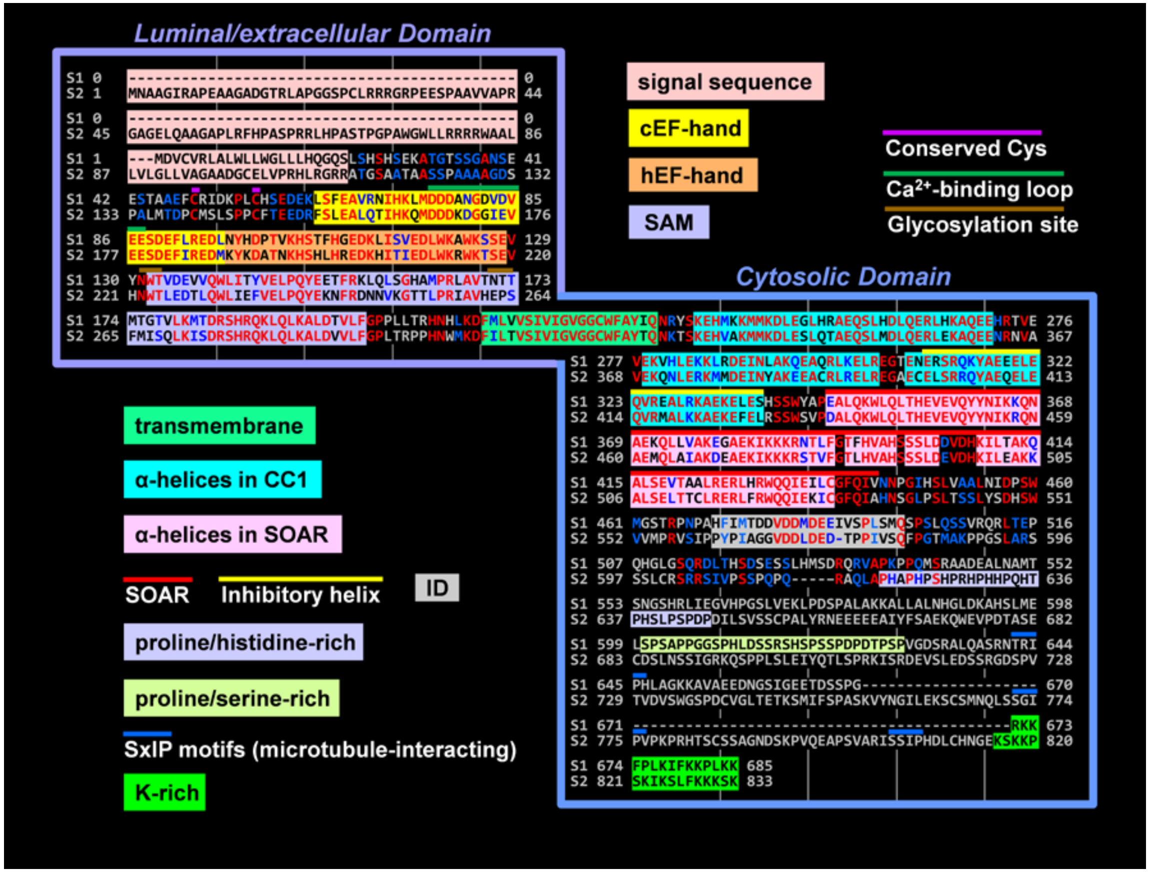

Supplementary information S1 (Figure) | **Sequence alignment of stromal interaction molecule1 STIM1 and STIM2.** Identity (red), similarity (blue) or differences (black and grey) between STIM1 and STIM2 are shown. Major structural features are also described and as shown in Fig. 1a. Note: the existence of an extended signal peptide in STIM2 is based on recent findings[1] that disproved earlier suggestions of an alternative translational start site (TTG; L86) for STIM2 (REF. 2). Based on this new evidence, STIM2 has been renumbered to start at its originally predicted Kozak sequence (Accession AAI71766.1). The three α-helices of the first coiled-coil domain (CC1) are predicted based on sequence analysis using JPred3 (REF. 3). The third of these helices (inhibitory helix) is supported by homology with the recently solved *C. elegans* structure[4]. cEF, canonical EF-hand hEF, hidden EF-hand ID, inhibitory domain SOAR, STIM Orai activating region.

1. Graham, S. J., Dziadek, M. A. & Johnstone, L. S. A cytosolic STIM2 preprotein created by signal peptide inefficiency activates ORAI1 in a store-independent manner. *J. Biol. Chem.* **286**, 16174–16185 (2011).
2. Williams, R. T. *et al.* Identification and characterization of the STIM (stromal interaction molecule) gene family: coding for a novel class of transmembrane proteins. *Biochem. J.* **357**, 673–685 (2001).
3. Cole, C., Barber, J. D. & Barton, G. J. The Jpred 3 secondary structure prediction server. *Nucleic Acids Res.* **36**, W197–201 (2008).
4. Yang, X., Jin, H., Cai, X., Li, S. & Shen, Y. Structural and mechanistic insights into the activation of Stromal interaction molecule 1 (STIM1). *Proc. Natl Acad. Sci. USA* (2012).