Ligand Docking of Lincomycin and *E. Tenella*

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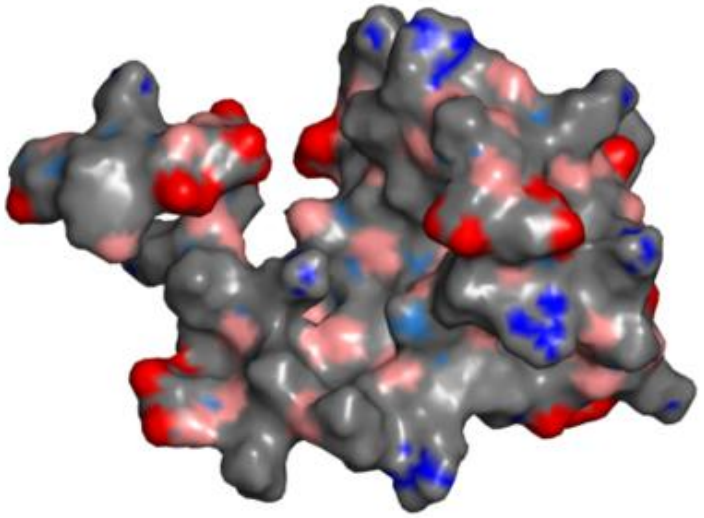
Outline

- Introduction
- Method
- Results
- Analysis
- Conclusion
- Acknowledgements

Introduction

Coccidiosis

- Caused by *Escherichia Tenella*
- *One major factor of economic loss in the poultry industry*
- *Prevalent amongst herd-raised animals*

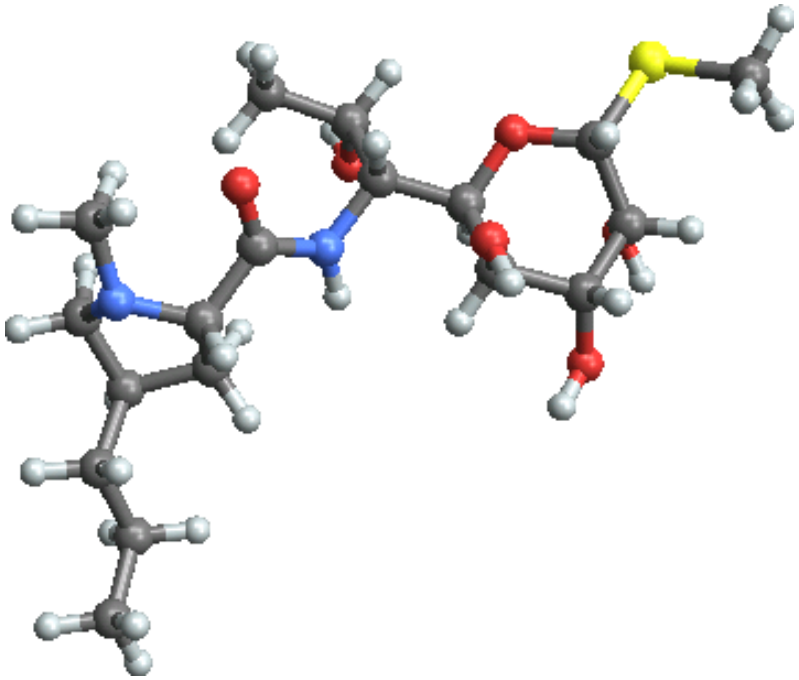


Picture of *E. Tenella in Python Molecular View*

Introduction

Lincomycin

- Lincosamide antibiotic
- Multiple forms of dosage
- Effective treatment of Coccidiosis

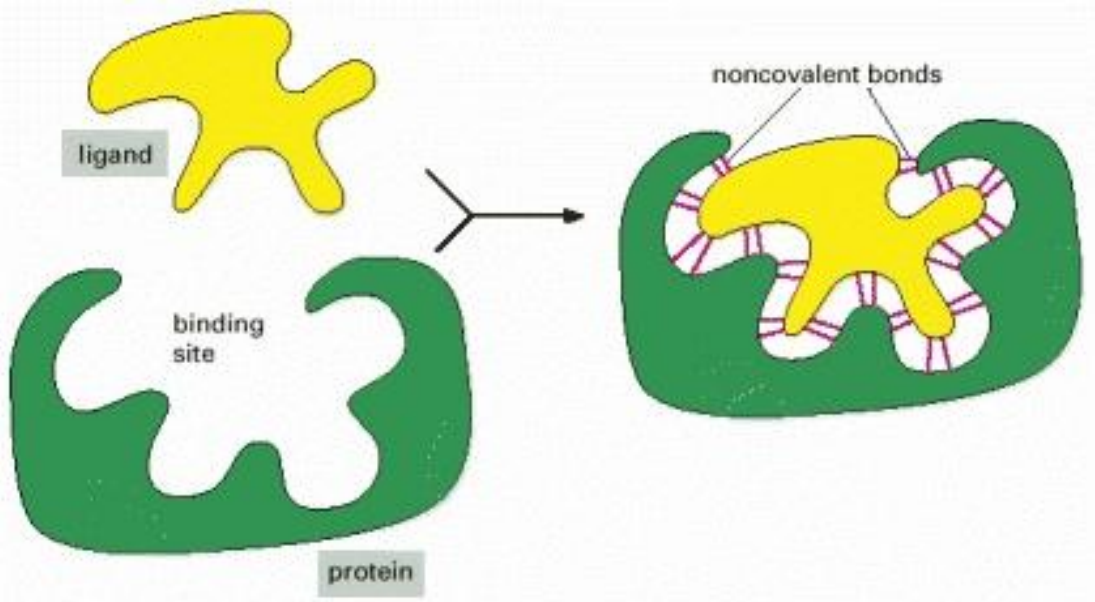


3-D molecular view of Lincomycin

Introduction

Ligand Docking

- Molecular complex of two molecules
- Lock-and-key system
- Based on the Free Energy Function



"Protein Function." *NCBI Bookshelf*. Web. 21 Jul 2011. <http://www.ncbi.nlm.nih.gov/books/NBK26911/>.

Free Energy Function

- Semiempirical free-energy force field to evaluate conformations during docking simulations.
- Evaluates dispersion/repulsion, hydrogen bonding, electrostatics, and desolvation.

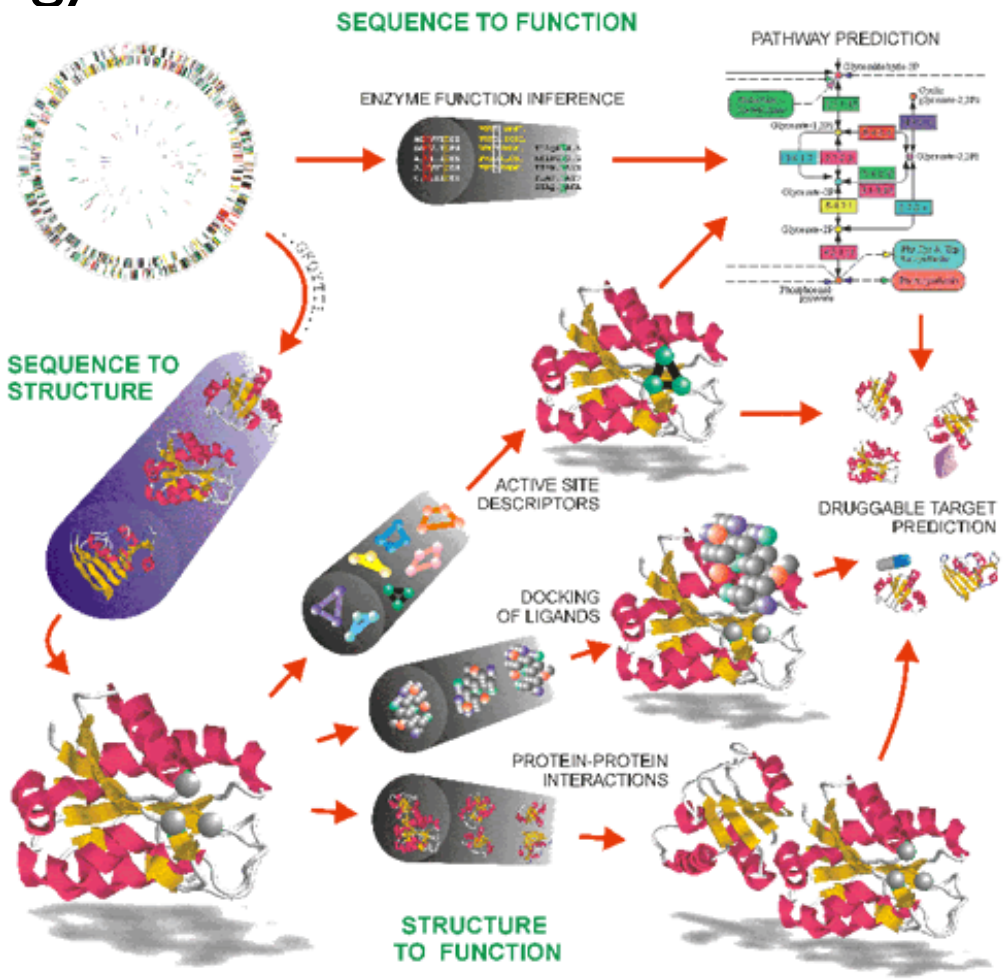
$$\Delta G = (V^{L-L}_{\text{bound}} - V^{L-L}_{\text{unbound}}) + (V^{P-P}_{\text{bound}} - V^{P-P}_{\text{unbound}}) + (V^{P-L}_{\text{bound}} - V^{P-L}_{\text{unbound}} + \Delta S_{\text{conf}})$$

$$V = W_{\text{vdw}} \sum_{i,j} \left(\frac{A_{ij}}{r_{ij}^{12}} - \frac{B_{ij}}{r_{ij}^{6}} \right) + W_{\text{hbond}} \sum_{i,j} E(t) \left(\frac{C_{ij}}{r_{ij}^{12}} - \frac{D_{ij}}{r_{ij}^{10}} \right) + W_{\text{elec}} \sum_{i,j} \frac{q_i q_j}{\varepsilon(r_{ij}) r_{ij}} + W_{\text{sol}} \sum_{i,j} (S_i V_j + S_j V_i) e^{(-r_{ij}^2/2\sigma^2)}$$

"6604793e1." *British Journal of Cancer*. Web. 21 Jul 2011.

Advantages of Ligand Binding

- Advances technology of drug design
- Qualitative over quantitative
  - Protein flexibility
  - Drug effectiveness
  - Drug toxicity

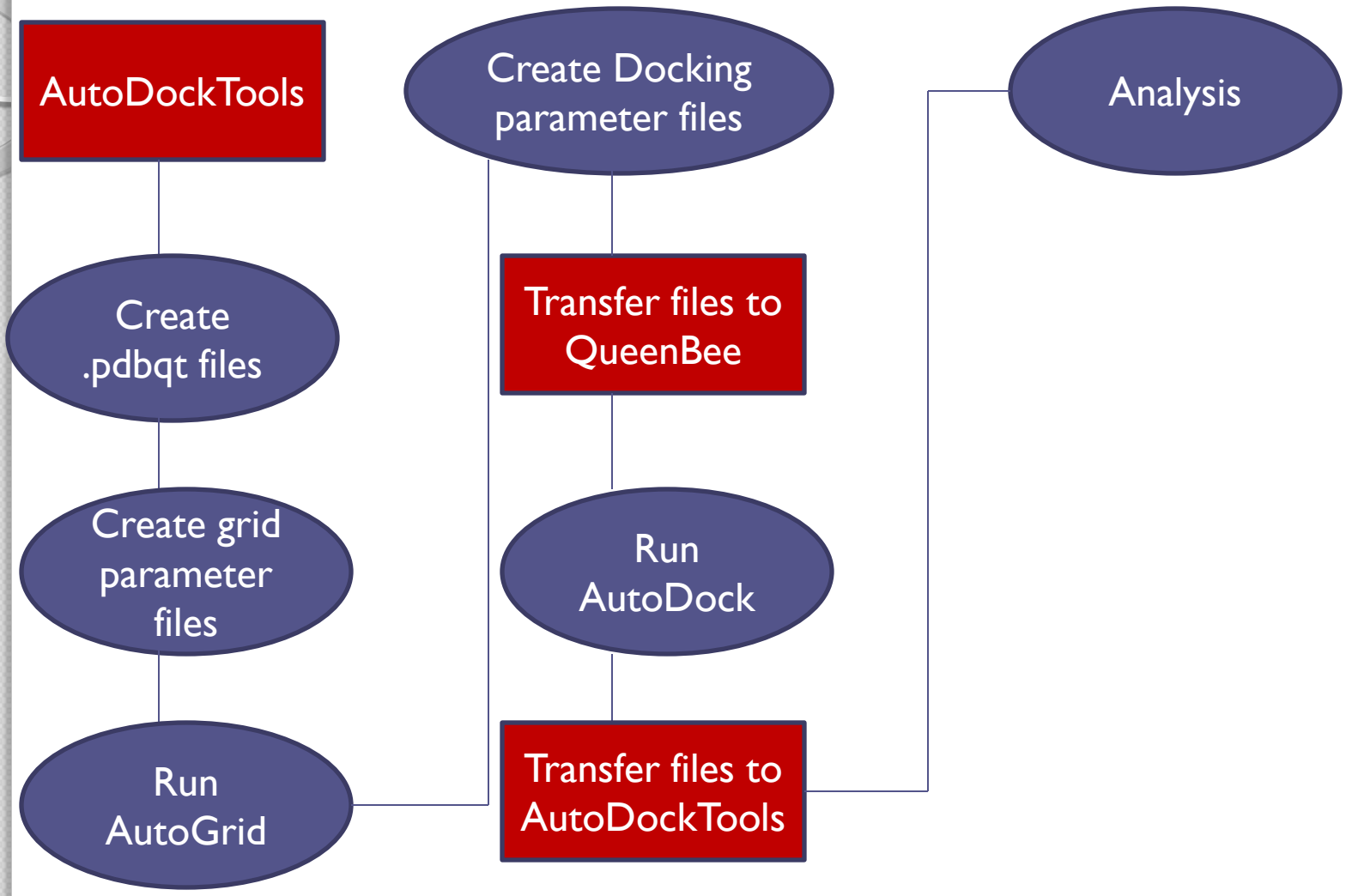


" Sequence of Drug Design." *Chemistry & Biochemistry*. Web. 21 Jul 2011. <http://www.chemistry.gatech.edu/faculty/Skolnick/>.

Method

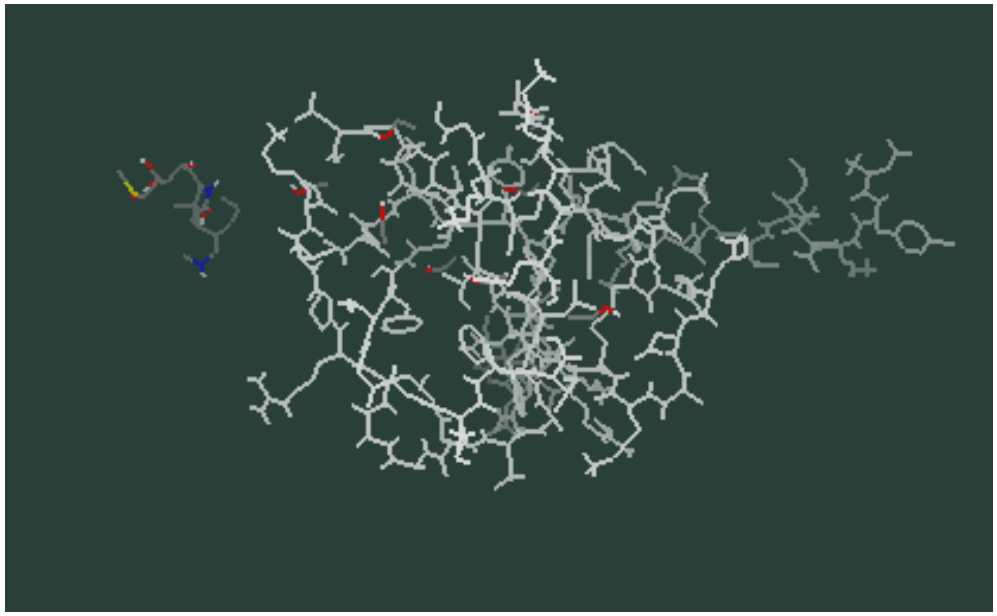
This experiment was conducted using AutoDock and AutoDockTools, software created by the Scripps Research Institute. Docking was performed on QueenBee, HPC supercomputer.

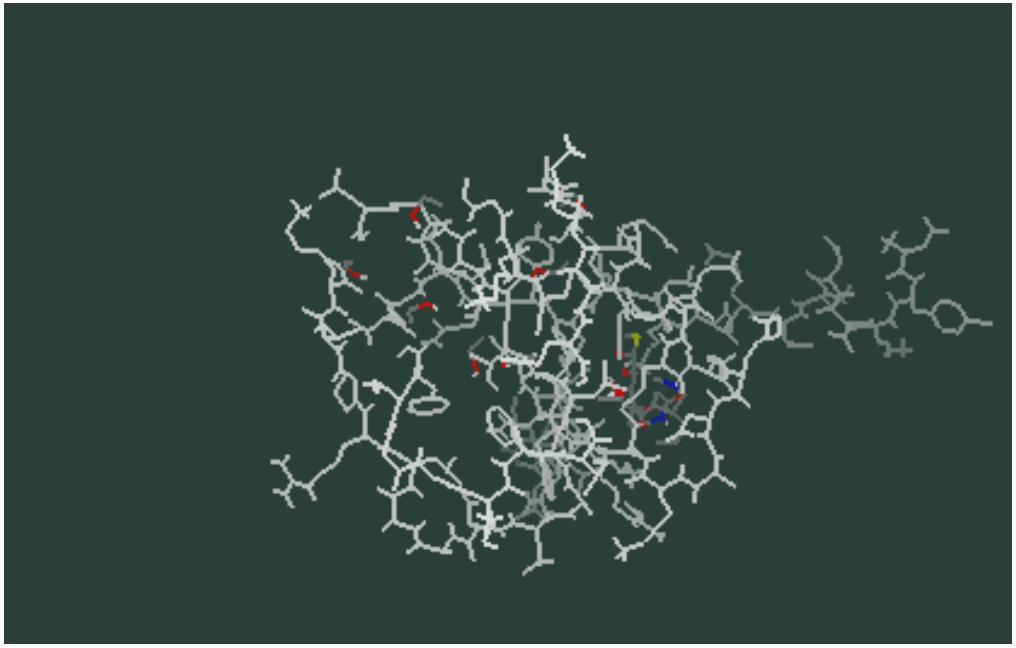
Method


AutoDockTools
Create .pdbqt files
Create grid parameter files
Run AutoGrid
Create Docking parameter files
Transfer files to QueenBee
Run AutoDock
Transfer files to AutoDockTools
Analysis

Results

Lincomycin successfully docked to *Escherichia Tenella*.





Analysis

- **Binding energy (Kcal/mol) is the sum of the intermolecular energy and the torsional free-energy penalty.**
- **Docking energy is the sum of the intermolecular energy and the ligand's internal energy.**
- **Torsional_energy is the number of active torsions**

This slide's information is per reference:
"Using AutoDock with AutoDockTools"

Conclusion & Future Work

Ligand docking is able to give a qualitative visualization of Lincomycin treating Coccidiosis. Through this visualization, scientists are able to see a precise pathway of Lincomycin affecting the parasite in an effort to treat it. Although the length of treatment can not be determined at this time, the results can contribute to future work with Molecular Dynamics (MD) simulation. This type of simulation will generate accurate and quantitative results than with Ligand Docking.

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Questions?? Comments??

Thank you