

**Figure S1**

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DKVLYGPTPVVDGFKSLIQTI FG AsnN
VLYGPTPVVDGFISLIQTI FG LysCa
TKPGYINAAFRSSKNNEAYFFINDKYVLLDYAPGSCRDKV Nter
TKPGYINAAFRSSKNNEAYFFINDKYVLLDYAPGSSRDVLYGPTPVVDGFKSLNQTIFG
1          10          20          30          40          50          60

SYGIDKSNNTYSRXLF P
SYANXK
WSEDTENNEAFIFYCNFAALFDYAPHVKRCKIILCGPKKAR DegF
SYGIDCSFDTENNEAFIFYENFCALIDYAPHSKDKIILGPKKIADVFPFFEGTVFESGI
          70          80          90          100         110         120

VNKEIKSISSGYXPFRNTIFESGADAAAFAS CNBr
EISGIYNAFRNTIFESGADAAAFAS LysCb
DAAyrSTRGKEVYLFKGDQYARIDYGSNSMvNKEIKSISSGYPCFRNTIFESGADAAAFAS
          130         140         150         160         170         180

HKXXXNVYFFRL
HKTNEVYFFKDDCARVVLP
HKTNEVYFFKDDHYARVKVTPGGKLAIMDGVREIVDYWPSLKDIVPL
          190         200         210         220         227
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**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 (LysCa and LysCb), 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.