Bioinformatics Readings to Review

Lecture 14 – 197-202--Databases of Multiple Sequence Alignments

CDD paper http://www.ncbi.nlm.nih.gov/pubmed/23197659

388-396 Protein families, domains, motifs

406-411 Protein localization & function

Lecture 15 -- Pevsner 421{430 Stop at Tertiary Protein Structure

Lecture 16 -- Pevsner 430-441 🡪 stop at middle

447 (bottom) - end of chapter

Self-Test questions 11-1, 11-8, 11-9

Lecture 18 , 19 - Pevsner 354-363

Krieger2003 Homology Modeling

Kelley2009 Protein structure prediction on the web

Pevsner 354-363 Stop at Partitioning Methods

Lecture 20 – Pevsner 296-301

Pevsner 312-320 (micro-arrays)

Lecture 21 – Pevsner 331-335 stop at Reproducibility

Pevsner 343-345 stop at Robust Multi-array Analysis

Lecture 22 – Pevsner 346-351 stop at Significance Analysis of Microarrays (SAM)

Pevsner 354-363 Stop at Partitioning Methods

367-371 (end of chapter)

Lecture 23, 24-- Pevsner 495-507 start at Protein-Protein Interactions

Szilagyi.2007.ProteinFolding Sections 1-9