



Why Computational Chemistry?

- Can rapidly focus attention on compounds most likely to have the desired properties
 - Save time and \$\$
 - Less "trial and error"
- Human Genome Project
 - Genes identified
 - Can get AA sequences of proteins that genes code for
 - 3-D protein structure prediction needed
 - Experimental protein structure determination is difficult
 - X-ray, NMR, and now computation

Protein Data Bank		
PDB Content Growth: ~28,000 current proteins		
31000	Deposited structures for the year of Total analytic structures (incl. models)	1
30000		
2100		
20000		
15000		
1000	1	
6.000		
Year Lad contrast \$1500-305		



How Can We Use This Data?

- Visualization of structure
- Possible insight into mechanism
- Identify the active site
- Structure with ligand in place
 - Active site determination
 - Design new molecules to bind to active site

Computation

- Does new molecule bind more strongly than the natural occurring ligand?
 - MM or Semi-empirical calculation

The Process

- Structure known? <u>http://www.rcsb.org</u>
- Download the structural data
- .pdb file
- Clean it up
- Usually remove water molecules
- Find the ligand (or find the receptor?)
- Remove the ligand (or model the receptor site?)
- Insert our new ligand (drug candidate)
- Nontrivial process, orientation is crucial
- Does it bind more strongly to the receptor?

Example: Casodex and Prostate Cancer

Most common type of cancer (excluding skin cancer) among American men

- Over 70% of all prostate cancer diagnosed is in men over 65 years old
- In 2003, approximately 221,000 new cases were diagnosed in the U.S.
- Overall survival rate ~97%

Antiandrogen Therapy

- Most prostate cancers are driven by androgens (male hormones)
- Antiandrogen drugs block the body's ability to use androgens, such as testosterone
 - Eulexin, Casodex, and Nilandron are examples
- These drugs are also used following surgery to help prevent recurrence of the cancer
 - How do they work on the molecular level?
 - What protein do they interact with?

Human Androgen Receptor Protein Antiandrogen drugs compete with testosterone for the binding site of this protein An affinity label (Metribolone) is used for the human androgen receptor in the prostate and in prostatic tumors It binds strongly to the androgen receptor Metribolone is a synthetic androgen and an anabolic steroid

Protein Data Bank

- Search for "human androgen receptor" – Get six hits, two of which include metribolone
- Use 1E3G
- Download the file, "unzip", and rename with .pdb ending
- Open and view in CAChe Workspace
- Try various "View / Backbone Ribbon" commands
 Reveals ~26 associated water molecules
 - These were deleted to "clean up" the structure
 - Must also "Beautify / Valence" to add H atoms
- Viewing as a "ribbon" structure clearly shows the position of the Metribolone









Steps For Insertion of a New Ligand

- Separate the old ligand
 - Leave protein structure unchanged
- Orient the new ligand
 - Can superimpose the new ligand onto the old ligand
- Insert the new ligand
 - See if the fit is sterically "reasonable"

Minimize

- Use MM or Semiempirical method
- Find the energy difference







Where to Look

• Cache Users Guide 6.1 – Chapter 19

Further Tutorials and Credits

- <u>http://www.ch.ic.ac.uk/local/organic/</u>
- Department of Chemistry Local Teaching Pages: <u>http://teaching.ch.ic.ac.uk/</u>
- <u>MedChem Homology Modelling: Designing an anti-TB drug.</u> Copyright (c) H. S. Rzepa and ICSTM Chemistry Department, 2003 and Fujitsu/CAChe.
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