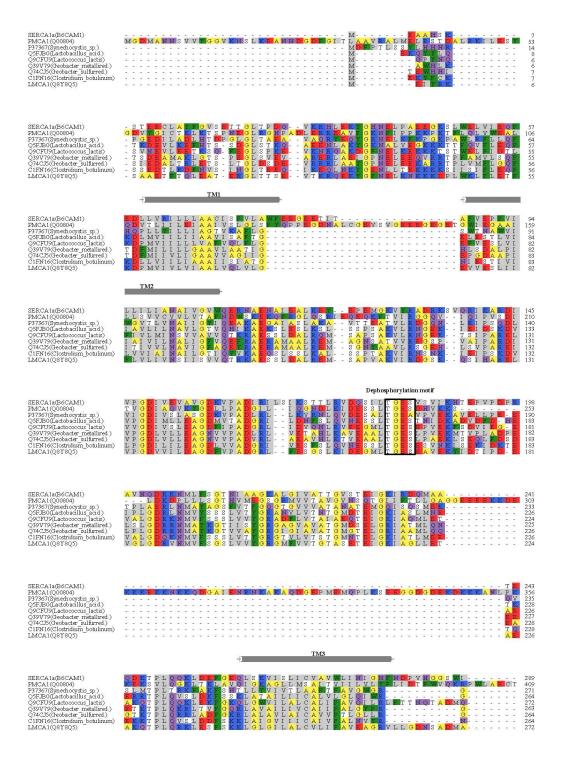
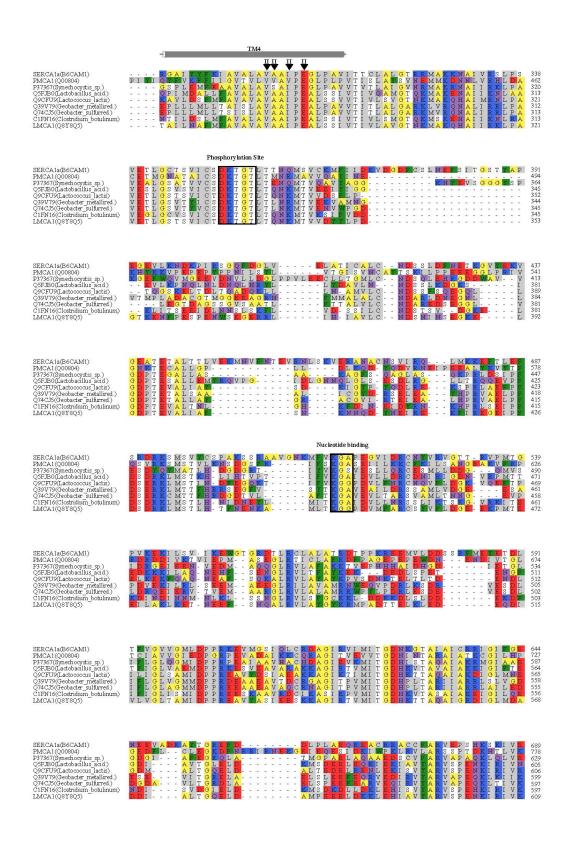
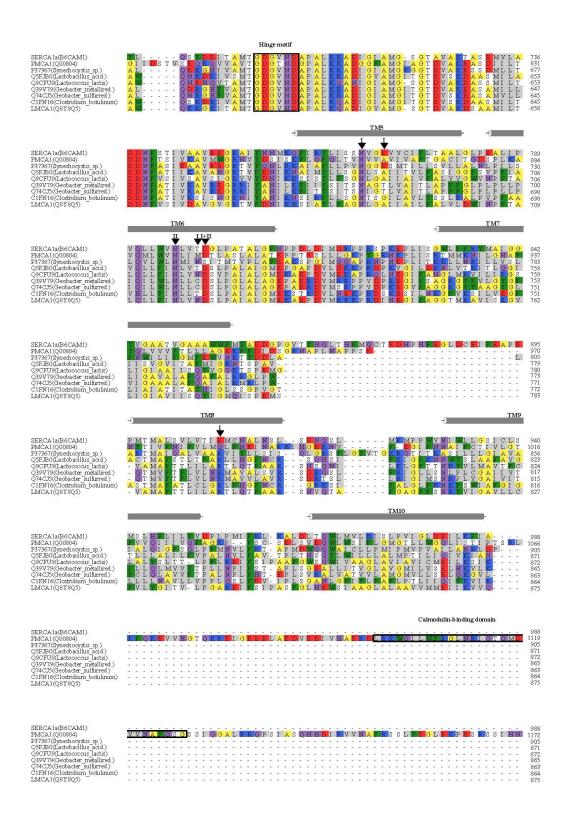
Figure S1







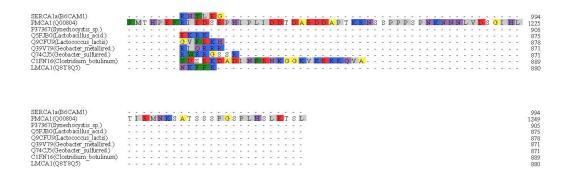


Figure S1: Multiple sequence alignment selected Ca²⁺ ATPases from rabbit and eubacteria generated by aligning 52 sequences of type IIa and IIb P-type ATPases in MUSCLE(1). The following amino acid groupings are indicated by colour schemes: positively charged (RK) shown on blue background; polar (QN) shown in purple; hydrophobic (CLIVM) with gray background; aromatic (FWY) with green background; small (TS) with a white background and tiny (AG) with yellow background. The dephosphorylation motif (TGES), phosphorylation motif (DKTGT), nucleotide binding motif (KGA), hinge motif (GDGXND) and calmodulin binding domain are highlighted in boxes. The residues involved in binding Ca²⁺ at site I and II are marked by black arrowheads. The structural elements of the transmembrane helices of SERCA1a (PDB: 1T5T) (2) are depicted in gray above the alignment.

Figure S2

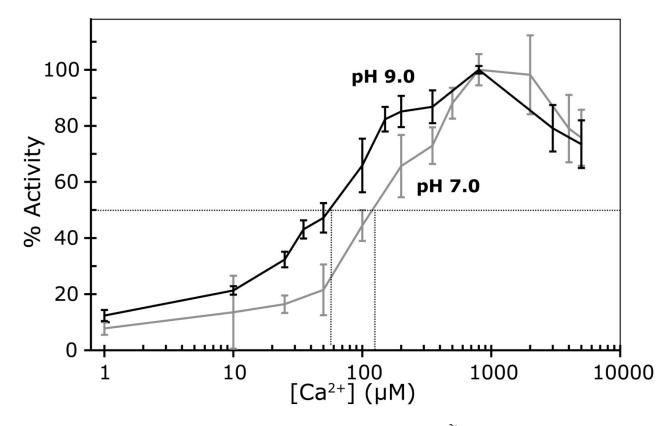


Figure S2. The ATPase activity of LMCA1 measured as a function of Ca²⁺-concentration at pH 7 (grey line) and 9 (black line).

- 1. Edgar, R. C. (2004) Nucl Acids Res 32, 1792-1797
- 2. Sorensen, T. L., Moller, J. V., and Nissen, P. (2004) Science 304, 1672-1675