

# **Lecture 16**

## Molecular Surface

# Molecular Surface

Jmol isosurface options

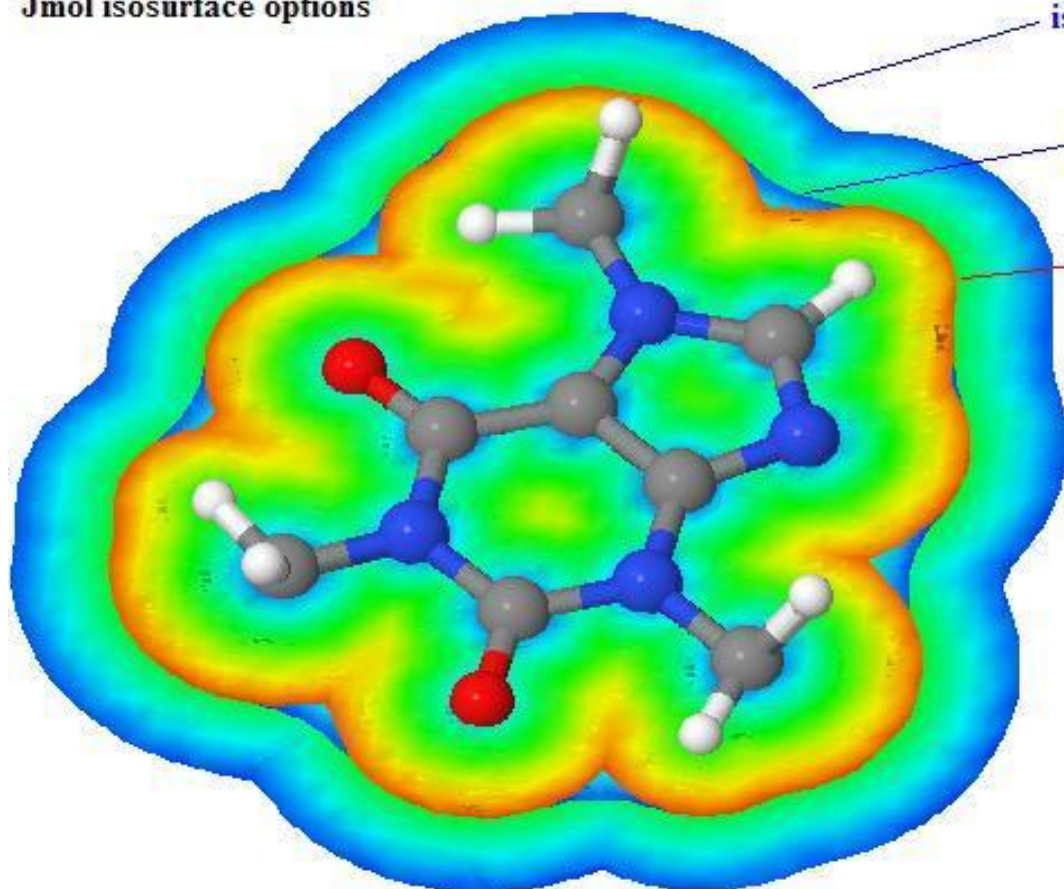
isosurface sasurface

isosurface molecular  
isosurface solvent 1.4

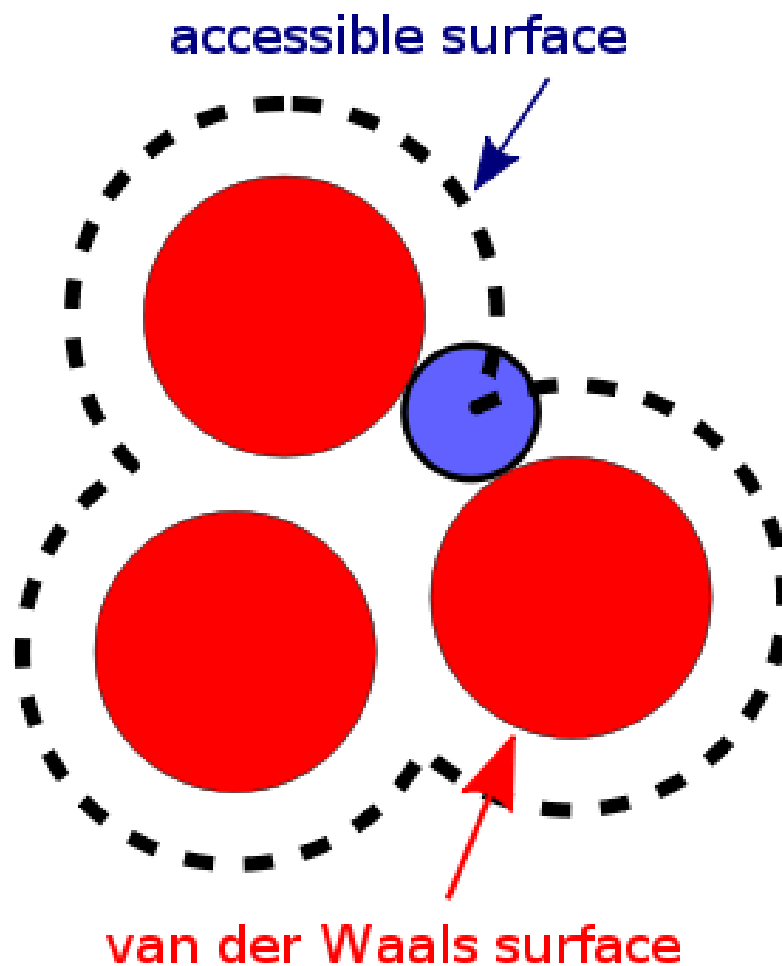
isosurface sasurface 0  
isosurface solvent 0

\*The difference between  
"molecular" and "solvent" is  
that:

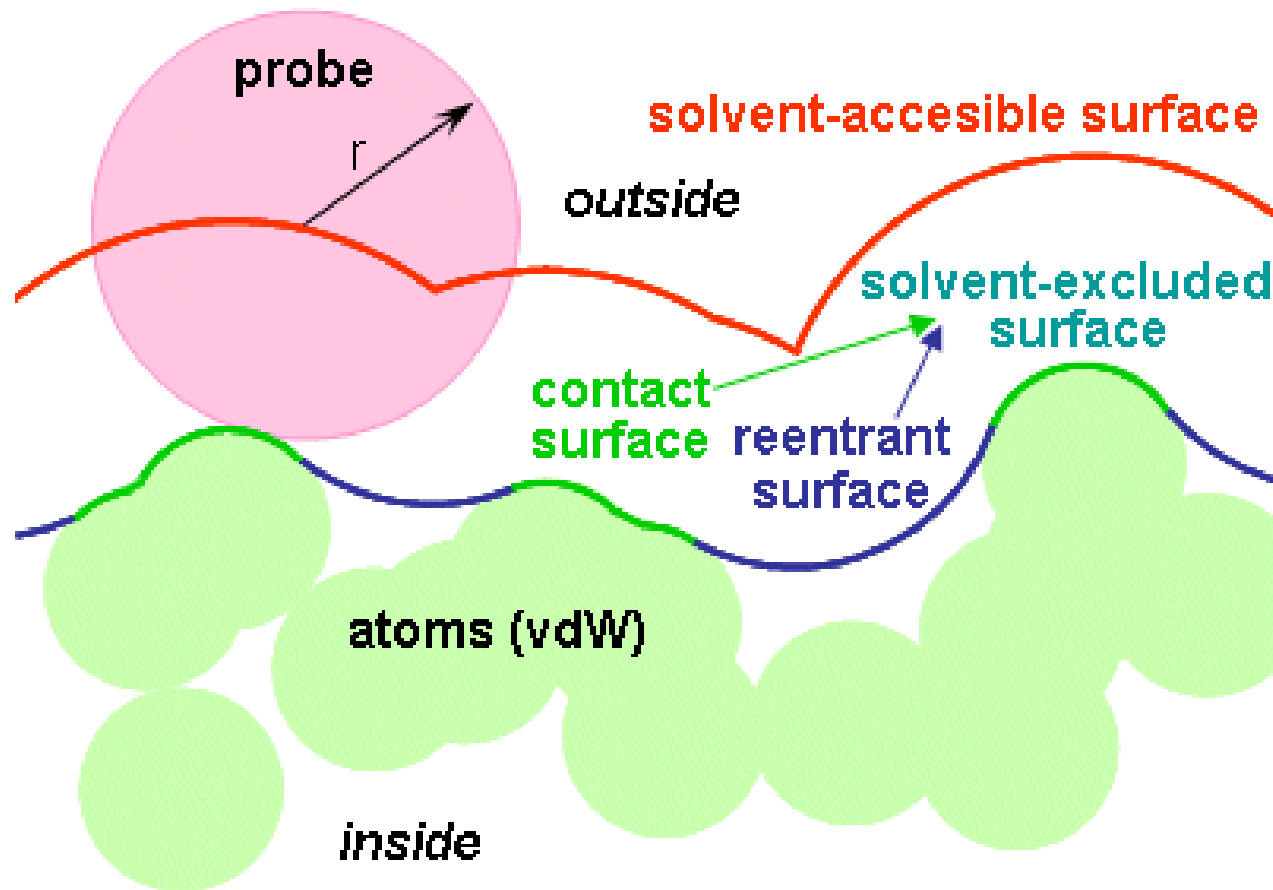
- 1) molecular doesn't take a  
probe radius parameter --  
it is fixed at a 1.4 Å.
- 2) solvent defaults to  
ignore(solvent) solvent 1.2



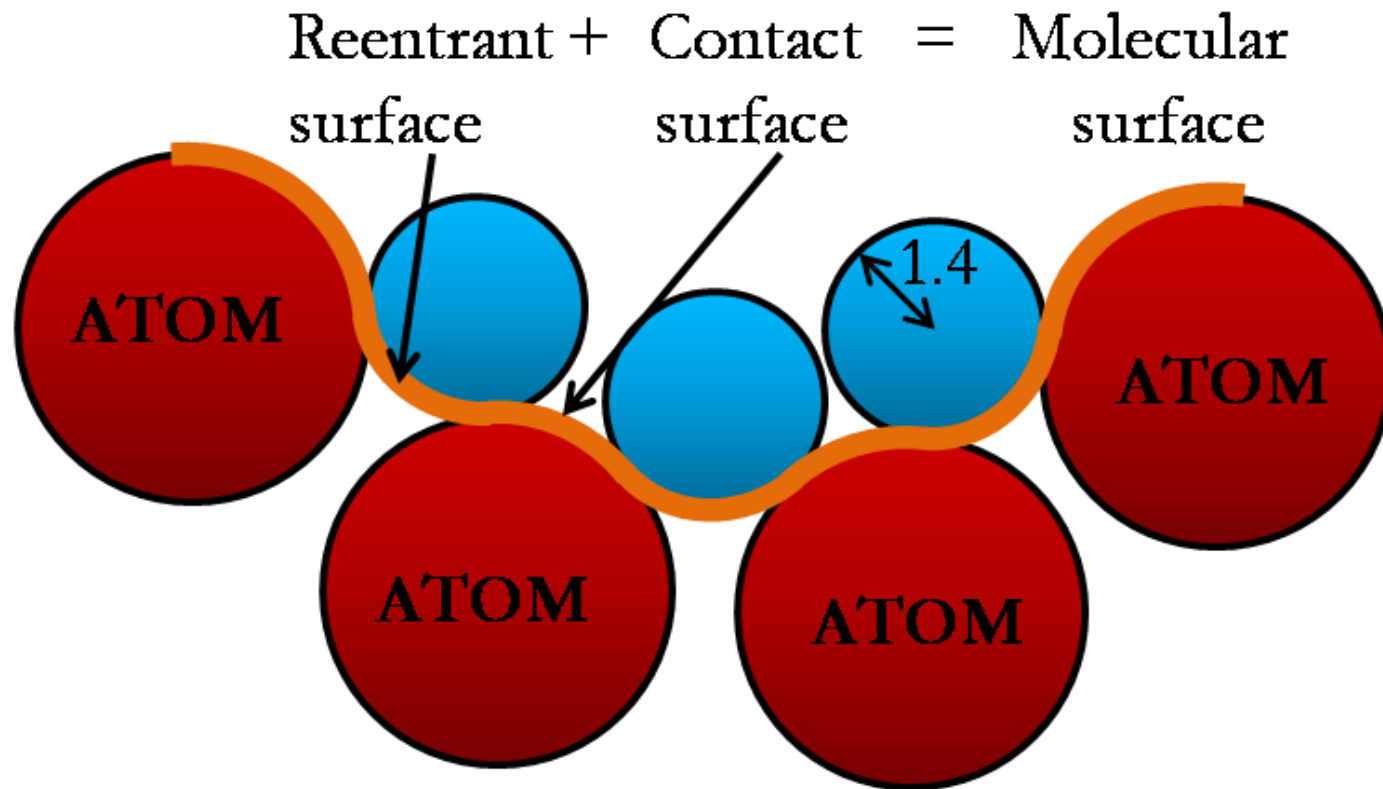
# Molecular Surface



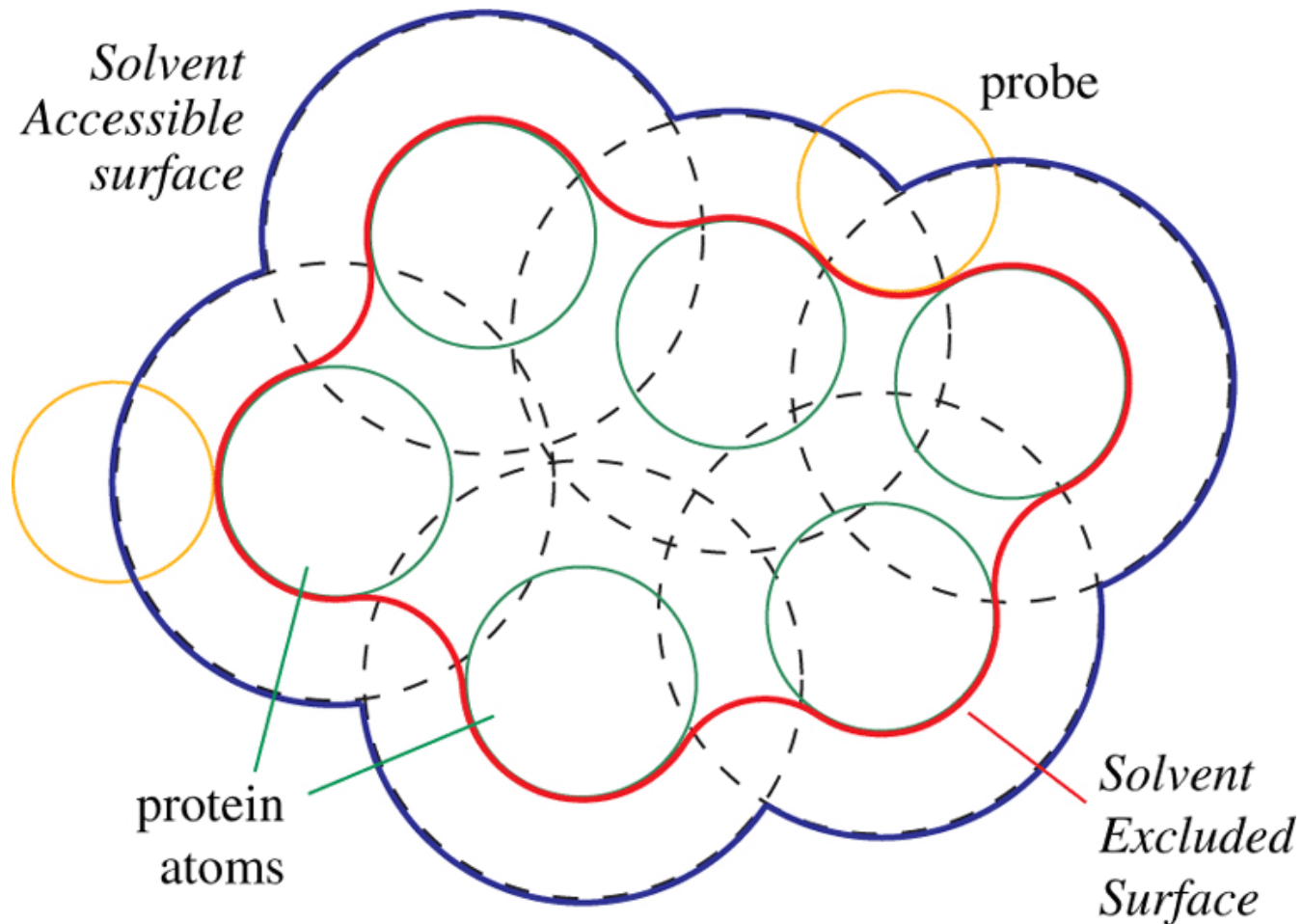
# Molecular Surface



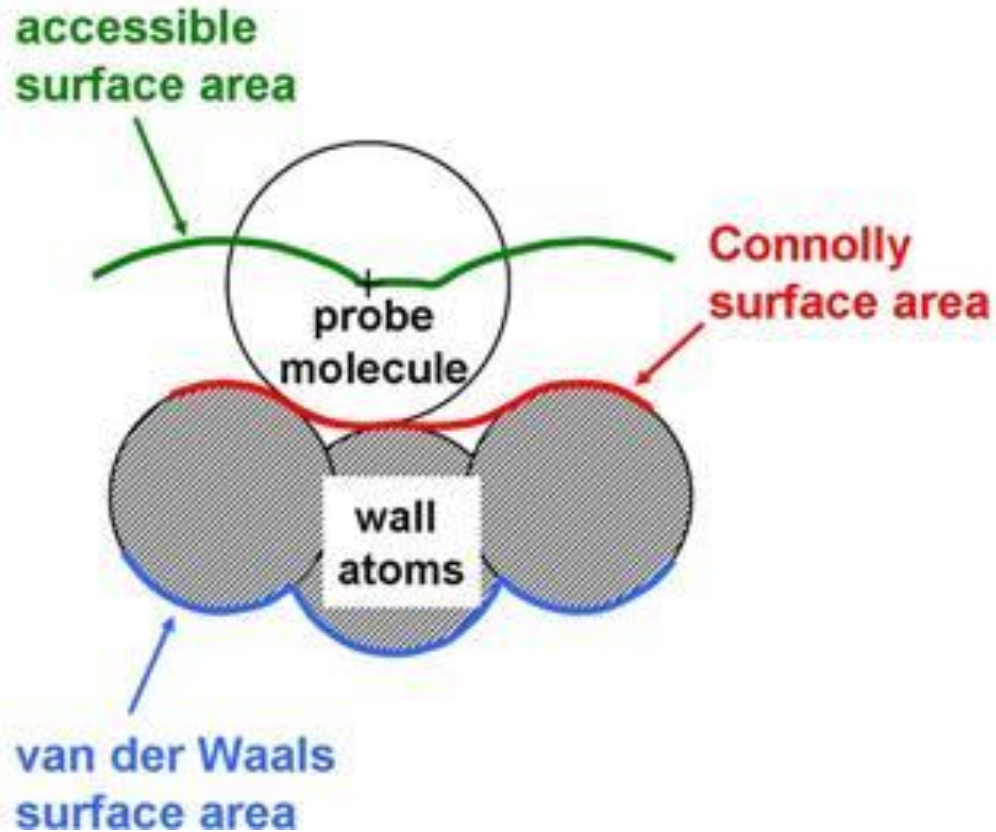
# Molecular Surface



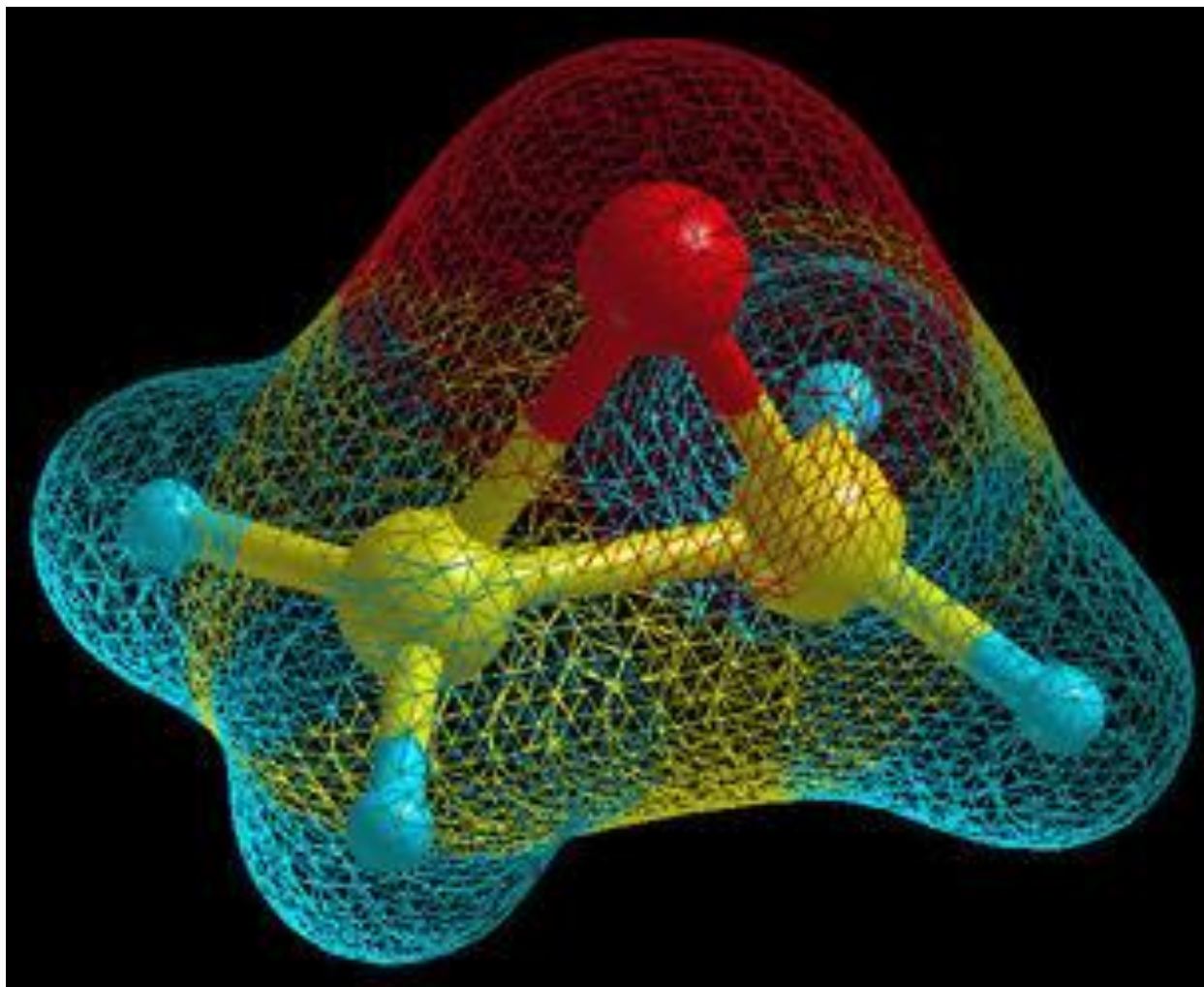
# Molecular Surface



# Molecular Surface

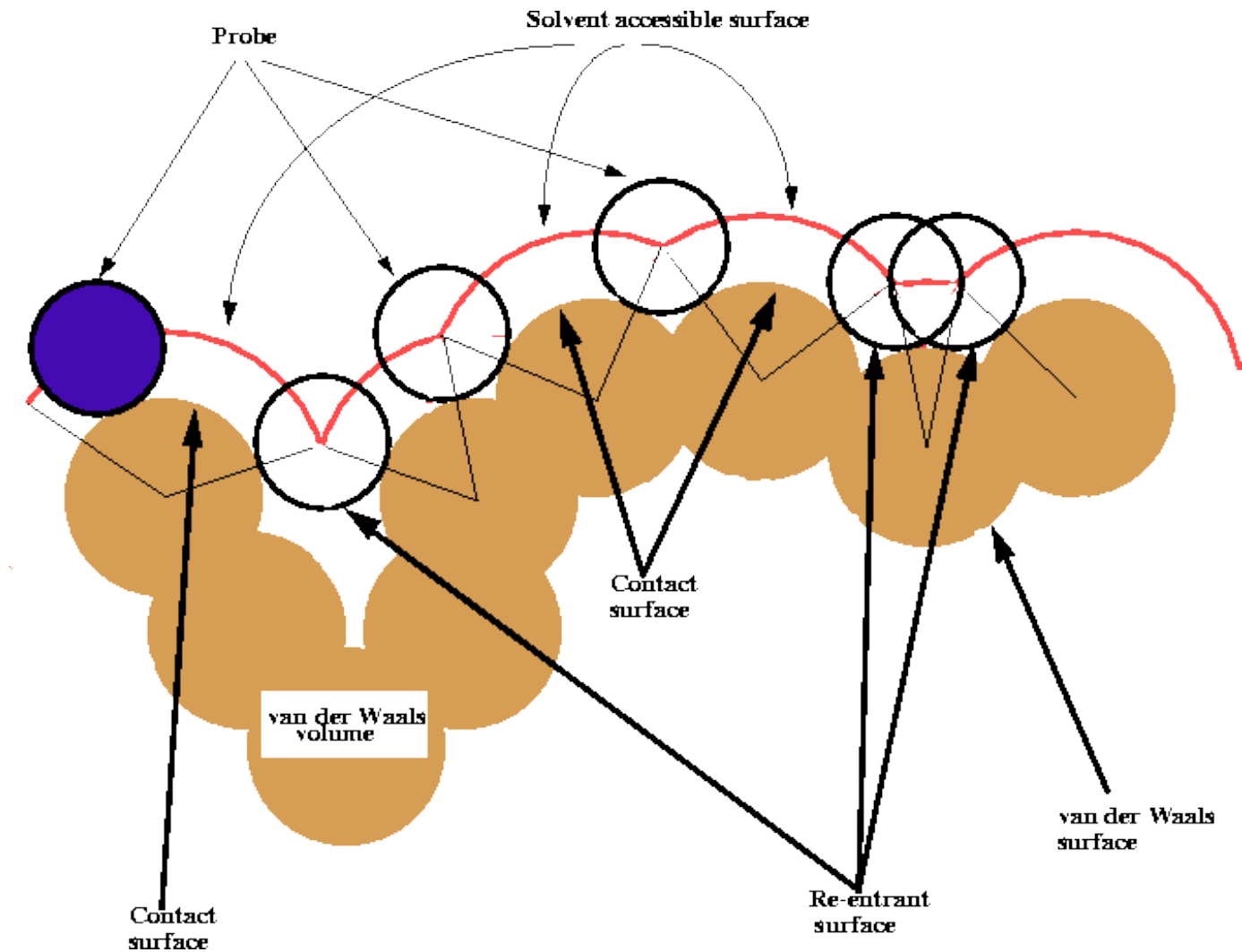


# Molecular Surface

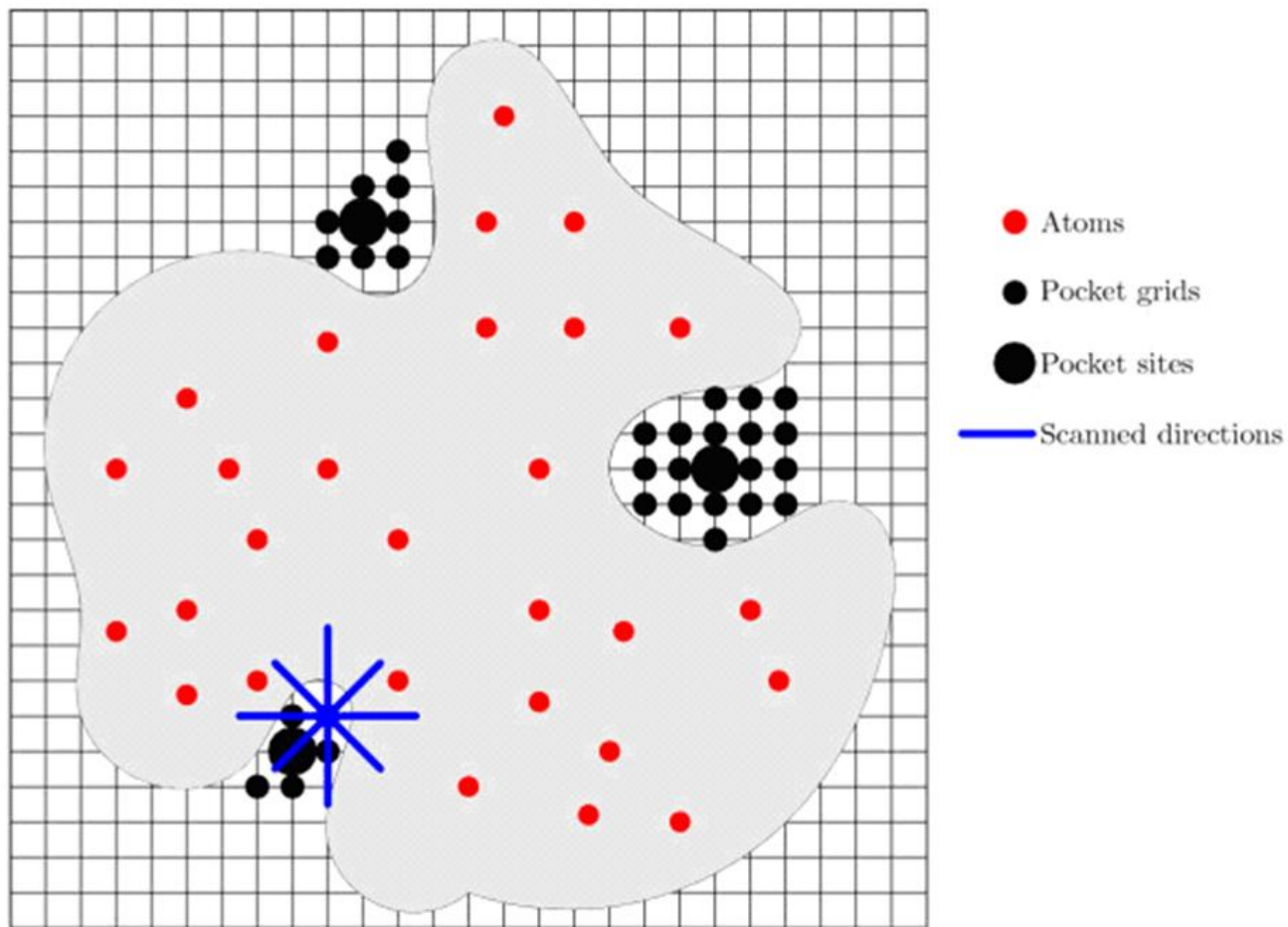




# Molecular Surface



# Molecular Surface

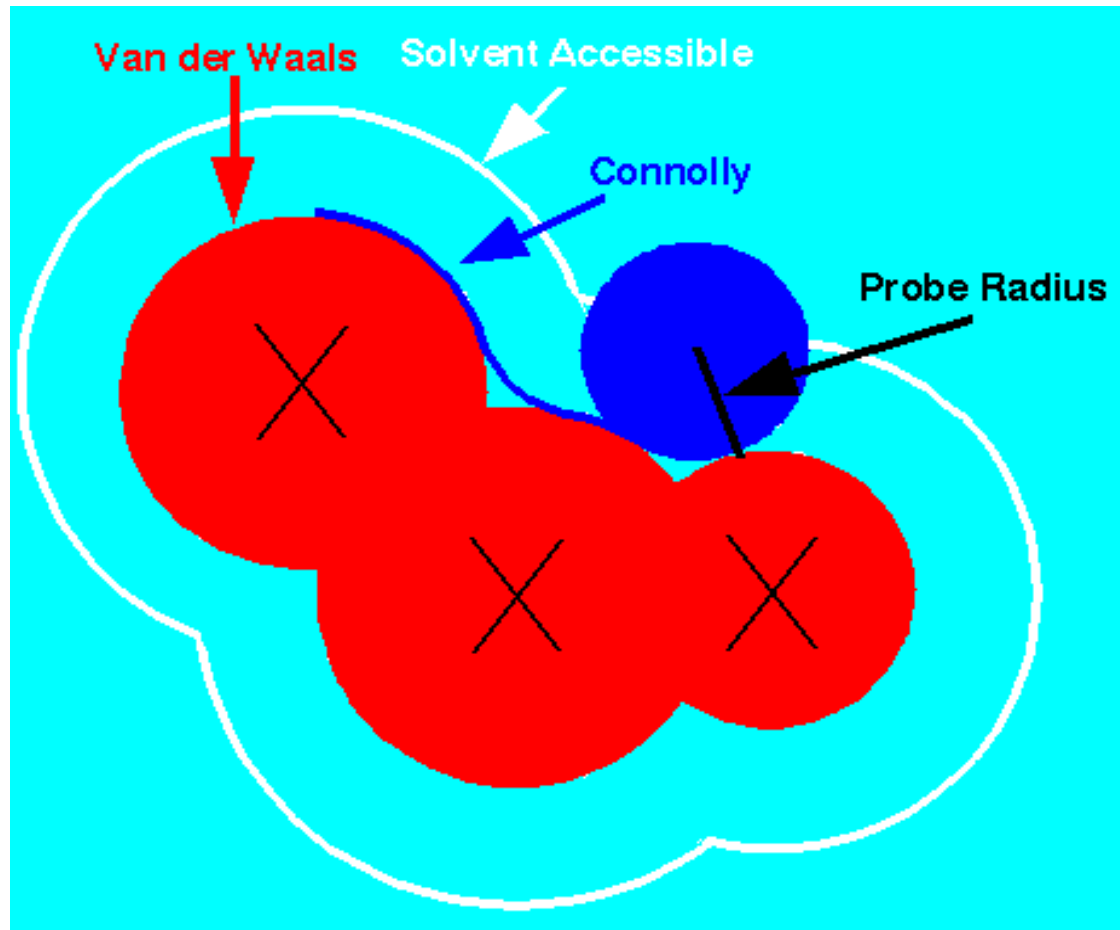


# Mathematical Models of Surface Representation

- Connolly surface
- NACCESS
- Surface Normal and Critical Points
- Grid Representation
- Advantage
  - Geometric Hashing based rigid-body programs

# Solvent Accessible Surface – SAS

## Connolly Surface



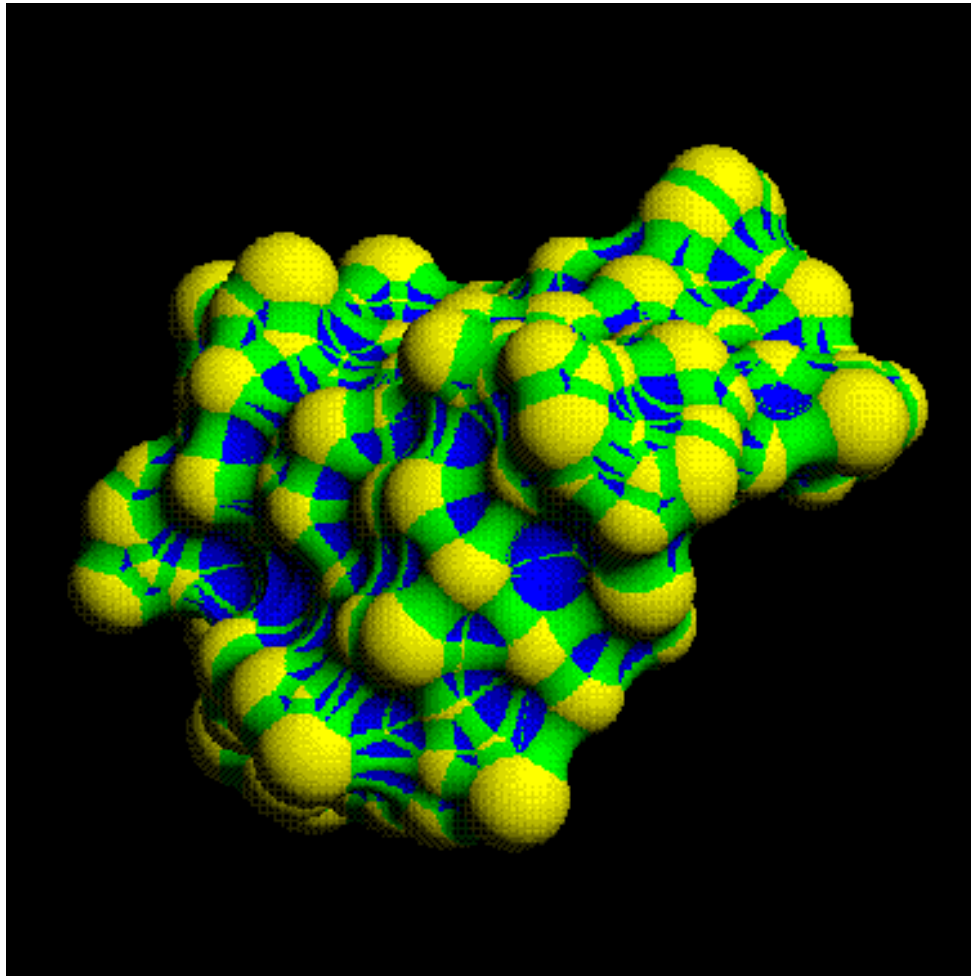
# Connolly's MS algorithm

- A 'water' probe ball (1.4-1.8 Å diameter) is rolled over the van der Waals surface.
- Smoothens the surface and bridges narrow 'inaccessible' crevices.

# Connolly's MS algorithm - cont.

- **Convex, concave** and **saddle** patches according to the no. of contact points between the surface atoms and the probe ball.
- ⚡ Outputs **points+normals** according to the required sampling density (e.g. 10 pts/Å<sup>2</sup>).

# Example - the surface of crambin

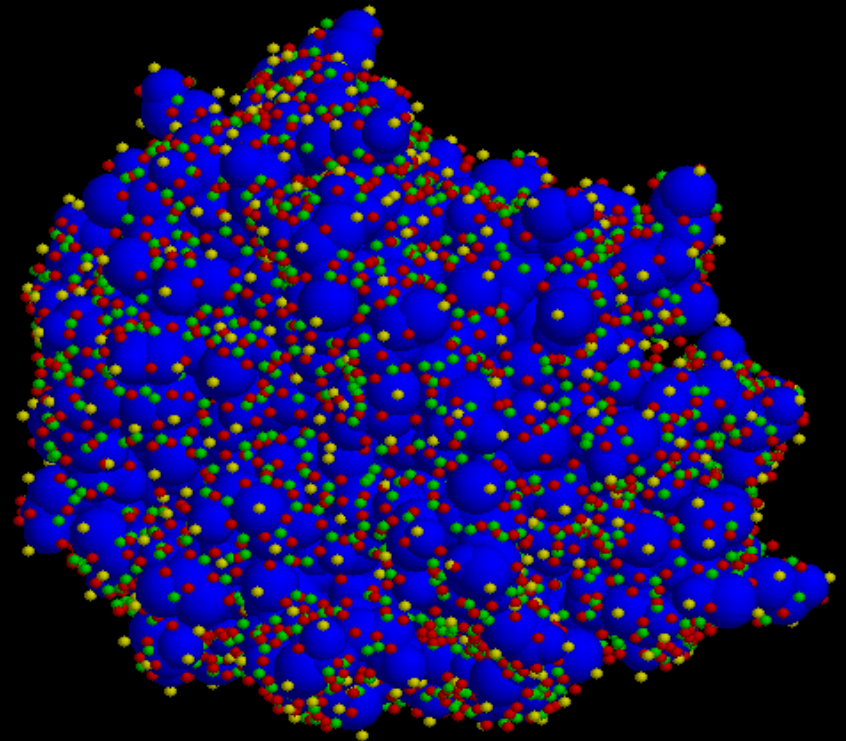
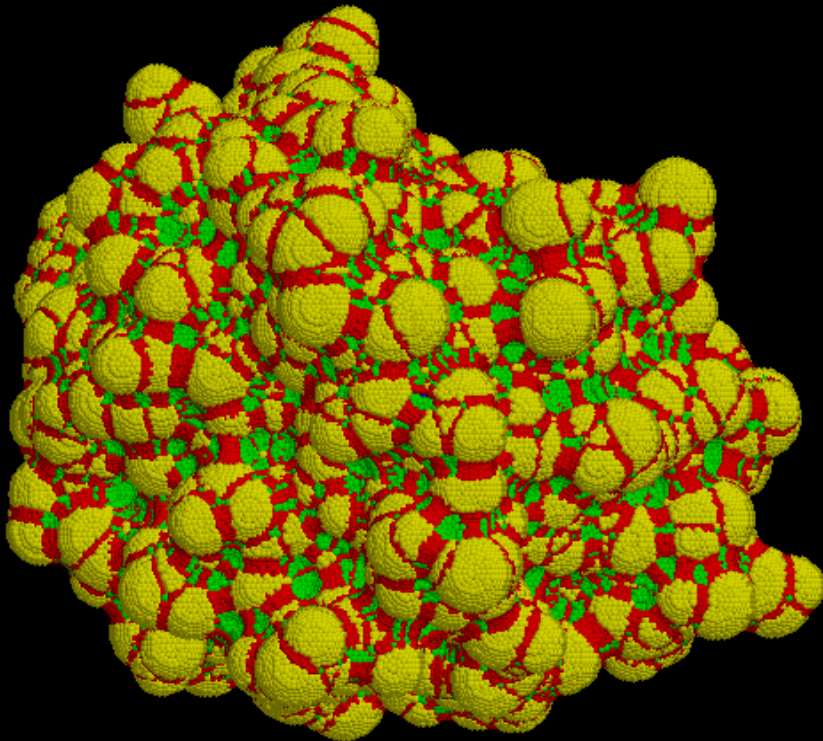


# **Critical points based on Connolly rep. (Lin, Wolfson, Nussinov)**

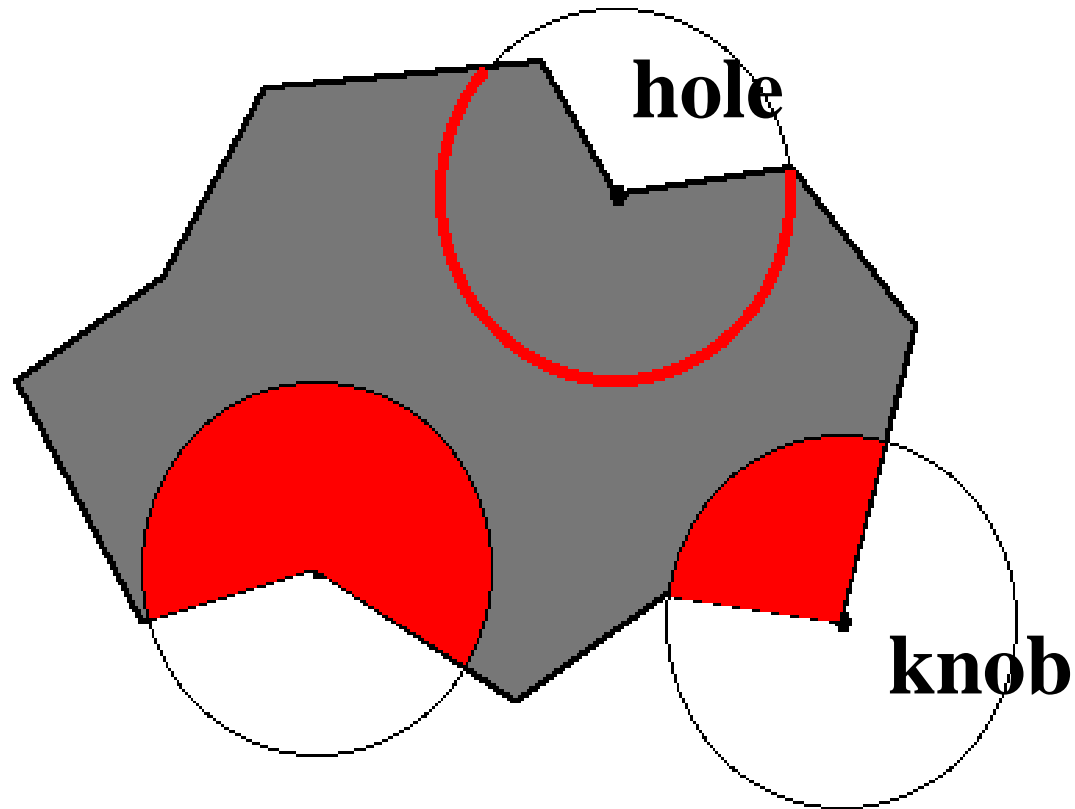
- Define a single point+normal for each patch.
- Convex-caps, concave-pits, saddle - belt.



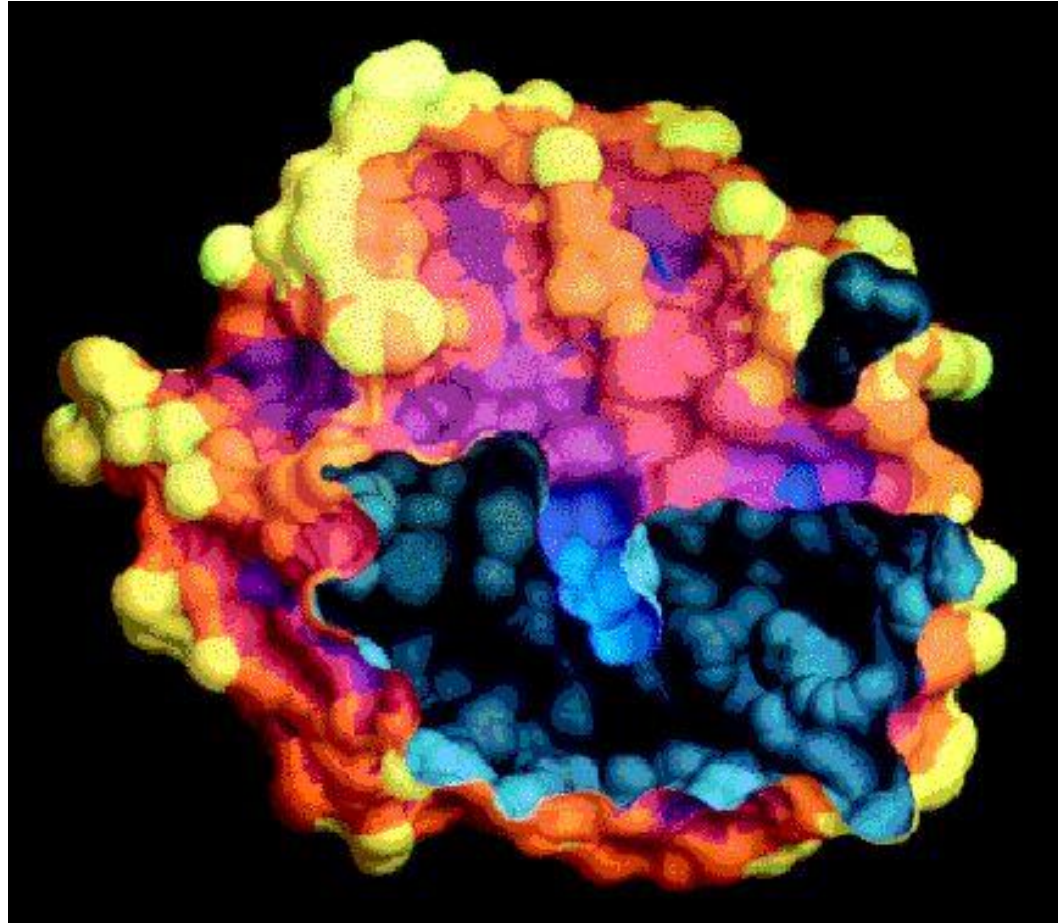
**Connolly => Shou Lin**



# Solid Angle local extrema



# Chymotrypsin surface colored by solid angle (yellow-convex, blue-concave)



# Definition of Protein Surface

- Roll the probe over the protein molecule using NACCESS program to compute the accessible surface area (ASA) (also called as SASA – surface accessible surface area)
- If an atom's accessible surface area (ASA) is more than  $0.1 \text{ \AA}^2$  then that is defined as surface atom.

# Definition of Protein Interface Area

- The surface area where two protein molecules interact during complex formation is called as the interface region.
- If an atom loses its ASA by more than  $0.1 \text{ \AA}^2$  then we call that as an interface atom. The total loss of ASA by all the interface atoms are the interface area.
- Sometimes, we take the average for interface area to call it as interface area per protein molecule.
- How to compute identify interface atoms? How to compute interface area?
  - Run the NACCESS on individual protein molecules
  - Run the NACCESS on the protein complex
  - Identify the atoms that loses its ASA by more than  $0.1 \text{ \AA}^2$

# Definition of Protein Interface Area

