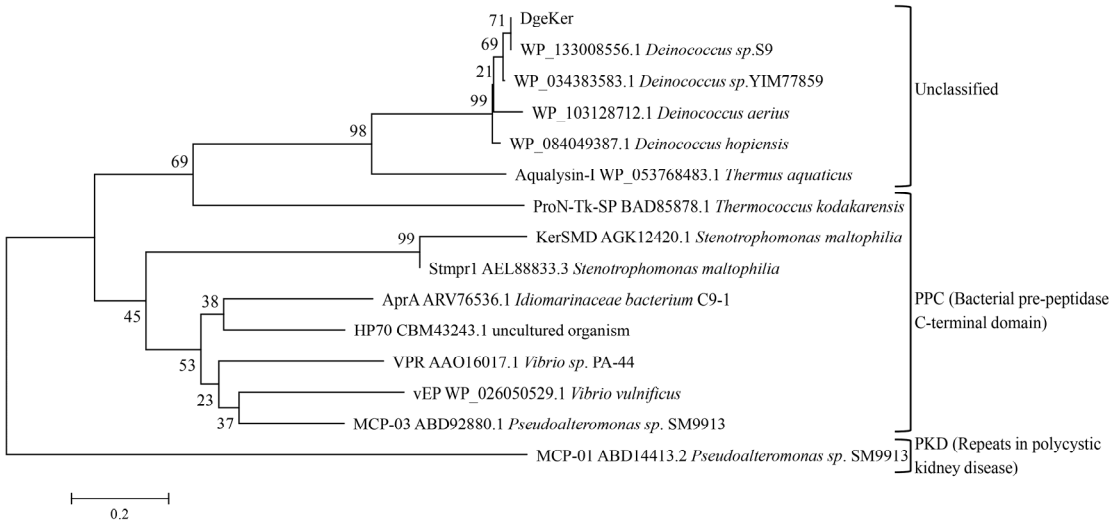# A novel thermostable keratinase from D*einococcus geothermalis* with potential application in feather degradation

Yin Tang[1], Leizhou Guo[1], Mingming Zhao[2,] Yuan Gui[1], Jiahui Han[2], Qilin Dai[1], Shijie Jiang[1], Min Lin[2], Zhengfu Zhou[2,*], Jin Wang[1,2,*]

Figure S1. Phylogenetic analysis of C-terminal extension of DgeKer and other keratinases. The C-terminal extension used were from Aqualysin-I, ProN-Tk-SP and other keratinases. The name and GenBank accession No. for each kerainase are in front of the Latin name of each strain. The classification of C-terminal extension is shown following one-sided brackets. The phylogenetic tree derived by the Neighbor-Joining method. The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches.
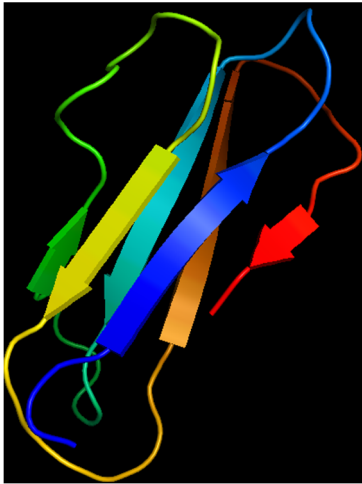
Figure S2. Modeled structured of C-terminal extension of DgeKer using Pymol software. Structure of ProN-Tk-SP from Thermococcus kodakaraensis (PDB ID: 3AFG) was used as template. The secondary structural elements are represented in cartoon model.