THE BIOLOGICAL PHYSICIST

The Newsletter of the Division of Biological Physics of the American Physical Society

Vol 4 № 3 August 2004

In this Issue

As the academic year starts,
THE BIOLOGICAL PHYSICIST
once again brings you a blockbuster issue! In addition to our regular features like PRE Highlights, and DBP updates from Peter Jung and Shirley Chan, we bring you the results of a survey of DBP members conducted jointly by PRE and DBP. And, we bring you a profile of pioneering biochemist Jane Richardson.

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Results from Survey of Members of the Division of Biological Physics

by Margaret Foster,
Senior Assistant Editor, Physical Review E

In June 2003, editors of Physical Review E and the chair of the Division of Biological Physics sent a survey to members of the APS Division of Biological Physics. The questions were intended to ascertain how well the section of Biological Physics serves the community and to solicit suggestions for enhancing the quality and usefulness of the section. Seventy-nine responses were received, and we would like to thank all who participated. We present here results from selected questions, as well as some information concerning submissions during 2003. All responses were tabulated, although respondents did not always answer all questions.

We asked how important various considerations were when members were selecting a journal for submitting their work on biological physics. We found interesting that respondents rated a fair review as somewhat more important than a timely review. The readership and the prestige of the journal were also rated as important. (See Fig. 1)

When asked where they had submitted work in the past 3 years, respondents listed 77 different journals. The Biophysical Journal and PNAS topped the list, with Physical Review Letters and Physica Review E following closely behind. Nature and Science were next, followed by Macromolecules, Journal of Neuroscience, Journal of Theoretical Biology, and Journal of Chemical Physics. (See Fig. 2)

When asked about their research interests in biological physics, DBP members indicated a large interest in theory, followed by interests in biomolecules, subcellular and cellular structures and processes, and multicellular phenomena. There was interest also in bioinformatics, properties of higher organisms, and ecology and evolution. (See Fig. 3)

Topics of papers submitted in 2003 to the Biological Physics Section in Physical Review E may be seen in Fig. 4. The papers were characterized by their principal PACS number. The largest number of papers were submitted on biomolecules, followed by properties of higher organisms, theory, and subcellular and cellular structure and processes. Bioinformatics does not explicitly appear, since there is no corresponding PACS number. Otherwise, submission topics may be compared to research interests of the respondents in the survey.

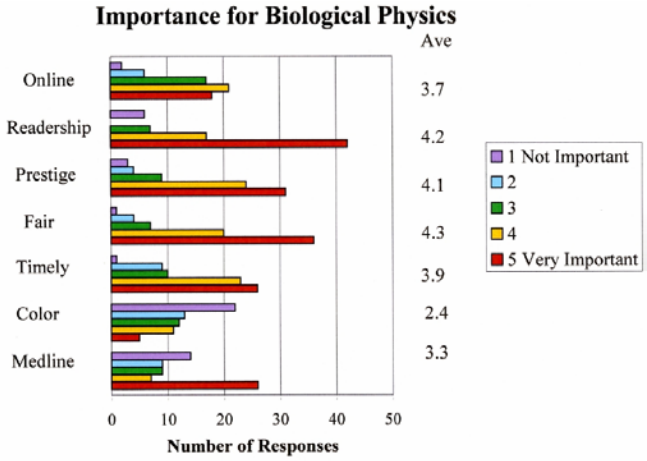

Fig. 1. Results for survey question: Please rate on a scale of 1-5 (1: not important, 5: very important) the importance of the following criteria when selecting a journal for submission of biological physics articles:

- *indexing in MEDLINE*
- *Color online*
- *timely reviews*
- *fair and helpful reviews*
- *prestige of journal*
- *readership of journal*
- *availability of online journal*

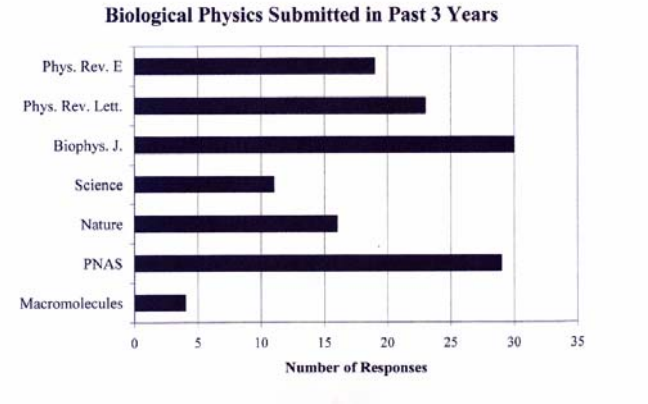

Fig. 2. Results for survey question: In the past three years, where have you submitted your work in biological physics? Please check all that apply:

- *Physical Review E*
- *Physical Review Letters*
- *Biophysical Journal*
- *Science*
- *Nature*
- *PNAS*
- *Macromolecules*
- *Other (please specify)*

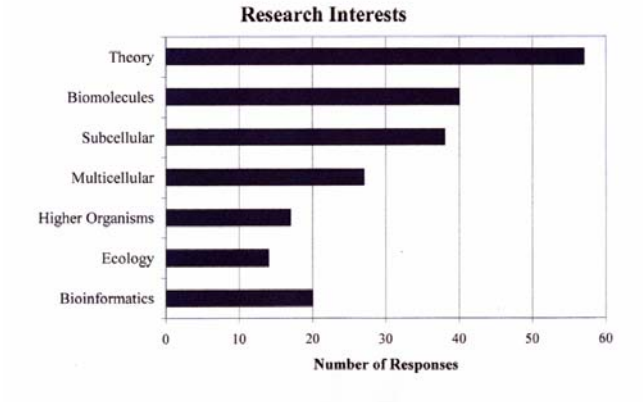

Fig. 3. Results for survey question: Please indicate your research interests in biological physics (check all that apply)

- *theoretical and mathematical aspects of biological physics*
- *biomolecules*
- *subcellular and cellular structure and processes*
- *multicellular phenomena*
- *properties of higher organisms*
- *ecology and evolution*
- *bioinformatics*
- *other (please specify)*

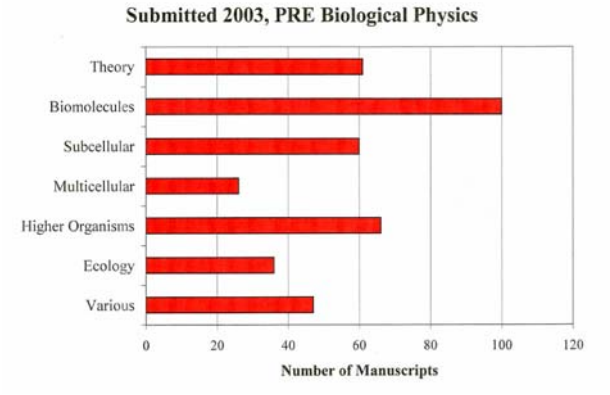

Fig. 4. Topics of papers submitted in 2003 to the Biological Physics Section in Physical Review E. Papers were characterized by the topic indicated by their principal PACS numbers

Average Time from Receipt to Acceptance
Published 2003 Direct Submissions

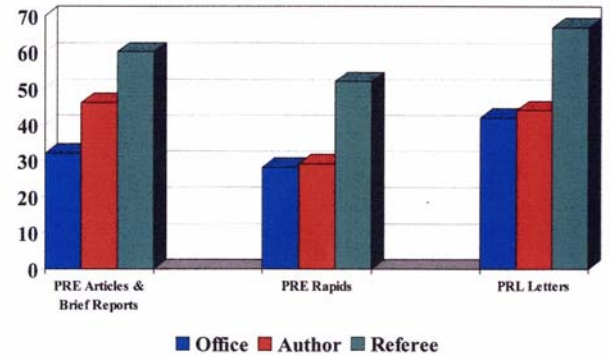

Fig. 5. Average times, in days, from receipt to acceptance, for manuscripts to reside in the office, with authors, and with referees, for papers submitted directly to Physical Review E and to Physical Review Letters and published in these journals in 2003.

We consider it a strength that the Biological Physics Section of Physical Review E does not restrict topics for submission and publication. The section welcomes submissions of biologically inspired physics papers reporting new results. Guidelines are given in the memo "Biological Physics papers in Physical Review E," available from <http://forms.aps.org/author.html>. The new results may involve any of the following:

(i) advances in fundamental physical understanding of biological systems.

(ii) new physical phenomena in a biological system.

(iii) better theoretical and experimental methods for physical analysis of biological data.

(iv) new physical instrumentation relevant to biology.

Within these guidelines, we are trying to improve the quality of papers published in the Biological Physics section. We thank the referees for sharing their expertise. Average times from receipt to acceptance for manuscripts published in 2003 in PRE and PRL are indicated in Fig. 5.

Last Call for Symposium Proposals
from Program Chair and Chair-Elect
Peter Jung

There is still time to submit a proposal for an invited symposium at the APS March meeting. The deadline is September 1. When you put one together, please follow the instructions below. I am looking forward to your ideas!

Instructions for submission of proposals for DBP symposia at the 2005 March meeting in LA

A. Symposium Title: Please don't forget that we would like to attract a large audience to each symposium and that we compete with many parallel events. If a title is too technical – as grand as the content of the symposium may be – it is likely that we will not attract a large audience.

B. Organizer:

Name:
Affiliation:
Phone:
Email:
Postal Address:

C. Description of Symposium:
This description is the basis upon which the program committee will select proposals.

Please describe the symposium in non technical terms (so that the committee members with a diverse background can understand the relevance). Write it like you write the proposal summary of an NSF proposal. Describe the role of each speaker and what she/he will present and how it complements the other speakers. In other word, we would like to see an overall plan and coherence between the speakers. Like an NSF summary, please stay within 1 page.

D. For each speaker:

Name:
Affiliation:
Phone:
Email:
Postal Address:

E. Session chair: It is very important that a session chair is selected at the time of proposal submission. The organizer can be session chair. The chair needs to be absolutely committed to attend the March meeting and chair the session.

Name:
Affiliation:
Phone:
Email:
Postal Address:

The DBP program committee (6 members of the executive committee) will select proposals for invited sessions. Submit by email to the program-chair by 09/01 to: Peter Jung, jung@helios.phy.ohiou.edu.

Ribbon Diagrams and Protein Taxonomy:

a profile of Jane S. Richardson

by S. Bahar

"I was an amateur astronomer all through elementary and high school," recalls Jane Richardson, "counting meteors, building a telescope, traveling to eclipses, and calculating the orbit of Sputnik from my own observations to earn a Science Talent Search Award." When she enrolled at Swarthmore College, near Philadelphia, she began in mathematics, physics and astronomy, but then switched to philosophy, keeping a math/physics minor. When she began graduate studies in philosophy at Harvard, however, she quickly realized that the most active research areas in philosophy were those she liked least: modern philosophy, rather than the classics.

Meanwhile, Richardson explains, she had enrolled in "several excellent courses in plant taxonomy and evolution in the Harvard botany department, [which was] very gracious to an interested outsider. I then tried high school teaching, which didn't work because when I concentrated on something I became completely oblivious to anything else. Then I joined, as a technician, the chemistry lab at MIT where my husband, David, was working on a PhD."

David Richardson, who had met Jane at Swarthmore, had become fascinated with the recently determined crystal structures of myoglobin and hemoglobin during his senior year, and, as a beginning graduate student, was researching protein structure in Al Cotton's laboratory at MIT. "Soon", says Jane Richardson, "I became hooked as well, and we've worked together on various aspects of 3D molecular structure ever since. Protein crystallography appealed to Dave's talent for making machinery (and, later, software) work right, and it appealed to my love of complex primary data and what is essentially a new kind of natural history."

It was the beginning of a remarkable collaboration that would spark a revolution in our understanding of protein structure. In 1963, future Nobel Laureate Chris Anfinsen was looking for someone to determine the crystal structure of Staphylococcal nuclease, which he thought would serve as a powerful model system for the study of protein folding. Dave Richardson took the project on for his doctoral thesis, collaborating with postdoc Ted Hazen, a protein chemist who worked on protein purification and crystal growth.

With one master's degree in philosophy and another in teaching, Jane Richardson played for a

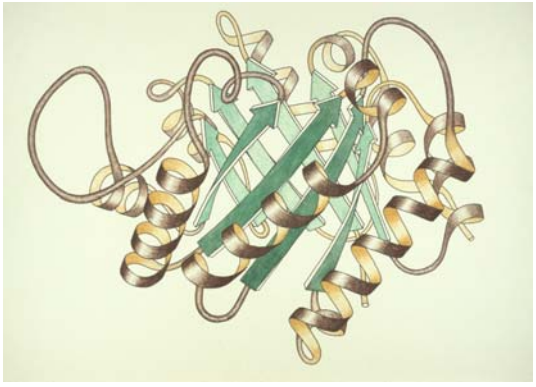

Figure 1. One of Jane Richardson's early hand-drawn ribbon schematics: a side view of triose phosphate isomerase (the classic "TIM barrel" structure" with a twisted cylinder of 8 green beta strands in the center ringed by 8 brown alpha-helices), colored with pastels.

time what she describes as "the role of a relatively invisible hanger-on". But that didn't last long. Her studies of taxonomy and evolution resonated in the protein structure studies she, her husband, and their colleagues were publishing in the late 1960s and early 70s [1-4]. She soon realized that the recurring structural motifs they kept finding in their crystallographic studies could fit into a general classification scheme for protein structure. She was driven, she says, by an

approach of "exhaustively *looking*, in detail, at each beautifully quirky and illuminating piece of data with a receptive mind and eye, as opposed to the more masculine strategy of framing an initial hypothesis, writing a computer program to scan the reams of data, and obtaining an objective and quantitative answer to that one question while missing the more significant answers which are suggested only by entirely unexpected patterns in those endless details." One can gain fruitful insights through "the inherent charm of close acquaintance with the phenomena". Painstakingly, Richardson began to construct an almost Linnean taxonomy of protein structure. During this process, she realized that she had to learn to draw the structures she wanted to classify. "I spent two years," she says, "learning how to make drawings that captured the simplicity and elegance I found in those structures." [5]

In Richardson's careful sketches, a remarkable array of structural motifs and rules

Figure 2. A ribbon drawing produced by David Richardson's Mage program: four subunits of Cu,Zn superoxide dismutase (shown as they pack in the crystal). The structure of this protein was solved in the Richardson laboratory.

emerged. She described these in a seminal *Nature* paper, "β-sheet topology and the relatedness of proteins", in 1977 [6], focusing on the topological classification of β-sheets. The article, which also had the cover picture, a powerful illustration of a "Greek key" structure in the polypeptide backbone of prealbumin, juxtaposed with a photograph of a Greek key structure along the edge of a 450 B.C. Greek amphora, solidified Richardson's reputation. And it also revolutionized biophysicists' understanding of protein structure. Combining observations of taxonomy from earlier papers, and adding many new insights, Richardson presented a table of schematic diagrams for all the topologically distinct β-pleated sheets found in protein structures which had been crystallized up to that time. From her careful observations, she was able to postulate general rules, most of which still appear valid today.

Richardson found that there were two possible types of backbone connections between β strands: "hairpin" connections, in which the backbone chain re-enters the same end of the β sheet it left, and "crossover" connections, where the chain loops around and re-enters the sheet from the opposite end. Crossover connections, she found, were always right-handed [4]. Parallel β structures occurred in large sheets, protected from the solvent by α helices. In contrast, anti-parallel β structures were found as partially unprotected twisted ribbons of two strands. Moreover, all observed β topologies could be described as a relatively limited subset of all possible combinations of connections (hairpins and crossovers). These observations led Richardson to speculate on the energetic landscapes that could lead to such a subset of possible structures. She proposed that

> …it may be that one reason that these structures are favourable is because they can fold correctly by many alternative pathways and therefore tend to fold rapidly and reliably. The idea that some broad features of protein structure are determined by essentially kinetic factors during folding (such as the dominance of near-neighbor strand interactions) is not incompatible with the requirement that the stable native conformation of a protein should be in the global free energy minimum. During its evolution, once a protein finds a reasonably stable, kinetically accessible, minimum energy conformation, it is then subject to natural selection for its stability. Selection will dig that particular local energy minimum as deep as possible by adjusting the amino acid sequence to approach optimal fit for the native conformation, and

> at the same time probably will raise all the other local energy minima whose stability is not being selected for. The result is very likely to be a genuine global energy minimum, in spite of the influence of kinetic requirements. [6]

The stage was set for a new generation of biophysicists and structural biochemists to investigate the energetics and evolution of protein folding. Furthermore, a new picture of protein topology had entered the scientific canon: the ribbon diagram. Elegant and simple, ribbon diagrams (also called Richardson diagrams) convey the basic outlines of molecular structure in a powerful and immediate visual form (Figure 1). Richardson still expresses amazement that she has "a whole generation of scientists see[ing] protein structure through my eyes".

In the years that followed, Jane and Dave Richardson, working at Duke University Medical Center expanded their studies to include other aspects of 3D protein structure. In addition to looking for broad structural motifs, they were led to investigate de novo protein design, as a method of testing theoretical predictions about the determinants of protein folding [7]. De novo design, explains Richardson, is "sort of like doing prediction backwards. Instead of working from natural structures, we look at whole categories of structures to find one that is relatively simple, that we think we understand, and that we can try to isolate as a sort of simplest-case paradigm structure. We then use that structure to design a sequence of amino acids that is not related to any natural structures. And then we actually try to make the new structure, either by direct chemical synthesis or by cloning and expression. At that point, you are able to see if it does actually fold up into something that resembles what you expected." [8]

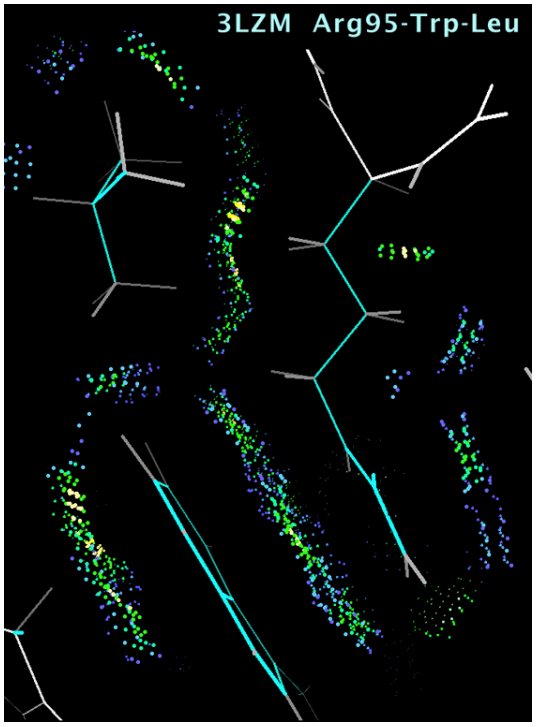

Figure 3. An example of the Richardsons' current all-atom contact analysis for the packing of three sidechains in T4 lysozyme, where the dot surfaces outline the places where two atoms are in contact.

The Richardsons have also become pioneers of developing software methods for the representation of protein and nucleic acid structures. They develop software in order, as they write on their lab's website, "to fill what we see as unmet needs, most notably **kinemages** (molecular graphics optimized for the communication of specific ideas in 3D) and the associated Mage and KiNG display programs, free software on Mac, PC and Unix, widely used for teaching, textbooks, journals, and databases as well as for research." For more details on these software packages, visit http://kinemage.biochem.duke.edu.

Most recently they have developed a method for studying the detailed contacts where atoms touch (Figure 3; [9]). It is used to study the packing inside and between molecules and also to find and correct errors in the experimental models of protein [10] and nucleic acid [11] structures.

Twenty one years ago, Jane Richardson wrote that she "never got a PhD, and I don't have tenure and probably never will." Today, she is a James B. Duke Professor of Biochemistry. "I think", she says, "that you can be intensely ambitious in science on very non-establishment terms that have nothing at all to do with running your own lab, with getting tenure and lots of grant money, or even with getting explicit recognition for your ideas. The first big reward is the excitement of attaining a new insight, independent of whether it is shared with anyone else. But if later work proves you right and if everyone else eventually ends up adopting and using your ideas, then that is *success*, and it can

in some ways add to the fun if they don't always realize who started it. I want immortality from both my biological and my intellectual children, but I don't think they would be as much worth procreating and nurturing if they were always busy thinking of me as their source."

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Jane S. Richardson.

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PRE HIGHLIGHTS

Biological Physics Articles from Physical Review E

(Statistical, Nonlinear, and Soft Matter Physics)

June 2004
Volume 69, Number 6, Articles (06xxxx)
http://scitation.aip.org/dbt/dbt.jsp?KEY=PLEEE8&Volume=69&Issue=6

ARTICLES

Extinction dynamics of Lotka-Volterra ecosystems on evolving networks

F. Coppex, M. Droz, and A. Lipowski
Published 1 June 2004 (*6 pages*)
061901

Combined Monte Carlo and quantum mechanics study of the hydration of the guanine-cytosine base pair
Kaline Coutinho, Valdemir Ludwig, and Sylvio Canuto
Published 1 June 2004 (*7 pages*)
061902

Diffusion in correlated random potentials, with applications to

DNA
Michael Slutsky, Mehran Kardar, and Leonid A. Mirny
Published 1 June 2004 (*11 pages*)
061903

Replica model for an unusual directed polymer in 1 + 1 dimensions and prediction of the extremal parameter of gapped sequence alignment statistics
Yi-Kuo Yu
Published 1 June 2004 (*31 pages*)
061904

Non-Euclidean properties of spike train metric spaces
Dmitriy Aronov and Jonathan D. Victor
Published 2 June 2004 (*9 pages*)
061905

Soft *Listeria*: Actin-based propulsion of liquid drops
Hakim Boukellal, Otger Campás, Jean-François Joanny, Jacques Prost, and Cécile Sykes
Published 2 June 2004 (*4 pages*)
061906

Statistical mechanics of double-helical polymers
Alvise De Col and Tanniemola B. Liverpool
Published 2 June 2004 (*5 pages*)
061907

Unzipping of DNA with correlated base sequence
A. E. Allahverdyan, Zh. S. Gevorkian, Chin-Kun Hu, and Ming-Chya Wu
Published 4 June 2004 (*16 pages*)
061908

Host-parasite coevolution and optimal mutation rates for semiconservative quasispecies
Yisroel Brumer and Eugene I. Shakhnovich
Published 4 June 2004 (*7 pages*)
061909

Hydrodynamic interactions between rotating helices
MunJu Kim and Thomas R. Powers
Published 4 June 2004 (*5 pages*)
061910

Random walks of molecular motors arising from diffusional encounters with immobilized filaments
Theo M. Nieuwenhuizen, Stefan Klumpp, and Reinhard Lipowsky
Published 9 June 2004 (*19 pages*)
061911

Analytical description of finite size effects for RNA secondary structures
Tsunglin Liu and Ralf Bundschuh
Published 9 June 2004 (*10 pages*)
061912

Chain persistency in single-stranded DNA
Anirban Sain, Bae-Yeun Ha, Heng-Kwong Tsao, and Jeff Z. Y. Chen
Published 15 June 2004 (*4 pages*)
061913

Analytical analysis of a vesicle tumbling under a shear flow
F. Rioual, T. Biben, and C. Misbah
Published 15 June 2004 (*10 pages*)
061914

Measure profile surrogates: A method to validate the performance of epileptic seizure prediction algorithms
Thomas Kreuz, Ralph G. Andrzejak, Florian Mormann, Alexander Kraskov, Harald Stögbauer, Christian E. Elger, Klaus Lehnertz, and Peter Grassberger
Published 15 June 2004 (*9 pages*)
061915

Semiconservative replication in the quasispecies model
Emmanuel Tannenbaum, Eric J. Deeds, and Eugene I. Shakhnovich
Published 16 June 2004 (*14 pages*)
061916

Pattern formation and nonlocal logistic growth

Nadav M. Shnerb
Published 22 June 2004 (*6 pages*)
061917

Transition path sampling study of flip-flop transitions in model lipid bilayer membranes
Jordi Martí and Félix S. Csajka
Published 22 June 2004 (*7 pages*)
061918

Electrostatic contribution to twist rigidity of DNA
Farshid Mohammad-Rafiee and Ramin Golestanian
Published 22 June 2004 (*11 pages*)
061919

Effect of chain connectivity on the structure of Lennard-Jones liquid and its implication on statistical potentials for protein folding
W. C. Lu, C. Z. Wang, and K. M. Ho
Published 23 June 2004 (*8 pages*)
061920

Diffusion of actin filaments within a thin layer between two walls
Guanglai Li and Jay X. Tang
Published 23 June 2004 (*5 pages*)
061921

Rupture of a liposomal vesicle
Marco A. Idiart and Yan Levin
Published 23 June 2004 (*8 pages*)
061922

Phase shifts of synchronized oscillators and the systolic-diastolic blood pressure relation
L. Angelini, G. Lattanzi, R. Maestri, D. Marinazzo, G. Nardulli, L. Nitti, M. Pellicoro, G. D. Pinna, and S. Stramaglia
Published 23 June 2004 (*6 pages*)
061923

Solvent-induced micelle formation in a hydrophobic interaction model
S. Moelbert, B. Normand, and P. De Los Rios
Published 24 June 2004 (*11 pages*)
061924

BRIEF REPORTS

Simple swimmer at low Reynolds number: Three linked spheres
Ali Najafi and Ramin Golestanian
Published 16 June 2004 (*4 pages*)
062901

July 2004
Volume 70, Number 1, Articles (01xxxx)
http://scitation.aip.org/dbt/dbt.jsp?KEY=PLEEE8&Volume=70&Issue=1

RAPID COMMUNICATIONS

Sorting mesoscopic objects with periodic potential landscapes: Optical fractionation
K. Ladavac, K. Kasza, and D. G. Grier
Published 20 July 2004 (*4 pages*)
010901(R)

Bubble relaxation dynamics in double-stranded DNA
D. J. Bicout and E. Kats
Published 28 July 2004 (*4 pages*)
010902(R)

ARTICLES

Fast spike pattern detection using the correlation integral
M. Christen, A. Kern, A. Nikitchenko, W.-H. Steeb, and R. Stoop
Published 1 July 2004 (*7 pages*)
011901

Markovian model of growth and histologic progression in prostate cancer
R. Peirolo and M. Scalerandi
Published 2 July 2004 (*9 pages*)
011902

Mechanism for neuronal spike generation by small and large ion channel clusters
Shangyou Zeng and Peter Jung
Published 7 July 2004 (*8 pages*)
011903

Refolding of lysozyme by quasistatic and direct dilution

reaction paths: A first-order-like state transition
Chia-Ching Chang, Xu-Cheng Yeh, Hui-Ting Lee, Po-Yen Lin, and Lou-Sing Kan
Published 7 July 2004 (*8 pages*)
011904

Near-field-magnetic-tweezer manipulation of single DNA molecules
Jie Yan, Dunja Skoko, and John F. Marko
Published 12 July 2004 (*5 pages*)
011905

Pulse propagation in discrete excitatory networks of integrate-and-fire neurons
Laurent Badel and Arnaud Tonnelier
Published 12 July 2004 (*7 pages*)
011906

Effect of the refractive index mismatch on light propagation through diffusive layered media
Fabrizio Martelli, Samuele Del Bianco, and Giovanni Zaccanti
Published 12 July 2004 (*10 pages*)
011907

Clustering through postinhibitory rebound in synaptically coupled neurons
D. T. W. Chik, S. Coombes, and Z. D. Wang
Published 15 July 2004 (*9 pages*)
011908

Dynamics of gene regulatory networks with cell division cycle
Luonan Chen, Ruiqi Wang, Tetsuya J. Kobayashi, and Kazuyuki Aihara
Published 15 July 2004 (*13 pages*)
011909

Overstretching and force-driven strand separation of double-helix DNA
Simona Cocco, Jie Yan, Jean-Francois Léger, Didier Chatenay, and John F. Marko
Published 20 July 2004 (*18 pages*)
011910

Spatially uniform and nonuniform analyses of electroencephalographic dynamics, with application to the topography of the alpha rhythm
S. C. O'Connor and P. A. Robinson
Published 21 July 2004 (*19 pages*)
011911

Density functional study on the structures and thermodynamic properties of small ions around polyanionic DNA
Ke Wang, Yang-Xin Yu, and Guang-Hua Gao
Published 28 July 2004 (*10 pages*)
011912

Electronic structures of *A*- and *B*-type DNA crystals
Masateru Taniguchi and Tomoji Kawai
Published 29 July 2004 (*8 pages*)
011913

Synchronization measures of bursting data: Application to the electrocorticogram of an auditory event-related experiment
Mark A. Kramer, Erik Edwards, Maryam Soltani, Mitchel S. Berger, Robert T. Knight, and Andrew J. Szeri
Published 29 July 2004 (*10 pages*)
011914

Nucleosome interactions in chromatin: Fiber stiffening and hairpin formation
Boris Mergell, Ralf Everaers, and Helmut Schiessel
Published 29 July 2004 (*9 pages*)
011915

Stochastic model for the species abundance problem in an ecological community
Simone Pigolotti, Alessandro Flammini, and Amos Maritan
Published 30 July 2004 (*5 pages*)
011916

Stretching of homopolymers and contact order
Marek Cieplak, Trinh Xuan Hoang, and Mark O. Robbins
Published 30 July 2004 (*8 pages*)
011917

BRIEF REPORTS

Spreading of families in cyclic predator-prey models
Mária Ravasz, György Szabó, and Attila Szolnoki
Published 12 July 2004 (*4 pages*)
012901

Simulations of a small protein in a specifically designed generalized ensemble
Ulrich H. E. Hansmann
Published 15 July 2004 (*4 pages*)
012902

Changes in the Hurst exponent of heartbeat intervals during physical activity
M. Martinis, A. Knežević, G. Krstačić, and E. Vargović
Published 21 July 2004 (*4 pages*)
012903

COMMENTS

Comment on "Theory of high-force DNA stretching and overstretching"
Pui-Man Lam
Published 2 July 2004 (*2 pages*)
013901

Reply to "Comment on 'Theory of high-force DNA stretching and overstretching' "
Cornelis Storm and Philip Nelson
Published 2 July 2004 (*2 pages*)
013902

CONFERENCE ANNOUNCEMENT

The 24th annual Dynamics Days conference (Dynamics Days 2005)
will be held
Jan. 7 - 10, 2005 in Long Beach, CA.
The meeting will be hosted by
U. C. Irvine. Dynamics Days is an annual conference organized to gather a variety of researchers with overlapping interests in nonlinear dynamics. Participants span the fields of mathematics, physics, biology, chemistry, ecology, engineering, and geology. For more information and registration, please see the conference website: http://www.physics.uci.edu/dynamicsdays2005/.

(Dynamics Days is not a DBP or APS event.)

DBP Leadership Update From Secretary-Treasurer Shirley Chan

Current members of DBP's election nominating committee:

Raymond Goldstein, as the Chair, one-year term, expires in March 2005,
Herbert Levine, two-year term, expires in March 2005.
Ned Wingreen, two-year term, expires in March 2005.
Andre Longtin, two-year term, expires in March 2006.
Aihua Xie, APS Council-appointee, one-year term, expires in March 2005.