**ALLEGATO A**

**UNIVERSITÀ DEGLI STUDI DI MILANO**
**Procedura di valutazione per la chiamata a professore di I fascia da ricoprire ai sensi dell'art. 24, comma 6, della Legge n. 240/2010 per il settore concorsuale 02/B2,**
**(settore scientifico-disciplinare FIS/03)**
**presso il Dipartimento di Fisica, Codice concorso 5353**

# Guido Tiana
# CURRICULUM VITAE

## INFORMAZIONI PERSONALI

| | |
|---|---|
| **COGNOME** | **TIANA** |
| **NOME** | **GUIDO** |
| **DATA DI NASCITA** | 25 LUGLIO 1972 |

Formazione

1997, Laurea in Fisica, Università degli Studi di Milano, 110 e lode
2000, PhD in Physics, Niels Bohr Institute, University of Copenhagen

Cronologia dell'attività di ricerca

1997, durante la tesi di laurea sono stato visiting student presso l'Università di Giessen (Germania) nel gruppo del prof. A. Bunde.
Aprile 1997-agosto 1997, visiting scientist al Center for Biological Sequence Analysis (CBS) a Lyngby (Denmark) della Danmarks Tekniske Universitet, nel gruppo di S. Brunak.
Agosto 1997-dicembre 1997, research assistant al Dipartimento di Chimica e Chimica Biologica della Harvard University, nel gruppo di E. Shakhnovich.
Gennaio 1998-luglio 1998, research assistant al Dipartimento di Fisica della Danmarks Tekniske Universitet, nel gruppo di J. Bohr.
Agosto 1998-giugno 2000, ho lavorato per la mia tesi dottorale al Niels Bohr Institute di Copenhagen sotto la supervisione di Kim Sneppen.
Agosto 2000-gennaio 2005, sono stato assegnista di ricerca al Dipartimento di Fisica dell'Università degli Studi di Milano.
2009-2013, fondatore e research manager dello spin-off Foldless s.r.l.
Gennaio 2005-settembre 2016, ricercatore al Dipartimento di Fisica dell'Università degli Studi di Milano.
2012-ora, Principal Investigator del Laboratorio di Biofisica Teorica nel Dipartimento di Fisica dell'Università degli Studi di Milano.
Ottobre 2016-ora, professore associato al Dipartimento di Fisica dell'Università degli Studi di Milano.

Interessi di ricerca

L'obiettivo principale della mia ricerca è capire il comportamento dei sistemi biologici da un punto di vista fisico. Proteine, DNA e cellule sono sistemi complessi finiti, che tipicamente mostrano comportamenti collettivi. Sono complessi perché l'interazione tra le loro parti è così eterogenea che il profilo di energia libera risultante è tipicamente molto frastagliato. Sono sistemi piccoli, che non rientrano nel limite termodinamico. Per non essere abbandonati a fluttuazioni casuali, le varie parti di questi sistemi cooperano per stabilizzarsi a vicenda, producendo fenomeni collettivi. In particolare, ho studiato: 1) **Il ripiegamento delle proteine**. Le proteine sono catene costituite da 20 tipi di amminoacidi che ripiegano in una conformazione unica di equilibrio. In breve, i miei risultati riguardano l'importanza di poche selezionate regioni della proteina per determinare la sua capacità di ripiegare. 2) **Disegno di inibitori del ripiegamento**. Peptidi con la stessa sequenza di segmenti specifici di proteine dannose sono utilizzati per inibirle. Questo approccio è stato

utilizzato contro la proteasi del virus HIV-1, responsabile per l'AIDS. 3) **Aggregazione di proteine**. Un esito pericoloso del ripiegamento delle proteine è la loro aggregazione in oggetti grandi, la cui energia di stabilizzazione è ordini di grandezza maggiore di quella delle proteine solubili. Questo è per esempio il caso del peptide Aß, una piccola proteina che causa il morbo di Alzheimer, e del prione, che causa il morbo di Creutzfeld-Jacob (la cosiddetta mucca pazza nel caso dei bovini). 4) **Evoluzione molecolare**. L'evoluzione delle sequenze proteiche attraverso i secoli può essere descritta attraverso processi di Markov, con l'obiettivo di capire quali parti delle proteine sono meno suscettibili a mutazioni. 5) **Network di regolazione genica**. Proteine e DNA formano network complessi che possono essere descritti in termini di equazioni differenziali che controllano le concentrazioni delle diverse specie nella cellula. In particolare, ho studiato le oscillazioni temporali di trascritti legati al cancro, associando queste oscillazioni al ritardo intrinseco nei segnali. 6) **Termodinamica del controllo trascrizionale**. I nodi nel network trascrizione sono spesso proteine chiamate fattori di trascrizione, che legano segmenti specifici del DNA. Il meccanismo di attivazione della trascrizione non è banale e coinvolge il legame cooperativo e una mutua esclusione tra diverse specie, dando luogo ad un comportamento termodinamico complesso. 7) **Rappresentazione spaziale operata dal cervello**. Diversi neuroni nel cervelletto sono usati per creare una rappresentazione spaziale dello spazio intorno a noi e per sviluppare strategie per muoversi in esso. Mi occupo di studiare semplici modelli fisici per capire come questo possa realizzarsi. 8) **Struttura e dinamica della cromatina**. Basandomi su dati sperimentali, ho sviluppato un modello per ottenere le proprietà strutturali della cromatina sulla scala delle kilobasi, in particolare per studiare le fluttuazioni conformazionali e la loro rilevanza biologica.
Le tecniche che uso sono quelle della meccanica statistica, sia analitiche che computazionali. Per tutti problemi menzionati sopra ho sviluppato semplici modelli che catturano gli ingredienti fisici fondamentali che controllano il sistema da studiare.
Ho sviluppato nuovi algoritmi per il sampling termodinamico e per generare traiettorie molecolari ad alta probabilità, scrivendo inoltre programmi in C per implementare tali algoritmi. Ho inoltre svolto e coordinato una piccola attività sperimentale nella biofisica di proteine (cf. lista articoli sottostante).
Un importante aspetto della mia ricerca è la creazione di modelli teorici basati su dati sperimentali, spesso nel framework del principio di massima entropia. Questo implica la collaborazione con colleghi sperimentali biofisici (con A. Podestà, UNIMI, M. Manno, CNR Palermo), biochimici (con M. A. Vanoni e S. Ricagno UNIMI, F. Chiti UNIFI), biologici (con G. Natoli, IEO-IFOM, E. Heard, Institut Curie, L. Giorgetti, FMI Basel) e preclinici (con M. Clerici and A. Clivio, UNIMI).
Oltre alla ricerca di base, nel periodo 2009-2013 ho portato avanti un'attività nella ricerca industriale, fondando Foldless s.r.l., un'azienda per sviluppare inibitori virali. Le attività svolte si estendevano dal design computazionale, ai trial preclinici, coinvolgendo ricerca computazionale, organizzazione ed interpretazione di esperimenti in biochimica, biologia cellulare, preclinica e company management. Foldless s.r.l. ha ottenuto un finanziamento di 1,320,701 euro.

Informazioni sul gruppo di ricerca

Dal 2012 sono il Principal Investigator del Laboratorio di Biofisica Computazionale nel Dipartimento di Fisica dell'Università di Milano. Qui sono l'unico membro con una posizione permanente, e ho supervisionato due post-doc (Martina Caldarini e Valentina Naddeo), cinque dottorandi, 31 laureandi magistrali e 19 laureandi triennali. Sono inoltre responsabile del parco computer del gruppo.

Raccolta fondi

• EU FP5 attività "human potential" HPCF-CT-2001-00426-01 "Protein folding and aggregation", 48000 euro.
• FIRB 2004 "Molecular recognition in protein-ligand, protein-protein and protein-surface interactions: development of integrated experimental and computational approaches to the study of systems of pharmaceutical interest", 68493 euro, coordinatore di unità.
• PUR 2009 Università di Milano, 11000 euro, responsabile.

• Attraverso lo spin-off Foldless s.r.l. 1,320,701 euro nel periodo 2009-2013; di questi circa 75,000 euro sono stati trasferiti a Unimi come ricerca conto terzi per 3 assegni di ricerca di cui sono stato responsabile scientifico
• 2 assegni “dote ricerca applicata” (circa 25,000 euro, cofinanziati da Foldless S.r.l.) della regione lombardia di cui sono stato responsabile scientifico.
• Dal 2006 dall’iniziativa specifica dell’INFN TO61/biophys, un finanziamento totale di circa 50,000 euro.
• Nel 2020, 30,000 euro programma SEED dell’Università di Milano per lo sviluppo di inibitori dell’emagglutinina, PI.

Brevetti

• EUR 05015597.7 Methods for the identification of protein folding inhibitors. Inventori: R. A. Broglia e G. Tiana
• USA 186924 A folding inhibitor of HIV-1 Protease as antiviral drug. Inventori: R. A. Broglia, D. Provasi e G. Tiana

Attività Istituzionali

2006-ora, Responsabile Locale dell’Iniziativa Specifica TO61/Biophys del’INFN.
2007-2010, membro della Giunta del Dipartimento di Fisica.
2011-2012, membro del Collegio di Dottorato della European School in Molecular Medicine.
2009-2013 co-fondatore, socio e research manager dello spin-off Foldless s.r.l., svolgendo attivita’ di coordinamento della ricerca.
2013-2018, 2022-ora collegio di dottorato del Dottorato in Fisica dell’Università di Milano.
2020-ora, Referente del Percorso in Fisica dei Dati nel Corso di Laurea Magistrale in Fisica.

Seminari scientifici

In totale ho dato 5 contributed talks, 55 invited talks e 9 invited lectures.

1. "Models for aggregation of proteins" (contributed talk) at Summer School "Physics of Molecular Biology", organized in Krogerup (Denmark) by Nordita (1998)
2. Topology of the space of good folder sequences (contributed talk) at Topical Meeting on Biophysics-Biological Physics, at the Niels Bohr Institute of Copenhagen (1999)
3. Designability of Model proteins (invited talk) at Third Fractal Meeting, Sils-Maria (Switzerland) (2000)
4. Energy landscape of folding sequences (invited talk) at ISI workshop, Villa Gualino (2000)
5. The protein folding problem (invited talk) at Workshop on Theoretical Nuclear and Many Body Physics, Cortona, Italy (2000)
6. Prediction of 3D structure of proteins (lecture) at International School of Physics "E. Fermi", Varenna, Italy (2000)
7. The protein folding problem: from 1D to 3D (invited talk) at Workshop in Protein Folding, Structure and Design at ICTP, Trieste (2001)
8. Folding, design and evolution of dimeric proteins (invited seminar) at CNR Palermo (2002)
9. Time delay as a key to apoptosis induction in the p53 network (invited talk) at Conference on Dynamics of Biological Systems, Humlebaek, Denmark (2002)
10. Design, thermodynamics and kinetics of small proteins (contributed talk) at Congresso Nazionale della Societa Italiana di Fisica, Alghero (2002)
11. Dynamics of the p53 genetic network (invited talk) at Conference on First Exit Problems in Turbulence, Climate and Genomics (2002)
12. Computational aspects of protein folding (invited seminar) at Universita' di Milano-Bicocca (2003)
13. Protein Folding and Drug Design (invited talk) at IF-Symposium, University of Frankfurt (2003)

14. Model study of resistance proof, folding-inhibitor drugs (invited talk) at International Workshop on "Proteomics: Protein Structure, Function and Interactions", ICTP, Trieste (2003)
15. Oscillations and robustness in the p53 genetic network (invited talk) at Workshop on complexity and criticality in memory of Per Bak, Copenhagen (2003)
16. Physics of protein folding and drug design (invited talk) at INFN workshop, Ferrara (2003)
17. The thermodynamics of protein folding (Lecture) at PhD course in Complex systems in post-genomic biology, Torino (2004)
18. The evolution dynamics of model proteins (invited speaker) at Second International Conference "From solid state to Biophysics", Dubrovnik, Croatia (2004)
19. Theoretical design and experimental test of folding inhibitors of HIV protease (contributed talk) at Workshop Theoretical Physics Methods in Quantitative Biology, Universita Milano Bicocca (2004)
20. A physical model for amyloid aggregation (invited talk) at Conference of the Italian Society for Pure and Applied Biophysics. Pisa (2004)
21. Oscillatory dynamics of tumor-suppressor protein p53 (lecture) at PhD course in Complex systems in post-genomic biology, Torino (2005)
22. Design of a folding inhibitor of the HIV-1 Protease (invited seminar) at Web-based conference "Protein Folding & Misfolding: Applications to Drug Discovery", organized by Echeminfo (2005)
23. Folding inhibitors of HIV Protease (invited seminar) at Workshop on Biophysical technologies organized by ST Microelectronics, Torino (2005)
24. (Invited talk) at FB11 Meeting of INFN, Bari (2005)
25. Folding inhibitors of HIV-1 Protease (Invited talk) at Second P2P Symposium, Padova (2005)
26. Oligarchy in protein folding: the upper and lower classes in protein chains (lecture) at International School of Physics "E. Fermi" on Protein Folding and Drug Design, Varenna (Italy) (2006)
27. Design of HIV-protease inhibitors which do not create resistance: blocking the folding of single monomers (invited seminar) at University of Parma (2006)
28. Design of HIV-1 Protease inhibitors which do not create resistance (invited seminar) at XVIII Congress of the Italian Society for Pure and Applied Biophysics, Palermo (Italy) (2006)
29. Design and characterization of folding inhibitors of lysozyme (invited talk), Workshop on protein folding, Harvard University, December 2007.
30. Protein Folding Inhibitors: from simplified models to the cell (invited talk) P2P workshop, University of Padova (2008)
31. Protein Folding: from simplified models to the design of folding inhibitors (invited talk) CSFI Conference on Scientific Computation in Physics, Rimini (2008)
32. Folding inhibitors of hen egg lysozyme (invited seminar) ETH Zurich, prof. Parrinello's Group (2008)
33. Protein folding and folding inhibitors (invited talk) at Young Investigators Symposium, Oak Ridge National Laboratories, Oak Ridge, TN, USA (2008).
34. Folding inhibitors: a new kind of drug (lecture), PhD course in complexity and post-genomic biology, Candiolo, 27 February 2009
35. Protein folding inhibitors: the case of HIV-1 protease (invited seminar), University of Trento, 15 April 2010
36. Protein folding and evolution (invited seminar), CNRS Annecy, France, 6 May 2010
37. Evolution of HIV-1 protease (invited talk), Workshop "The application of theoretical physics methods in biology", ECT* Trento, 29 June 2010
38. Tools to model, simulate and control protein folding (invited lecture), XV School of Pure and Applied Biophysics, Venice, 24-28 January 2011
39. Studying the mechanism of protein folding without parallel computers (invited talk), Kallen talk series, University of Lund (Sweden), 27 September 2011
40. Determination of the structure of chromatin from 5C data (invited seminar), Institute Curie, Paris, February 2012

41. "Obtaining structures from biological data: chromatin and other stories" (invited talk) at S. Raffaele Scientific Institute (2013)
42. "Conformational fluctuations in the X chromosome inactivation center" at Workshop on Chromatin Structure, SISSA Trieste (2013)
43. "Describing conformational fluctuations in chromatin: the case of the X inactivation centre (XIC)" (lecture) at the PhD Course "Genome structure and functional dynamics: physics-based computational approaches", Università di Torino (2014)
44. "Obtaining structures from biological data: the case of the Inactivation Centre of the X-Chromosome " (invited talk) at Dipartimento di Bioscienze, UNIMI
45. Describing conformational fluctuations in chromatin (invited tak), Advanced Workshop on Interdisciplinary Views on Chromatin Structure and Function, ICTP Trieste (15 september 2014)
46. The Complex Structure of chromatin (invited talk), Workshop Excursions in Complexity, The Royal Academy of Science Copenhagen (4 June 2015)
47. Structure and Function in chromatin domains (invited talk), Summer School “models of life”, Krogerup, Denmark (2-8 august 2015)
48. Structure and function in chromatin domains (invited talk), Conference “Living systems: from interaction patterns to critical behaviour”, San Servolo, Venice, 16-19 September 2015
49. Structure and function in chromatin domains (invited talk), Conference FisMat 2015, Palermo 28/9-2/10 2015
50. Structure and function in chromatin domains (invited talk), Mini-Workshop on Statistical and Molecular Physics, SISSA Trieste, 12-13 October 2015
51. The complex structure of chromatin (invited talk), EPFL Lausanne, 15 March 2016
52. The complex structure of chromatin (invited talk), Conference “Quantitative Laws II”, Como 16 June 2016.
53. Getting more from NMR data: the conformational ensemble of antitumoral peptidomimetics (invited talk), 2nd Workshop of the Center for Complexity and Biosystems, Milano, 5 October 2016
54. Physical models highlight a strong correlation between chromosome structure and transcription (invited talk), qBio Workshop, IFOM Milano 20-21 February 2017
55. Modelling data with the Maximum Entropy Principle (invited talk), University of Torino, 15 March 2017
56. “Maximum-entropy techniques to model complex biological molecules” and “The complex structure of chromatin” (invited lectures) at Lake Como School of Advanced Studies “Advances in Complex Systems”, 7 and 9 July 2017.
57. “Maximum-entropy modelling of biomolecules” (contributed talk) at Congress of the Department of Physics, 29 June 2017.
58. “Describing Chromosome Structure by the Principle of Maximum Entropy” (invited talk), Scuola Normale Superiore, Pisa, 25 September 2017
59. “Maximum entropy modelling of biomolecules” (invited talk) at FisMat 2018, ICTP Trieste, 5 October 2017
60. “Data-driven coarse-grained models of biomolecules”, (invited talk) CECAM Workshop “Computational biophysics on your desktop: is that possible?”, 3-6 September 2018
61. “Determination of conformational ensembles of proteins by NOEs (including the case of spin diffusion), (invited talk) DIBIT San Raffaele, 15 April 2019
62. “The complex structure of chromatin”, (invited lecture) Pre-dotctoral School in Quantitative Biology, IFOM Milano, 8 July 2019
63. “The information flow in protein folding”, (invited talk) Meeting Biophys & PlexNet, Napoli 25 September 2019
64. “Data-driven simulations of biopolymers” (Physics Colloquiuum) Università dell’Insubria, 11 maggio 2020 (telematico)
65. “The complex conformational dynamics of the genome” (invited talk), INFN Biophys 2022, Firenze, 14-16 September 2022

66. “The complex conformational dynamics of the genome” (invited talk), SISSA Trieste, 30 September 2022
67. Lectures on Molecular Dynamics simulations of proteins (5h, invited lectures), Winter School on Physics of the Cell, University of Trento 17-18/1/2023
68. “Data-based modelling of biomolecules” (contributed talk), Condensed Matter Highlights, Unimi, 14/2/2023
69. “Statistical Physics of Biomolecules throughout the Enrico Fermi Schools” (invited talk), Passion for Physics 2023, Varenna, 23/6/2023

Attività di valutazione

Sono stato referee di numerosi progetti per l’Anvur (VQR), il Miur (PRIN e FIRB), la Regione Sardegna e l’Agence Nationale de la Recherche (Francia).
Membro di una commissione di ammissione al Dottorato in Fisica (Università di Milano 2011), membro di una commissione per posizione RTD/B (Università di Padova, 2019) e RTD/A (Università di Milano, 2022).

Attività didattiche

*Didattica integrativa:*
• Esercitazioni in Statistical Mechanics (corso tenuto da P. Bak, University of Copenhagen, 1999)
• Esercitazioni in Elettromagnetismo (corso tenuto da A. Bracco, Chimica Industriale, Universita' di Milano, 2000)
• Esercitazioni in Elettromagnetismo (corso tenuto da P. Magni, Ingegneria, Politecnico di Milano, 2001-2003)
• Lezioni del corso serale di Elettromagnetismo (fisica, Universita' di Milano, 2001)
• Lezioni del corso di Fisica delle Proteine 1 & 2 (corso tenuto da R.A. Broglia, Fisica, Universita' di Milano, 2002-2004)

*Didattica come responsabile:*
• Laboratorio di Calcolo 2 (CL in Fisica, Università di Milano, 2005-2007, totale 18 CFU)
• Fisica applicata alla biologia (CL in Bioscienze, Università di Milano, 2006-2009, totale 12 CFU)
• Fisica delle Proteine 1 (CL in Fisica, Università di Milano, dal 2005, totale 108 CFU)
*Per questo corso ho scritto le note “Physics of Protein Folding”, 185 pp. disponibili sul sito ARIEL*
• Biofisica Computazionale (CL in Fisica, Università di Milano, dal 2009, totale 84 CFU)
*Per questo corso ho scritto le note “Lecture Notes on Computational Biophysics”, 111 pp. disponibili sul sito ARIEL*
• Fisica (CL in Biotecnologie, Università di Milano, 2010-2020, totale 60 CFU)
*Per questo corso ho scritto le note “Appunti di Fisica per Biotecnologi”, 136 pp. disponibili sul sito ARIEL*
• Processi Stocastici (CL in Fisica, del 2021, Università di Milano, totale 18 CFU)
• Stochastic Processes and Simulations in Natural Sciences (Università Bocconi, 2023, 32 ore)

*Relatore e correlatore di Tesi*
• correlatore 13 tesi di laurea quadriennale/magistrale: A. Amatori (2002), R. Berera (2002), M. Colombo (2003), F. Simona (2003), M. Becchi (2004), L. Sutto (2004), R. Siliprandi (2004), M. Zanotti (2004), P. Cerri (2005), S. Colacino (2005), G. Vicari (2005), C. Camilloni (2005), M. Caldarini (2006),
• relatore 35 tesi di laurea quadriennale/magistrale: L. Ferrari (2008), A. Bugada (2008), S. Biffi (2008), F. Carbonchi (2009), F. Cabassi (2009), P. Sormanni (2011), M. Villa (2012), L Bachschmid Romano (2012), C. Paissoni (2012), S. Lui (2013), R. Meloni (2013), R. Capelli (2014), Y. Zhan (2015), G. Sormani (2015), A. Contini (2015), F. Villa (2015), F. Marchetti (2015), A. Possenti

(2016), M. Negri (2017), P. Valena (2017), P. Longo (2017), A. Guidarelli (2019), C. Ugolini (2019), M. Cagiada (2019), M Crippa (2020), D. Oriani (2020), M. Arrighetti (2020), S. Terzoli (2020), C. Paternoster (2021), M. Bonamassa (2021), M. Tajana (2022), A. Pivetta (2022), F. Borando (corrente), R. Beccaria (corrente), A. Zambon (Corrente).
• correlatore di 2 tesi di laurea triennale: V. Perelli (2005), F. Carbonchi (2007),
• relatore di 22 tesi di laurea triennale: M. E. Orselli (2008), C. Ciceri (2008), M. Rossi (2009), A. Gambaro (2010), M. Villa (2010), A. Contini (2011), G. Sormani (2012), P. Bertollo (2014), L. Bonati (2015), S. Franzini (2015), A. Fancelli (2016), M. Crippa (2017), S. Terzoli (2017), G. Franco (2018), M. Bonamassa (2018), L. Maldera (2019), D. Andreghetti (2020), R. Beccaria (2021), L. Cesari (2021), M Sardena (2022), F. Pecis (2023), T. Talpo (corrente)
• correlatore di 4 tesi di dottorato: A. Amatori (2006), L. Sutto (2007), C. Camilloni (2008), M. Caldarini (2009),
• relatore di 5 tesi di dottorato: A. Sanzeni (2016), R. Meloni (2017), R. Capelli (2017), F. Cola (2018), E. Marchi (corrente)
• Opponent della tesi PhD di Simon Mitternacht, University of Lund (Sweden), 2009, I. Cataudella, University of Copenhagen (2013), E. Sarti (SISSA, Trieste), Pia Cordsen, University of Copenhagen (2014), Marco Giulini (Università di Trento 2022), Alex Abraham (Università di Napoli 2023).

Organizzazione di Conferenze e Scuole

1. In October 1999 co-direttore del workshop "Pathways in Protein Folding and Protein Aggregation" al Niels Bohr Institute, Copenhagen.
2. Segretario scientifico del CXLV course in "Protein Folding, Evolution and Design", July 2000, at the International School of Physics "E. Fermi", in Varenna (Italy).
3. Organizzatore del "Topical Meeting on Biophysics-Biological" at Niels Bohr Institute, April 2000.
4. Direttore della School in Protein Aggregation, Les Houches 9-18 April 2002.
5. Segretario Scientifico del CLXV course in "Protein Folding and Drug Design", July 2006, at the International School of Physics "E. Fermi", in Varenna (Italy).
6. Organizzatore del Workshop "Physics of Protein Folding and Aggregation", Bressanone (Italy) 11-12 February 2010
7. Organizzatore del Workshop "Physics of Protein Folding and Aggregation", Bressanone (Italy) 16-18 February 2012
8. Organizzatore del Workshop "Protein Physics: Structure, Dynamics and Function", Bressanone (Italy) 6-8 February 2014
9. Organizzatore del Workshop " Physics of biomolecules: structure, dynamics, and function", Bressanone (Italy) 3-6 February 2016
10. Organizzatore del Workshop "Physics of biomolecules: structure, dynamics, and function", Bressanone (Italy) 7-10 February 2018
11. Organizzatore del Workshop "Interdisciplinary aspects of biomolecular modelling", Università di Milano, 26 giugno 2019
12. Organizzatore del Workshop "Physics of biomolecules: structure, dynamics, and function", Bressanone (Italy) 5-8 February 2020
13. Co-direttore della scuola "Statistical Physics of Deep Learning", Lake Como School of Advanced Studies, Como, 13-17 June 2022
14. Organizzatore del Workshop "Physics of biomolecules: structure, dynamics, and function", Bressanone (Italy) 5-8 September 2022

Trasferimento Tecnologico

- Cofondatore, socio e research manager dello spin-off Foldless s.r.l (2009-2013)
- Coautore di due brevetti (vedi sopra)
- Co-organizzatore del discussion forum su Quantum Technologies all' ISIQ 2017, 10a Conferenza Italiana su Quantum Information, Firenze (13/9/2017)

- Co-direttore della scuola DeepTech Entrepreneurship, Milano 27-29 Settembre 2021 (http://www.deeptechschool.it) e seconda edizione 21-23 Novembre 2022.

Attività Editoriale

Dal 2022 Associated Editor di Frontiers in Molecular Biosciences (IF=6.1). Ho svolto attività di referee per qualche centinaio di articoli su riviste internazionali (PRL, PRE, JCP, Proteins, etc.). Nominated "Outstanding referee" by the American Physical Society in 2021.

Pubblicazioni

Autore di 130 pubblicazioni in totale, di cui 111 pubblicazioni su riviste soggette a referaggio (di cui 73 come corresponding author), h-index 29 (Scopus), totale citazioni 2735 (Scopus). Queste includono 1 Nature (IF=69.5), 1 Cell (IF=66.8), 1 Molecular Cell (IF=19.3), 2 PNAS (IF=11.2), 1 JACS (IF=16.3), 2 PRL (IF=9.2), 1 Nature Str Mol Biol (IF=15.3). 1 Genome Res. (IF=11.1), 1 Nature Genetics (IF=41.3).

PUBBLICAZIONI IN GIORNALI CON REFEREE

1. M. Skorobogatiy and G. Tiana, Mapping of Mutation-sensitive Sites in Proteinlike Chain, Phys. Rev. E, 58(1998) 3572 (IF=2.7, citaz=8)
2. G. Tiana, R. A. Broglia, H. E. Roman, E. Vigezzi and E. Shakhnovich, Folding and Misfolding of Designed Protein-like Folding and Misfolding of Designed Protein-like Chains with Mutations, J. Chem. Phys, 108(1998) 757 (IF=4.3, citaz=68)
3. R.A. Broglia, G. Tiana, S. Pasquali, H. E. Roman, E. Vigezzi, Folding and Aggregation of Designed Protein Chains, Proc. Natl. Acad. Sci. USA, 95(1998) 12930 (IF=11.2, citaz=80)
4. R. A. Broglia, G. Tiana, H. E. Roman, E. Vigezzi and E. Shakhnovich, Stability of Designed Proteins against Mutations, Phys. Rev. Lett., 82(1999) 4727 (IF=9.2, citaz=32)
5. G. Tiana, R. A. Broglia and E. I. Shakhnovich, Hiking in the energy landscape in sequence space: a bumpy road to good folders, Proteins., 39(2000) 244 (IF=4.0, citz=57)
6. G. Tiana, R. A. Broglia and E. I. Shakhnovich, Energy Profile of the Space of Model Protein Sequences, J. Biol. Phys., 27(2001) 147 (IF=1.6, citaz=1)
7. R. A. Broglia and G. Tiana, Predicting the Three Dimensional Structure of a Lattice Designed Model Protein from its Primary Structure, J. Biol. Phys., 27(2001) 161 (IF=1.6)
8. R. A. Broglia and G. Tiana, Reading the three-dimensional structure of a protein from its amino acid sequence, Proteins., 45(2001) 421 (IF=4.0, citaz=17)
9. G. Tiana, R. A. Broglia and D. Provasi, Designability of lattice model heteropolymers, Phys. Rev. E, 64(2001) 11904 (IF=2.7, citaz=9)
10. R. A. Broglia and G. Tiana, Hierarchy of Events in the folding of model proteins, J. Chem. Phys, 114(2001) 7267 (IF=4.3, citaz=43)
11. G. Tiana and R. A. Broglia, Statistical Analysis of Native Contact Formation in the Folding of Designed Model Proteins, J. Chem. Phys., 114(2001) 2503 (IF=4.3, citaz=42)
12. J. Borg, M. H. Jensen, K. Sneppen and G. Tiana, Hydrogen bonds in polymer folding, Phys. Rev. Lett., 86(2001) 1031 (IF=9.2, citaz=26)
13. G. Tiana and R. A. Broglia, Design and Folding of dimeric proteins, Proteins 49(2002) 82 (IF=4.0, citaz=28)
14. G. Tiana, M. H. Jensen and K. Sneppen, Time delay as a key to Apoptosis Induction in the p53 Network, Eur. Phys. J. B, 29(2002) 135 (IF=1.4, citaz=101)
15. M. H. Jensen, K. Sneppen and G. Tiana, Sustained oscillations and time delays in gene expression of protein Hes1, FEBS Letters, 541(2003) 176 (IF=3.1, citaz=127)
16. G. Tiana, D. Provasi and R. A. Broglia, Role of bulk and of interface contacts in the behaviour of model dimeric proteins, Phys. Rev. E, 67(2003) 51909 (IF=2.7, citaz=2)
17. R. A. Broglia, G. Tiana and R. Berera, Resistance proof, folding-inhibitor drugs, J. Chem. Phys., 118(2003) 4754 (IF=4.3, citaz=18)
18. G. Tiana, B. E. Shakhnovich, N. Dokholyan and E. I. Shakhnovich, Imprint of evolution on protein structures, Proc. Natl. Acad. Sci. USA , 101(2004) 2846 (IF=11.2, citaz=48)
19. G. Tiana, N. V. Dokholyan, R. A. Broglia and E. I. Shakhnovich, The evolution dynamics of model proteins, J. Chem. Phys., 121(2004) 2381 (IF=4.3, citaz=9)
20. Isabella Daidone, Fabio Simona, Danilo Roccatano, Ricardo A. Broglia , Guido Tiana, Giorgio Colombo

and Alfredo Di Nola, Beta-hairpin conformation of fibrillogenic peptides: structure and alpha-beta transition mechanism revealed by molecular dynamics simulations, Proteins , 57(2004) 198 (IF=4.0, citaz=89)

21. R. A. Broglia, G. Tiana and D. Provasi, Simple model of protein folding and of non-conventional drug design, Journal of Physics Condensed Matter, 16(2004) 111 (IF=2.7, citaz=18)
22. G. Tiana, M. Colombo, D. Provasi, R. A. Broglia, Deriving amino acid contact potentials from their apparence frequencies in proteins: an inverse thermodynamical problem., J. Phys Cond Mat , 16(2004) 2551 (IF=2.7, citaz=8)
23. G. Tiana, F. Simona, R. A. Broglia and G. Colombo, Thermodynamics of beta-amyloid fibril formation, J. Chem. Phys., 120(2004) 8307 (IF=4.3, citaz=23)
24. G. Tiana, F. Simona, G. M. S. De Mori, R. A. Broglia and G. Colombo, Understanding the determinants of stability and folding of small globular proteins from their energetics, Protein Science, 13(2004) 113 (IF=4.0, citaz=70)
25. F. Simona, G. Tiana, R. A. Broglia and G. Colombo, Modelling the alpha-helix to beta-hairpin transition mechanism and the formation of oligometric aggregates of the fibrillogenic peptide A-beta(12-28), J. Mol. Graph. and Model. 23(2004) 263 (IF=2.9, citaz=27)
26. A. Amatori, G. Tiana, L. Sutto, J.Ferkinghoff-Borg, A. Trovato and R. A. Broglia, Design of amino acid sequences to fold into C_alpha-model proteins, J. Chem. Phys., 123(2005) 54904 (IF=4.3, citaz=5)
27. G. Tiana, R. A. Broglia, L. Sutto and D. Provasi, Design of a folding inhibitor of the HIV-1 Protease, Mol. Simul. 31(2005) 765 (IF=2.3, citaz=3)
28. R. A. Broglia, G. Tiana, L. Sutto, D. Provasi and F. Simona, Design of HIV-1-PR inhibitors which do not create resistance: blocking the folding of single monomers, Protein Sci., 14(2005) 2668 (IF=6.9, citaz=32)
29. R. A. Broglia, D. Provasi, F. Vasile , G. Ottolina, R. Longhi and G. Tiana , A folding inhibitor of the HIV-1 Protease, Proteins, 62(2006) 928 (IF=4.0, citaz=32)
30. A. Podesta, G. Tiana, P. Milani and M. Manno, Early events in insulin fibrillization studied by time-lapse atomic force microscopy, Biophys. J. 90(2006) 589 (IF=3.7, citaz=44)
31. S. Colacino, G. Tiana, R. A. Broglia and G. Colombo, The Determinants of Stability in the Human Prion Protein: Insights into Folding and Misfolding from the Analysis of the Change in the Stabilization Energy Distribution in Different Conditions, Proteins, 62(2006) 698 (IF=4.0, citaz=38)
32. A. Amatori, J.Ferkinghoff-Borg, G. Tiana, R. A. Broglia, Thermodynamic features characterizing good and bad folding sequences obtained using a simplified off-lattice protein model, Phys. Rev. E, 73(2006) 61905 (IF=2.7, citaz=5)
33. S. Colacino, G. Tiana and G. Colombo, Similar folds with different stabilization mechanisms: the cases of prion and doppel proteins, BMC Structural Biology, 6(2006) 17 (IF=2.2, citaz=22)
34. L. Sutto, G. Tiana and R. A. Broglia, Sequence of events in folding mechanism: Beyond the Go model, Protein Sci., 15(2006) 1638 (IF=6.9, citaz=33)
35. M. Manno, E. F. Craparo, A. Podesta, D. Bulone, R. Carrotta, V. Martorana, G. Tiana and P. L. San Biagio, Kinetics of different processes in human insulin amyloid formation, J. Mol. Biol. , 366(2007) 258 (IF=5.1, citaz=145)
36. R. A. Broglia, G. Tiana, L. Sutto, D. Provasi, F. Simona, The physics of protein folding and of non-conventional drug design: Attacking AIDS with its own weapons, La Rivista del Nuovo Cimento, 29(2007) 1 (IF=3.6, citaz=5)
37. R. A. Broglia, G. Tiana, L. Sutto, D. Provasi, V. Perelli, Low-throughput model design of protein folding inhibitors, Proteins, 67(2007) 469 (IF=4.0, citaz=11)
38. G. Tiana, S. Krishna, S. Pigolotti, M. H. Jensen and K. Sneppen, Oscillations and temporal signalling in cells, Physical Biology, 4(2007) 1 (IF=2.9, citaz=106)
39. Lo Cicero, M., Laface, A. E.,Ferramosca, S., Sirianni, F., Cesana, E., Provasi, D., Tiana G, Galli, M., Moroni, M., Clivio, A.,Broglia, R. A., Rusconi, S., In vitro activity of a non-conventional (folding) protease inhibitor on human immunodeficiency virus type-1 replication, Antiviral Therapy 12, S19-S19 (2007) (IF=2.1)
40. G. Tiana, L. Sutto and R. A. Broglia, Use of the Metropolis algorithm to simulate the dynamics of protein chains, Physica A, 380(2007) 241 (IF=3.7, citaz=50)
41. C. Camilloni, D. Provasi, G. Tiana and R. A. Broglia, Optical absorption of a Green Fluorescent Protein variant: environment effects in a density functional study, J. Phys. Chem. B, 111(2007) 10807 (IF=3.4, citaz=5)
42. M. Bonomi. F. Gervasio, G. Tiana, D. Provasi, R. A. Broglia and M. Parrinello, Insight in the folding inhibition of HIV-1 protease by a small peptide, Drugs of the future, 32, 14 (2007) (IF=0.1)
43. S. Ferramosca, M. Lo Cicero, A. Laface, F. Sirianni, E. Cesana, D. Provasi, G. Tiana, M. Galli, M. Moroni, A. Clivio. R. A. Broglia and S. Rusconi, The non-conventional (folding) protease inhibitor

blocks the human immunodeficiency virus type-1 replication without evidence of resistance during in vitro passage, Antiviral Therapy 13, 4, A34 (2008) (IF=2.1)

44. A. Amatori, G. Tiana, J.Ferkinghoff-Borg and R. A. Broglia, The denatured state is critical in determining the properties of model proteins designed on different folds, Proteins 70(2008) 1047 (IF=4.0, citaz=3)
45. M. Bonomi, F. L. Gervasio, G. Tiana, D. Provasi, R. A. Broglia and M. Parrinello, Insight in the folding inhibition of the HIV--1 Protease by a small peptide, Biophys. J., 93(2007) 2813 (IF=3.7, citaz=33)
46. R. A. Broglia, Y. Levy and G. Tiana, HIV-1 Protease folding and the design of drugs which do not create resistance, Curr. Opin. Struct. Biol. 18(2008) 60 (IF=6.9, citaz=34)
47. C. Camilloni, D. Provasi, G. Tiana, R. A. Broglia, Exploring the Protein G Helix Free Energy Surface by Solute Tempering Metadynamics , Proteins 71(2008) 164 (IF=4.0, citaz=51)
48. G. Verkhivker, G. Tiana, C. Camilloni, D. Provasi and R. A. Broglia, Exploring the molecular basis of folding inhibition for unconventional HIV-1 protease inhibitors: a mechanism of structural mimicry in atomistic simulations of biomolecular binding, Biophys. J. 95(2008) 550 (IF=3.7, citaz=9)
49. F. Marini, C. Camilloni, D. Provasi, R. A. Broglia and G. Tiana, Metadynamic sampling of the free energy landscapes of proteis coupled with a Monte Carlo algorithm, Gene 422(2008) 37-40 (IF=2.5, citaz=4)
50. C. Camilloni, A. Guerini Rocco, I. Eberini, E. Gianazza, R. A. Broglia, G. Tiana, Urea and guanidinium chloride denature Protein L in different ways in molecular dynamics simulations, Biophys. J. 94(2008) 4654 (IF=3.7, citaz=138)
51. G. Tiana, Estimation of microscopic averages from metadynamics, Europ. Phys. J. B 63(2008) 235 (IF=1.4, citaz=13)
52. C. Camilloni, L. Sutto, D. Provasi, G. Tiana and R. A. Broglia, Early events in protein folding: Is there something more than hydrophobic burst? Protein Science, 17(2008) 1424-1432 (IF=6.9, citaz=14)
53. M. Caldarini, F. Vasile, D. Provasi, R. Longhi, G. Tiana, R. A. Broglia, Identification and characterization of folding inhibitors of hen egg lysozyme: an example of a new paradigm of drug design, Proteins 74(2009) 390 (IF=4.0, citaz=7)
54. G. Tiana and R. A. Broglia, The molecular evolution of HIV-1 Protease simulated at atomic detail, Proteins 76 (2009) 895-910 (IF=4.0, citaz=3)
55. G. Tiana, Protein folding: Can high-performance computing improve our understanding?, Il Nuovo Cimento C 32, 9 (2009) (IF=0.2)
56. L. Giorgetti, T. Siggers, S. Yaeger, G. Tiana, G. Caprara, P. Milani, M. Bulyk, G. Natoli, A Graded Response of a Transcription Factor to Increasing Doses of External Stimuli: A Thermodynamic Framework Describing the Behavior of NF-kB, Biophysical J., 96, Pages 304a-305a (2009) (IF=3.7)
57. S. Ferramosca, M. Lo Cicero, A. E. Laface, F. Sirianni, E. Cesana, D. Provasi, G. Tiana, M. Galli, M. Moroni, A. Clivio, R. A. Broglia and S. Rusconi, In vitro efficacy of a non-conventional (folding) HIV-1 protease inhibitor without selection of resistance. Infection 37 (2009) 23 Supplement 2 (IF=2.7)
58. M. Caldarini, L. Sutto, C. Camilloni, F. Vasile, R. A. Broglia and G. Tiana, Identification of the folding inhibitors of hen-egg lysozyme: gathering the right tools, Europ. Biophys. J. 39, 911 (2010) (IF=2.1, citaz=8)
59. L. Giorgetti, T. Siggers, G. Tiana, G. Caprara, S. Notarbartolo, T. Corona, M. Pasparakis, P. Milani, M. L. Bulyk, G. Natoli, Noncooperative Interactions between Transcription Factors and Clustered DNA Binding Sites Enable Graded Transcriptional Responses to Environmental Inputs, Molecular Cell 37 (2010) 418-428 (IF=19.3, citaz=114)
60. C. Camilloni, R. A. Broglia and G. Tiana, Hierarchy of folding and unfolding events of protein G, CI2, and ACBP from explicit-solvent simulations, J. Chem. Phys. 134, 045105 (2011) (IF=4.3, citaz=33)
61. G. Tiana and L. Sutto, Equilibrium properties of realistic random heteropolymers and their relevance for globular and naturally unfolded proteins Phys. Rev. E 84 (2011) 061910 (IF=2.7, citaz=7)
62. S. Kimura, R. A. Broglia, G. Tiana, Thermodynamics of strongly allosteric inhibition, Europ. Biophys. J. 41, 991 (2012) (IF=2.1)
63. P. Heidarsson, I. Calpapuram, C. Camilloni, A. Imparato, G. Tiana, F. Poulsen, B. Kragenlund, C. Cecconi, A Highly compliant protein native state with a spontaneous-like mechanical unfolding pathway, J. Am. Chem. Soc. 134, 17068 (2012) (IF=16.3, citaz=24)
64. G. Tiana and C. Camilloni, Ratcheted molecular-dynamics simulations identify efficiently the transition state of protein folding. J. Chem. Phys. 137, 235101 (2012) (IF=4.3, citaz=9)
65. G. Tiana and M. H. Jensen, The dynamics of genetic control in the cell: the good and bad of being late, Philos. Trans. A 371, 20120469 (2013) (IF=3.1, citaz=11)
66. S. Lui and G. Tiana, The network of stabilizing contacts in proteins studied by coevolutionary data, J. Chem. Phys. 139, 155103 (2013) (IF=4.3, citaz=26)
67. S. Kimura, M. Caldarini R. A. Broglia, N. Dokholyan and G. Tiana, The maturation of HIV-1 protease

precursor studied by discrete molecular dynamics, Proteins 82, 633 (2014) (IF=4.0, citaz=10)

68. R. Meloni, C. Camilloni and G. Tiana, Sampling the denatured state of polypeptides in water, urea and guanidine chloride to strict equilibrium conditions with the help of massively parallel computers, J. Chem. Theo. Comp. 10, 846-854 (2014) (IF=6.5, citaz=5)
69. R. Capelli, C. Paissoni, P. Sormanni and G. Tiana, Iterative derivation of effective potentials to sample the conformational space of proteins at atomistic scale, J. Chem. Phys. 140, 195101 (2014) (IF=4.3, citaz=5)
70. L. Giorgetti, R. Galupa, E. P. Nora, T. Piolot, F. Lam, J. Dekker, G. Tiana and E. Heard, Predictive polymer modeling reveals coupled fluctuations in chromosome conformation and trascription, Cell, 157, 950 (2014) (IF=66.8, citaz=285)
71. M. Caldarini, P. Sonar, I. Valpapuram, D. Tavella, C. Volontè, V. Pandini, M. A. Vanoni, A. Aliverti, R. Broglia, G. Tiana and C. Cecconi, The complex folding behavior of HIV-1-protease monomer revealed by optical-tweezer single-molecule experiments and molecular-dynamics simulations, Biophys. Chem. 195, 32 (2014) (IF=2.0, citaz=15)
72. G. Tiana, F. Villa, Y. Zhan, R. Capelli, C. Paissoni, P. Sormanni, E. Heard, L. Giorgetti, R. Meloni, MonteGrappa: an iterative Monte Carlo program to optimize biomolecular potentials in simplified models, Comp. Phys. Comm 186, 93 (2015) (IF=4.7, citaz=11)
73. E. Molteni, G. Onida and G. Tiana, Conformational dependence of the circular-dichroism spectra of single amino acids from plane-waves-based density-functional theory calculations, J. Phys. Chem. B 119, 4803 (2015) (IF=3.4, citaz=9)
74. A. Contini and G. Tiana, A many-body term improves the accuracy of effective potentials based on protein coevolutionary data, J. Chem. Phys. 143, 025103 (2015) (IF=4.3, citaz=12)
75. G. Tiana, Effect of disorder on the contact probability of elongated conformations of biopolymers, Phys. Rev. E. 92, 010702(R) (2015) (IF=2.7, citaz=1)
76. A. Sanzeni, A. Celani, G. Tiana, M. Vergassola, Theory of feedback controlled brain stimulations for Parkinson's disease, Physica A 441, 121 (2016) (IF=3.8, citaz=1)
77. R. Capelli, F. Villemont, E. Moroni, G. Tiana, A. van der Vaart and G. Colombo, Assessment of mutational effects on peptide stability through confinement simulations, J. Phys. Chem. Lett. 7, 126 (2016) (IF=6.9, citaz=9)
78. G. Tiana, A. Amitai, T. Pollex, T. Piolot, D. Holcman, E. Heard, L. Giorgetti, Structural fluctuations of the chromatin fiber within topological associating domains, Biophys. J. 110, 1234 (2016) (IF=3.7, citaz=40)
79. F. Vasile, M. Civera, L. Belvisi, D. Potenza, G. Tiana, Thermodynamically-Weighted Conformational Ensemble of Cyclic RGD Peptidomimetics From NOE Data, J. Phys. Chem. B 120, 7098 (2016) (IF=3.4, citaz=15)
80. Y. Zhan, L. Giorgetti, G. Tiana, Looping probability of random heteropolymers helps to understand the scaling properties of biopolymers, Phys. Rev. E 94, 032402 (2016) (IF=2.7, citaz=4)
81. J. Marangon, M. S. Christodoulou, F. Casagrande, G. Tiana, L. Dalla Via, A. Aliverti, D. Passarella, G. Cappelletti, S. Ricagno, Tools for the rational design of bivalent microtubule-targeting drugs, Biochem. Biophys. Res. Comm. 479, 48 (2016) (IF=3.0, citaz=10)
82. A. Sanzeni, V. Balasubramanian, G. Tiana and M. Vergassola, Complete coverage of space favors modularity of the grid system in the brain, Phys. Rev. E 94, 062409 (2016) (IF=2.7, citaz=6)
83. R. Meloni, C. Camilloni and G. Tiana, Properties of low-dimensional collective variables in the molecular dynamics of biopolymers, Phys. Rev. E 94, 052406 (2016) (IF=2.7, citaz=2)
84. R. Capelli, F. Marchetti, G. Tiana and G. Colombo, SAGE: a Fast Computational Tool for Linear Epitope Grafting onto a Foreign Protein Scaffold, J. Chem. Inf. Model. 57, 6-10 (2017) (IF=6.1, citaz=7)
85. Y. Zhan, L. Giorgetti and G. Tiana, Modelling Genome-wide Topological Associating Domains of Mouse Embryonic Stem Cells, Chromosome Res. 25, 5 (2017) (IF=4.6, citaz=10)
86. Y. Zhan, L. Mariani, I. Barozzi, E. G. Shultz, N. Bluthgen, M. Stadler, G. Tiana and L. Giorgetti, Reciprocal insulation analysis of Hi-C data shows that TADs represent a functionally but not structurally privileged scale in the hierarchical folding of chromosomes, Genome Res. 27, 479 (2017) (IF=11.1, citaz=101)
87. H. I. Rösner, M. Caldarini, A. Prestel, M. A. Vanoni, R. A. Broglia, A. Aliverti, G. Tiana and B. B. Kragelund, Cold denaturation of the HIV-1 protease monomer, Biochemistry 56, 1029 (2017) (IF=2.1,citaz=5)
88. R. Meloni and G. Tiana, Thermodynamic and Structural Effect of Urea and Guanidine Chloride on the Helical and on a Hairpin fragment of GB1 from Molecular Simulations, Proteins 85, 753 (2017) (IF=4.3, citaz=2)
89. F. Cola, F. Marchetti and G. Tiana, How likely are oscillations in a genetic feedback loop with delay?

, Europ. Phys. J. E 40 , 74 (2017) (IF=2.1)

90. S. A. Ghadami, F. Bemporad, B. M. Sala, G. Tiana, S. Ricagno and F. Chiti, FRET studies of the conformational states adopted by transthyretin for amyloid fibrl formation, Cell. Mol. Life Sci. 74 , 3577 (2017) (IF=6.5, citaz=6)
91. G. Tiana and L. Giorgetti, Integrating experiment, theory and simulation to determine the structure and dynamics of mammalian chromosomes, Curr. Opin. Struct. Biol. 49, 11 (2018) (IF=7.8, citaz=13)
92. F. Vasile, M. Padigada, A. Siccardi, D. Potenza, G. Tiana, A combined NMR-computational study of the interaction between influenza-virus Hemagglutinin and sialic derivatives from human and avian receptors on the surface of transfected cells, Int. J. Mol. Sci. 19, 1267 (2018) (IF=4.5, citaz=11)
93. R. Capelli, G. Tiana and C. Camilloni, An implementation of the maximum-caliber principle by replica-averaged time-resolved restrained simulations, J. Chem. Phys. 148, 184114 (2018) (IF=4.3, citaz=10)
94. A. Possenti, M. Vendruscolo, C. Camilloni, G. Tiana, A method for partitioning the information contained in a protein sequence between its structure and function, Proteins 86, 956-964 (2018) (IF=4.3, citaz=1)
95. M. Negri, M. Gherardi, G. Tiana, M. Cosentino Lagomarsino, Spontaneous domain formation in disordered copolymers as a mechanism for chromosome structuring, Soft Matter 14, 6128 (2018) (IF=4.0)
96. G. Franco, M. Cagiada, G. Bussi and G. Tiana, Statistical mechanical properties of sequence space determine the efficiency of the various algorithms to predict interaction energies and native contacts from protein coevolution, Phys. Biol. 16, 046007 (2019) (IF=2.9, citaz=4)
97. S. Bonfanti, M. C. Lionetti, M. R. Fumagalli V. R Chirasani, G. Tiana, N. V. Dokholyan, S. Zapperi, C. A. M. La Porta, Molecular mechanisms of heterogeneous oligomerization of huntingtin proteins, Sci. Rep. 9, 7615 (2019) (IF=4.3, citaz=10)
98. J. Redolfi, Y. Zhan, C. Valdes-Quezada, M. Kryzhanovska, I. Guerreiro, V. Iesmantavicius, T. Pollex, R. S. Grand, E. Mulugeta, J. Kind, G. Tiana, S. A. Smallwood, W. de Laat and L. Giorgetti, DamC reveals principles of chromatin folding in vivo without crosslinking and ligation, Nature Str. Mol. Biol. 26, 471-480 (2019) (IF=15.3, citaz=40)
99. F. Vasile and G. Tiana, Determination of Structural Ensembles of Flexible Molecules in Solution from NMR data Undergoing Spin Diffusion, J. Chem. Inf. Model 59, 2973 (2019) (IF=6.1, citz=5)
100. F. Cuturello, G. Tiana and G. Bussi, Assessing the accuracy of direct-coupling analysis for RNA contact prediction, RNA Journal 26, 637 (2020) (IF=4.7, citaz=11)
101. S. Pigolotti, M. H. Jensen, Y. Zhan and G. Tiana, Chromosome contact maps are bifractal, Phys. Rev. Res. 2 , 043078 (2020) (citaz=1)
102. M. Crippa, Y. Zhan, G. Tiana, Effective model of loop extrusion predicts chromosomal domains , Phys. Rev. E 102 , 032414 (2020) (IF=2.7, citaz=1)
103. M. C. Lionetti, F. Cola, O. Chepizhko, M. R. Fumagalli, F. Font-Clos, R. Ravasio, S. Minucci, P. Canziano, M. Camera, G. Tiana, S. Zapperi, C. La Porta, MicroRNA-222 regulates melanoma plasticity , J. Clin. Med. 9 , 2573 (2020) (IF=1.8, citaz=3)
104. S. Terzoli and G. Tiana, Molecular Recognition Between Cadherins Studied by a Coarse-Grained Model Interacting With a Coevolutionary Potential , J. Phys. Chem. B 124 , 4079 (2020) (IF=3.4)
105. F. Zenk, Y. Zhan, P. Kos, E. Loeser, N. Atinbayeva, M. Schaechtle, G. Tiana, L. Giorgetti, N. Iovino, HP1 drives de novo 3D genome reorganization in early Drosophila embryos, Nature 593, 289 (2021) (IF=69.5, citaz=21)
106. M. Crippa, D. Andreghetti, R. Capelli and G. Tiana, Evolution of Frustrated and Stabilising Contacts in Reconstructed Ancient Proteins, Europ. Biophys. J. 50, 699-712 (2021) (IF=2.1)
107. H. I. Rösner, M. Caldarini, G. Potel, D. Malmodin, M. A. Vanoni, A. Aliverti, R. A. Broglia, B. B. Kragelund, G. Tiana, The denatured state of HIV-1 protease under native conditions , Proteins 90 , 96-109 (2022) (IF=4.3)
108. M. Tajana, A. Trovato and G. Tiana, Key interaction patterns in proteins revealed by cluster expansion of the partition function , Europ. Phys. J. E 45 , 95 (2022) (IF=1.6)
109. P. Mach, P. I. Kos, Y. Zhan, J. Cramard, S. Gaudin, J. Tünnermann, E. Marchi, J. Eglinger, J. Zuin, M. Kryzhanovska, S. Smallwood, L. Gelman, G. Roth, E. P. Nora, G. Tiana, L. Giorgetti, Live-cell imaging and physical modeling reveal control of chromosome folding dynamics by cohesin and CTCF , Nature Genetics 54 , 1907-1918 (2022) (IF=41.3)
110. L. Viverit, C. Y. Heo, L. N. Pereira, G. Tiana, Application of machine learning to cluster hotel booking curves for hotel demand forecasting , Int. J. Hospital. Manag. 111 , 103455 (2023) (IF=10.4)
111. E. Marchi, Y. Zhan and G. Tiana, Locality of contacts determines the subdiffusion exponents in

polymeric models of chromatin , Phys. Rev. E 107 , 064406 (2023) (IF=2.7)

BOOKS AND BOOK CHAPTERS

112. Y. Zhan, L. Giorgetti and G. Tiana, Polymer Folding Simulations from Hi-C Data, in Hi-C Data Analysis, Eds. F. Ferrari and S. Bicciato, Springer Methods ISBN 978-1-0716-1389-4 (2021)
113. G. Tiana and L. Giorgetti, Modelling the 3D conformations of genomes, Series in Computational Biopysics, Taylor and Francis Books, Inc. ISBN 9781138500792 (2019)
114. G. Tiana and L. Giorgetti, Coarse graining of a giant molecular system: the chromatin fiber, in Biomolecular Simulations Methods and Protocols, Eds. M. Bonomi and C. Camilloni, Springer ISBN 978-1-4939-9608-7 (2019)
115. G. Tiana, E. Heard and L. Giorgetti, From chromosome capture to polymer physics and back: investigating he three-dimensional structure of chromatin within topological associating domains, in Epigenetics and System Biology, Ed. L. Ringrose, Elsevier ISBN: 9780128030752 (2017)
116. R. A. Broglia and G. Tiana, Protein Folding and Aggregation, Encyclopedia of Condensed Matter Physics, Eds. F. Bassani, J. Liedl and P. Wyder, Elsevier Press ISBN: 9780123694010 (2005)

PROCEEDINGS

117. R. A. Broglia and G. Tiana, Mechanism of folding and aggregation of proteins, p. 69-98, Proc. Int. School. Phys. E. Fermi, IOS Press (2001)
118. R. A. Broglia and G. Tiana, Complementary pictures for proteins: designability and foldability, are they equivalent?, p. 103-116, Proc. Int. School. Phys. E. Fermi, IOS Press (2001)
119. R. A. Broglia and G. Tiana, The Protein Folding Problem, Theoretical Nuclear Physics in Italy, p. 157, Proc. of the VIIIth Conference on Problems in Theoretical Physics, Cortona, World Scientific, (2001)
120. R. A. Broglia and G. Tiana, From atomic nuclei to drug design, p. 419, Proceedings INFN workshop on Theoretical Nuclear and Many Body Systems, World Scientific (2002)
121. R. A. Broglia and G. Tiana, Physical Models for Protein Folding and Drug Design, p. 23-33, Proceedings Idea--Finding Symposium, Frankfurt Institite for Advanced Studies, Ep Systema, Hungary (2003)
122. R. A. Broglia and G. Tiana, Protein folding and non-conventional drug design: a primer for nuclear structure physicists, p. 117, Proceedings of the International Conference on Labirinth in Nuclear Structure, Crete, AIP Press (2004)
123. M.H. Jensen, K. Sneppen and G. Tiana, Oscillating Gene Expressions in Regulatory Networks, proceedings of the Geilo ASI School on "Forces, Growth and Form in Soft Condensed Matter: At the Interface between Physics and Biology", eds. A.T. Skjeltorp and A.V. Belushkin, Kluwer Academic, Dordrecht, p. 195-202 (2004)
124. R. A. Broglia and G. Tiana, The physics of protein folding and drug design, p. 595-602, Proceedings of the 8th spring seminar on nuclear physics, Ed. A. Covello, Paestum, World Scientific (2005)
125. G. Tiana, S. Krishna, M. H. Jensen and K. Sneppen, Time oscillations in gene expression, Proceedings of the Geilo ASI School on ""Evolution from Cellular to Social Scales, eds. A.T. Skjeltorp and A.V. Belushkin, Kluwer Academic, Dordrecht (2008), p. 61-81
126. G. Tiana, D. Provasi, A. Amatori, L. Sutto and R. A. Broglia, Oligarchy in protein folding: the upper and lower classes in protein chains, p. 161-174, Proceedings of the CLXV course of the E. Fermi School on Protein Folding and Drug Design, Varenna (Italy), 4-14 July 2006, IOS Press (2007)
127. R. A. Broglia, G. Tiana,D. Provasi and L. Sutto, Molecular recognition through Local Elementary Structures: transferability of simple models to real proteins, p. 85-112, Proceedings of the CLXV course of the E. Fermi School on Protein Folding and Drug Design, Varenna (Italy), 4-14 July 2006, IOS Press (2007)
128. D. Provasi, G. Tiana and R. A. Broglia, Folding inhibition of HIV Protease: an experimental glance, p. 283-291, Proceedings of the CLXV course of the E. Fermi School on Protein Folding and Drug Design, Varenna (Italy), 4-14 July 2006, IOS Press (2007)
129. Stefano Rusconi, Mirko Lo Cicero, A. E. Laface, S. Ferramosca, E. Cesana, G. Tiana, D. Provasi, F. Sirianni, M. Galli, M. Moroni, A. Clivio, and R. A Broglia, Susceptibility to a Non-Conventional (Folding) Protease Inhibitor of Human Immunodeficiency Virus Type 1 Isolates In Vitro, p. 293-297, Proceedings of the CLXV course of the E. Fermi School on Protein Folding and Drug Design, Varenna (Italy), 4-14 July 2006, IOS Press (2007)
130. Luca Giorgetti, Trevor Siggers, Guido Tiana, Greta Caprara, Samuele Notarbartolo, Teresa Corona, Manolis Pasparakis, Paolo Milani, and G. Natoli, Non-Cooperative Interactions Between Transcription Factors and Clustered DNA Binding Sites Enable Graded Transcriptional Responses To Environmental

Inputs, Biophysical Journal 98, 68a (2010)

| Data | 10/7/2023 | Luogo | Milano |
|---|---|---|---|