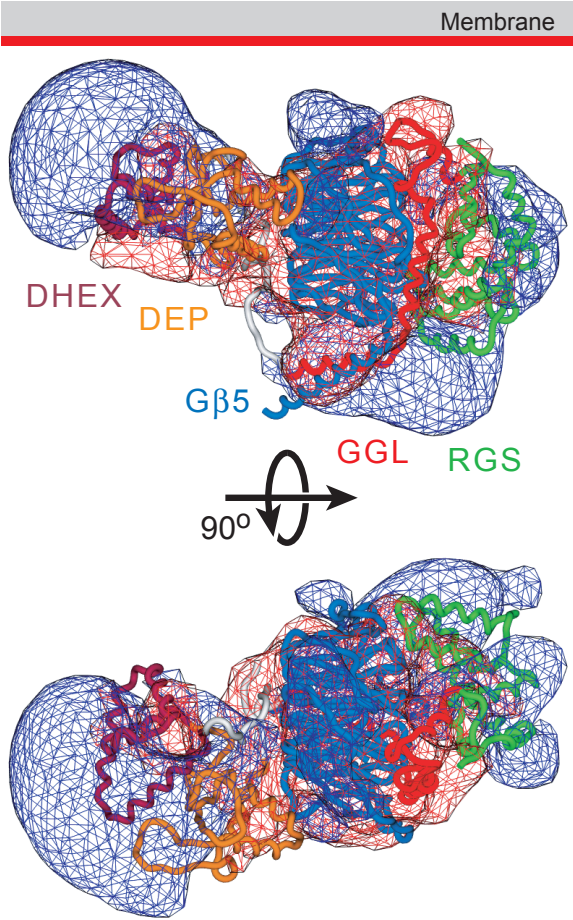
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Supplementary Figure 2



Supplementary Figure 2 Specific contacts between residues of RGS9 and G β 5 residues. Diagram illustrating specific intermolecular contacts between RGS9 and G β 5 (blue) residues. The RGS9 contact residues are colored based on their positions in the N-terminal tail (light-grey), DHEX-GGL linker (dark-grey), DEP domain (orange), GGL domain (red) and RGS domain (green).

Supplementary Figure 3



Supplementary Figure 3 The electrostatic potential of G β 5–RGS9 supports the membrane orientation model. Electrostatic potential maps, calculated at $\pm 2 kT$, and depicted as positive (blue) and negative (red) contours, are superposed on the G β 5–RGS9 structure backbone trace colored as in **Figure 1**. **Top**, Oriented as in **Figure 6a** relative to the membrane. **Bottom**, The structure is rotated 90° around the X-axis with respect to the **top** image.