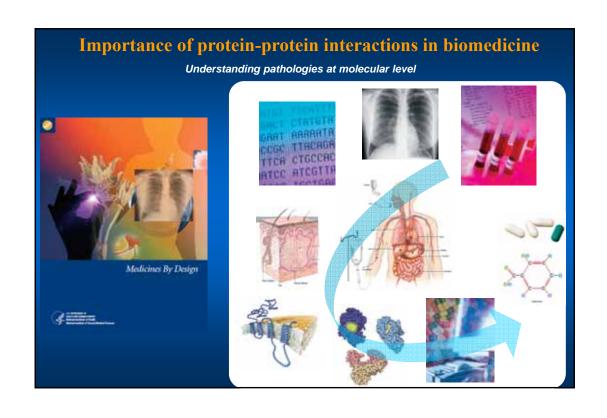
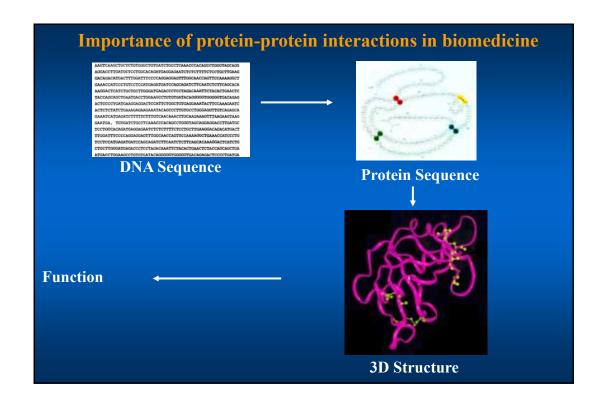
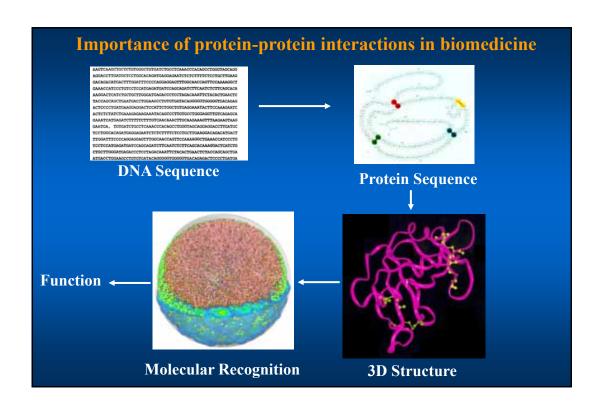
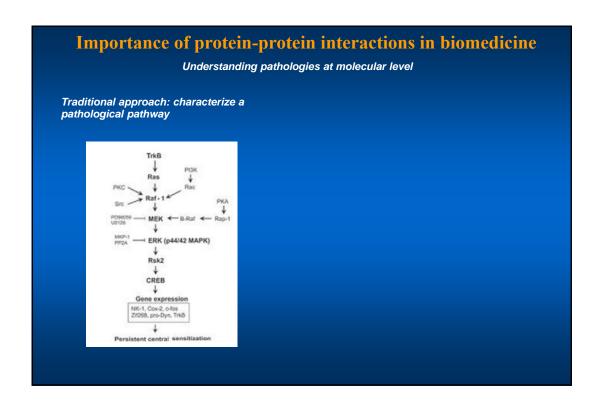


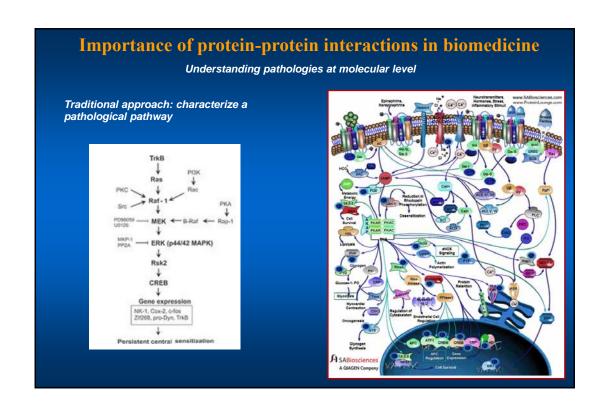
- Importance of protein interactions in biomedicine
- Study of protein-protein interactions
- Computational approaches
- Applications

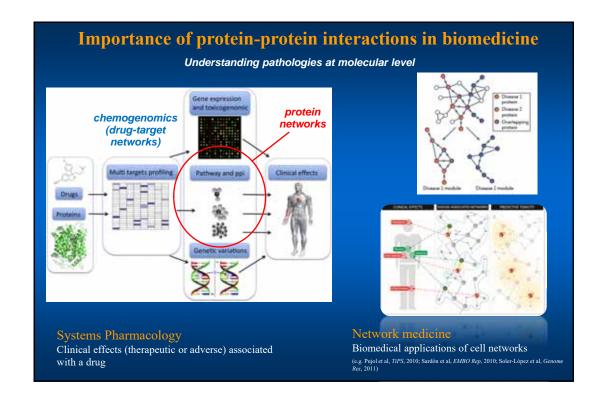


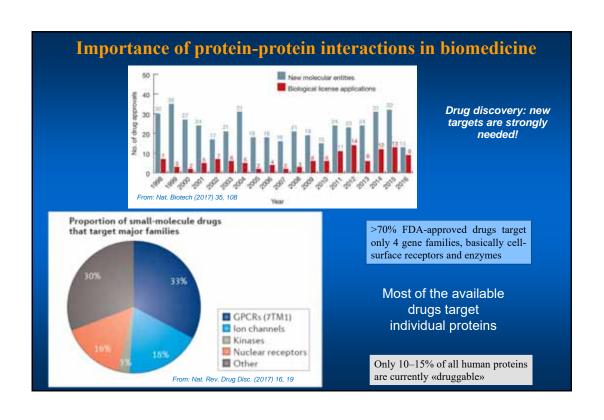


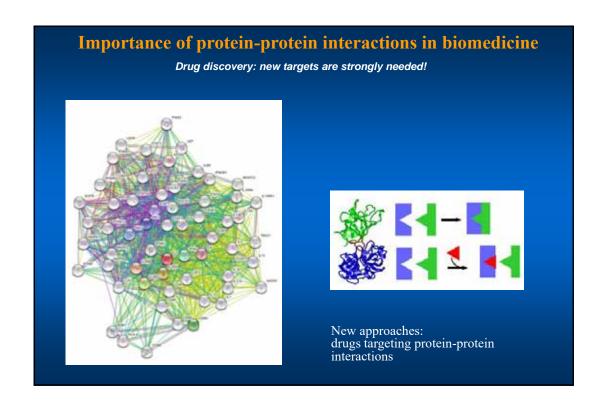


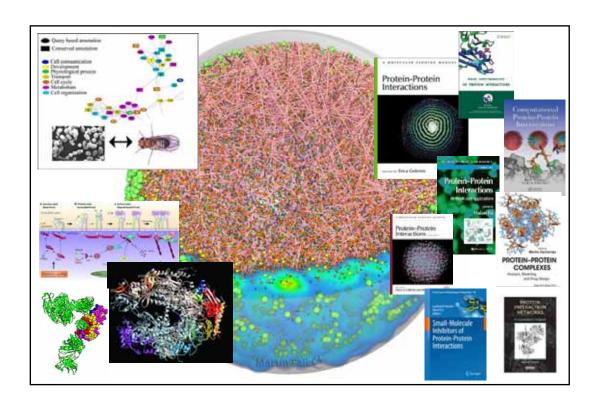




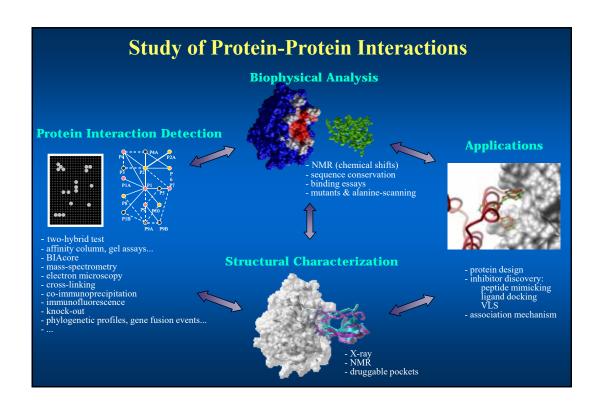


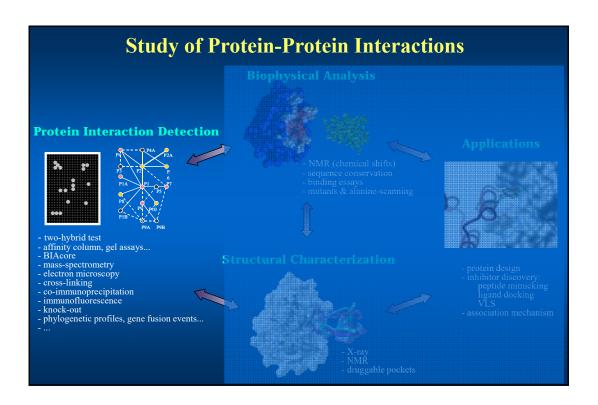


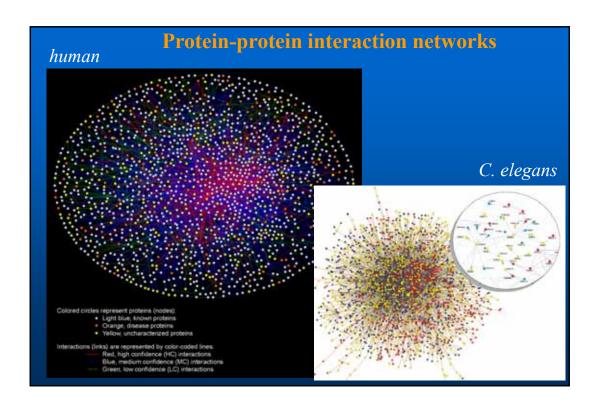




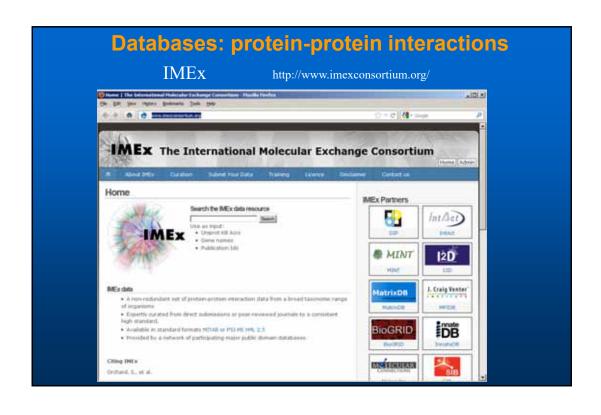
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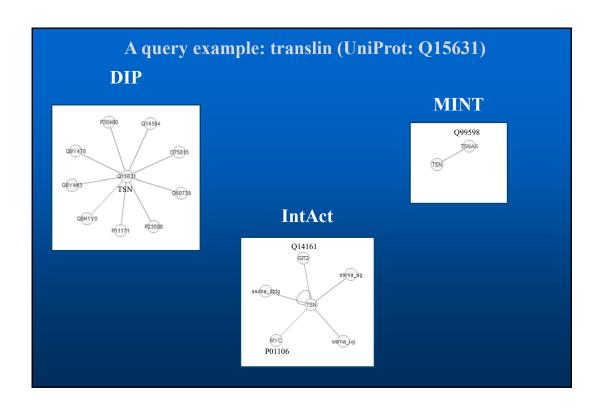


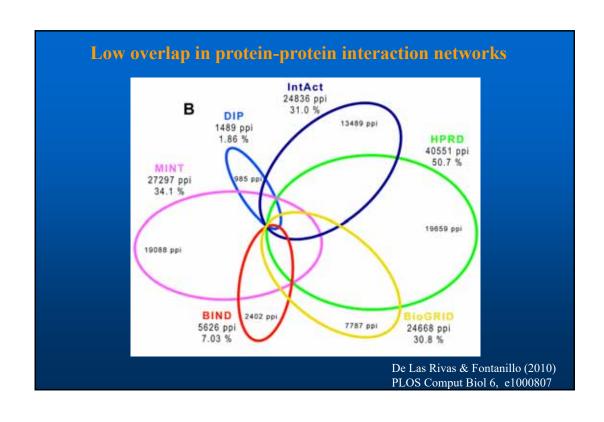


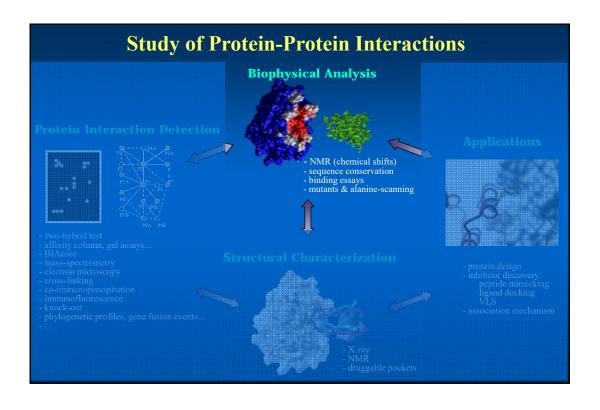


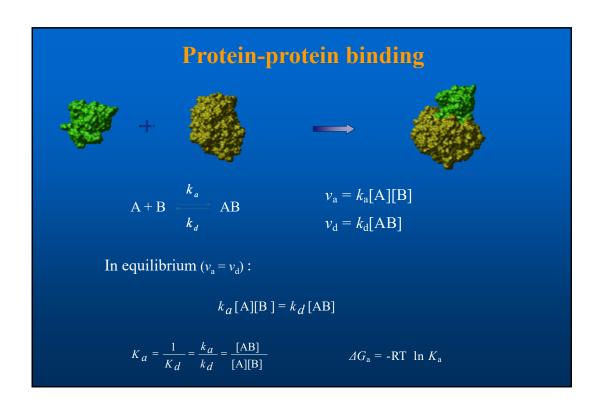
Databases: protein-protein interactions	
IntAct	(http://www.ebi.ac.uk/intact/)
BioGRID	(http://thebiogrid.org/)
DIP	(http://dip.doe-mbi.ucla.edu/dip)
MINT	(http://mint.bio.uniroma2.it/mint)
InnateDB	(http://www.innatedb.com/)
BINDTranslation	(http://baderlab.org/BINDTranslation)
HPRD	(www.hprd.org/)
MatrixDB	(http://matrixdb.ibcp.fr/)

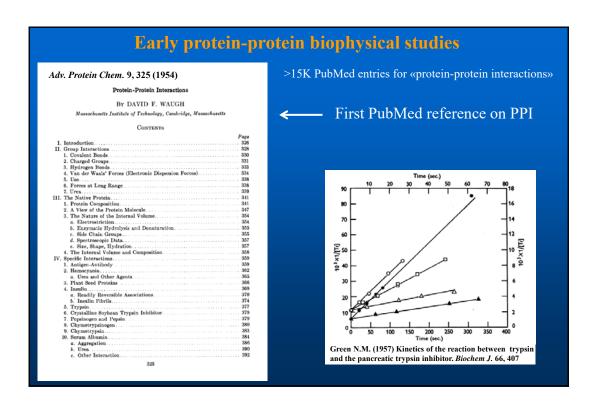


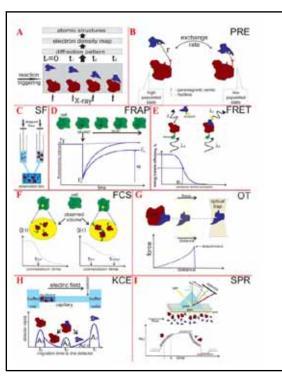






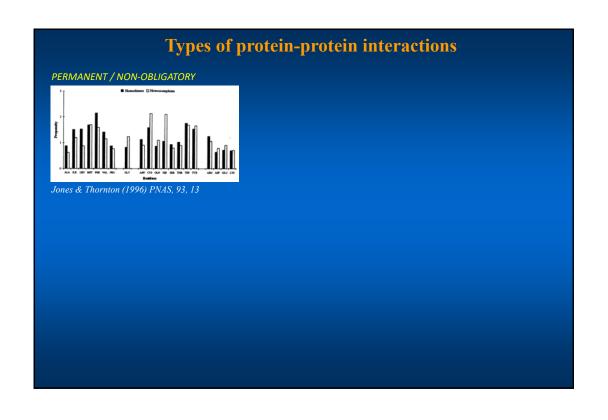


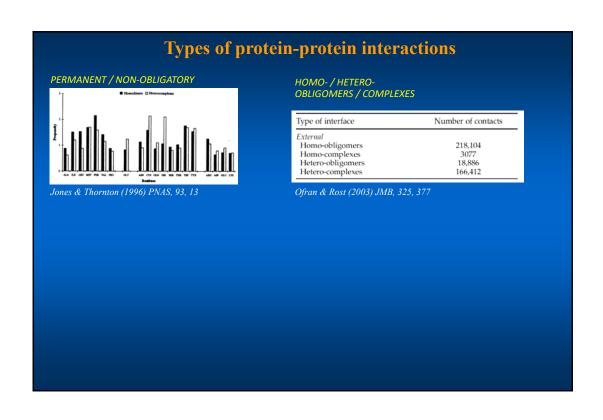


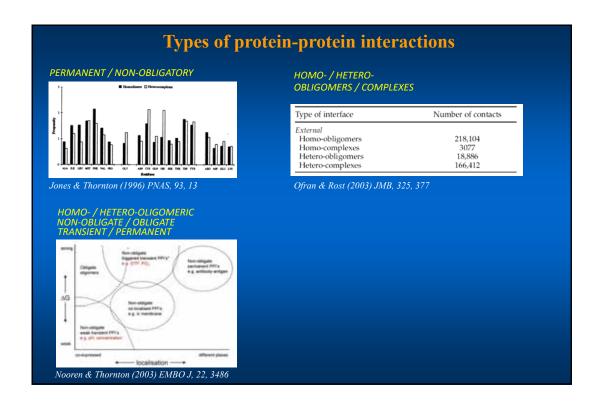


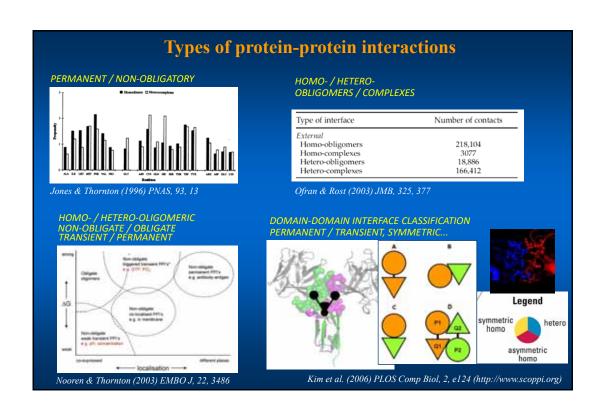
Protein-protein interactions: Biophysical methods

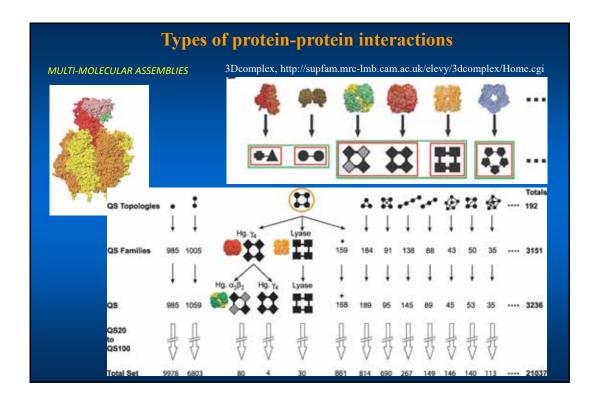
- · X-ray crystallography
- NMR
- Stopped-flow methods
- Fluorescence Recovering After Photobleaching
- Fluorescence Resonance Energy Transfer
- Fluorescence Correlation Spectroscopy
- Optical Tweezers / AFM / Biocore
- Electrophoresis
- Surface Plasmon Resonance (SPR)
- Isothermal Titration Calorimetry (ITC)

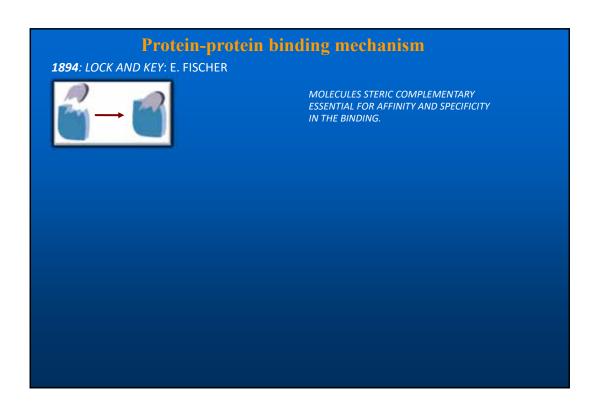


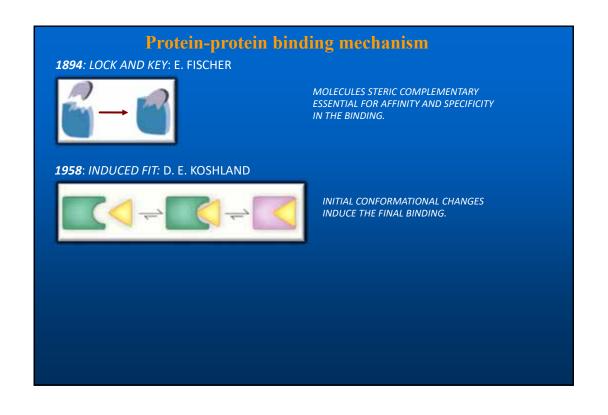


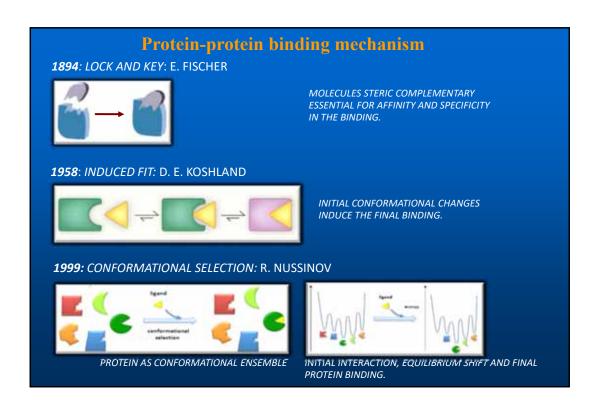


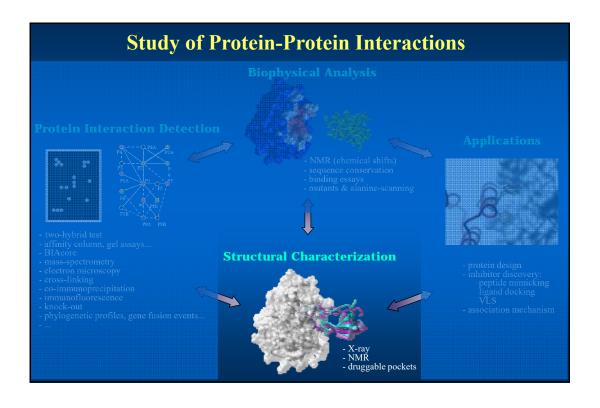


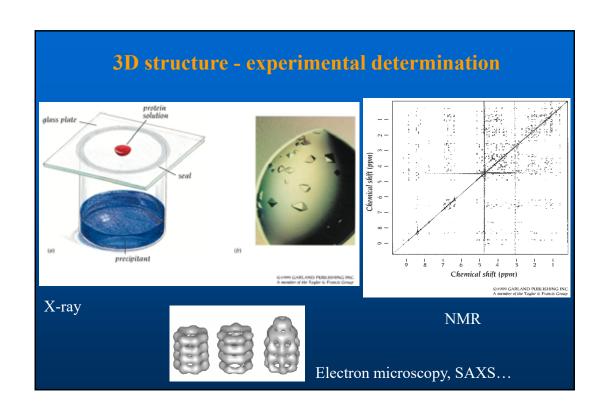


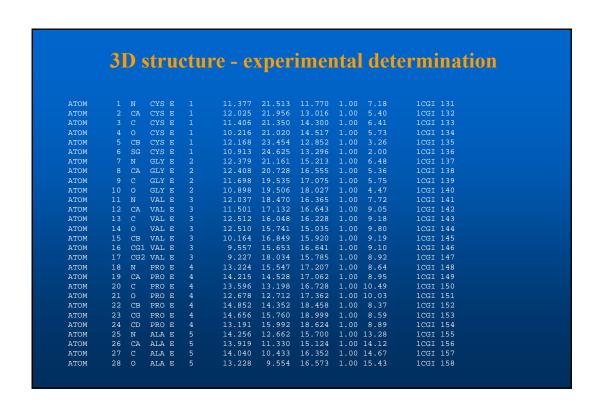




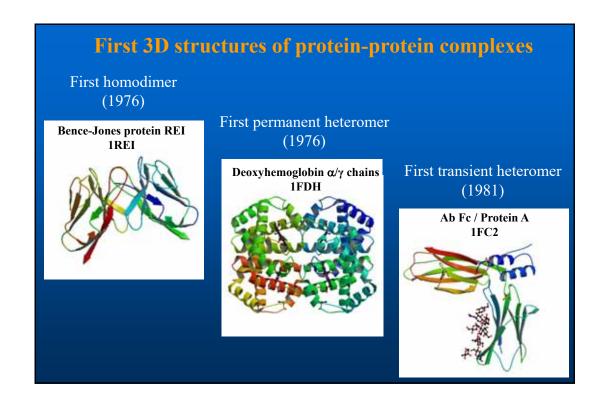


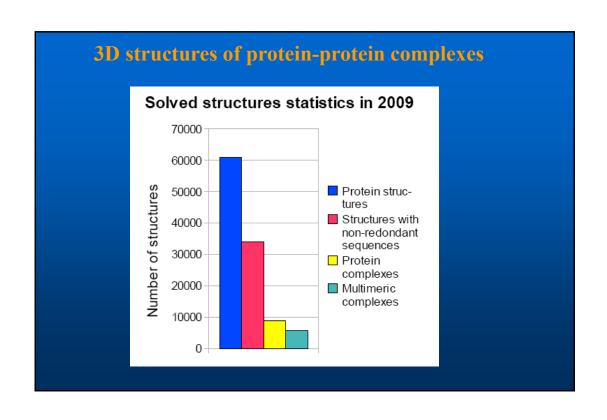


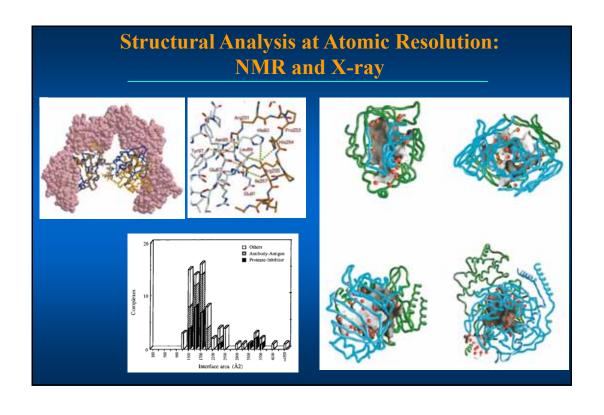


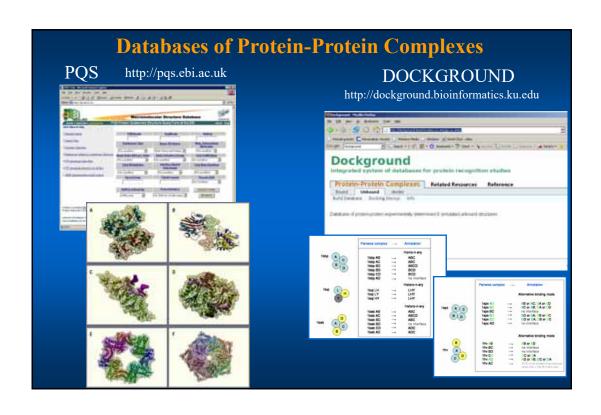


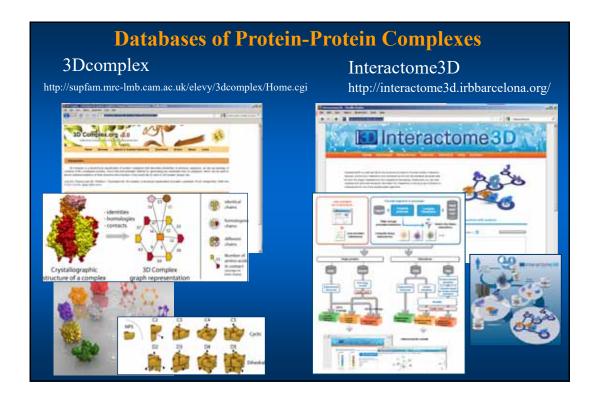




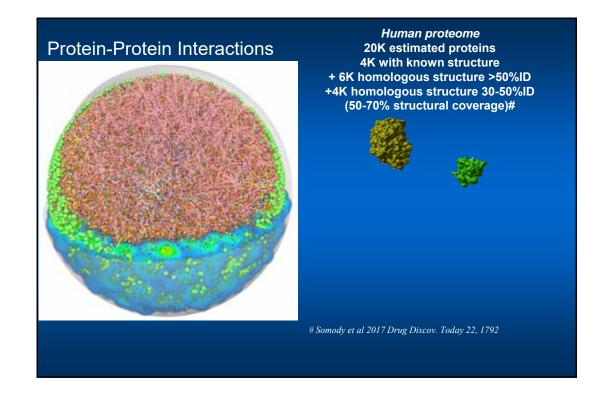


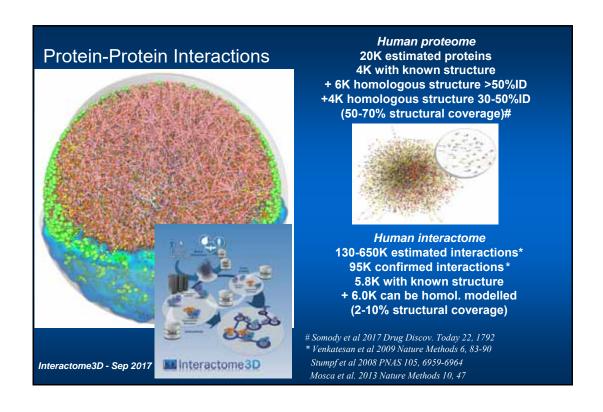




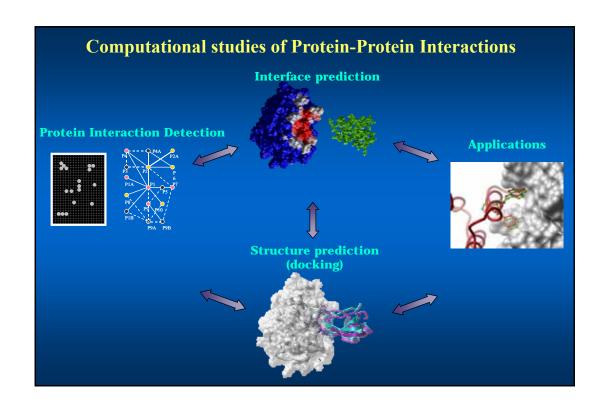


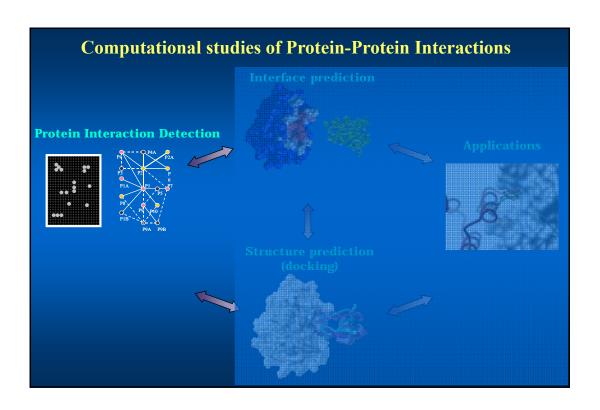
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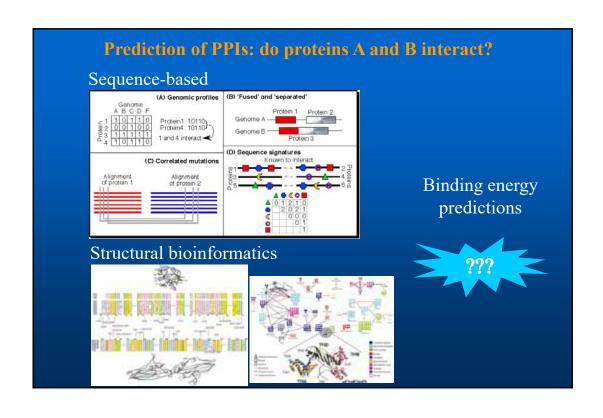


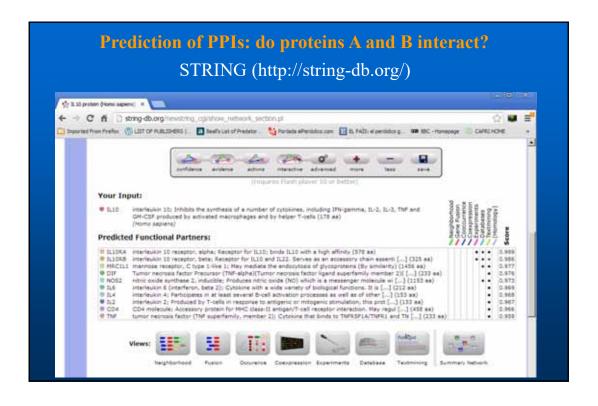


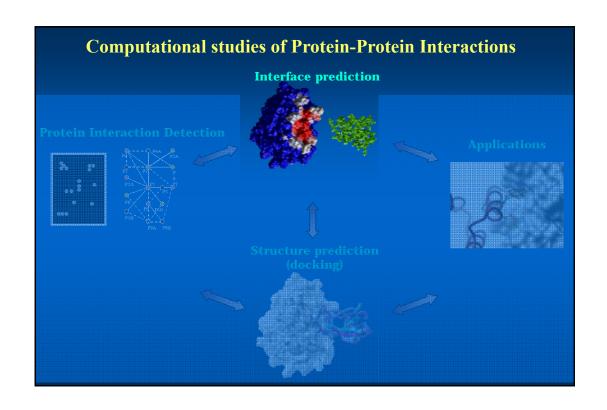
First computer studies on protein-protein interactions Proc. Nat. Acad. Sci. USA Vol. 72, No. 4, pp. 1330-1334, April 1975 Hemoglobin Interaction in Sickle Cell Fibers I: Theoretical Approaches to the Molecular Contacts (model buildine/protein interactions/computer graphics) CYRUS LEVINTHAL, SHOSHANA J. WODAK, PETER KAHN, AND ARTEM K. DADIVANIAN Department of Biological Sciences, Columbia University, New York, N.Y. 10027 Contributed by Cyrus Levinthal, January 10, 1978 Wodak SJ, Janin J (1978). "Computer Analysis of Protein-Protein Interactions". Journal of Molecular Biology 124 (2): 323-42.

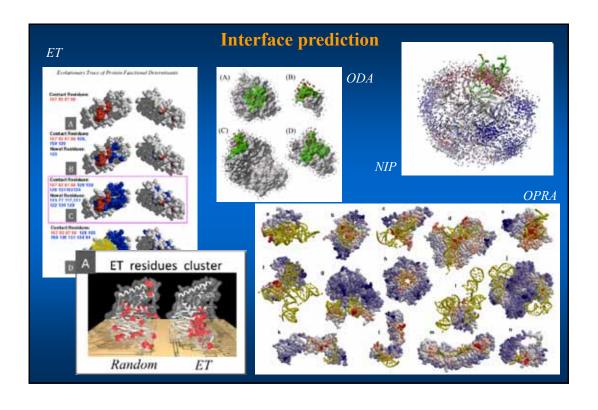


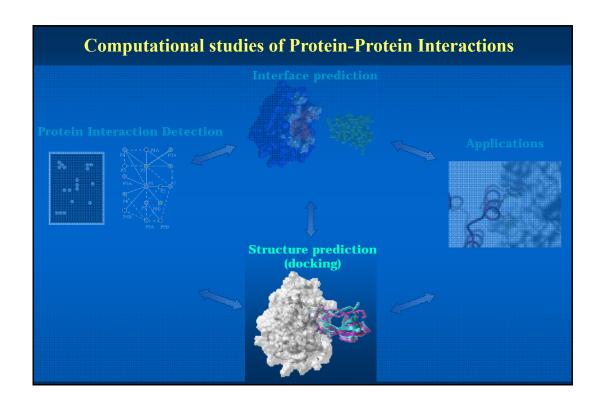


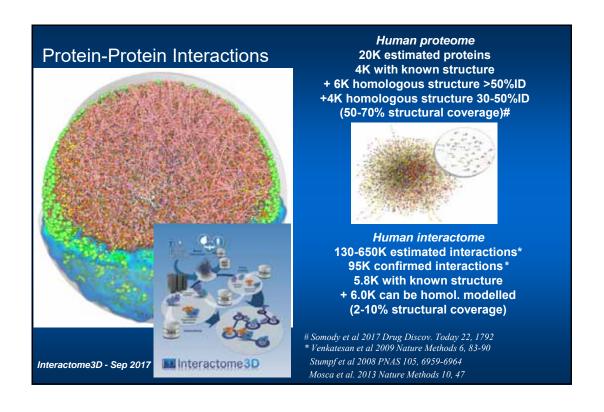


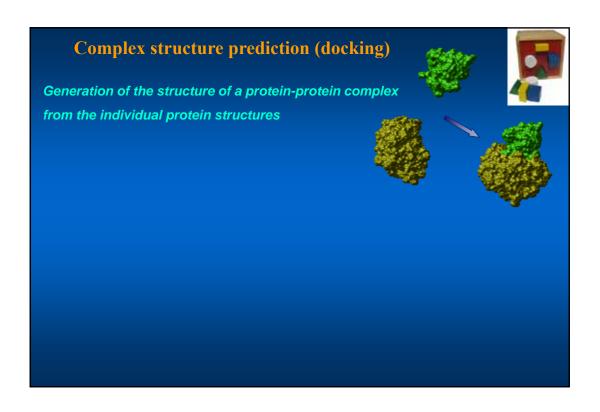


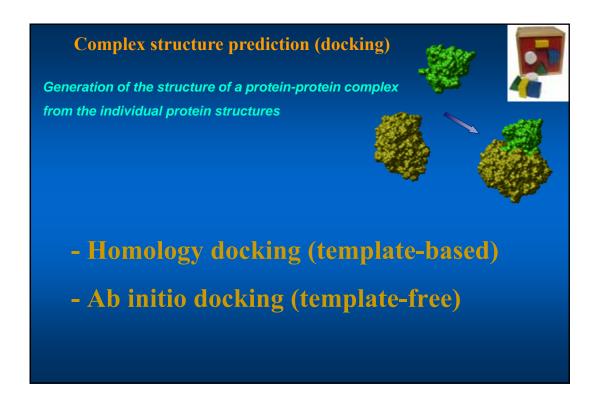


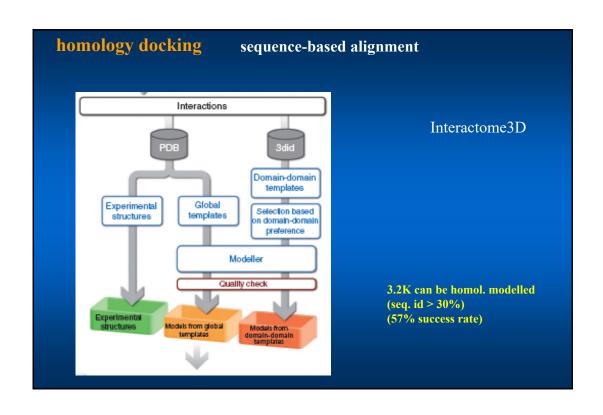


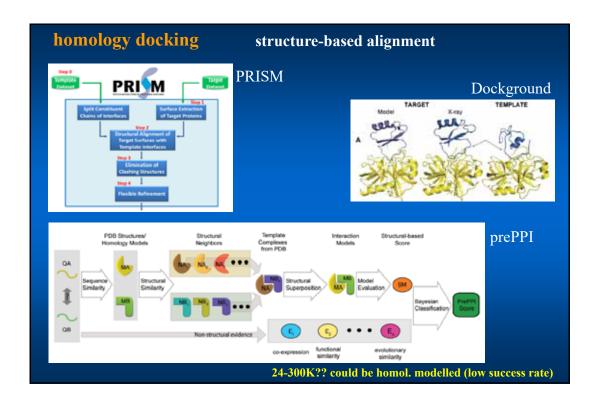












Why Is Docking A Hard Problem? • Large Search Space → "Hard" • "The Curse of Dimensionality" • Sequence Alignment: 1D - Easy! • Structure Alignment: 3-6D - Hard • Rigid Body Docking: 6D - Hard! • Flexible Docking: 3N - "Impossible!" • Sequence Space: Discrete • Structure Space: Continuous

