Supplementary information

Table S1: Comparison of data in ProThermDB and MPTherm databases

Mutation type	Data size		Fold increase in ProThermDB
	ProThermDB	MPTherm	
Total	31580	7181	4.39
Wild-type	12050 (38.15)	3808 (53.02)	3.16
Single	16028 (50.75)	2330 (32.44)	6.87
Double	2046 (6.47)	362 (5.06)	5.65
Multiple (>=3)	1456 (4.63)	681 (9.48)	2.14

Note: Percentage of data in each classification is shown in parenthesis

Table S2: Description of data items in ProThermDB with an example entry showing the experimental thermodynamic data of carbonic anhydrase 2 protein. Underline indicates hyperlinks to other databases

Description	**Example**
Entry	27543
Protein name	Carbonic anhydrase 2
Source name	Homo sapiens (Human)
UniProt ID	P00918
Sequence length	260
Mutation (UniProt)	G145R
Mutation type	Single
PDB ID	12CA
Solvent accessibility	0.0
Secondary structure	Helix
Temperature (℃)	25.0
pH	7.5
Buffer name	-
Buffer concentration	-
Ion	-
Ion concentration	-
Additives	-
Protein concentration	-
Measure	Fluorescence
Method	GdnHCL
Remarks	Parameters computed during native (N) to intermediate state (I) unfolding transition
ΔG^{H2O}(kcal/mol)	3.58 (1.58)
$\Delta\Delta G_{H2O}$	-0.36
ΔG (kcal/mol)	-
ΔΔG (kcal/mol)	-
m (kcal/mol/M)	6.23 (2.29)
Cm (M)	0.58
Tm (℃)	-
ΔTm (℃)	-
ΔH (kcal/mol	-
ΔHvH (kcal/mol)	-
ΔC_p (kcal/mol)	-
State	3
Reversibility	Yes
PubMed id	31778702
Authors	Gupta, P., Mahlawat, P. and Deep, S
Reference	Int J Biol Macromol 143, 472-482 (2020) PMID: 31778702
Location of the data	Table 2, p.479
Keywords	Carbonic anhydrase deficiency syndrome; Human carbonic anhydrase II; Mutant; Protein destabilization