for the curved edges. Lastly, the internal control points used for the Gregory patches are determined.

The resultant molecular surface is easily malleable and hence useful in describing receptor sites for scientists performing molecular modeling studies. Key properties of our new molecular surface generation technique are as follows: (1) the surface is closed and generated about a volume, (2) the surface is smooth and continuous, and (3) the surface can be manipulated in real time. Generation of an equilateral triangular net and accompanying control points about the surface have allowed for the creation of a smooth and continuous parametric patch surface based on Gregory patches. Gregory patch surfaces successfully and efficiently meet the above criteria and provide the basis for an implementation of a real-time malleable surface for molecular modeling applications.

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As the Helix Turns, or, Rational Design of Sequence Specific DNA Minor Groove Binding Drugs

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In seeking DNA binding drugs that can be targeted to specific sequences, minor groove binders are preferable to intercalators because they are more strongly sequence-specific. X-ray structural analysis of DNA/drug complexes — for example, CGCGAATTCGCG with the antibiotic netropsin — reveals the basis for the preference of most minor groove binders for regions of the DNA containing A.T. base pairs. The presence of the N2 amino of guanine in the minor groove sterically prevents a drug from settling down against the floor of the groove. Since reversals of base pairs are not distinguishable in the minor groove, the floor of the groove reads essentially as binary code: A hydrogen bond donating group is either absent or present for an A.T. or a G.C. base pair, respectively. The substitution of an imidazole for one of the pyrrole rings of netropsin (creating a "lexitropsin") is a possible way to read a G.C. in the minor groove: The hydrogen bond donating amino can be accommodated by a cleft in the drug, which also provides a hydrogen bond acceptor. However, such a change in drug structure may not result in a G.C. requirement but simply permit it.

In an animated film, the details of the crystal structures of the dodecamer CGCGAATTCGCG, and of netropsin complexed with it, are presented as bond skeletons and van der Waals dotted surfaces using vector graphics. Cartoon representations of the DNA and drugs are used to illustrate the rational, for the design of hypothetical sequence-specific minor groove binders.

Automated Protein Structure Data Bank Similarity Searches and Their Use in Molecular Modeling with MIDAS

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Active site modeling of proteins and molecular structure prediction are important approaches in molecular biology. An automated approach for structure predictions of novel sequences is a search for complete or partial match of the new protein sequence against the sequences of known three-dimensional (3D) structures. Data analysis is further aided by fast and accurate pictorial representation of the 3D structures.

The most widely used protein database for sequence searches, PIR (Protein Identification Resource, developed at NBRF, National Biomedical Research Foundation, Washington, DC), does not contain any 3D structure information. The Brookhaven Protein Data Bank does contain 3D coordinates, but it is not formatted for extensive similarity searches. We have generated a protein sequence database with the format and structural advantages of PIR and the Brookhaven Protein Data Bank. Modifications were made to PSQ (Protein Sequence Query program, VMS version,