



T H E
S C R I P P S
R E S E A R C H
I N S T I T U T E

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Biocomplexity Faculty Search Committee
c / o Prof. Rob de Ruyter van Steveninck
Department of Physics
Indiana University
Bloomington IN, 47405-7105

Dear Members of the Search Committee,

I am writing to apply for the Biocomplexity Faculty position in the College of Arts and Sciences at Indiana University Bloomington that was advertised in the Oct 21, 2004 issue of *Nature*. I am currently a post-graduate researcher at The Scripps Research Institute where I am working with Prof. Charles L. Brooks III.

My PhD work was carried out in the Laboratory of Quantum Physics at the University Paul Sabatier (France) under the direction of Dr. Yves-Henri Sanejouand and in the Theoretical Chemistry group at Kyoto University (Japan) under the direction of Professor Nobuhiro Go. My PhD work was dedicated to the theoretical studies of large amplitude motions in small proteins.

At The Scripps Research Institute with Professor Charles L. Brooks III, my research has been primarily focused on the exploration of the dynamical and mechanical properties of macromolecular assemblies of proteins related to the expression of their functions using computational models with different level of complexity. I have worked on the ribosome in collaboration with Prof. Joachim Frank and on myosin II in collaboration with Prof. Kenneth Taylor, to answer questions related to the mechanism of experimentally observed conformational changes in these systems. The opportunities to work in close relation with experimental groups have been of great importance for my research. More recently, I have also been developing new methodologies to assist the interpretation of low-resolution structures as obtained from cryo electron microscopy.

I intend to pursue active collaborations with experimental groups to approach questions arising from structural proteomics. My research proposal centers on combining computational approaches and experimental data for the determination and subsequent dynamical studies of supra-molecular assemblies of proteins, which are critical for the machinery of the cell. In addition, I am eager to approach biophysical problems related to these systems from a more theoretical perspective, since a physicochemical understanding of their dynamics will surely deepens our knowledge of the machinery of these biological systems.

I truly believe that the outstanding interdisciplinary research conducted at Indiana University Bloomington would provide the most stimulating environment to undertake my future research as well as to establish fruitful collaborations. As a member of the College of Arts and Sciences, I would be committed to excellence in research.

Please find enclosed my CV, list of publications, a summary of research accomplishments and plans and a statement of teaching interests. You will receive letters from five referees in support of this application: Prof. CL. Brooks III, my current advisor, Prof. N. Go and Dr. YH. Sanejouand, my PhD advisors; Prof. J. Frank and Prof. K. Taylor with who I have collaborated.

Thank you for considering my application. I am entirely at your disposal should you require further information. I look forward to hearing from you.

Dr. Florence Tama

Curriculum Vitae

Florence Tama

30 years old

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EDUCATIONAL BACKGROUND

- 2000:** **PhD degree** Theoretical studies of large amplitude motions of proteins.
Paul Sabatier University (France)
- 1997:** **M. Sc** in Chemistry of biological molecules, Paul Sabatier University (France)
- 1996:** **B. Sc** in Chemistry and Physics, Paul Sabatier University (France)

RESEARCH EXPERIENCE

- 01/01-present** **Postdoctoral research associate** with Prof. Charles L. Brooks III
The Scripps Research Institute, La Jolla (**USA**)
- Computational studies of large biological assemblies: Development of “multiresolution” motional models for large-scale virus capsid dynamics, ribosome and myosin conformational change based on reduced basis normal mode calculations.
 - Development of computational techniques to interpret cryo-electron microscopy data.
- 01/98-06/98** **Graduate student** with Dr. Yves-Henri Sanejouand
- 01/99-06/99** LPQ Paul Sabatier University (**France**)
- 06/00-12/00**
- Study of proteins dynamics (especially conformational change upon ligand binding or compressibility) by theoretical methods such as molecular dynamics simulation and normal mode analysis.
- 07/98-12/98** **Graduate student** with Prof. Nobuhiro Go
- 07/99-05/00** Kyoto University (**Japan**)
- 1998-1999** **Teaching assistant**, Paul Sabatier University, Toulouse
(150 hours)
- First, second and third year College students

Fellowships

- 09/97-09/00:** Graduate fellowship (MENRT) from the French Ministry of education and research.
- 07/99-09/99:** Monbusho Fellowship from the Japanese Government for young exchange researcher.
- 09/99-03/00:** Fellowship from Paul Sabatier University (France) for mission in Japan.

Publications list

1. A building block approach for determining low-frequency normal modes of macromolecules. **F. Tama**, F.X. Gadea, O. Marques and Y.H. Sanejouand. *Proteins* **41**: 1-7 (2000)
2. Molecular dynamics simulation shows large volume fluctuation of proteins. **F. Tama**, O. Miyashita, A. Kitao and N. Go, *Eur. Biophys. J.* **29**: 472-480 (2000)
3. Conformational change of Proteins arising from Normal Mode Analysis. **F. Tama** and Y.H. Sanejouand. *Protein. Eng.* **14**: 1-6 (2001)
4. Exploring Large-Scale Conformational Changes in Virus Maturation. **F. Tama** and CL. Brooks III. *J. Mol. Biol.* **318**: 733-747 (2002)
5. Exploring global distortions of biological macromolecules from low-resolution structural information and elastic network theory. **F. Tama**, W. Wriggers and CL. Brooks III. *J. Mol. Biol.* **321**: 297-305 (2002)
6. Normal mode analysis with simplified models to investigate the global dynamics of biological systems. **F. Tama**. *Prot. Pept. Let.* **10**: 119-132 (2003)
7. Mega-dalton biomolecular motion captured from electron microscopy reconstructions. P. Chacon, **F. Tama** and W. Wriggers. *J. Mol. Biol.* **326**: 485-492 (2003)
8. Understanding the ratchet-like inter-subunit reorganization of the ribosome. **F. Tama**, M. Valle, J. Frank and CL Brooks III. *Proc. Natl. Acad. Sci. USA* **100**: 9319-9323 (2003)
9. Topology representing Neural Networks reconcile biomolecular shape structure and dynamics. W. Wriggers, P. Chacon, J. Kovacs, **F. Tama** and S. Birmanns. *Neurocomputing* **56**: 365-379 (2004)
10. Flexible multi-scale fitting of atomic structures into low-resolution electron density maps with elastic network normal mode analysis. **F. Tama**, O. Miyashita and CL. Brooks, III. *J. Mol. Biol.* **337**: 985-999 (2004)
11. NMFF: Flexible high-resolution annotation of low-resolution experimental data from cryo-EM maps using normal mode analysis. **F. Tama**, O. Miyashita and CL. Brooks III, *J. Struct. Biol.* **147**: 315-326 (2004)
12. Motions of the ribosome modulate electrostatic properties. J. Trylska, R. Konecny, **F. Tama**, CL. Brooks III and JA McCammon. *Biopolymers* **74**: 423-431 (2004)
13. Diversity and identity of mechanical properties of icosahedral viral capsids studied with elastic network normal mode analysis. **F. Tama** and CL. Brooks III. *J. Mol. Biol.* (2004) **in press**
14. The Requirement for Mechanical Coupling Between Head and S2 Domains in Smooth Muscle Myosin ATPase Regulation and its Implications for Dimeric Motor Function **F. Tama**, M. Feig, CL. Brooks, III and KA. Taylor. *J. Mol. Biol.* (2004) **in press**

- 15.** Electrostatic properties of Cowpea Chlorotic Mottle Virus, R. Konecny, J. Trylska, **F. Tama**, D. Zhang, NA Baker, CL. Brooks III and JA McCammon. *Submitted to Proteins*
- 16.** The 13 Å Structure of a Chaperonin GroEL-Protein Substrate complex by Cryo-Electron Microscopy. S. Falke, **F. Tama**, CL. Brooks III, EP. Gogol and MT. Fisher. *Submitted to J. Mol. Biol.*

Book chapter:

Unveiling molecular mechanisms of biological functions in large macromolecular assemblies using elastic network normal mode analysis. **F. Tama** and CL Brooks III in Normal Mode Analysis: Theory and Applications to Biological and Chemical Systems, Mathematical Biology Series, CRC Press (2004).

Invited presentations at conference and workshops

1. Simulation on larger length and longer time scale: Elastic Network Normal Mode Analysis. F. Tama. Theory and Computation in Molecular Biological Physics, CTBP & TSRI, La Jolla, USA, August 9-20 2004.
2. Exploration of functionally important motions of biological assemblies: application to the ribosome. F. Tama and C.L. Brooks III. Annual Meeting of the Molecular Biology Society of Japan, Kobe, Japan, December 11-14 2003.
3. Dynamical Properties of Low-resolution Structure (Cryo-EM) Studied with Elastic Network Normal Mode Analysis. F. Tama. Electron-Phase Microscopy and its Applications, December 8-9, Okazaki, Japan, 2003.
4. NMFF: Flexible fitting of atomic structures into low-resolution EM maps using elastic network normal mode analysis. F. Tama, A practical Course in Molecular Microscopy, CIMBio, TSRI, La Jolla, USA, November 12-20 2003
5. Exploring global distortions of biological macromolecules and assemblies by normal mode analysis. F. Tama. Multiscale Modeling in Biology, University of Notre Dame, USA, August 14-17 2003
6. Exploring large-scale structural rearrangements in viruses, the ribosome and other molecular machines. C.L. Brooks III and F. Tama. ACS National meeting, New-Orleans, USA, March 2003
7. Introduction to Normal mode analysis. F. Tama. Situs EM/X-tal Fitting and Modeling Workshop, San Diego, USA, February 3-5 2003.
8. Studies of protein flexibility using normal mode analysis. F. Tama and Y.H. Sanejouand. CECAM Workshop, Dynamics of proteins on a continuous energy, Lyon, May 2002
9. Reconciling shape with structure: morphometric strategies for multi-resolution flexing. W. Wriggers, S. Birmanns, F. Tama, J. Kovacs and P. Chacon. Biophysical Society Discussion. Frontier in Structural Cell Biology, How can we determine the structures of large subcellular machines at atomic resolution? Asilomar, CA, USA, April 2002
10. Exploring Large-Scale Conformational Changes in Virus Maturation. F. Tama and C.L. Brooks III. SIAM conference on Life Science 2002, Boston, USA, March 2002.
11. Fast and accurate approximations of low-frequency normal modes. F. Tama and Y.H. Sanejouand. CECAM Workshop, Calculation of concerted motions in biomolecules, Lyon, October 1999.

References

Post-doctoral studies: advisor

Prof. Charles L. Brooks III

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Post-doctoral studies: collaborators

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