International Tables for Crystallography (2006). Vol. F, Figure 22.1.2.3, p. 544.

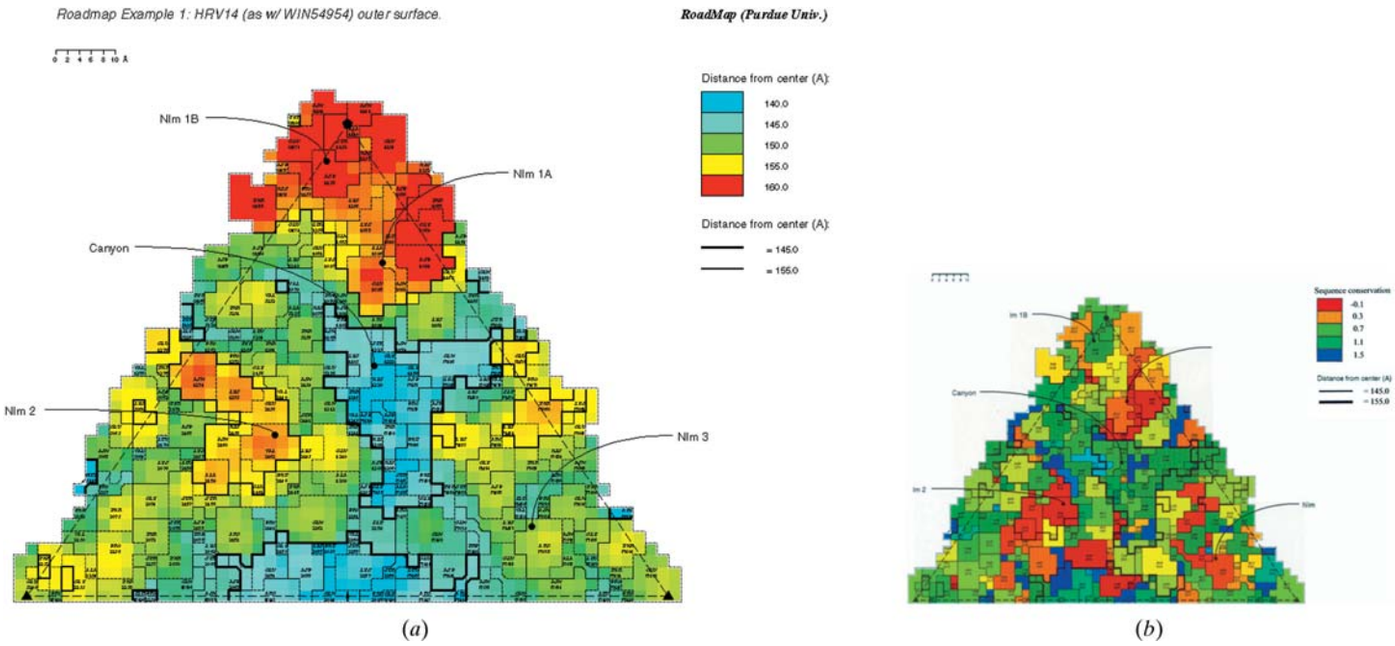

Fig. 22.1.2.3. (*a*) Solvent-accessible surface topology of a rhinovirus 14–drug complex (Kim *et al.*, 1993). The triangle shows one of the 60 symmetry-equivalent faces of an icosadeltahedron that constitute the entire virus surface. The surface is coloured and contoured according to distance from the centre of the virus, red being the most elevated. Residues are marked with dotted lines and labelled with residue type and number. A letter starting the residue label indicates a symmetry equivalent. The first numeral indicates the protein number (1 to 4), which is followed by the three-digit residue number. A depression, the 'canyon', is where the cellular receptor is bound (Olson *et al.*, 1993). The locations of the dominant neutralizing immunogenic (NIm) sites were determined through the sequencing of escape mutants (Sherry & Rueckert, 1985; Sherry *et al.*, 1986) and are labelled 'NIm'. (*b*) The same view is coloured according to sequence similarity (Palmenberg, 1989; Chapman, 1994), with blue being the most conserved rhinoviral amino acids and red being the most variable. Comparison of diagrams like these suggested the 'canyon hypothesis' (Rossmann, 1989). The prediction has proved largely true in that the sites of receptor attachment in several picornaviruses would be depressed areas whose sequences could be more highly conserved because they were partially inaccessible to antibodies and therefore not under the same selective pressure to mutate. In this and other applications, the schematic nature of these diagrams has helped in the collation of structure with data arising from the known phenotypes of site-directed or natural mutants. Part (*b*) is reproduced from Chapman (1993). Copyright (1993) The Protein Society. Reprinted with the permission of Cambridge University Press.

Many other properties can be mapped to the surface. These include properties of the atoms associated with that part of the surface (such as thermal factors), curvature of the surface calculated from adjacent atoms (Nicholls & Honig, 1991), or distance to the nearest part of the surface of an adjacent molecule. *GRASP* is now used to illustrate complicated molecular structures, in part because it also supports the superimposition of other objects over the molecular surface. These include the representation of molecules with CPK spheres and/or bonds, and the representation of electrostatic potentials with field lines, dipole vectors *etc.*

22.1.2.4.1.5. *Implementations in popular packages*

Commercial packages use variants of the methods discussed above. For example, surfaces are drawn in the *Insight* II molecular modelling system using the Connolly dot algorithm (Molecular Structure Corporation, 1995).

22.1.2.4.2. *Schematic and two-dimensional representations such as 'roadmap'*

For their work on viruses, Rossmann & Palmenberg (1988) introduced a highly schematic representation in which individual amino acids were labelled. The methods were extended by Chapman (1993) to other proteins and to the automatic display of features such as topology, sequence similarity and hydrophobicity. Roadmaps sacrifice a realistic impression of shape for the ability to show the locations and properties of constituent surface atoms or residues. This has been important in combining the power of structure and molecular biology in understanding function. Potential sites of mutation are readily identified without substantial molecular-graphics resources, and phenotypes of mutants are readily mapped to the surface and compared with the physiochemical properties to reveal structure–function correlations.

For a set of projection vectors, the intersection points with the first van der Waals (or solvent-accessible) surface of an atom are calculated by basic vector algebra. The atom is identified so that when the projection is mapped to a plane for display, the boundaries of each atom or amino acid can be determined. The atoms or amino acids can then be coloured, shaded, outlined, contoured, or labelled according to parameters that are either calculated from the coordinates (such as distance from the centre of mass), read from a file (such as sequence similarity), or follow properties that are dependent on the residue type (*e.g.* hydrophobicity) or atom type [*e.g.* atomic solvation parameters (Eisenberg & McLachlan, 1986)].

Several types of projections can be used. The simplest is similar to that used by most other surface-imaging programs. A set of parallel projection vectors is mapped to a 2D grid. An example is shown in Fig. 22.1.2.3. This view avoids distortions, but only one side of the molecule is visualized. Roadmaps are flat, two-dimensional projections that cannot be rotated in real time to reveal other views. Three-dimensionality is limited to an extension by Jean-Yves Sgro that maps the parallel projection of one view to a three-dimensional surface shell that can be rotated with interactive graphics and/or viewed with stereo imaging (Harber *et al.*, 1995; Sgro, 1996). However, the schematic nature of roadmaps leads to the ability to view all parts of the molecule simultaneously.

To view all parts of the molecule, cylindrical projections are used that are similar to those used in atlases. This is possible because the

references