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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 α -carbon to the next is 1.5 angstrom

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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, β -sheet, α -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.