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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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This is a single–particle cryo-EM study. The number of raw particles and particles included in the different refining steps as well as the final particles included in the final 3D reconstruction are stated in the Results, Materials and Methods sections and can be found in Table 1, Figure 1-figure supplement 1D.

Sample size and statistical methods for determining significance in difference for functional testing using Rb efflux essays and patch-clamp recordings are detailed in Materials and Methods and in the legends for Figure 7 and Figure 7-figure supplement 1. For these experiments, no power analysis was used and the sample size of ≥3 is considered adequate for performing statistical analysis using the standard methods stated in the manuscript.

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Biological repeats for experiments shown in Figure 7 and Figure 7-figure supplement 1 are as described in the corresponding figure legend.

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* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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Software and algorithms used for processing of the single particle data are described in Materials and Methods, Key resources table, Table 1, and Figure 1-figure supplement 1.

Statistical tests, sample size, mean and SEM of functional tests used in experiments presented in Figure 7 and Figure 7-figure supplement 1 are described in the corresponding figure legends.

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Source data of the 3D reconstruction and model will be deposited into the Protein data bank upon acceptance of the manuscript.