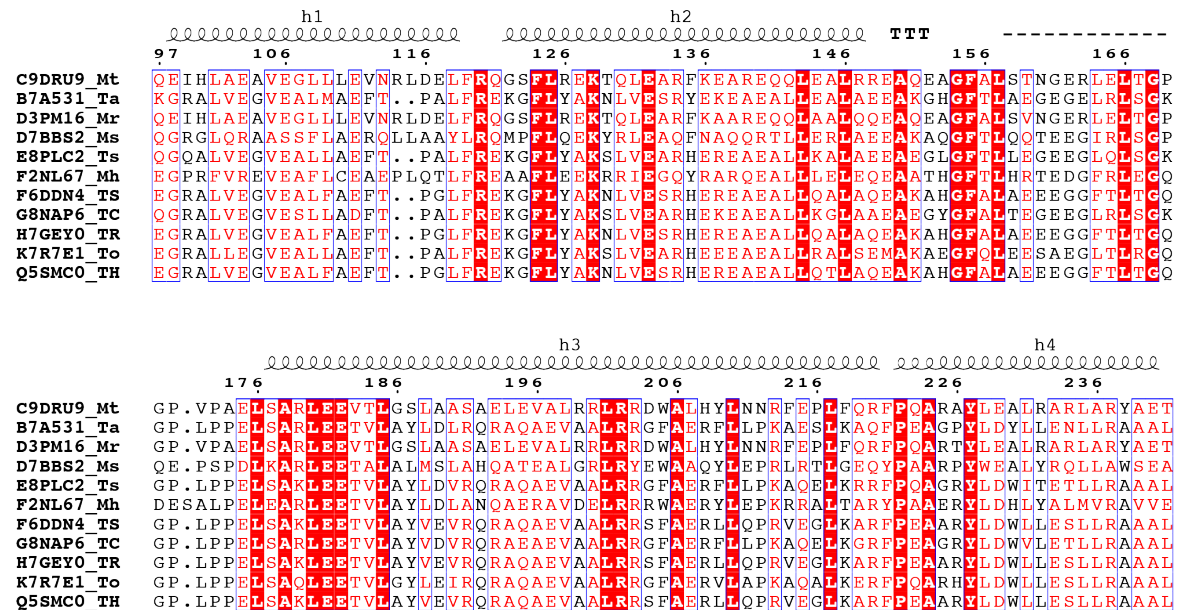


Supplemental Figure S1 by Li et al.:



Supplemental Figure S1. Sequence alignment of the HHE regions of LonC proteases from different species. Sequences of the HHEs of LonC proteins from *Meiothermus taiwanensis* (Mt), *Thermus aquaticus* (Ta), *Meiothermus rubber* (Mr), *Meiothermus Silvanus* (Ms), *Thermus scotoductus* (Ts), *Marinithermus hydrothermalis* (Mh), *Thermus thermophilus* strain SG0.5JP17-16 (TS), *Thermus* sp. CCB_US3_UF1 (TC), *Thermus* sp. RL (TR), *Thermus oshimai* (To), *Thermus thermophilus* strain HB8 (TH), were aligned using T-coffee (Notredame *et al.*, 2000). The UniProtKB/TrEMBL accession numbers of the proteins are given in front of the abbreviations for the organisms. The secondary structure of the HHE as defined by the structure of MtaLonC-N is shown on top of the aligned sequences. Helical coils and TTT denote α -helices and strict α -turns, respectively. Dashed lines indicate the region where the electron density map is not interpretable. Strictly conserved residues are colored in white characters on a red background. Conserved residues defined based on their physico-chemical properties as higher than 70% are colored in red on a white background and framed in blue boxes. The figure was created with ESPrnt (Gouet *et al.*, 1999).

Supplemental Reference:

Gouet, P., Courcelle, E., Stuart, D. I. & Metoz, F. (1999). *Bioinformatics* **15**, 305-308.
 Notredame, C., Higgins, D. G. & Heringa, J. (2000). *J. Mol. Biol.* **302**, 205-217.