ProTherm: Thermodynamic Database for Proteins and Mutants

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1 Introduction

Thermodynamic data for proteins are important for understanding the mechanism of protein stability as well as protein engineering. Recently, several mutation databases have been developed for specific objectives. On the other hand, there are no electronically accessible databases for thermodynamic data on protein stability. Thus, we have developed a database, Thermodynamic Database for Proteins and Mutants (ProTherm) [1], which includes several thermodynamic data, structural information, measuring methods, experimental conditions and literature information. This database will help to understand the mechanism of protein stability. A WWW interface will enable users to search the database through the Internet.

2 Contents of the database

Each entry in the database is identified by a serial number and includes the following information: (i) *Structural information*: protein name, enzyme code, Protein Mutant Database (PMD) numbers, Protein Data Bank (PDB) code for wild and mutant structures, wild and mutant residue names with residue number showing the nature of mutation, information on monomeric and oligomeric states, secondary structure, accessibility and number of transition states. (ii) *Thermodynamic data obtained from denaturant denaturation experiments*: unfolding Gibbs free energy change in the absence and presence of denaturant (ΔG^{H2O}, ΔG), difference in unfolding Gibbs free energy changes in the absence and presence of denaturant ($\Delta\Delta G^{\mathrm{H2O}}$, $\Delta\Delta G$), Temperature (T), midpoint of denaturant concentration (C_{m}) and slope of denaturation curve (m). (iii) *Thermodynamic data obtained from thermal denaturation experiments*: unfolding Gibbs free energy change (ΔG), difference in Gibbs free energy changes ($\Delta\Delta G$), transition temperature (T_{m}), transition temperature change (ΔT_{m}), enthalpy change (ΔH) and heat capacity change (ΔC_{p}). (iv) *Experimental methods and conditions*: pH, measurements and method. (v) *Functional information*: enzyme activity, binding constants etc. (vi) *Literature information*: keywords, reference, authors and remarks.

3 Search options

A WWW interface enables users to search data based on various conditions with different sorting options for outputs. (i) retrieving data for a particular protein. (ii) specifying the type of mutation as single, double, multiple or wild type. Further, specifying any wild type residue and/or mutant residue is possible. (iii) specifying secondary structures having mutations, helix (H), strand (S), turn (T) and coil (C). (iv) searching data based on solvent accessible surface area (ASA; in % or Å^2) of relevant residue. The mutations are classified into buried (ASA $< 20\%$), partially buried ($20\% \leq ASA \leq 50\%$) and exposed (ASA $> 50\%$). (v) extracting data for a particular measurement (CD, DSC, Fl etc.) and a specific method (Thermal, GdnHCl, Urea etc.), (vi) limiting data for a particular range of T, $T_{\rm m}$, $\Delta T_{\rm m}$, ΔG, $\Delta\Delta G$, $\Delta G^{\rm H2O}$, $\Delta\Delta G^{\rm H2O}$, ΔH, $\Delta C_{\rm p}$ and pH. (vii) extracting data with authors, publication year and key words. (viii) specifying output format by selecting various output items and by sorting with publication year, wild type residue, mutant residue, residue number, secondary structure, accessibility, pH, T, $T_{\rm m}$, $\Delta T_{\rm m}$, ΔH, ΔG, $\Delta\Delta G$, m, $C_{\rm m}$, $\Delta G^{\rm H2O}$ and $\Delta\Delta G^{\rm H2O}$.

4 Links to other databases

ProTherm is cross-linked with NCBI PUBMED literature database, Protein Mutant Database, Enzyme code and Protein Data Bank structural database. Moreover, all the mutation sites associated with each PDB structure are automatically mapped and can be directly viewed through 3DinSight developed in our laboratory.

5 Availability

The database is freely available at the URL, http://www.rtc.riken.go.jp/protherm.html.

References

[1] Gromiha, M.M., An, J., Kono, H., Oobatake, M., Uedaira, H. and Sarai, A., ProTherm: Thermodynamic database for proteins and mutants, *Nucleic Acids Res.*, 1999 (in press).