Curriculum Vita

Homayoun Valafar, PhD
University of South Carolina
Associate Professor of Computer Science and Engineering, University of South Carolina
Adjunct Associate Professor of Bioengineering, Clemson University
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Last Modified: May 7, 2010

Education

PURDUE UNIVERSITY   **West Lafayette, IN**
May 1995
   Ph.D. in Electrical and Computer Engineering
   Thesis Topic: Distributed Global Optimization and its Applications to Neural Networks

PURDUE UNIVERSITY   **West Lafayette, IN**
August 1990
   MS in Electrical and Computer Engineering
   Thesis Topic: Parallel Self-organizing Consensual Neural Networks

MICHIGAN TECHNOLOGICAL UNIVERSITY   **Houghton, MI**
May 1988
   BS in Electrical and Computer Engineering,

Positions

1995-1998	Postdoctoral Research Associate, Dr. Peter Albersheim, CCRC, UGA, Athens, GA
1998-2000	Postdoctoral Research Associate, Dr. James H. Prestegard, UGA, Athens, GA
2000-2004	Project Coordinator, Southeast Collaboratory for Structural Genomics, UGA, Athens, GA
2004-2009	Assistant Professor, Comp. Sci. and Eng., University of South Carolina, Columbia, SC
2007-2010	Graduate director, Biomedical Eng. , University of South Carolina, Columbia, SC
2009-Present	Associate Professor, Comp. Sci. and Eng., University of South Carolina, Columbia, SC
2010-Present	Adjunct Associate Professor, Bioengineering, Clemson University, Clemson, SC

Areas of Research Interest

Special interests:
Bioinformatics and Computational Biology
Computational Medicine
High Performance Computing
Artificial Neural Networks
Optimization

General Interests
Pattern recognition and classification
Computer hardware design
Quantum Computing

Honors and Awards

1984	Member of Engineering National Honor Society Eta Kappa Nu
1984	Member of National Honor Society Phi Kappa Phi
1984-1995	Dean's List for outstanding college students
1995-1998	Member of IEEE computer society
1997-1998	Member of National Dean's List
2002	IR7 (highest) level specialist award from the International Technology Institute, in recognition of research contributions to the field of Bioinformatics. Diploma No.: IR7-02062456
2002-2006	Achievement award from 03-06 International Multi-Conferences in Computer Science and Computer Engineering
2006-Present	Member of Upsilon Pi Epsilon honor society
2007	NSF Career Award
2008	Young research investigator award, College of Engineering, USC

Research Support

ONGOIN

PI: Homayoun Valafar Project Number: MCB-0644195 Source: NSF CAREER Title: "Career: Assessment of Structural Novelty of an Unknown Protein Using Unassigned Residual Dipolar Coupling Data"	Project Date: 01/01/07-12/31/11
PI: Homayoun Valafar Project Number: MCB-0733968 Source: NSF Title: "NSF REU Supplement to Existing Career Grant (MCB-0644195): Assessment of the Structural Novelty of an Unknown Protein Using Unassigned RDC Data"	Project Date: 01/01/07-12/31/09
PI: Homayoun Valafar Project Number: 1R01GM081793-01 Source: NIH Title: "Structure and Dynamics of Membrane Proteins from NMR Orientational Constraints"	Project Date: 08/01/07-06/30/11
PI: Homayoun Valafar Project Number: 1R01GM081793-01 Source: NIH Title: "Administrative Supplement: Structure and Dynamics of Membrane Proteins from NMR Orientational Constraints"	Project Date: 08/01/07-06/30/11
PI: Jijun Tang Project Number: CNS-0708391 Source: NSF Title: "CRI: CRD Acquisition of a High-Performance Shared-Memory Computer for Biological and Medical Research in South Carolina"	Project Date: 06/12/07-6/11/10
PI: Homayoun Valafar Project Number: Magellan Source: USC-SAM Title: "MGS: Locating the Active Sites of Proteins Using Multiple Structure Alignment"	Project Date: 5/2010-4/2011
PI: Lucia Pirisi-Creek Source: NIH Title: "South Carolina IDeA Network of Biomedical Research Excellence"	Project Date: 5/10-4/15

Invited Lectures

- Target Selection Using Probability Density Profile Analysis of Backbone RDC Data, Rutgers, New Jersey, 5/16/2009, Dr. Guy Montelione (host)
- Generating 3D Structures from RDC Data, Northeast Structural Genomics Consortium, 6/16/09
- Contributions of RDC to High-Throughput Characterization of Protein Structure and Dynamics, University at Buffalo, NY, 7/20/09, Dr. Thomas Szyperski (host)
- Simultaneous Study of Structure and Motion of Proteins with REDCRAFT, Northeast Structural Genomics Consortium, 11/1/09
- REDCRAFT: A computational Approach for Simultaneous Investigation of Structure and Dynamics of Proteins from Residual Dipolar Couplings, NIGMS Enabling Technology Workshop, NIH, Bethesda, 4/19/10
- Estimation of principal order parameters from unassigned data, Rutgers and the northeast structural genomics consortium, 5/09 &11/09
- Structure Determination of Membrane Proteins Using REDCRAFT, Roadmap Membrane Protein Meeting, UCSF, 5/09
- Protein engineering with multiple structure alignment, Bioinformatics Symposium, Columbia, SC, 4/09
- Structure determination of membrane proteins using REDCRAFT, 3/09, UCSF
- Multiple structure alignment with msTALI, JHP symposium, UGA, 3/09
- Estimation of molecular anisotropy in the absence of structure and assignment, 10/08, UCSD
- Advances in analysis of RDC data, 8/08, UGA
- Analysis of RDC data using REDCAT, 10/07, Rutgers and the northeast structural genomics consortium
- Utility of RDC data in structure determination and study of internal motion, 3/07, Southeast collaboratory for Biomolecular NMR
- Structure Validation of Membrane Proteins Using REDCAT, UCSD, 6/19/06
- Study of Dynamics of Membrane Proteins Using REDCRAFT, Burnham Institute, 6/21/06
- Simultaneous Characterization of Structure and Motion of Biomolecules from Residual Dipolar Couplings, Complex Carbohydrate Research Center, UGA, 5/05.
- Rapid Classification to a Protein Fold Family Using a Statistical Analysis of Dipolar Couplings, Institute of Bioinformatics, UGA, 6/06.
- Contributions of RDC to High-Throughput Characterization of Protein Structure and Dynamics, NIEHS/NIH, Research Triangle Park, NC, 10/05.
- Rapid Classification to a Protein Fold Family Using Statistical Analysis of Residual Dipolar Couplings, Faculty Forum in Scientific Computing, USC, 11/05.
- Monosaccharide Decomposition Analysis of Complex Carbohydrates Using Multi-Level Neural Networks, CCRC/UGA, 11/05
- Introduction to REDCAT / REDcRAFT Software Suit, NIEH/NIH, Research Triangle Park, NC, 5/09/05
- Optimization and pattern recognition tools in structural genomics, Michigan Technological University, Department of Electrical/Computer Engineering, 3/12/2004.
- Applications of optimization and pattern recognition tools in structural genomics, University of Georgia, Department of Engineering, 2/18/2004.
- Computational methods in structural genomics: high throughput protein structure determination from NMR spectra, San Diego State University, Departments of Computer Science, Mathematics, Chemistry and Biochemistry Colloquium, 10/17/2003.
- Structural Genomics Initiative at the SECSG, Eastern Connecticut State University, Departments of Computer Science and Mathematics, 5/07/03.

- Computational Developments of the NMR Core of the Southeast Collaboratory for Structural Genomics (SECSG) , Bioinformatics Seminar Series at UGA, University of Georgia, Computer science and Bioinformatics institute Colloquium, 12/06/02.
- GeneFormatics, Rapid Protein Fold recognition Using Backbone ^{15}N-H Residual Dipolar Couplings, 6/2000

Teaching History at USC

Fall 2004	**CSCE 590F, Topics in Bioinformatics and Medical Informatics**
Spring 2005	**CSCE 245, Object-Oriented Programming Techniques**
Fall 2005	**CSCE 790R, Structural Protein Bioinformatics**
Spring 2006	**CSCE 245, Object-Oriented Programming Technique**
Fall 2006	**CSCE 790S, Protein Folding and Dynamic**
	CSCE 590G, Topics in Computational Medicine
Spring 2007	**CSCE 245, Object-Oriented Programming Techniques**
	CSCE 500, Computer Programming & Applications
Spring 2008	**CSCE 245, Object-Oriented Programming Techniques**
	CSCE 500, Computer Programming & Applications
Fall 2008	**CSCE 206, Scientific Applications Programming**
Spring 2009	**CSCE 245, Object-Oriented Programming Techniques**
	CSCE 769, Computational Structural Biology
Spring 2010	**CSCE 769, Computational Structural Biology (broadcast to Clemson & MUSC)**
Fall 2010	**CSCE 240, Introduction to Software Engineering**

Committees and Professional Service

2000-2002	Session chair, annual International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS)
2000-Present	Member of the organizing and reviewing committee, annual international conference of Parallel Distributed Processing Techniques and Application (PDPTA).
2000-Present	Editor of the Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS).
2002-Present	Active referee to the Journal of Artificial Intelligence in Medicine.
2003-2005	Co-chair, annual International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS)
2006	Co-chair, annual International Conference on Bioinformatics and Computational Biology (BioComp06)
2005-2006	Annual panel review, National Defense Science and Engineering, 2/19/2005.
2007	Chair of scientific review committee and award committee, IEEE 7th international conference on Bioinformatics and Bioengineering

Member of Advisory/Examination Committee

Primary Research Advisor

Xijiang Miao
Thesis title: Homology Protein Structure Detection using Unassigned RDC Data from Multiple Alignment Media
Degree: PhD
Graduation date: 12/07

Matthew Fawcet
Thesis title: Computational Protein Folding from First Principles
Degree: PhD
Graduation date: 5/09

Rishi Mukhopadhyay
Thesis title: Provably Optimal Structure Determination of Proteins from a Minimum Set of RDCs and Order Tensor Estimates
Degree: PhD
Graduation date: 12/10

Paul Shealy
Thesis title: Multiple Protein Structure Alignment as a Tool for Study of Evolutionary Relation and Discovery of Active Sites
Degree: PhD
Graduation date: 5/11

Ryan Yandle
Thesis title: Computational Homologous Protein Structure Identification Using Unassigned Two-Dimensional Residual Dipolar Couplings
Degree: MS
Graduation date: 5/11

Mikhail Simin
Thesis title: Computational and Methodological Improvement to Protein Structure Determination from Orientational Restraints
Degree: PhD
Graduation date: 5/12

Arjang Fahim
Thesis title: Undecided
Degree: PhD
Graduation date: 5/15

Research Committee Advisor

Feng Yu
Degree: PhD, Computer Science
Graduation date: 5/08

Achraf El-Allali
Degree: PhD, Computer Science
Graduation date: 6/08

Suman Pakala
Degree: PhD, Computer Science
Graduation date: 8/08

Stephanie Zierke
Degree: MS, Computer Science
Graduation date: 8/08

Ozan Karaman
Degree: MS, Biomedical Engineering
Graduation date: 12/09

Stephanie Irausquin
Degree: PhD, Biology
Graduation date: 12/10

Gargi Dayama
Degree: PhD, Public Health
Graduate date: 5/12

Books and Conference Proceedings

1. H.R. Arabnia, **H. Valafar**: Proceedings of the 2006 International Conference on Bioinformatics & Computational Biology, BIOCOMP'06, Las Vegas, Nevada, USA, June 26-29, 2006 CSREA Press 2006

2. F. Valafar, **H. Valafar**: Proceedings of The 2005 International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences, METMBS 2005, Las Vegas, Nevada, USA, June 20-23, 2005, CSREA Press 2005

3. F. Valafar, **H. Valafar**: Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences, METMBS '04, June 21-24, 2004, Las Vegas, Nevada, USA ISBN number: 1-932415-43-2 (470 pages). CSREA press, USA, 2004.

4. F. Valafar, **H. Valafar**: Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences, METMBS '03, June 23 - 26, 2003, Las Vegas, Nevada ISBN number: 1-932415-04-1 (518 pages). CSREA press, USA, 2003.

5. Associate editor of the *Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences* (*METMBS*). ISBN numbers: 1-892512-31-9 (Volume I, 600 pages), 1-892512-32-7 (Volume II, 315 pages), and 1-892512-33-5 (complete set, 915 pages). CSREA press, USA, 2002.

6. Associate editor of the *Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences* (*METMBS*). ISBN number: 1-892512-77-7 (523 pages). CSREA press, USA, 2001.

7. Associate editor of the *Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences* (*METMBS*). ISBN numbers: 1-892512-60-2 (Volume I, 408 pages), 1-892512-61-0 (Volume II, 346 pages), and 1-892512-62-9 (complete set, 754 pages). CSREA press, USA, 2000.

Journal Publications

1. Shealy P, Simin M, Park SH, Opella SJ, **Valafar H,** Simultaneous Structure and Dynamics of a Membrane Protein using REDCRAFT: Membrane-bound form of Pf1 Coat Protein, *Journal of Magnetic Resonance*, 2010 Nov;207(1):8-16. Epub 2010 Jul 30, PMID: 20829084

2. Park SH, Son WS, Mukhopadhyay R, **Valafar H**, Opella SJ., Phage-Induced Alignment of Membrane Proteins Enables the Measurement and Structural Analysis of Residual Dipolar Couplings with Dipolar Waves and lambda-Maps, J Am Chem Soc. 2009 Oct 14;131(40):14140-1

3. Mukhopadhyay R, Miao X, Shealy P, **Valafar H,** Efficient and accurate estimation of relative order tensors from λ-*maps*, *J Magn Reson*. Volume 198, Issue 2, June 2009, Pages 236-247, PMC Journal – in process

4. Miao X, Mukhopadhyay R, **Valafar H**, Estimation of relative order tensors, and reconstruction of vectors in space using unassigned RDC data and its application, *J Magn Reson*. 2008 Oct;194(2):202-11, PMC2669903

5. Miao X, Waddell PJ, **Valafar H**, TALI: local alignment of protein structures using backbone torsion angles, J Bioinform Comput Biol. 2008 Feb;6(1):163-81.

6. Bansal S, Miao X, Adams MW, Prestegard JH, **Valafar H**, Rapid classification of protein structure models using unassigned backbone RDCs and probability density profile analysis (PDPA). *J Magn Reson*. 2008 Feb 12, PMC2699457

7. Bryson M, Tian F, Prestegard JH, **Valafar H**, REDCRAFT: A tool for simultaneous characterization of protein backbone structure and motion from RDC data. *J Magn Reson*. 2008 Apr;191(2):322-34, PMC2728087

8. Prestegard JH, Mayer KL, **Valafar H**, Benison GC., Determination of protein backbone structures from residual dipolar couplings, Methods Enzymol. 2005;394:175-209, PMC1808351

9. Wang J, **Valafar H**, Prestegard JH, Assessment of protein alignment using 1H-1H residual dipolar coupling measurements, J Magn Reson, 2005 Jan;172(1):85-90

10. Di Lello P, Benison GC, **Valafar H**, et al., NMR structural studies reveal a novel protein fold for MerB, the organomercurial lyase involved in the bacterial mercury resistance system, *BIOCHEMISTRY* 43 (26): 8322-8332 JUL 6 2004

11. **Valafar H**, Mayer KL, Bougault CM, LeBlond PD, Jenney FE Jr, Brereton PS, Adams MW, Prestegard JH, Backbone solution structures of proteins using residual dipolar couplings: application to a novel structural genomics target, J Struct Funct Genomics. 2004;5(4):241-54, PMC1815388

12. **H. Valafar**, Arabnia H.R., Distributed Global Optimization and its Potential Implementation on the MultiRing Network. *Journal of Neural, Parallel and Scientific,* Vol. 12, no. 4, pp. 465-490. Dec. 2004

13. L. C. Morris, **Valafar H.**, Prestegard J. H., Assignment of Backbone Resonances from Minimal NMR Data Using Connectivity, Torsion Angle Constraints, and Chemical Shifts. *Journal of Biomolecular NMR* 29: 1-9, 2004.

14. **H. Valafar**, Prestegard J.H., REDCAT: A Residual Dipolar Coupling Analysis Tool. *Journal of Magnetic Resonance* 167 (2004) 228-241

15. K. Umemoto, Leffler H., Venot A., **Valafar H.**, Prestegard J., Conformational Differences in Liganded and UnligandedStates of Galectin-3. *Biochemistry*, 2 (13): 3688-3695 APR 8 2003

16. **H. Valafar**, Presetegard J., Rapid Classification of a Protein Fold Family Using a Statistical Analysis of Dipolar Couplings. Bioinformatics, 2003 Aug 12:19(12):1549-55

17. Ford MG, **Valafar H**, Prestegard JH, Utilizing molecular symmetry and dipolar couplings to assign the resonances of a 33kDa protein complex, *BIOPHYSICAL JOURNAL* 84 (2): 276A-276A Part 2 Suppl. S FEB 2003

18. **H. Valafar**, Valafar F., J. Prestegard, Data-mining protein structure databanks for crystallization patterns of proteins, Techniques in Bioinformatics and Medical Informatics, *Annals of the New York Academy of Sciences*, 980: 13-22 2002

19. **H. Valafar**, Valafar F., Data Mining and Knowledge Discovery in Proton Nuclear Magnetic Resonance (^{1}H-NMR) Spectra using Frequency to Information Transformation (FIT). KNOWL-BASED SYST 15 (4): 251-259 Sp. Iss. SI MAY 2002

20. Fang T, **Valafar H.**, and Prestegard J., A Dipolar Coupling Based Strategy for Simultaneous Resonance Assignment and Structure Determination of Protein Backbones, *Journal of the American Chemical Society*; 2001

21. Prestegard JH, **Valafar H**, Glushka J, Tian F, Nuclear magnetic resonance in the era of structural genomics, Biochemistry. 2001 Jul 31;40(30):8677-85

22. Al-Hashimi HM, **Valafar H**, et al., Variation of molecular alignment as a means of resolving orientational ambiguities in protein structures from dipolar couplings. *J MAGN RESON* 143: (2) 402-406 APR 2000.

23. **H. Valafar**, Valafar F et al., Predicting the effectiveness of hydroxyurea in individual sickle cell anemia patients. *ARTIF INTELL MED* 18: (2) 133-148 FEB 2000.

24. Valafar F, **Valafar H**. CCRC-Net: an Internet-based spectral database for complex carbohydrates using artificial neural networks search engines. *TRAC-TREND ANAL CHEM* 18: (8) 508-512 AUG 1999.

25. Cherniak R, Valafar H, et al., Cryptococcus neoformans chemotyping by quantitative analysis of H-1 nuclear magnetic resonance spectra of glucuronoxylomannans with a computer-simulated artificial neural network. CLIN DIAGN LAB IMMUN 5: (2) 146-159 MAR 1998, PMC121351

Conferences and Symposia Publications

1. Mukhopadhyay R., Simin M., Valafar H., Calculation of structure and trajectory of motion of mobile domains in proteins from residual dipolar couplings, *Keystone Symposia: Frontiers of NMR in Biology*, January 8 - 13, 2011 Big Sky Resort, Big Sky, Montana

2. Mukhopadhyay R., **Valafar H.**, Dynafold: A provably optimal algorithm for protein structure determination from N-H and C_α-H_α Residual Dipolar Couplings collected in two alignment media, 51th *Experimental Nuclear Magnetic Resonance Spectroscopy Conference,* Daytona Beach, Florida, April 18-23, 2010

3. Simin M., **Valafar H.**, Algorithmic and Methodology Improvements of REDCRAFT, 51th *Experimental Nuclear Magnetic Resonance Spectroscopy Conference,* Baytona Beach, Florida, April 18-23, 2010

4. Schmidt C., Mukhopadhyay R., **Valafar H.**, REDCAT Improvements and XplorGUI Introduction, 51th *Experimental Nuclear Magnetic Resonance Spectroscopy Conference,* Daytona Beach, Florida, April 18-23, 2010

5. Mukhopadhyay R., Yandle R., **Valafar H.**, nD-PDPA: Structural Similarity Assessment of Proteins From Unassigned Residual Dipolar Couplings, Protein Structure Initiative: 2010 NIGMS Workshop: Enabling Technologies in Structure and Function, April 19-21, 2010, Natcher Building Bethesda, Maryland

6. Simin M., Shealy P., **Valafar H.**, REDCRAFT: A computational Approach for Simultaneous Investigation of Structure and Dynamics of Proteins from Residual Dipolar Couplings, Protein Structure Initiative: 2010 NIGMS Workshop: Enabling Technologies in Structure and Function, April 19-21, 2010, Natcher Building Bethesda, Maryland

7. Shealy P., **Valafar H.**, Aligning Multiple Protein Structures using Biochemical and Biophysical Properties, *International Conference on Bioinformatics and Computational Biology (BioComp09)*, Las Vegas July 13-16, 2009

8. Yandle R., Mukhopadhyay R., **Valafar H**., Using Residual Dipolar Couplings from Two Alignment Media to Detect Structural Homology, *International Conference on Bioinformatics and Computational Biology (BioComp09)*, Las Vegas July 13-16, 2009

9. Simin M., **Valafar H**., Alternative Metric System and Data Sensitivity for Protein Structure Determination with REDCRAFT, *International Conference on Bioinformatics and Computational Biology (BioComp09)*, Las Vegas July 13-16, 2009

10. Mukhopadhyay R., Shealy P., **Valafar H**., Study of Structure and Dynamics of Proteins from Unassigned RDC Data, *Keystone Symposia: Frontiers of NMR in Biology, Mew Mexico*, February 15-20, 2009

11. Shealy P., Mukhopadhyay R., Park S.H., Opella S., **Valafar H.**, Minimum RDC Data Requirements for Protein Folding Using REDCRAFT with Angular Constraints, *50th Experimental Nuclear Magnetic Resonance Spectroscopy Conference,* Monterey March 29-April 3, 2009

12. R. Mukhopadhyay, Yandle R., **H. Valafar**, 2-D Probability Density Profile Analysis: Identifying Structure of an Unknown protein From Unassigned Residual Dipolar Couplings, *50th Experimental Nuclear Magnetic Resonance Spectroscopy Conference,* Monterey March 29-April 3, 2009

13. X. Miao; R. Mukhopadhyay ; **H. Valafar***, Estimation of order parameters and relative orientation of an unknown protein from unassigned, correlated 2D-RDC data. *49th Experimental Nuclear Magnetic Resonance Spectroscopy Conference,* Monterey March 9-14

14. P. Shealy; S. Smith; **H. Valafar ,** Order Tensor Estimation and Assignment of Backbone Resonances Using Residual Dipolar Couplings. *49th Experimental Nuclear Magnetic Resonance Spectroscopy Conference,* Monterey March 9-14

15. E. Timko, P. Shealy, M. Bryson, and **H. Valafar**, Minimum Data requirements and Supplemental Angle Constraints for Protein Structure Prediction with REDCRAFT, *BioComp08*, Las Vegas July 14-16

16. P. Shealy, R. Mukhopadhyay, S. Smith, **H. Valafar**, Automated Assignment of Backbone Resonances Using Residual Dipolar Couplings Acquired from a Protein with Known Structure, *BioComp08*, Las Vegas July 14-16

17. R. Mukhopadhyay, P. Shealy, **H. Valafar,** Protein Fold Family Recognition From Unassigned Residual Dipolar Coupling Data, *BioComp08*, Las Vegas July 14-16

18. S. Bansal, X. Miao**,** J. H. Prestegard, H. Valafar, Rapid Classification of Protein Structure Models using Unassigned NMR Data, *21st Symposium of The Protein Society*, July 21, 2007, Boston, Massachusetts.

19. S. Bansal, **H. Valafa**r, K.L. Mayer, P. LeBlond, G. Sciortino; J.H. Prestegard, Target Selection for NMR vs X-Ray Structure Determination using 1D NMR Screen, *47th ENC*, April 23-28, 2006.

20. X. Miao, M. Bryson, **H. Valafar**, TALI: Protein Structure Alignment Using Backbone Torsion Angles. *BIOCOMP 2006: 3-9*

21. M. Bryson, X. Miao, **H. Valafar**: Process of Efficiently Parallelizing a Protein Structure Determination Algorithm. *PDPTA 2006*: 320-326

22. **H. Valafar**, Mayer K. L., LeBlond P. D., Bougault, C., Prestegard J.H., Residual Dipolar Couplings in High Throughput Backbone Solution Structure Determination of Proteins, *International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'2004).* June 21-24, Las Vegas, Nevada.

23. **H. Valafar**, Prestegard JH, Fold Family Recognition Based on Unassigned Residual Dipolar Couplings, *Computational Aspects of Biomolecular NMR, Gordon Research Conference*, January 18-23, 2004, Ventura, California.

24. **H Valafar** ; Prestegard JH, A New Program for RDC Analysis and Structure Validation. *44th ENC* Program March 30 - April 4, 2003, Savannah, Georgia

25. LC Morris ; **Valafar H**; Prestegard JH, Assignment of Backbone Resonances from Minimal NMR Data Sets Using Connectivity, Torsion Angle Constraints, and Chemical Shifts. *44th ENC* Program March 30 - April 4, 2003, Savannah, Georgia

26. KL Mayer ; **Valafar H**; et. al., NMR Structure Determination Using Residual Dipolar Couplings,. *44th ENC* Program March 30 - April 4, 2003, Savannah, Georgia

27. MG Ford ; **Valafar H**; Prestegard JH, Residual Dipolar Coupling Assisted Assignment for HSQC Based Ligand Titration Data on Galectin-1. *44th ENC* Program March 30 - April 4, 2003, Savannah, Georgia

28. RD Seidel; Juan-Carlos Amor; **H Valafar**; Richard A. Kahn; James H. Prestegard, Conformational Changes in human Arf1 on Nucleotide Exchange and Deletion of the N-terminal Helix using Residual Dipolar Coupling. *44th ENC* Program March 30 - April 4, 2003, Savannah, Georgia

29. K. Mayer, **H. Valafar**, et al, NMR Structure Determination and Validation using Residual Dipolar Couplings, *ISGO International Conference on Structural Genomics*, Oct 10-13, 2002 Berlin

30. K. Mayer, **H. Valafar**, et al, The Roles of NMR in Structural Genomics at the SECSG, *43rd Experimental NMR Conference (ENC 43)*, April 14-19, 2002 Asilomar, CA

31. **H. Valafar**, Tian F., Prestegard J. H., Rapid Classification of Protein Fold Families Using a Statistical Analysis of Dipolar Couplings. *42st Experimental Nuclear Magnetic Resonance Conference (ENC 42), 2001*.

32. F. Tian; **Valafar H**.; Prestegard J. H.; A Dipolar Coupling Based Strategy for Simultaneous Protein Resonance Assignment and Structure Determination. *42st Experimental Nuclear Magnetic Resonance Conference (ENC 42), 2001*.

33. J. H. Prestegard, Tian F., **H. Valafar**, High Through-put NMR Analysis of Proteins at the Southeast Collaboratory for Structural Genomics. *42st Experimental Nuclear Magnetic Resonance Conference (ENC 42), 2001*.

34. **H. Valafar**, Valafar F.; Knowledge Discovery in ^{1}H-NMR spectra of Complex Carbohydrates using Frequency to Information Transformation (FIT). *International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'2001), p61-66*.

35. **H. Valafar**, Valafar F., Prestegard J. H.; One and Two Dimensional Statistical Data-Mining of Protein Databank for Crystallization Patterns of Proteins. *International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'2001), p67-72*.

36. **H. Valafar**, Tian F., Prestegard J. H., Rapid Classification of Protein Fold Families Using a Statistical Analysis of Dipolar Couplings. *International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'2001), p146-151*.

37. **H. Valafar**, Valafar F, Reduction in the complexity of 1D ^{1}H-NMR spectra by the use of Frequency to Information Transformation. *International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'2000)*, p207-212

38. **H. Valafar**, Muti-leveled output Neural Networks in Monosaccharide decomposition Analysis of N-linked Oligosaccharides, *International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'2000)*, p219-224

39. **H. Valafar**, Prestegard J, Data-mining of Protein Structure Databank for Crystallization patterns of Proteins. *International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences (METMBS'2000),* p193-200

40. H. Al-Hashimi, **Valafar H.**, et al., Resolving Orientational Ambiguities in Protein Structures Using Dipolar Couplings and Variation of Molecular Alignment*, 41st Experimental Nuclear Magnetic Resonance Conference (ENC), 2000*.

41. J. Glushka, Q. Teng, E. R. Zartler, **Valafar H.**, J. Prestegard, Rapid and automated evaluation of proteins as candidates for structure determination, *41st Experimental Nuclear Magnetic Resonance Conference (ENC), 2000*.

42. Valafar, F., **Valafar H.** 1999. A Comparative study of Artificial Neural Networks Using Reinforcement learning and Multidimensional Bayesian Classification Using Parzen Density Estimation for Identification of GC-EIMS Spectra of Partially Methylated Alditol Acetates on the World Wide Web. International Join Conference on Artificial Intelligence International Joint Conference on Neural Networks (IJCNN 1999), Washington, DC, July 10-16, 1999

43. Valafar, F., **Valafar H.** 1999. Identification of ^{1}H-NMR Spectra of Xyloglucan Oligosaccharides: A Comparative Study of Artificial Neural Networks and Bayesian Classification Using Non-parametric Density Estimation. International Joint Conference on Neural Networks (IJCNN 1999), Washington, DC, July 10-16, 1999

44. **H. Valafar**, F. Valafar. 1999. Identification of ^{1}H-NMR Spectra of N-Linked Oligosaccharides Using Artificial Neural Networks. *First Joint BMES/EMBS Conference 99*, p157-158.

45. **Valafar, H.**, F. Valafar. 1999. Prediction of a Patient's Response to a Specific Drug Treatment Using Artificial Neural Networks. *First Joint BMES/EMBS Conference 99*, p72-73.

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