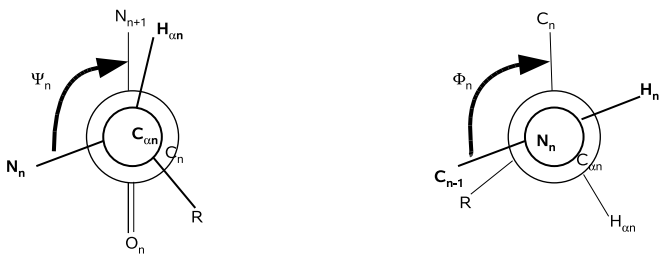


Conformation of a polypeptide chain

- Rotate around the N-C α and C α -C bonds \Rightarrow Many conformations
- Some rotations lead to clashes between atoms (backbone or side chains)
- Described by *dihedral angles* around bond
- ω : C $\alpha(n)$ - C n - N $n+1$ - C $\alpha(n+1)$:
Nearly always *trans* ($\omega = 180^\circ$) except for a few next to proline which may be *cis* ($\omega = 0^\circ$)
- ϕ C $n-1$ - N n - C $\alpha(n)$ - C n
- ψ N n - C $\alpha(n)$ - C n - N $n+1$

1

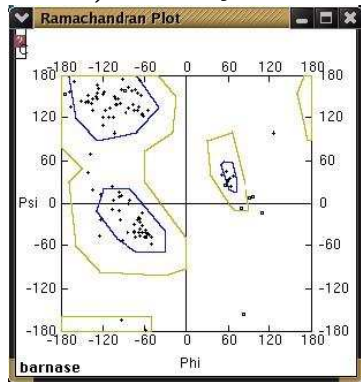
Definition of dihedral angles:



Angle can be between -180° and $+180^\circ$ according to the protein/IUPAC convention. (Polymer chemists use an opposite definition). The value of the the dihedral angle is *independent of the viewing direction*

2

An example of a Ramachandran(Φ/Ψ) plot (for the protein “bar-nase”..) made by the “Swiss PDB viewer” (spdbv)



Angles Ψ (Psi) and Φ (Phi)

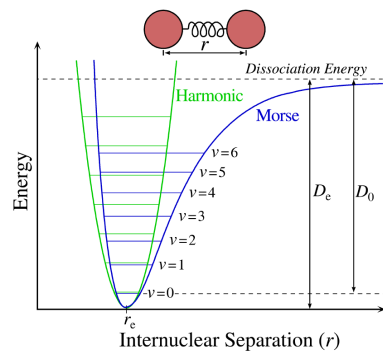
(\square refer to gly, $+$ refer to other residues)

With one exception all non-gly residues fall within the α -helix (around $\phi = -57^\circ, \psi = -47^\circ$), β -strand (large region around $\phi = -120^\circ, \psi = +120^\circ$) or left-handed helix (around $\phi = +40^\circ, \psi = +40^\circ$) regions.

3

Important interactions for proteins

- Covalent bonds - within chains and disulphide bridges between chains
 - Model by Morse potential: $E_{ij}(r_{ij}) \approx D_e(1 - e^{-(r-r_e)})^2$
(can in principle model bond breaking)
 - For small deviations: $E_{ij}(r_{ij}) = C(r_{ij} - r_{eq})^2$



(Graph from Wikipedia)

4

- van der Waals attractions
 - permanent dipole-permanent dipole (freely rotating),
 - permanent dipole - induced (temporary) dipole
 - induced dipole-induced dipole (dispersion forces)

$$E_a(r_{ij}) = -4\epsilon_{ij} \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6$$

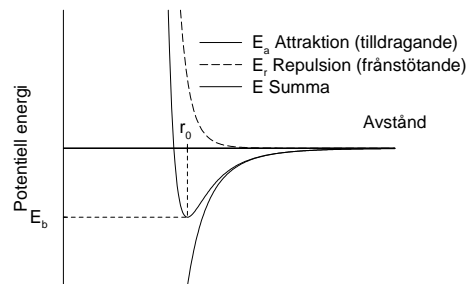
- “Exchange repulsion” Quantum mechanical - modelled as

$$E_r(r_{ij}) = +4\epsilon_{ij} \left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12}$$

(or $E_r(r_{ij}) = A_{ij}e^{-r_{ij}/\sigma_{ij}}$ - best at large r_{ij})

5

Växelverkan mellan två atomer i (t.ex.) vätska



Simple intermolecular potentials

Lennard-Jones (6-12)

$(E_b = \epsilon_{ij}, r_0 = \sigma_{ij}/\sqrt[6]{2})$

$$E_{LJ}(r_{ij}) = 4\epsilon_{ij} \left[\left(\frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6 \right]$$

Buckingham (exp-6)

Softer than L-J

$$E(r_{ij}) = A_{ij}e^{-r_{ij}/\sigma_{ij}} - B_{ij} \left(\frac{\sigma_{ij}}{r_{ij}} \right)^6$$

6

- Charge-charge interactions $E_{ij}(r_{ij}) = \frac{k Q_i Q_j}{\epsilon_r r_{ij}}$
(NB! Strange notation in Whitford regarding ϵ_0, ϵ)
Dipoles (like H₂O) described by “partial charges” on the atoms.
- Hydrogen bonding: Mixture of charge-charge and quantum-chemical bonded interaction. Between (electronegative atoms) O,N or F and hydrogen covalently bound to O,N or F (lone pair - hydrogen).
- Hydrophobic effect [Very important in aqueous solution]

7

Hydrophobic interaction

In liquid water: hydrogen bond network between water molecules

⇒

Very unfavourable to introduce (part of) molecule into water that cannot form hydrogen bonds (or at least charge interactions) since water molecules forced to form hydrogen bonds in “fewer directions”.

⇒ “Entropic favouring” of phase separation. Molecules “hydrophobic” (water fearing)

Hydrophobic effect the most important interaction for protein folding, formation of biological membranes etc. etc. (But can **not** be described by atom-atom interactions)

8

Repetition

Secondary structure elements are arranged in space in hierarchy

Super secondary structure = A few secondary structure elements arranged in frequent motifs (like β -barrels,

Tertiary structure = The arrangement of secondary structure elements (sheets, helices, loops) of one chain in space

Quaternary structure = The arrangement of the different chains (subunits) of multichain proteins in space. Allows active site formation *between* subunits

9

The Protein Data Bank (<http://www.rcsb.org/pdb>)

Deposition of 3-D structures of proteins from X-ray crystallography (contains only non-hydrogen atoms) and nmr

Identification of protein by 4-character code beginning with digit

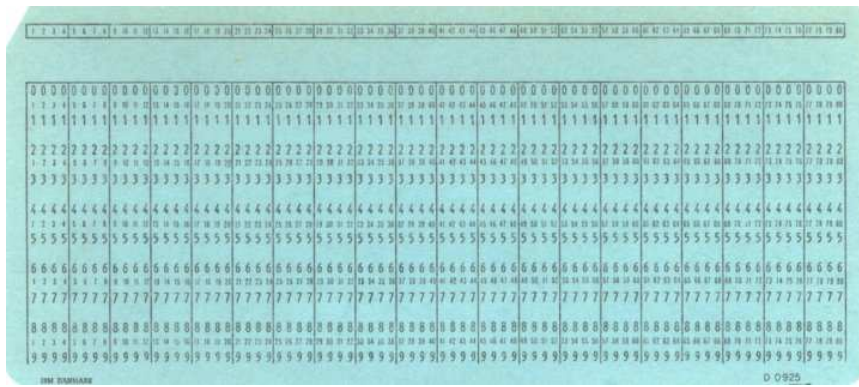
Special format adopted to punch cards:

- Header with information about the structure
- Sequence of amino acids
- Crystal data (size etc)
- ATOM records with names, coordinates (Ångström) and "temperature factors", cf. Ch.10
- HETATM similar records with non-protein atoms (like metal ions)

More information about the punch card based PDB-format can be found at

http://www.rcsb.org/pdb/file_formats/pdb/pdbguide2.2/guide2.2_frame.html

(cf. also table 3.19, p. 51 in Whitford)



(picture of a punch card from Wikipedia)