Macromolecular Electron Microscopy and Fatty Acid Synthase

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5.08 Recitation
Week 6 (March 10-11, 2016)

Discussion questions

1. Why do reconstructions of biological molecules not achieve resolutions limited by the electron microscope?

2. Why is EM a suitable approach for visualizing FAS?

3. What are the advantages and limitations with the way EM specimens of FAS were prepared and imaged?

4. How certain are you that FAS catalytic domains were correctly modeled in the EM reconstructions?

5. How might the observed conformations facilitate interaction with the ACP domain?

Bonus questions

1. Why might eukaryotes have adopted the multifunctional FAS architecture? Why would bacteria use discrete FAS enzymes but multifunctional PKS architecture?

2. To what extent do you think we can extrapolate from FAS structures to polyketide synthase modules that are FAS-like, but lack enoyl reductase, dehydratase, and/or methyltransferase domains?

3. Why do you think FAS has a non-functional methyltransferase domain?

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