Figure S1

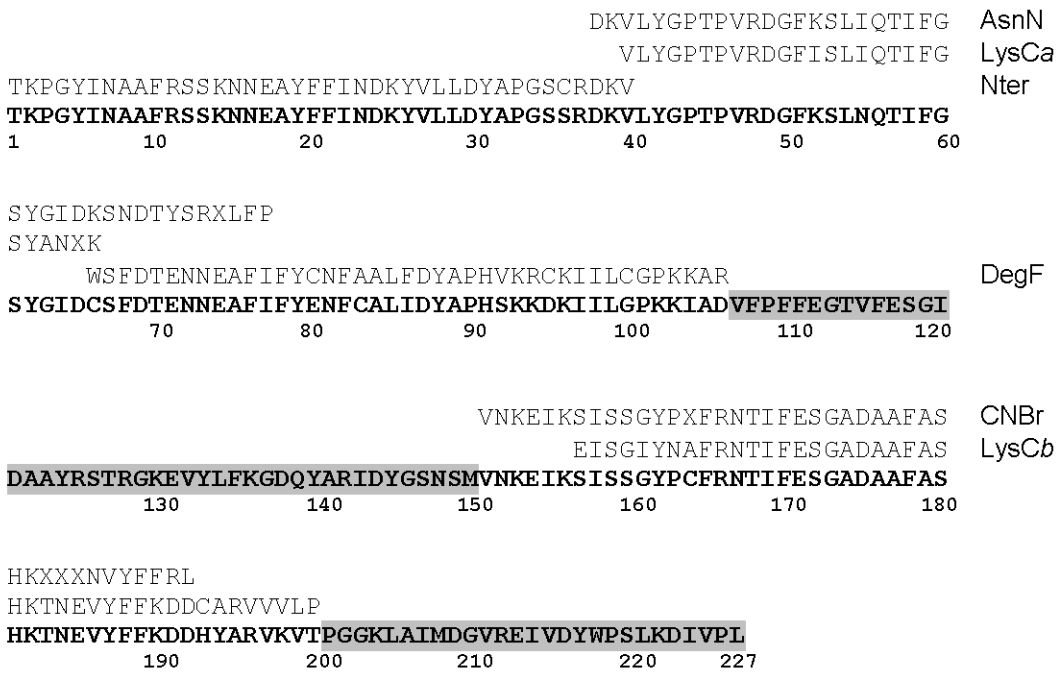

Figure S1. Amino acid sequence of LS-24. LS-24 sequence derived on the basis of internal sequencing and the interpretation of electron density map calculated using *ab initio* phases at 2.2Å resolution. The N-terminal sequences of LS-24 (Nter), fragments obtained by natural proteolysis (DegF), proteolysis by endoproteinase Lys-C (LysC*a* and LysC*b*), endoproteinase Asn-N (AsnN) and chemical modification using CNBr (CNBr) have been aligned. The portions of the sequence interpreted from electron density map are highlighted in grey.