Conformational energy maps of amino acids with a side chain C^{β} atom derived from high-resolution protein structures

Govardhan A. Balaji[1,†], H. G. Nagendra[1], Vitukudi N. Balaji[1] and Shashidhar N. Rao[2,3,*]

[1]Department of Biotechnology, Sir M. Visvesvaraya Institute of Technology, Bengaluru 562 157 India
[2]Department of Chemistry and Chemical Biology, Rutgers University, Piscataway, NJ 08552 USA
[3]Present address: Department of Bioengineering, University of California, San Diego, CA 92093, USA

Experimental protein energy maps in the (ϕ, ψ) space for the dipeptides of 20 naturally occurring amino acids using the current collections of high-resolution entries in the protein data bank (PDB) are presented here. Data sets were generated for hydrogen bond distance cut-off values of 2.7 Å and 3.1 Å. Neighborhood effects of proline residues on the (ϕ, ψ) maps have been examined. The impact of disulphide bridges on these maps has been critically examined. The comparisons of experimental maps with those obtained using various molecular mechanics and molecular dynamics methods were published earlier. The comparison metrics are: (i) locations of global and secondary minima, (ii) percentage areas enclosed by isoenergy contours, (iii) energy-based RMSD and (iv) barriers to conformational transitions. The experimental maps for individual amino acid dipeptide motifs show a higher degree of qualitative consistency with theoretical maps derived using molecular mechanics when compared to those from molecular dynamics methods. We also demonstrate that a majority of backbone conformations observed in the structures of small peptides in the Cambridge Crystallographic Database are within the allowed regions of the experimental Ramachandran maps. A few protein models obtained from NMR spectroscopy were evaluated in terms of the amino acid outlier energies using the experimental maps.

and their consistency with experimental observations has been evaluated and reviewed[1–12]. Following studies by Pohl[13], we have recently presented extensive analyses of these conformational parameters in the X-ray structures obtained from the protein data bank (PDB) in terms of (ϕ, ψ) energy maps (referred to interchangeably as Pohl's maps, experimental conformational energy maps and empirical protein energy maps (henceforth as EPEMs)) as a function of X-ray resolution, sequence homology and distances between atoms involved in main chain hydrogen bonds[14]. Finkelstein *et al.*[15,16] demonstrated that this quasi energy originates from the Boltzmann-like statistics of stable folds of random heteropolymeric proteins that exhibit mutational changes of residues. They also showed that the corresponding conformational temperature of such statistics can be estimated as the protein melting temperature arising from an 'all-or-none' melting transition, which is, in turn dependent on the properties of diverse amino acid residues. Such maps were obtained by converting the Boltzmann distribution of backbone dihedral occurrences into energy. These analyses focused on four separate motifs: alanyl dipeptide, glycyl dipeptide, prolyl dipeptide and a combination of all non-glycyl non-prolyl dipeptides. It was demonstrated that the features of experimental energy maps such as positions of minima, per cent occupancy of energy contours, the barrier to transitions from one mini-