

## BIOL 01.24.17

### 2nd, 3rd, 4th structures

1. Ionic: strong.
2. Hydrogen bonding: hydration shell.
  - responsible for 2ndary structures.
3. Van der Waals: weak
4. Hydrophobic interactions: **NOT BONDS**, reducing needs for highly ordered water molecules.
  - Bond strength:
    1. Van
    2. Ionic
    3. Hbond
    4. C-C
    5. C=C

### 2ndary structure's rules

1. X-ray diffraction: interatomic bond distances, angles of amino acids chains.
2. Theoretical analysis of angles
3. **Something else here yo.**
  - Planar rotation limitations
    1.  $\phi\psi$
2. Alpha-helix with **3.6** amino acids/turn
  - Rise from one  $\alpha$ -carbon to the next is 1.5 angstrom

### Jan 26, 2017

5. Pitch is 5.4 Angstrom
6. Linus' mistake
  - L stereoisomer
  - Right handed helix
7. Helix or not?
  1. Similarly charged residues disrupts helix formation.
  2. If too many large amino acids consecutively, helix disrupted.
  3. Bonding between R groups 3-4 residues apart stabilize.
  4. P stabilizes helix; **Proline destabilizes.**
  5. Negative N terminus, positive C terminus stabilizes helix.
    - Leads to dipole across peptide bond.
8. Circular dichroism
  - Random coil,  $\beta$ -sheet,  $\alpha$ -helix interact with light differently.
  - Measures amount of secondary structures.

9. Betasheet
  - 3.5 angstrom between adjacent amino acids, vs. 1.5 in alphahelix.
  - Fully extended.
  - Antiparallel arrangemet of adjacent betastrands.
  - Adjacent polypeptide strands an be parallel or antiparallel.
10. Folding
  - Fewer than 1/billion random polypeptides folds into organized structures.
  - Folding energy is low; most protein close to unfolded state.
  - Genes encoded for folding seleted by evolution.
  - Folded diffently every time.