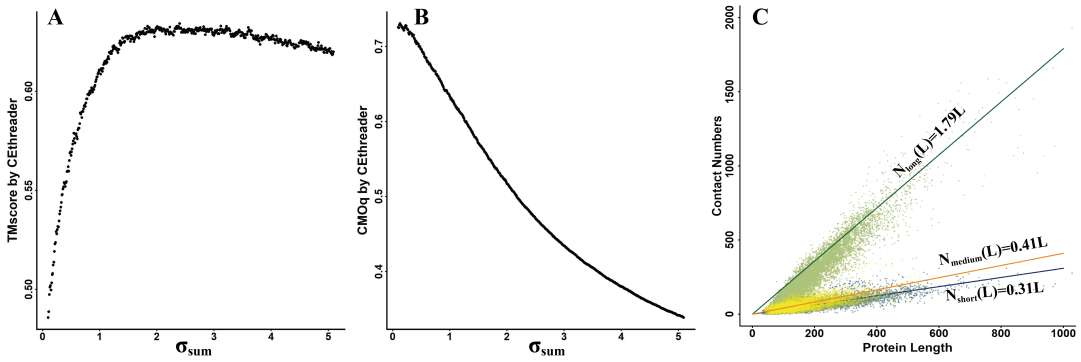

Figure S4. Optimization of the number of predicted contacts to be used by CEthreader. (A, B) TM-score and *CMOq* as a function of σ_{sum} by CEthreader on 905 training protein pairs. (C) Correlation between the number of contacts and the sequence length for 9,896 non-redundant domains from the SCOPe database with a pair-wise sequence identity cutoff of <30%. The linear regression with fitted σ_{cr} parameters coincides well with the experimental structure data.