NAME: **RITA CASADIO**
Citizenship: **Italian**
Residence: **Bologna Italy**

POSITION TITLE
Full Professor of **Biochemistry**, University of Bologna, Italy
Address: Department of Biology, Via San Giacomo 9/2, 40126 Bologna Italy; Tel.+39-051-2094005;
casadio@biocomp.unibo.it
rita.casadio@unibo.it
www.biocomp.unibo.it

EDUCATION/TRAINING

1) Maturità classica
2) Degree in Physics (Universita' degli Studi di Bologna)
3) Perfezionamento in Teoria e Applicazione delle Macchine Calcolatrici
4) Certificato di Studiosita' in Biofisica (Universita' degli Studi di Bologna)

Special courses and Fellowships

1973- Advanced Course on Computer Science (Universita' degli Studi di Bologna)
1976- FEBS Advanced Course n.41 on the Biochemistry of Cellular Membranes (Politecnico Federale Svizzero, Zurigo)
1977- 2nd International Course on the Bioenergetics of Biological Membranes (Gruppo Italiano di Bioenergetica ed Accademia dei Lincei, Roma)
1978- Human Biology (Medical Center, University of California, San Francisco)
1980- International Course on Bacteriorhodopsin (Science Academy, Szeged, Ungheria)
1980- Corso Avanzato di NMR applicata in Chimica Organica e Biologia (Universita' della Calabria, Rende)
1981- Short Term Embo Fellowship at the Department of Biophysics, University of Osnabruck (Germany)
1982- International School on Biothermokinetics (Biozentrum, Basel)
1983- Introduzione alla Scienza della Complessita': Processi Stocastici e Autoorganizzazione nei Sistemi Complessi (Istituto di Aggiornamento e formazione dell'ENI-TEMA, Castelgandolfo)

Academic Positions

1974 - 1981 Assegnista Ministeriale, **University of Bologna**, Italy.
1978 - 1979 Assistant Research Biochemistry I, Cardiovascular Research Institute, **University of California**, San Francisco
1981 - 1987 Permanent Researcher, Matter Physics. **University of Bologna**, Italy
1987 -2001 Associate Professor of Biophysics. **University of Bologna**, Italy
2001(1/10)- on-going. Full Professor of Biophysics/Biochemistry. **University of Bologna**, Italy
2005- on-going. President of the International Bologna Master in Bioinformatics. **University of Bologna,** Italy

Teaching Activities, Societies, Appointments

RC is presently the President of the International Bologna Master in Bioinformatics, a two year 2nd level course at the Bologna University, giving courses of Bioinformatics, Biophysics and computational Biology (since 2005). She is also invited to give lectures to undergraduate and graduate students in different PHD and Master courses in Italy, Europe and extraEU countries (such as Oman (Sultan Quaboos University-College of Medicine and Health), China (Shanghai Jiao Tong University-Department of Automation) and Turkey (Sabanci University, Istanbul). RC is member of the American Biophysical Society, of the Protein Society, and of the Italian Societies of Biochemistry, Biophysics and Bioinformatics. She is member of the board of directors of I.N.B.B, an Italian InterUniversity Consortium for Researches in Biostructures and Biosystems, acting also as a representative of the Italian Minister of MIUR; she has been a member of the board of directors of ISCB, the International Society of Computational Biology, comprising over 800 researchers and in 2008-2011, she coordinated the project Bioinformatics for the Italian National Research Council

(Department of Life Science). RC with the Biocomputing Unit of Bologna is active in organizing International Schools on Bioinformatics (www.biocomp.unibo.it) and the Bologna Master in Bioinformatics. The Biocomputing unit has been a node of a network of excellence (BIOSAPIENS) within the VIth European Community framework (2004-2009) and a node of the National platform LIBI for Bioinformatics (2003-2011). Presently it is involved in an European Cost Action activity for the Rabbit Genome (2011-ongoing, RC is the national representative) and an Italian National project for operative research in animal genetics. RC acts as a referee for scientific journals such as Proteins, Protein Science, Bioinformatics, FEBS Lett, Proteomics, European Journal Biochemistry, EMBO J, NAR, and for PRIN, NIH and EC research projects. She is also regularly included in the reviewing committee of several international meeting such as ISMB, WABI (co-chaired in 2005), BIRD, all devoted to different computational aspects of Bioinformatics and Computational Biology. Presently she is a member of the Editorial Board of BMC Bioinformatics; BioDataMining; Advances in Bioinformatics; BMC Research Notes; Journal of Biomedicine and Biotechnology, Advanced Studies in Biology, The Open Chemical and Biomedical Methods Journal; she has been guest editor Guest Editor to the Special Section on Computational Biology and Bioinformatics (WABI) -- Part 1 and 2 on Lecture Notes in Bioinformatics (Lecture Notes in Computer Science). RC is a member of the Academy of Science of the Bologna Institute. She is presently also a member of the ANVUR-GEV05.

Research Activities and Acknowledgments
RC has been working mainly in the fields of membrane and protein Biophysics (particularly with bacteriorhodopsin from Halobacterium Halobium and F1F0 ATPases from mesophilic organisms), both experimentally and theoretically, including mechanisms of energy conservation in bacteria.
She is interested in Bioinformatics and Computational Biology, developing computer modelling of relevant biological processes, such as protein folding, protein-protein and protein-DNA interactions. Her researches have been devoted to different aspects of protein modelling, including prediction of secondary and tertiary structures with neural networks, hidden Markov models and genetic algorithms, molecular docking and drug design (for details see http://lipid.biocomp.unibo.it). One major field of research has been the implementation and developments of tools out of machine-learning approaches for the prediction of secondary and tertiary structure of proteins from their aminoacid residue sequences, particularly of membrane proteins and their transmembrane topology. Projects focused on the prediction of contact maps, of protein-protein and protein-DNA interaction, of the bonding state of cysteines and their topology. Presently her researches are mainly devoted to the specific development of tools out of machine learning based approaches for problem solving of relevant biomedical and biotechnological problems for large scale analysis of genomic, proteomic and interactomic data (for details see http://lipid.biocomp.unibo.it), focusing also on the the implementation and developments of tools for the prediction subcellular localisation of proteins, particularly of membrane proteins, for the genome and SNPs annotation and the prediction of mutation effect on protein stability and interaction. Projects are devoted to the analysis of interactomes and their relation with protein-protein interaction at the molecular levels. RC is the author of over 200 scientific papers, one international patent of a peptidomimetic molecule, and presented her work at several (over 300) national and international meetings (for some details see http://lipid.biocomp.unibo.it/casadio/cv.html).
    About the Biocomputing Unit of the University of Bologna (group leader Rita Casadio). Since 1995 Rita Casadio is the group leader of the Biocomputing Unit of the University of Bologna, in the Department of Biology. The group became officially active in 1995, when the Interdepartmental Center for the Biotechnological Research of the University of Bologna (CIRB) supported the establishment of a Biocomputing Center. Since then research interests focus on different aspects of protein sequence analysis, mainly the development and implementation of predictive algorithms based on methods out of machine learning approaches. The results of these works have been selected several times for presentation at the International Forum of Bioinformatics "Intelligent Systems for Molecular Biology (ismb)". A method (CORNET) developed in the lab for the prediction of contact maps of proteins (a relevant step for the ab initio prediction of protein 3D structure) has been scored the best of its category in the Critical Assessment of Techniques for Protein Structure Prediction (CASP) No 4 and No 5 (Asimolar, California, 2000 and 2002). A

method for predicting the topography of outer membrane proteins based on HMM and sequence profile has been acknowledged with the SGI best award at ismb02 (Edmonton, Canada, August 3-7, 2002). The unit is member of the European bioinformatics Community (ECBB), and is also active in organizing international training courses since 1999 (Bologna Winter Schools) on Bioinformatics (www.biocomp.unibo.it). In 2006 the Group organized BITS, the Annual Conference of the Italian Society of Bioinformatics.

Special recognitions to our work are listed below:

1) SGI Best Paper Award at the International Conference on Intelligent Systems for Molecular Biology 2002, (ISMB2002) Edmonton (Canada) August 3-7, 2002:Martelli PL, Fariselli P, Krogh A, Casadio R –A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins-Bioinformatics 18: S46-S53 (2002)

2) Selection for the Human Mutation Virtual Issue "Evaluating Mutation Patogenicity"; Tavtigian SV and Greenblatt MS, eds; May 2010: Calabrese R, Capriotti E, Fariselli P, Martelli PL, Casadio R –Functional annotations improve the predictive score of human disease-related mutations in proteins- Hum Mutat 30:1237-1244 (2009) (Selected for the Human Mutation Virtual Issue "Evaluating Mutation Patogenicity";Tavtigian SV and Greenblatt MS, eds; May 2010)

3)Evaluated as Recommended by Faculty of 1000, Biology reports: Fariselli P, Finelli M, Marchignoli D, Martelli PL, Rossi I, Casadio R -MaxSubSeq: an algorithm for segment-length optimization. The case study of the transmembrane spanning segments- Bioinformatics 19:500-505 (2003)

4)Evaluated as Recommended by Faculty of 1000, Biology reports:Martelli PL, Fariselli P, Krogh A, Casadio R-A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins-Bioinformatics 18: S46-S53 (2002)

The computational facilities of the group comprises:

i) one cluster for high performance computing consisting of 5 dual Xeon core2 servers, for a total of 28 processors and 15 TB of data storage capacity;

ii) a computing cluster that consists of 2 servers dual Opteron dual core and 6 server dual xeon CPU;

iii) 2 File servers;

iv) 8 Linux workstation.

Funding to RC

Patents:

1) Antonio Facchiano, Francesco Facchiano, Ivan Rossi, Rita Casadio
"Molecole non peptidiche analoghe al peptide RGD con effetto inibitorio sulla adesione, la migrazione e la proliferazione cellulare" Domanda n. RM2001A000089 depositata il 21.02.2001 a ROMA per Brevetto Nazionale (Italy)

2) Antonio Facchiano, Francesco Facchiano, Ivan Rossi, Rita Casadio
"RGD-analog non-peptidic molecules having anti-adhesive, Anti-migration anti-proliferative effects" Domanda n. WO 02/066421A1 depositata il 29.08.2002 a Agente: SARPI Maurizio, Studio Ferrario, Via Collina 36 00187 ROMA ITALIA per Brevetto "Europeo" in ARIPO PATENT, EUASIAN PATENT, EUROPEAN PATENT, OAP PATENT (European Patent) Assegnatari: Istituto Dermopatico dell'Immacolata, Roma

3) Antonio Facchiano, Francesco Facchiano, Ivan Rossi, Rita Casadio
"RGD-analog non-peptidic molecules having anti-adhesive, anti-migration anti-proliferative effects" Domanda n. US20020119932A1 depositata il 29.08.2002 a YOUNG & THOMPSON, 745 South 23rd Stren 2nd Floor, Arlington, VA, 22202 per Brevetto Nazionale (United States of America) in United States of America

Selected Publications (from http://www.biocomp.unibo.it)

1. Martelli PL, Fariselli P, Balzani E, Casadio R -Predicting cancer-associated germline variations in proteins- BMC Genomics Jun 18;13 Suppl 4:S8 (2012)
2. Vaccarelli G, Antonacci R, Tasco G, Yang F, El Ashmaoui HM, Hassanane MS, Massari S, Casadio R, Ciccarese S. Generation of diversity by somatic mutation in the Camelus dromedarius T-cell receptor gamma (TCRG) variable domains - Eur J Immunol (2012, in press)
3. Fontanesi L, Galimberti G, Calò DG, Fronza R, Martelli PL, Scotti E, Colombo M, Schiavo G, Casadio R, Buttazzoni L, Russo V -Identification and association analysis of several hundred single nucleotide polymorphisms within candidate genes for backfat thickness in Italian Large White pigs using a selective genotyping approach- J Anim Sci, Aug;90(8):2450-64 (2012)
4. Casadio R, Vassura M, Tiwari S, Fariselli P, Martelli PL -Correlating disease related mutations to their effect on protein stability: a large scale analysis of the human proteome- Hum Mutat Hum Mutat. 32:1161-70 (2011)
5. Pippucci T, Benelli M, Magi A, Martelli PL, Magini P, Torricelli F, Casadio R, Seri M, Romeo G -EX-HOM (EXome-HOMozygosity): a proof of principle- Hum Hered. 72:45-53 (2011)
6. Savojardo C, Fariselli P, Alhamdoosh M, Martelli PL, Pierleoni A, Casadio R-Improving the prediction of disulfide bonds in Eukaryotes with machine learning methods and protein subcellular localization- Bioinformatics 27:2224-2230 (2011)
7. Piovesan D, Luigi Martelli P, Fariselli P, Zauli A, Rossi I, Casadio R -BAR-PLUS: the Bologna Annotation Resource Plus for functional and structural annotation of protein sequences- Nucleic Acids Res 39:W197-W202 (2011)
8. Pierleoni A, Indio V, Savojardo C, Fariselli P, Martelli PL, Casadio R -MemPype: a pipeline for the annotation of eukaryotic membrane proteins- Nucleic Acids Res 39:W375-W380 (2011)
9. Pantaleo MA, Astolfi A, Indio V, Moore R, Thiessen N, Heinrich MC, Gnocchi C, Santini D, Catena F, Formica S, Martelli PL, Casadio R, Pession A, Biasco G -SDHA Loss-of-Function Mutations in KIT-PDGFRA Wild-Type Gastrointestinal Stromal Tumors Identified by Massively Parallel Sequencing- J Natl Cancer Inst 103:983-987 (2011)
10. Pierleoni A, Martelli PL, Casadio R .(2011)-MemLoci: predicting subcellular localization of membrane proteins in Eukaryotes- Bioinformatics 27:1224-30.
11. Di Lena P, Fariselli P, Margara L, Vassura M, Casadio R -Is there an optimal substitution matrix for contact prediction with correlated mutations?- IEEE/ACM Trans Comput Biol Bioinform 8: 1017-28 (2011)
12. Vassura M, Di Lena P, Margara L, Mirto M, Aloisio G, Fariselli P, Casadio R -Blurring contact maps of thousands proteins: what we can learn by reconstructing 3D structure- BioData Min 4:1 (2011)
13. Martelli PL, D'Antonio M, Bonizzoni P, Castrignanò T, D'Erchia AM, D'Onorio De Meo P, Fariselli P, Finelli M, Licciulli F, Mangiulli M, Mignone F, Pavesi G, Picardi E, Rizzi R, Rossi I, Valletti A, Zauli A, Zambelli F, Casadio R, Pesole G - ASPicDB: a database of annotated transcript and protein variants generated by alternative splicing- Nucleic Acids Res 39:D80-D85 (2011)
14. Iacopetta D, Madeo M, Tasco G, Carrisi C, Curcio R, Martello E, Casadio R, Capobianco L, Dolce V -A novel subfamily of mitochondrial dicarboxylate carrier from Drosophila melanogaster: Biochemical and computational studies- Biochim Biophys Acta (Bioenergetics) 1807:251-261 (2011)
15. Fontanesi L, Beretti F, Martelli PL, Colombo M, Dall'Olio S, Occidente M, Portolano B, Casadio R, Matassino D, Russo V -A first comparative map of copy number variations in the sheep genome- Genomics 97:158-165 (2011)
16. Bartoli L, Martelli PL, Rossi I, Fariselli P, Casadio R -The prediction of protein-protein interacting sites in genome-wide protein interaction networks: The Test Case of the Human Cell Cycle- Curr Protein Pept Sci 11:601-608 (2010)
17. Fontanesi L, Martelli PL, Beretti F, Riggio V, Dall'Olio S, Colombo M, Casadio R, Russo V, Portolano B -An initial comparative map of copy number variations in the goat (Capra hircus) genome- BMC Genomics 11:639 (2010).
18. Di Lena P, Fariselli P, Margara L, Vassura M, Casadio R -Fast overlapping of protein contact maps by alignment of eigenvectors- Bioinformatics 26:2250-2258 (2010)
19. Bergamini CM, Dondi A, Lanzara V, Squerzanti M, Cervellati C, Montin K, Mischiati C, Tasco G, Collighan R, Griffin M, Casadio R -Thermodynamics of binding of regulatory ligands to tissue transglutaminase- Amino Acids 39:297-304 (2010)
20. Ricci G, Dondi A, Belotti T, Baldi E, Tartarini S, Paris R, Pagliarani G, Serafini-Fracassini D, Casadio R, Giannetti A, Masi M -Allergenicity of different apple cultivars assessed by means of skin prick test and sensitisation to recombinant allergens Mal d 1 and Mal d 3 in a group of Italian apple-allergic patients. Int J Food Sci Tech 45:1517-1523 (2010)
21. Bartoli L, Martelli PL, Rossi I, Fariselli P, Casadio R -Prediction of protein-protein interacting sites: how to bridge molecular events to large scale protein interaction networks- Lect Notes Comp Sci 5688:1-17 (2009)
22. Fariselli P, Savojardo C, Martelli PL, Casadio R -Grammatical-Restrained Hidden Conditional Random Fields for Bioinformatics applications- Algorithms Mol Biol 22:4-13 (2009)
23. Bartoli L, Fariselli P, Krogh A, Casadio R (2009) -CCHMM_PROF: a HMM-based coiled-coil predictor with evolutionary information- Bioinformatics 25:2757-2763 (2009)
24. Bartoli L, Montanucci L, Fronza R, Martelli PL, Fariselli P, Carota L, Donvito G, Maggi G, Casadio R -The Bologna Annotation Resource: a non-hierarchical method for the functional and structural annotation of protein sequences relying on a comparative large-scale genome analysis- J Proteome Res 8:4362-4371 (2009)
25. Calabrese R, Capriotti E, Fariselli P, Martelli PL, Casadio R -Functional annotations improve the predictive score of human disease-related mutations in proteins- Hum Mutat 30:1237-1244 (2009)
26. Di Lena P, Vassura M, Margara L, Fariselli P, Casadio R -On the reconstruction of three-dimensional protein structures from contact maps- Algorithms 2:76-92 (2009)
27. Ezkurdia I, Bartoli L, Fariselli P, Casadio R, Valencia A, Tress ML -Progress and challenges in predicting protein-protein interaction sites- Brief Bioinform 10:233-246 (2009)
28. Juncker AS, Jensen LJ, Pierleoni A, Bernsel A, Tress ML, Bork P, von Heijne G, Valencia A, Ouzounis CA, Casadio R, Brunak S -Sequence-based feature prediction and annotation of proteins- Genome Biol 10:206 (2009)
29. Vassura M, Margara L, Fariselli P, Casadio R -A graph theoretic approach to protein structure selection- Artif Intell Med 45:229-237 (2009)

30. Serafini-Fracassini D, Della Mea M, Tasco G, Casadio R, Del Duca S -Plant and animal transglutaminases: do similar functions imply similar structures?- Amino Acids 36:643-657 (2009)

31. Pierleoni A, Martelli PL, Casadio R -PredGPI: a GPI anchor predictor- BMC Bioinformatics 9:392 (2008)

32. Carota L, Bartoli L, Fariselli P, Martelli PL, Montanucci L, Maggi G, Casadio R - High Throughput Comparison of Prokaryotic Genomes- Lect Notes Comp Sci 4967:1200-1209 (2008)

33. Vassura M, Margara L, Di Lena P, Medri F, Fariselli P, Casadio R -Reconstruction of 3D structures from protein contact maps- IEEE/ACM Trans Comput Biol Bioinform 5:357-367 (2008)

34. Montanucci L, Fariselli P, Martelli PL, Casadio R -Predicting protein thermostability changes from sequence upon multiple mutations- Bioinformatics 24:i190-i195 (2008)

35. Mirto M, Ferramosca A, Tartarini D, Romano S, Negro A, Tasco G, Fiore S, Zara V, Casadio R, Aloisio G -A protein structure prediction service in the ProGenGrid system- Stud Health Technol Inform 138:135-146 (2008)

36. Capriotti E, Fariselli P, Rossi I, Casadio R -A three-state prediction of single point mutations on protein stability changes- BMC Bioinformatics 9 Suppl 2:S6 (2008)

37. Vassura M, Margara L, Di Lena P, Medri F, Fariselli P, Casadio R -FT-COMAR: fault tolerant three-dimensional structure reconstruction from protein contact maps- Bioinformatics 24:1313-1315 (2008)

38. Montanucci L, Fariselli P, Martelli PL, Rossi I, Casadio R -In Silico Evidence of the Relationship Between miRNAs and siRNAs- Open Appl Inf Journal 2:9-13 (2008)

39. Casadio R, Martelli PL, Pierleoni A -The prediction of protein subcellular localization from sequence: a shortcut to functional genome annotation- Brief Funct Genomic Proteomic 7:63-73 (2008)

40. Sommaruga S, De Palma A, Mauri PL, Trisciani M, Basilico F, Martelli PL, Casadio R, Tortora P, Occhipinti E -A combined approach of mass spectrometry, molecular modeling, and site-directed mutagenesis highlights key structural features responsible for the thermostability of Sulfolobus solfataricus carboxypeptidase- Proteins 71:1843-1852 (2008)

41. Bartoli L, Fariselli P, Casadio R -The effect of backbone on the small-world properties of protein contact maps- Phys Biol 4:L1-L5 (2008)

42. Capriotti E, Arbiza L, Casadio R, Dopazo J, Dopazo H, Marti-Renom MA -Use of estimated evolutionary strength at the codon level improves the prediction of disease-related protein mutations in humans- Hum Mutat 29:198-204 (2008)

43. Bartoli L, Capriotti E, Fariselli P, Martelli PL, Casadio R -The pros and cons of predicting protein contact maps. Methods Mol Biol. 413:199-217 (2008)

44. Vassura M, Margara L, Medri F, Di Lena P, Fariselli P, Casadio R -Reconstruction of 3D structures form protein contact maps- Lect Notes Comp Sci 4463:578-589 (2007)

45. Vassura M, Margara L, Fariselli P, Casadio R -A graph theoretic approach to protein structure selection- Lect Notes Comp Sci 4578:497-504 (2007)

46. Vassura M, Margara L, Di Lena P, Medri F, Fariselli P, Casadio R -Fault tolerance for large scale protein 3D reconstruction from contact maps- Lect Notes Comp Sci 4645:25-37 (2007)

47. Mirto M, Rossi I, Epicoco I, Fiore S, Fariselli P,Casadio R, Aloisio G -High throughput protein similarity searches in the LIBI Grid problem solving environment- Lect Notes Comp Sci 4743:414-423 (2007)

48. Fariselli P, Molinini D, Casadio R, Krogh A - Prediction of Structurally-Determined Coiled-Coil Domains with Hidden Markov Models- Lect Notes Comp Sci 4414:292-302 (2007)

49. Fermani S, Sparla F, Falini G, Martelli PL, Casadio R, Pupillo P, Ripamonti A, Trost P -The molecular mechanism of thioredoxin regulation in photosynthetic A2B2-glyceraldehyde-3-phosphate dehydrogenase- Proc Natl Acad Sci USA 104:11109-11114 (2007)

50. Casadio R, Fariselli P, Martelli PL, Tasco G -Thinking the impossible: how to solve the protein folding problem with and without homologous structures and more- Methods Mol Biol 350:305-320 (2007)

51. Montanucci L, Martelli PL, Fariselli P, Casadio R -Robust determinants of thermostability highlighted by a codon frequency index capable of discriminating thermophilic from mesophilic genomes- J Proteome Res 6:2502-2508(2007)

52. Tress ML, Martelli PL, Frankish A, Reeves GA, Wesselink JJ, Yeats C, Olason PL, Albrecht M, Hegyi H, Giorgetti A, Raimondo D, Lagarde J, Laskowski RA, Lopez G, Sadowski MI, Watson JD, Fariselli P, Rossi I, Nagy A, Kai W, Storling Z, Orsini M, Assenov Y, Blankenburg H, Huthmacher C, Ramirez F, Schlicker A, Denoeud F, Jones P, Kerrien S, Orchard S, Antonarakis SE, Reymond A, Birney E, Brunak S, Casadio R, Guigo R, Harrow J, Hermjakob H, Jones DT, Lengauer T, Orengo CA, Patthy L, Thornton JM, Tramontano A, Valencia A -The implications of alternative splicing in the ENCODE protein complement- Proc Natl Acad Sci USA 104:5495-54500 (2007)

53. Pierleoni A, Martelli PL, Fariselli P, Casadio R -BaCelLo: a Balanced subCellular Localization predictor- Nature Protocols DOI:10.1038/nprot.2007.165 (2007)

54. Fariselli P, Rossi I, Capriotti E, Casadio R -The WWWH of remote homolog detection: The state of the art- Brief Bioinform 8:78-87 (2007)

55. Tassoni A, Franceschetti M, Tasco G, Casadio R, Bagni N -Cloning, functional identification and structural modelling of Vitis vinifera S-adenosylmethionine decarboxylase- J Plant Physiol 164:1208-1219 (2007)

56. Bartoli L, Calabrese R, Fariselli P, Mita D, Casadio R -A computational approach for detecting peptidases and their specific inhibitors at the genome level- BMC Bioinformatics 8:S3 (2007)

57. Capriotti E, Casadio R -K-Fold: a tool for the prediction of the protein folding kinetic order and rate- Bioinformatics 23:385-386 (2007)

58. Pierleoni A, Martelli PL, Fariselli P, Casadio R -eSLDB: eukaryotic subcellular localization database- Nucleic Acids Res 35:D208-12 (2007)

59. Grandi F, Sandal M, Guarguaglini G, Capriotti E, Casadio R, Samori' B -Hierarchical mechanochemical switches in angiostatin- Chembiochem 7:1774-82 (2006)

60. Capriotti E, Calabrese R, Casadio R -Predicting the insurgence of human genetic diseases associated to single point protein mutations with support vector machines and evolutionary information- Bioinformatics 22:2729-34 (2006)

61. Pierleoni A, Martelli PL, Fariselli P, Casadio R -BaCelLo: a balanced subcellular localization predictor- Bioinformatics 22:e408-416 (2006)
62. Amico M, Finelli M, Rossi I, Zauli A, Elofsson A, Viklund H, von Heijne G, Jones D, Krogh A, Fariselli P, Martelli PL, Casadio R -PONGO: a web server for multiple predictions of all-alpha transmembrane proteins- Nucleic Acids Res 34(Web server issue):169-172 (2006)
63. Occhipinti E, Bec N, Gambirasio B, Baietta G, Martelli PL, Casadio R, Balny C, Lange R, Tortora P -Pressure and temperature as tools for investigating the role of individual non-covalent interactions in enzymatic reactions Sulfolobus solfataricus carboxypeptidase as a model enzyme- Biochim Biophys Acta (Proteins and Proteomics) 1764:563-572 (2006)
64. Marani P, Wagner S, Baars L, Genevaux P, de Gier JW, Nilsson I, Casadio R, von Heijne G -New Escherichia coli outer membrane proteins identified through prediction and experimental verification- Protein Sci 15:884-889 (2006)
65. Milanesi L, Petrillo M, Sepe L, Boccia A, D'Agostino N, Passamano M, Di Nardo S, Tasco G, Casadio R, Paolella G - Systematic analysis of human kinase genes: a large number of genes and alternative splicing events result in functional and structural diversity- BMC Bioinformatics 6 (Suppl 4): S20 (2005)
66. Fariselli P, Martelli PL, Casadio R -A new decoding algorithm for hidden Markov models improves the prediction of the topology of all-beta membrane proteins- BMCBioinformatics 6 (Suppl 4): S12(2005)
67. Scotto d'Abusco A, Casadio R, Tasco G, Giangiacomo L, Giartosio A, Calamia V, Di Marco S, Chiaraluce R, Consalvi V, Scandurra R, Politi L -Oligomerization of Sulfolobus solfataricus signatured amidase is promoted by acidic pH and temperature- Archaea 1:411-423 (2005)
68. Becker L, Bannwarth M, Meisinger C, Hill K, Model K, Krimmer T, Casadio R, Truscott KN, Schulz GE, Pfanner N, Wagner R -Preprotein Translocase of the Outer Mitochondrial Membrane: Reconstituted Tom40 Forms a Characteristic TOM Pore- J Mol Biol 345:1011-1020 (2005)
69. Capriotti E, Fariselli P, Calabrese R, Casadio R -Predicting protein stability changes from sequence with Support Vector Machines- Bioinformatics 21:ii54-ii58 (2005)
70. Morozzo della Rocca B, Miniero DV, Tasco T, Dolce V, Falconi M, Ludovico A, Cappello AR, Sanchez P, Stipani I, Casadio R, Desideri A, Palmieri F -Substrate-induced conformational changes of the mitochondrial oxoglutarate carrier: a spectroscopic and molecular modelling study- Mol Membr Biol 22:443452 (2005)
71. Fariselli P, Finelli M, Rossi I, Amico M, Zauli A, Martelli PL, Casadio R -TRAMPLE: the transmembrane protein labelling environment- Nucl Acids Res 33:W198-W201 (2005)
72. Capriotti E, Fariselli P, Casadio R -I-Mutant2.0: predicting stability changes upon mutation from the protein sequence or structure- Nucl Acids Res 33:W303-W305 (2005)
73. Calonghi N, Cappadone C, Pagnotta E, Boga C, Bertucci C, Fiori J, Tasco G, Casadio R, Masotti L -Histone deacetylase 1: a target of 9-hydroxystearic acid in the inhibition of cell growth in human colon cancer- J Lipid Res 46:1569-1603 (2005)
74. Gianni T, Martelli PL, Casadio R, Campadelli-Fiume G -The Ectodomain of Herpes Simplex Virus Glycoprotein H Contains a Membrane {alpha}-Helix with Attributes of an Internal Fusion Peptide, Positionally Conserved in the Herpesviridae Family J Virol 79:2931-2940 (2005)
75. Aguzzi MS, Facchiano F, Ribatti D, Gaeta R, Casadio R, Rossi I, Capogrossi MC, Facchiano A -A novel RGDS-analog inhibits angiogenesis in vitro and in vivo- Biochem Biophys Res Commun 321:809-814 (2004)
76. Compiani M, Capriotti E, Casadio R -Dynamics of the minimally frustrated helices determine the hierarchical folding of small helical proteins- Phys Rev E 69:051905.1-051905.8 (2004)
77. Capriotti E, Fariselli P, Casadio R -A neural-network-based method for predicting protein stability changes upon single point mutations- Bioinformatics 20:I63-I68 (2004)
78. Grano V, Tasco G, Casadio R, Diano N, Portaccio M, Rossi S, Bencivenga U, Compiani M, De Maio A, Mita DG - Reduction of active elastase concentration by means of immobilized inhibitors: a novel therapeutic approach- Biotechnol Prog 20:968-974 (2004)
79. Durante D, Casadio R, Martelli PL, Tasco G, Portaccio M, De Luca P, Bencivenga U, Rossi S, Di Martino S, Grano V, Diano N, Mita DG -Isothermal and non-isothermal bioreactors in the detoxification of waste waters polluted by aromatic compounds by means of immobilised laccase from Rhus vernicifera- J Mol Catal B: Enzym 27:191-206 (2004)
80. Aiello R, Messina A, Schiffler B, Benz R, Tasco G, Casadio R, De Pinto V -Functional characterization of a second porin isoform in drosophila melanogster: DmPorin2 forms voltage-independent cation selective pores- J Biol Chem 279:25364-25373 (2004)
81. Martelli PL, Fariselli P, Casadio R -Prediction of disulfide-bonded cysteines in proteomes with a hidden neural network- Proteomics 4:1665-1671 (2004)
82. Berezin C, Glaser F, Rosenberg J, Paz I, Pupko T, Fariselli P, Casadio R, Ben-Tal N -ConSeq: the identification of functionally and structurally important residues in protein sequences- Bioinformatics 20:1322-1324 (2004)
83. Capriotti E, Fariselli P, Rossi I, Casadio R -A Shannon entropy-based filter detects high-quality profile-profile alignments in searches for remote homologues- Proteins 54:351-360 (2004)
84. Casadio R, Fariselli P, Martelli PL -In silico prediction of the structure of membrane proteins: Is it feasible?- Briefings Bioinf 4:341-348 (2003)
85. Fariselli P, Finocchiaro G, Casadio R -SPEPlip: the detection of signal peptide and lipoprotein cleavage sites- Bioinformatics 19:2498-2499 (2003)
86. Fariselli P, Finocchiaro G, Casadio R -Prediction of Signal Peptide in Proteins with Neural Networks- Lect Notes Comp Sci 2859:237-244 (2003)
87. Martelli PL, Fariselli P, Tasco G, Casadio R -The prediction of membrane protein structure and genome structural annotation- Compar Funct Genom 4:406- 409 (2003)
88. Casadio R -The 4th Bologna Winter School: hot topics in structural genomics (Conference Report)- Compar Funct Genom 4:394-396 (2003)

89. Occhipinti E, Martelli PL, Spinozzi F, Corsi F, Formantici C, Molteni L, Amenitsch H, Mariani P, Tortora P, Casadio R - 3D structure of Sulfolobus solfataricus carboxypeptidase developed by molecular modeling is confirmed by site-directed mutagenesis and small angle X-ray scattering- Biophys J 85:1165-1175 (2003)

90. Martelli PL, Fariselli P, Casadio R -An ENSEMBLE machine learning approach for the prediction of all-alpha membrane proteins- Bioinformatics 19:I205-I211 (2003)

91. Casadio R, Fariselli P, Finocchiaro G, Martelli PL -Fishing new proteins in the twilight zone of genomes: The test case of outer membrane proteins in Escherichia coli K12, Escherichia coli O157:H7, and other Gram-negative bacteria- Protein Sci 11:1158-1168 (2003)

92. De Pinto V, Messina A, Accardi R, Aiello R, Guarino F, Tomasello MF, Tommasino M, Tasco G, Casadio R, Benz R, De Giorni F, Ichas F, Baker M, Lawen A -New functions of an old protein: the eukaryotic porin or voltage dependent anion selective channel (VDAC). Minireview- Ital J Biochem 52:17-24 (2003)

93. Fariselli P, Finelli M, Marchignoli D, Martelli PL, Rossi I, and Casadio R -MaxSubSeq: an algorithm for segment-length optimization. The case study of the transmembrane spanning segments- Bioinformatics 19:500-505 (2003)

94. Juan D, Grana O, Pazos F, Fariselli P, Casadio R, Valencia A. -A neural network approach to evaluate fold recognition results- Proteins 50:600-608 (2003)

95. Martelli PL, Fariselli P, Malaguti L, Casadio R. -Prediction of the disulfide-bonding state of cysteines in proteins at 88% accuracy- Protein Sci 11 :2737-2739

96. Martelli PL, Fariselli P, Malaguti L, Casadio R. -Prediction of the disulfide bonding state of cysteines in proteins with hidden neural networks- Protein Eng. 15:951-953 (2002)

97. Scagliarini A, Ciulli S, Battilani M, Jacoboni I, Montesi F, Casadio R, Prosperi S -Characterisation of immunodominant protein encoded by the F1L gene of orf virus strains isolated in Italy Brief Report- Arch Virol 147: 1989-1995 (2002)

98. Griffin M, Casadio R, Bergamini C -Transglutaminases, nature's biological glues- Biocheml J 368:377-396 (2002)

99. Martelli PL, Fariselli P, Krogh A, Casadio R -A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins- Bioinformatics 18: S46-S53 (2002)

100. Fariselli P, Martelli P, Casadio R -A neural network based method for predicting the disulfide connectivity in proteins- Knowledge based intelligent information engineering systems and allied technologies (KES 2002), (Damiani E et al., eds), Vol 1, pp 464-468, IOS Press, Amsterdam (2002)

101. Casadio R, Jacoboni I, Messina A, De Pinto V -A 3D model of the voltage-dependent anion channel (VDAC)- FEBS Lett 520:1-7 (2002)

102. Casadio R, Compiani M, Facchiano A, Fariselli P, Martelli PL, Jacoboni I, Rossi I -Protein structure prediction and biomolecular recognition: from protein sequence to peptidomimetic design with the human beta 3 integrin- SAR QSAR Envir Res 13:473-486 (2002)

103. Menotti L, Casadio R, Bertucci C, Lopez M, Campadelli-Fiume G -Substitution in the murine nectin1 receptor of a single conserved amino acid at a position distal from the Herpes Simplex virus gD binding site confers high-affinity binding to gD- J Virol 76:5463-5471 (2002)

104. Bismuto E, Martelli PL, De Maio A, Mita DG, Irace G, Casadio R - Effect of molecular confinement on internal enzyme dynamics: Frequency domain fluorometry and molecular dynamics simulation studies- Biopolymers (Biospectroscopy) 67:85-95 (2002)

105. Pollastri G, Baldi P, Fariselli P, Casadio R -Prediction of coordination number and relative solvent accessibility in proteins- Proteins 47:142-53 (2002)

106. Casadio R, Martelli PL, Giordano A, Rossi M, Raia CA -A low-resolution 3D model of the tetrameric alcohol dehydrogenase from Sulfolobus solfataricus- Protein eng 15:215-223 (2002)

107. Fariselli P, Pazos F, Valencia A, Casadio R -Prediction of protein--protein interaction sites in heterocomplexes with neural networks- Eur J Biochem 269: 1356-1361 (2002)

108. El Masry MM, De Maio A, Martelli PL, Casadio R, Moustafa AB, Rossi S, Mita DG -Influence of the immobilization process on the activity of beta galactosidase bound to nylon membranes grafted with glycidyl methacrylate. Part 1. Isothermal behavior- J Mol Catal B:Enzym 16: 175-189 (2001)

109. Fariselli P, Olmea O, Valencia A, Casadio R -Progress in predicting inter-residue contacts of proteins with neural networks and correlated mutations- Proteins, Suppl 5: 157-162 (2001)

110. Fariselli P, Olmea O, Valencia A, Casadio R -Prediction of contact maps with neural networks and correlated mutations- Protein eng 14: 835-843 (2001)

111. Fariselli P, Casadio R -Prediction of disulfide connectivity in proteins- Bioinformatics 17: 957-964 (2001)

112. Pollastri G, Baldi P, Fariselli P, Casadio R -Improved prediction of the number of residue contacts in proteins by recurrent neural network- Bioinformatics 17, Suppl 1:234-242 (2001)

113. Casadio R, Frigimelica E, Bossu' P, Neumann D, Martin MU, Tagliabue A, Boraschi D. Model of interaction of the IL-1 receptor acessory protein Il-1RAcP with the IL-1B/IL-1RI complex. FEBS Letters 499: 65-68 (2001)

114. Battilani M, Scagliarini A, Tisato E, Turilli C, Jacoboni I, Casadio R, Prosperi S. Analysis of canine parvovirus sequences from wolves and dog isolated in Italy. J Gen Virol 82: 1555-1560 (2001)

115. Musiani F, Arnofi E, Casadio R, Ciurli S. -Structure based computational study of the catalytic and inhibition mechanisms of urease.J Biol Inorg Chem 6: 300-314 (2001)

116. El-Sherif H, Martelli PL, Casadio R, Portaccio M, Bencivenga U, Mita DG -Urease immobilization on chemically grafted nylon membranes. Part 1: Isothermal characterization- J Mol Catal B: Enzym 14: 15-29 (2001)

117. Fariselli P, Casadio R -RCNPRED: a server for the prediction of the residue co-ordination numbers in proteins- Bioinformatics 17: 202-203 (2001)

118. Jacoboni I, Martelli PL, Fariselli P, De Pinto V, Casadio R - Prediction of the transmembrane regions of beta barrel membrane proteins with a neural network based predictor- Protein Science 10: 779-787 (2001)

119. Casadio R., Compiani M., Fariselli P., Jacoboni I. and Martelli P.L. -Neural Networks predict protein folding and structure: artificial intelligence faces biomolecular complexity- SAR and QSAR in env res 11: 149-182 (2000)

7

120. Jacoboni I, Martelli PL, Fariselli P, Compiani M, Casadio R - Predictions of protein segments with the same amino acid sequence and different secondary structure: a benchmark for predictive methods- Proteins 41: 535-544 (2000)

121. Bismuto E, Martelli PL, Casadio R, Irace G - Tryptophanil fluorescence lifetime distribution of hypertermophilic b-glycosidase from molecular dynamics simulation: a comparison with the experimental data- Protein Sci 9: 1730-1742 (2000)

122. Sirangelo I, Tavassi S, Martelli PL, Casadio R, Irace - The effect of tryptophanyl substitution on folding and structure of myoglobin- Eur J Biochem 267: 3937-3945 (2000)

123. Fariselli P, Casadio R -Prediction of the number of residue contacts in proteins.Proc Int Conf Intell Syst Mol Biol.8:146-151 (2000)

124. Mariani P, Carsughi F, Spinozzi F, Romanzetti S, Meier G, Casadio R, Bergamini CM - Ligand-induced conformational changes in tissue transglutaminase: Monte Carlo analysis of small-angle scattering data - Biophys J 78: 3240-3251 (2000)

125. Casadio R, Polverini E, Mariani P, Spinozzi F, Flavio C, Fontana A, Polverino de Laureto P, Matteucci G, Bergamini CM - The structural basis for the regulation of tissue transglutaminase by calcium ions- Eur J Biochem 262: 672-679 (1999)

126. Casadio R, Compiani M, Fariselli P, Martelli PL -A data base of minimally frustrated alpha helical segments extracted from proteins according to an entropy criterion. Proc Int Conf Intell Syst Mol Biol. 68-76 (1999)

127. Fariselli P, Riccobelli P, Casadio R - The role of evolutionary information in predicting the disulfide bonding state of cysteines in proteins- Proteins 36: 340-346 (1999)

128. Fariselli P, Bottoni A, Bernardi F, Casadio R - Quantum mechanical analysis of oxygenated and deoxygenated states of hemocyanin: theoretical clues for a plausible allosteric model of oxygen bindig- Protein Sci 8: 1546-1550 (1999)

129. Fariselli P, Casadio R - Neural network based predictor of residue contacts in proteins - Prot Eng 12: 15-21 (1999)

130. Compiani M, Fariselli P, Martelli PL, Casadio R -Neural Networks to Study Invariant Features of Protein Folding- Theor Chem Acc 101: 21-26 (1999)

131. Arrigo P, Fariselli P, Casadio R - Can functional regions of proteins be predicted from their coding sequences? The case study of G-protein coupled receptors - Gene 221: 65-110 (1998)

132. Compiani M, Fariselli P, Martelli P and Casadio R - An entropy criterion to detect minimally frustrated intermediates in native proteins - Proc Natl Acad Sci USA 95: 9290-9294 (1998).

133. Di Bernardo S, Fato R, Casadio R, Fariselli P, Lenaz G - A high diffusion coefficient for coenzyme Q10 might be related to a folded structure- FEBS Lett 426: 77-80 (1998)

134. Polverini E, Casadio R, Neyroz P, Masotti L - Conformational changes of Neuromedin B and Delta sleep inducing peptide induced by their interaction with lipid membranes as revealed by spectroscopic techniques and molecular dynamics simulation- Arch Biochem Biophys 349: 225-235 (1998)

135. Vivarelli F, Fariselli P, Casadio R (1997) - The prediction of protein secondary structure with a cascade correlation learning architecture of neural networks- Neural Comp Appl 6: 57-62 (1997)

136. Arrigo P, Fariselli P, Casadio R. Self-organizing neural maps of the coding sequences of G-protein-coupled receptors reveal local domains associated with potentially functional determinants in the proteins. Proc Int Conf Intell Syst Mol Biol. 5:44-47 (1997)

137. Mariani P, Casadio R, Carsughi F, Ceretti M, Rustichelli F - Structural analysis of membranes from photosynthetic bacteria by SANS- Europhys Lett 37: 433-438 (1997)

138. Compiani M, Fariselli P, and Casadio R - Noise and randomlike behaviour of perceptrons: theory and applications to protein structure prediction- Phys Rev E 55: 7334-7343 (1997)

139. Rost B, Fariselli P, and Casadio R - Topology prediction for helical transmembrane proteins at 86% accuracy- Protein Sci 5: 1704-1718 (1996)

140. Rost B, Casadio R, Fariselli P- Refining neural network predictions for helical transmembrane proteins by dynamic programming. Proc Int Conf Intell Syst Mol Biol. 4:192-200 (1996)

141. Zanotti F, Casadio R, Perrucci C and Guerrieri F -DCCD sensitive proton permeability of bacterial photosynthetic membranes. Cross-reconstitution studies with purified bovine heart Fo subunits- Biochim Biophys Acta (Bioenergetics) 1276: 80-86 (1996)

142. Casadio R and Melandri BA -CaATP inhibits the MgATP-dependent proton pump (H-ATPase) in bacterial photosynthetic membranes with a mechanism of alternative substrate inhibition- J Biol Inorg Chem 1: 284-291 (1996)

143. Bernardi F, Bottoni A, Casadio R, Fariselli P and Rigo A - An ab-initio study of the mechanism of the binding process of triplet O2 to hemocyanin – Inorg Chem 35: 5207-5212 (1996)

144. Casadio R, Fariselli P, Taroni C and Compiani M - A predictor of a-helix trasmembrane domains of proteins based on neural networks- Eur Biophys J 24: 165-178 (1996).

145. Fariselli P and Casadio R -HTP: a neural network based method for predicting the topology of helical trasmembrane domains in proteins - Comput Applic Biosci 12: 41-48 (1996).

146. Bernardi F, Bottoni A, Casadio R, Fariselli P and Rigo A - An ab-initio study of dioxygen binding site of hemocyanin: a comparison between a CASSCF and DFT approach - Int J Quantum Chem 56: 109-116 (1996).

147. Polverini E, Neyroz P, Fariselli P, Casadio R and Masotti L -The effect of membranes on the conformation of neuromedin C- Biochim Biophys Res Commun 214: 663-668 (1995).

148. Casadio R, Di Bernardo S, Fariselli P, Melandri BA - Characterization of 9-aminoacridine interaction with chromatophore membranes and modelling of the probe response to artificially induced transmembrane DpH's- Biochim Biophys Acta (Biomembranes) 1237: 23-30 (1995)

149. Vivarelli F, Giusti G, Villani M, Campanini R, Fariselli P, Compiani M, Casadio R - LGANN: a parallel system combining a local genetic algorithm and neural networks for the prediction of secondary structure of proteins- Comp Appli Biosci 11: 253-260 (1995)

150. Rost B, Casadio R, Fariselli P, Sander C - Transmembrane helices predicted at 95% accuracy- Protein Sci 4: 521-533 (1995)

151. Casadio R, Compiani M, Fariselli P, Vivarelli F -Predicting free energy contributions to the conformational stability of folded proteins from the residue sequence with radial basis function networks.Proc Int Conf Intell Syst Mol Biol.3:81-88 (1995)

152. Fariselli P, Di Bernardo S and Casadio R - A mathematical model relating diffusion of hydrophobic ions to their adsorption on biological membranes as detected with a microdialyzer- J Biol Phys 19: 211-222 (1994)

153. Fregni V and Casadio R - Kinetic characterization of an ATP-dependent proton pump in bacterial photosynthetic membranes: a study with the fluorescent probe 9-amino-6-chloro-2-methoxyacridine- Biochim Biophys Acta (Bioenergetics) 1143: 215-222 (1993)

154. Fariselli P, Compiani M and Casadio R - Predicting secondary structures of membrane proteins with neural networks- Eur Biophys J 22: 41-51 (1993)

155. Casadio R – Measurements of transmembrane pH differences of low extents in bacterial chromatophores: a study with the fluorescent probe 9-amino, 6-chloro, 2-methoxy acridine- Eur Biophys J 19: 189-201 (1991)

156. Casadio R, Venturoli G and Melandri BA - Evaluation of the electrical capacitance in biological membranes at different phospholipid to protein ratios. A study based on electrochromic effects- Eur Biophys J 16: 243-253 (1988)

157. Casadio R -The oligomycin-sensitive Ca-ATPase of chromatophores from photosynthetic bacteria is not coupled to delta muH+ generation- Prog Clin Biol Res. 273:201-206 (1988)

158. Seren S, Casadio R and Sorgato K - Fusion of bacteriorhodopsin with submitochondrial particles yields a new system with retention of energy coupling and acquisition of photophosphorylation- Biochim Biophys Acta (Bioenergetics) 810: 370-376 (1985)

159. Casadio R and Wagner R - Rotational mobility and domain flexibility of bacterial coupling factors as detected with the triplet probe eosin isothiocyanate- Biochim Biophys Acta (Bioenergetics) 809: 215-222 (1985)

160. Casadio R and Melandri BA - Calibration of the response of 9-aminoacridine fluorescence to transmembrane pH differences in bacterial chromatophores- Arch Biochem Biophys 238: 219-228 (1985)

161. Casadio R, Venturoli G, Di Gioia A, Castellani P, Leonardi L and Melandri BA - Phospholipid enriched bacterial chromatophores: a system suited to investigate the ubiquinone mediated interactions of protein complexes in photosynthetic oxidoreduction processes- J Biol Chem 259: 9145-9157 (1984)

162. Casadio R and Wagner R - Rotational diffusion and domain flexibility of bacterial coupling factors as detected with the triplet probe eosin- Ital J Biochem 31: 361-369 (1982)

163. Baccarini Melandri A, Casadio R and Melandri BA - Electron transport, proton translocation and ATP synthesis in bacterial chromatophores- Curr Top Bioenerg 12: 197-258 (1981)

164. Casadio R, Venturoli G and Melandri BA - Light induced transmembrane potential difference in chromatophores of photosynthetic bacteria: measurements with a ion-selective minielectrode- Photobiochem Photobiophysics 2: 243-253 (1981)

165. Casadio R and Stoeckenius W - The effect of protein-protein interaction on light-dark adaptation of bacteriorhodopsin- Biochemistry 19: 3374-3381 (1980)

166. Casadio R, Gutowitz H, Mowery P, Taylor M and Stoeckenuis W - Light-dark adaptation in Triton-solubilized purple membranes- Biochim Biophys Acta (Bioenergetics) 590: 13-23 (1980)

167. Casadio R, Melandri BA, Piretti MV and Serazanetti GP - Phospholipid composition of photosynthetic membranes of Rhodopseudomonas capsulata- Ital J Biochem 28: 183-193 (1979)

168. Casadio R, Baccarini Melandri A and Melandri BA - Limited cooperativity in the coupling between electron flow and ATP synthesis: a comparative study in chromatophores phosphorylating at very different rates- FEBS Lett 87: 323-328 (1978)

169. Baccarini Melandri A, Casadio R and Melandri BA - Thermodynamics and kinetics of photophosphorylation in bacterial chromatophores and their relation with the transmembrane electrochemical potential difference of protons- Eur J Biochem 78: 389-402 (1977)

170. Melandri BA, Casadio R and Baccarini Melandri A - Bacterial photosynthetic phosphorylation under conditions of limited electron flow- Biochem Soc Trans 5: 495-499 (1977)

171. Casadio R and Melandri BA - The behaviour of 9-aminoacridine as an indicator of transmembrane pH difference in liposomes of natural bacterial phospholipids- J Bioenerg Biomembr 9: 17-29 (1977)

172. Casadio R, Baccarini Melandri A and Melandri BA - Electrochemical proton gradient and phosphate potential in bacterial chromatophores- FEBS Lett 49: 203-207 (1974)

173. Casadio R, Baccarini Melandri A and Melandri BA - On the determination of the transmembrane pH difference in bacterial chromatophores using 9-aminoacridine- Eur J Biochem 47: 121-128 (1974)