

France-Stanford Exchange Program Meeting at Institut Pasteur 2010

Organizers: Marc Delarue (IP), Seb Doniach (Stanford), Henri Orland (CEA)

1 Chromatin and chromosomes: Sept 7th, 2010

1.1 Morning. Batiment Roux, Salle Chamberland

10:00 J.A. Spakowitz, Stanford, USA. Target-site search by DNA binding proteins

11:00 C. Zimmer, IP, Paris. Imaging and simulating gene positioning in yeast nucleus

Lunch in Module 3 (Espace Congres)

1.2 Afternoon. Batiment Fernbach, Salle JP Aubert

2:00 J.L. Sikorav, CEA, France. DNA renaturation in homogeneous and heterogeneous systems

3:00 J. Lipfert, Delft, NL. Single molecule manipulations of proteins interacting with nucleic acids

3:30 M. Baaden, IBPC, Paris. Divalent cations assist DNase I in its biological function and are essential for DNA binding

4:00 Drinks

Dinner in Paris

2 Protein and Folding: Sept 8th, 2010

2.1 Morning. Batiment Roux, Salle Chamberland

10:00 V. Pande, Stanford, USA. Insight from atomistic simulations of protein folding and misfolding on the millisecond timescale and beyond

11:00 G. Bowman, Stanford, USA. Markov states: Protein folded states are kinetic hubs

Lunch in Module 3 (Espace Congres)

2.2 Afternoon. Batiment Fernbach, Salle JP Aubert

2:00 R. Netz, MPI, Munich, Germany. Hydrophobic effect and denaturation by urea: Insights into protein folding mechanisms from MD simulations

3:00 A. Blondel, IP, Paris. Modeling the conformational path transition can help drug design

3:30 F. Poitevin, IP, Paris. Testing the dipolar model of solvation with SAXS data