CURRICULUM VITAE

M. KOKKINIDIS

General:

Title:	Professor (Structural Biology)
Citizenship:	Greek
Family status:	Married, one child
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Fields of Research

- Protein Crystallography & development of crystallography methods
- Protein Folding: theory and structural studies (emphasis on coiled-coils and helical bundles)
- Protein Engineering & development of bio-inspired materials
- Structural studies of protein-DNA interactions & development of genome customization tools
- Studies of the structural basis of bacterial pathogenic mechanisms (Type III & VI secretion systems)
- Enzymatic mechanisms

Education

Degree	Discipline	University	Year of Award
Diploma (Dipl. Phys.)	Physics	Technical University, Munich, Germany	1977

(*Research topic of diploma thesis*: Study of the diffusion of hydrogen and its isotopes in metals)

PhD (Dr. rer. nat.)	Crystallography	Technical University, Munich, Germany & Max-Planck-Institut f. Biochemie, Martinsried	1981

(*Research topic of PhD Thesis*: Structure-function relationships of cholinergic agents)

Postdoctoral Training

Max-Planck-Institut f. Biochemie, Martinsried, Munich (1984)
EMBL, Heidelberg, Division of Biological Structures (1984-1987)

Academic Appointments

1982-1983 Visiting Professor, Univ. of Crete, Dept. of Physics (post held while on national service)
1987-1992 Assistant Professor, Univ. of Crete, Dept. of Biology
1992-2000 Associate Professor, Univ. of Crete, Dept. of Biology
2000-present Professor, Univ. of Crete, Dept. of Biology

Additional appointment: 1987-present: Senior Research Scientist at IMBB/FORTH, post held parallel to the appointment at the University of Crete.

Awards and fellowships:

1976	Fellowship, Technical University Munich
1977/80	Friedrich-Ebert Foundation (Stiftung) PhD studies Fellowship,
1984	Short term fellowship, Deutscher Akademischer Austauschdienst (DAAD)
1984/86	European Commission, postdoctoral fellowship, BEP program
1986	EMBL price for collaborative project (4-α-helical bundle proteins)
1986/87	Short term postdoctoral fellowship, European Molecular Biology Organization (EMBO)
1987/88	Short term fellowship (3 months), EMBO
1998/99	Short term fellowship (3 months), EMBO

Honours, memberships & selected administrative responsibilities

- Award of a REGPOT grant (coordinator) aiming to support and further develop the innovative capacity of Structural Biology Research at IMBB/FORTH
- National delegate for the FP7 ESFRI (Natural Sciences) Program
- Member of Users Committee, CALIPSO project for Transnational access to EU lightsources
- National delegate in ESUO (European Synchrotron Users Organization)
- Head of the Executive Board, Hellenic Pasteur Institute (2002-2004)
- National coordinator of the XFEL project
- National Focal Point Coordinator, ICGEB, Trieste, Italy
- EU delegate for the International Human Frontier Science Programme (HFSPO)-Post-doctoral programme (till 1996)
- Founding member of the SGI for Biological Macromolecules (European Crystallographic Association)
- Founding member of the Greek Crystallographic Association
- European Science Foundation, Network on the Crystallography of Biological Macromolecules
- Member of the EU-P.R. China Committee on Protein Engineering
- Evaluator of proposals for a) Research grants within the EU FP programmes, b) the SON (Netherlands Foundation for Chemical Research) programme, c) GSRT d) the HFSPO (Strasbourg/France) research programmes & post-doc programme (from 1998), e) MRC (UK) Research grants f) Netherlands ZonMw programmes
- Final evaluator of Greek the programmes STRIDE, ΙΣΤΟΣ
- Evaluator of NCSR "Demokritos" Research Centre, Athens
- Reviewer of manuscripts submitted to Nucl. Acids Res., FEBS J., J. Mol. Biol., J. Biol. Res., Acta Cryst. D, PLoS Pathogens, Protein Engineering Design and Selection, Biochemistry, J. Biol. Inorg. Chem., Protein Science etc; Lead Guest Editor of Journal X-Ray Optics and Instrumentation.

Research Publications

Total Number of Original Articles in Peer-reviewed Journals	107
Total Number of Non-Self Citations	>1600
h-index	22
Publications in Conference Proceedings	>50
Book translations	1
Presentations in Scientific Meetings	>100
Press-Releases Concerning Research	5

Research Funding

M. Kokkinidis has attracted competative funding of more than 6.5 M€ in the framework of approx. 40 national and international grants. He has in particular coordinated 6 international research consortia in connection with EU-funded projects, ICGEB projects etc.

Teaching responsibilities

Undergraduate program

"Protein crystallography" course, Depts. of Biology, Chemistry & Materials Sciences, University of Crete
"Biotechnology" course, Dept. of Biology & Materials Sciences, University of Crete
"Protein Engineering" course, Dept. of Biology, Chemistry & Materials Sciences, University of Crete
Graduate program Parts of four joint courses (**BIO501, BIO503, BIO505, BIO408**) of the Depts. of Biology & Chemistry and one course of the Medical School

Total degrees awarded or in progress:

Master's 15; **PhD** 13

SELECTED SIGNIFICANT PUBLICATIONS in refereed journals

Kokkinidis, M. & Gieren A., Cholinergic Neurotransmitter-Receptor Interactions, **Trends Pharm. Sci.**, 369-70 (1984)

Banner, D.W., Kokkinidis, M. & Tsernoglou, D., The Structure of the ColEl Rop Protein at 1.7 Angstroem resolution, **J. Mol. Biol. 196**, 657-75 (1987)

Castagnoli, L., Scarpa, M., Kokkinidis, M., Banner, D.W., Tsernoglou, D. & Cesareni, G., Genetic and Structural Analysis of the ColEl Rom (Rop) Protein, **EMBO J. 8**, 621-29 (1989)

Paliakasis, C.D. & Kokkinidis, M., Relationships between sequence and structure for the four-α-helix bundle tertiary motif in proteins, **Prot. Engineering 5**, 739-49 (1992)

Steif, Ch., Weber, P., Hinz, H.-J., Flossdorf, J., Cesareni, G. & Kokkinidis, M., Subunit interactions provide a significant contribution to the stability of the dimeric four-α-helical bundle protein ROP, **Biochemistry 32**, 3867-76 (1993)

Athanasiadis, A., Vlassi, M., Kotsifaki, D., Tucker, P., Wilson,K.S. & M. Kokkinidis, The crystal structure of *Pvu*II endonuclease reveals extensive structural homologies to EcoRV, **Nature Str. Biol. 1**, 469-75 (1994) (Comment entitled ***No limits on restriction*** was published in **Nature 370**, 78 (1994))

Vlassi, M., Steif, P. Weber, Tsernoglou, D., Wilson, K.S., H.-J. Hinz & Kokkinidis, M., Restored heptad pattern continuity does not alter the folding of a 4-α-helix bundle, **Nature Str. Biol. 1**, 706-14 (1994)

Gogos, J., Jin Jingmin, Wan, H., Kokkinidis, M. and Kafatos, F.C., Recognition of diverse Sequences by Class I Zinc Fingers: Asymmetries and indirect effects on specificity in the interaction between CF2II and A+T-rich sequence elements, **Proc. Natl. Acad. Sci. USA 93**, 2159-64 (1996)

M.W. Lassalle, H-J. Hinz, H. Wenzel, M. Vlassi, M. Kokkinidis & G. Cesareni, Dimer-to-Tetramer Transformation: Loop Excision Dramatically alters Structure and Stability of the ROP Four α-Helix Bundle Protein, **J. Mol. Biol. 279**, 987-1000 (1998)

M. Vlassi, K.S. Wilson & M. Kokkinidis, Structural Parameters for Proteins Derived from the Atomic-Resolution (1.09 Angstroem) Structure of a Designed Variant of the *ColE1* ROP Protein, **Acta Cryst. D54,** 1245-60 (1998)

M. Vlassi, G. Cesareni & M. Kokkinidis, A correlation between the loss of hydrophobic core packing interactions and protein stability, **J. Mol. Biol. 285,** 817-27 (1999)

Glykos, N.M., Cesareni, G. & Kokkinidis, M., Protein plasticity to the extreme: Changing the topology of a 4-α-helix bundle with a single amino-acid substitution. **Structure 7**, 597-603 (1999)

N.M.Glykos & M.Kokkinidis, Stochastic Approach to Molec. Replac., **Acta Cryst. D56,** 169-74 (2000)

N.M.Glykos & M. Kokkinidis, Multidimensional Molec. Replacement, **Acta Cryst. D57**, 1462-73 (2001)

N.M.Glykos & M. Kokkinidis, Structure determination of a small protein through a 23-dimensional molecular-replacement search, **Acta. Cryst. D59**, 709-718 (2003)

Mavromatis, K., Feller, G., Kokkinidis, M. and Bouriotis, V., Cold adaptation of a psychrophilic chitinase: a mutagenesis study, **Prot. Engng**. **16**, 497-503 (2003)

A.Spyridaki, C. Matzen, Th.Lanio, A.Jeltsch, A.Simoncsits, A.Athanasiadis, E.Scheuring-Vanamee, M. Kokkinidis & A. Pingoud, Structural and biochemical characterization of a new Mg 2+ binding site near Tyr94 in the restriction endonuclease *Pvu*II, **J. Mol. Biol**. 331, 395-406 (2003)
V.E. Fadouloglou, A.P. Tampakaki, N.M. Glykos, M.N. Bastaki, J.M. Hadden, S.E. Phillips, N.J. Panopoulos & M. Kokkinidis, Structure of $HrcQ_B$-C, a conserved component of the bacterial type III secretion systems, **Proc. Natl. Acad. Sci. USA 101**, 70-75 (2004)

N.M. Glykos & M. Kokkinidis, Structural polymorphism of a marginally stable 4-α-helix bundle. Images of a molten globule? **Proteins: Structure, Function and Bioinform. 56**, 420-425 (2004)

P. Tampakaki, V.E. Fadouloglou, A.D. Gazi, N. J. Panopoulos & M. Kokkinidis, Conserved Features of Type III Secretion, **Cellular Microbiology 6**, 805-816 (2004)

N.M. Glykos, Y. Papanikolau, M. Vlassi, D. Kotsifaki, G. Cesareni & M. Kokkinidis, Loopless Rop: structure and dynamics of an engineered homotetrameric variant of the Repressor of Primer protein, **Biochemistry 45**, 10905-10919 (2006)

V.E. Fadouloglou, A. Deli, N.M, Glykos, E. Psylinakis, V. Bouriotis and M. Kokkinidis, Crystal structure of the *Bc*ZBP, a zinc-binding protein from *Bacillus cereus* : Functional insights from structural data, **FEBS Journal 274**, 3044-3054 (2007)

Gazi , M. Bastaki, S.N. Charova, E.A. Gkougkoulia, E.A. Kapellios, N.J. Panopoulos and M. Kokkinidis, Evidence for a coiled-coil interaction mode of disordered proteins from bacterial type III secretion systems, **J. Biol. Chemistry**, 283: 34062-68 (2008)

A.Gazi , S.N.Charova, N.J.Panopoulos & M. Kokkinidis, Coiled-Coils in Type III Secretion Systems: Structural Flexibility, Disorder and Biological Implications. **Cell. Microbiol**. **11**: 719-29 (2009)

V.E. Fadouloglou, M.N. Bastaki, A.E. Ashcroft, S.E.V. Phillips, N.J. Panopoulos, N.M. Glykos and M. Kokkinidis, On the quaternary association of the type III secretion system $HrcQ_B$-C protein: Experimental evidence differentiates among the various oligomerization models, **J. Structural Biol**. **166**:214-25 (2009)

T.M.Geel, G. Meiss, B.T.F. van der Gun, B.J. Kroesen, L.F.M.H. de Leij, V. Siksnys, A. Šilanskas, M. Kokkinidis, A. Pingoud, M.H.J. Ruiters and P.M.J. McLaughlin, Endonucleases as tool to induce apoptosis in TRAIL-insensitive ovarian carcinoma cell. **Exp. Cell Res**. **315**, 2487-95 (2009)

N.M. Glykos, Stavrakoudis, A., Bouriotis, V. & Kokkinidis, M., Molecular dynamics simulations of BcZBP, a deacetylase from Bacillus cereus: Active site loops determine substrate accessibility and specificity, **J. Chem. Theory Comput. 5**, 3299-3311 (2009)

Schierling, A.-J. Noël, W. Wende, H.L. Tie, E. Kubareva, T. Oretskaya, M. Kokkinidis & A. Pingoud, Controlling the enzymatic activity of a restriction enzyme by light, **Proc. Natl. Acad. Sci. USA** 107:1361-1366 (2010).

A.P. Tampakaki, N.Skandalis, A.D. Gazi, M.N. Bastaki, P.F. Sarris, S.N. Charova, M. Kokkinidis, & N.J. Panopoulos, Playing the "Harp": Evolution of Our Understanding of *hrp/hrc* Genes, **Ann. Rev. Phytopath**. **48**, 347-370 (2010)

P.F. Sarris, N. Skandalis, M. Kokkinidis, N.J. Panopoulos, *In silico* analysis reveals multiple putative type VI secretion systems and effector proteins in *P. syringae* pathovars, **Mol. Plant Pathol. 11**, 795-804 (2010) [***selected among the top 50 articles*** *on P.syringae for the period 2006-2011*]

J. Dikić, C. Menges, S. Clarke, M. Kokkinidis, A. Pingoud, W. Wende, and P. Desbiolles, The rotation-coupled sliding of EcoRV, **Nucl. Acids Res.** 40: 4064-4070 (2012)

Fadouloglou VE, Kapanidou M, Agiomirgianaki A, Arnaouteli S, Bouriotis V, Glykos NM, **Kokkinidis** M., Structure determination through homology modelling and torsion-angle simulated annealing: application to a polysaccharide deacetylase from *Bacillus cereus*, **Acta Crystallogr D** 69 :276-83 (2013).

SIGNIFICANT RESEARCH ACHIEVEMENTS IN THE LAST 10 YEARS

1) Protein folding and novel biomaterials

The process of protein folding, while critical and fundamental to virtually all of biology, in many ways remains a mystery. Based on our previous work [Vlassi *et al*., Nature, Struct. Biol.1, 706 (1994)] in the last 10 years we used the ColE1 Rop protein as a model system to study the folding of a recurrent protein tertiary motif, the **4-α-helical bundle**. Rop is the paradigm of a canonical 4-α-helical bundle. Its structural simplicity has rendered it a model system to investigate the sequence-structure relationships and dynamics of the tertiary motif of α-helical bundles, including the frequently debated question concerning the **role of loops in protein folding**. Numerous mutations in the loop region of Rop have been produced and studied crystallographically with the aim to understand sequence-folding relationships. The most striking results include: a) one mutant ('loopless Rop'), which restores the 'heptad' periodicity with the deletion of five loop residues and thereby totally alters the native Rop folding, assembly and stability (it becomes hyperthermophile) of the protein and b) the replacement A31P which leads to a complete reorganization of the protein, which is converted from the canonical left-handed, all-antiparallel form to a right-handed mixed-parallel and antiparallel 4-α-helical bundle crystallizing in two discrete structural states and exhibiting properties of a molten globule. Our analysis suggests that the role of the loop is not to determine the fold, but to actively exclude some of the otherwise possible folding pathways. The establishment of **molten-globule-like states** was also shown for several other loop mutants, with properties that are reminiscent to those of highly interactive coiled-coil proteins in various biological systems (e.g. HrpO in T3SS). The knowledge obtained from these studies was recently exploited in the development of novel, protein-based materials e.g. **fibres with nano- to micron-scale features** which are assembled through the oligomerization of suitably designed, long α-helices. Potential field of applications: Materials science, nanobiotechnology. In addition, we have developed **helical protein scaffolds** for the attachment of enzymatic domains, e.g. the LLRop scaffold **which will be used in the ScafNu project**. Using these engineered scaffolds we have developed recently nucleases for genome modification/gene therapy (see next section). ***Selected publications*****: 1)** N.M. Glykos & M. Kokkinidis, Structural polymorphism of a marginally stable 4-α-helix bundle. Images of a molten globule?, Proteins: Structure, Function and Bioinformatics 56, 420425 (2004); **2)** N.M. Glykos *et al.* & M. Kokkinidis, Loopless Rop: structure and dynamics of an engineered homotetrameric variant of the Repressor of Primer protein, Biochemistry 45, 10905-19 (2006); **3)** M. Ambrazi *et al.* & M. Kokkinidis, Purification, crystallization, X-ray diffraction analysis and phasing of a loop variant of the ColE1 Rop protein, Acta Cryst.F 64**,** 432-34 (2008).

2) Enzymes for DNA modification and biomedical applications

The exploitation of the information generated by genomic sequencing efforts in biomedicine and biotechnology will depend (among other things) critically on the availability of DNA binding/modifying enzymes which can target and modify individual genes. Based the considerable experience and achievements of our group with DNA-binding enzymes (restriction endonucleases, DNA

methyltransferases, zinc fingers [Athanasiadis *et al*., Nature, Struct. Biol.1 469-75 (1994)]), we have put in the last 10 years a considerable effort in structural studies of these enzymes, and we have **coordinated several international initiatives** (in the framework of EU-funded consortia) aiming at their application in biomedicine. Our work has for the first time shed light on the **structural basis of the pathway** by which metal ions as essential cofactors enter the catalytic centre of restriction endonucleases. Furthermore, we have undertaken a major effort in the design and development of restriction endonucleases and DNA methyltransferases of **utmost and programmable specificity** for gene replacement, gene silencing etc. **Delivery of these enzymes to cell nucleus** has been demonstrated. In this context we also developed and studied a novel, **monomeric form of the PvuII** restriction endonuclease. Using helical scaffolds (see previous section) we developed **novel specificities for the I-CreI** homing endonuclease for targeting specific genes that are associated with genetic diseases. I-CreI is already **used by the company Cellectis (Paris) for gene therapy applications**. Furthermore we have been involved in the development of methods to make the activity of engineered nucleases **controllable by light**, *after* they have been delivered to the cell/nucleus; this is an extremely important step for the practical application of the enzymes in gene therapy. In addition, we have crystallized the DNA-free and the DNA-bound forms of M.BseCI DNA methyltransferase from *B. stearothermophilus* which methylates the N6 atom of the 3' adenine in the sequence 5'-ATCGAT-3'. The structure has been solved recently and we are in the process of obtaining an atomic model. ***Selected EU grants (coordinated by us)*** **1)** Restriction Endonucleases and DNA Methyltransferases: Structures, Interactions with DNA and Engineering of Novel Functions, EU, Biotechnology Programme 160.000 ecu; **2)** Development of Highly Specific Enzymes for Genome Manipulation, EU, Quality of Life Programme, € 240.000; **3)** MenuG: Meganucleases for Gene Replacement, EU, NEST/FP6 Programme, € 295.000. ***Selected publications:*** 1) A. Spyridaki *et al.* & M.Kokkinidis and A. Pingoud, Structural and biochemical characterization of a new Mg^{2+} binding site near Tyr94 in the restriction endonuclease *Pvu*II, J. Mol. Biol. 331, 395-406 (2003); 2) E. Kapetaniou *et al.* & M. Kokkinidis, Purification, crystallization and preliminary X-ray analysis of the *Bse*CI DNA methyltransferase from *Bacillus stearothermophilus* in complex with its cognate DNA, Acta Cryst.F 63, 12-14 (2007) 3) Ch. Meramveliotaki *et al.* & M. Kokkinidis, Purification, crystallization, X-ray diffraction analysis and phasing of an engineered single-chain PvuII restriction endonuclease, Acta Cryst. F 63, 836-838 (2007); 4) T.M.Geel *et al.* & M. Kokkinidis, A.Pingoud, M.H.J. Ruiters & P. McLaughlin, Endonucleases as tool to induce apoptosis in TRAIL-insensitive ovarian carcinoma cell Exp. Cell Res. 315, 2487-2495 (2009); 5) B. Schierling *et al.* & M. Kokkinidis & A. Pingoud, Controlling the enzymatic activity of a restriction enzyme by light, Proc. Natl. Acad. Sci. USA 107:1361-66 (2010); J. Dikić *et al.*, M. Kokkinidis, A. Pingoud, W. Wende, and P. Desbiolles, The rotation-coupled sliding of EcoRV, Nucl. Acids Res. 40: 4064-4070 (2012)

3) Studies of bacterial Type III (T3SS) and Type VI (T6SS) secretion systems

T3SS enable plant and animal bacterial pathogens to deliver virulence proteins into the cytosol of eukaryotic host cells causing a broad spectrum of diseases including bacteremia, septicemia, typhoid fever and bubonic plague in mammals and localized lesions, systemic wilting and blights in plants. In the last 10 years we studied structure and function of several T3SS proteins and their supramolecular assemblies. Among our achievements is the first **structure determination of a conserved T3SS core protein** ($HrcQ_B$ from *Pseudomonas syringae*), the first structural characterization of an **intrinsically disordered T3SS protein** (HrpO) and characterization of the structural basis of its interactions. In addition, we studied the role of the coiled-coil motif in T3SS and the importance of structural flexibility as a T3SS secretion signal. Other T3SS proteins studied (e.g. the HrpA protein of the *P.syringae* T3SS pilus) have produced technologically exploitable results, e.g. the **assembly of nano-fibres and hydrogels**. We have recently initiated the structural/functional study of T6SS, a bacterial secretion system whose function is poorly understood. ***Selected grants (coordinated by us)*** **1)** Study of bacterial pathogenicity mechanisms and development of computer tools for antimicrobials design, PEP program (Region of Crete, € 170.000, (2006-2008); **2)** Pathogenicity proteins and Chaperones III: novel antibacterial targets and applications in the classical genetic improvement of plants € 45.000 (2006-2008, Pythagoras II programme). ***Selected publications:*** 1) V.E. Fadouloglou *et al.* & M. Kokkinidis, Structural studies of the Hrp secretion system: expression, purification, crystallization and preliminary X-ray analysis of the C-terminal domain of the $HrcQ_B$ protein from *Pseudomonas syringae* pv. Phaseolicola , Acta Cryst. D57, 1689-91 (2001); 2) V.E. Fadouloglou *et al.* & M. Kokkinidis, Structure of $HrcQ_B$-C, a conserved component of the bacterial type III secretion systems, Proc. Natl. Acad. Sci.

USA 101, 70-75 (2004); 3) A. P. Tampakaki *et al.* & M. Kokkinidis, Conserved Features of Type III Secretion, Cellular Microbiology 6, 805-16 (2004); 4) A. Gazi *et al.* M. Kokkinidis, Evidence for a coiled-coil interaction mode of disordered proteins from bacterial type III secretion systems, J. Biol. Chemistry, 283: 34062-68 (2008); 5) A. Gazi *et al.* & M. Kokkinidis, Coiled-Coils in Type III Secretion Systems: Structural Flexibility, Disorder and Biological Implications. Cell. Microbiol. 11: 719–29 (2009); 6) V.E. Fadouloglou *et al.* & M. Kokkinidis, On the quaternary association of the type III secretion system $HrcQ_B$-C protein: Experimental evidence differentiates among the various oligomerization models, J. Structural Biol. 166:214-25 (2009); 7) A.P. Tampakaki *et al.* M. Kokkinidis & N.J. Panopoulos, Playing the "Harp": Evolution of Our Understanding of *hrp/hrc* Genes, Ann. Rev. Phytopath. 48, 347-370 (2010); 8) P.F. Sarris, N. Skandalis, M. Kokkinidis, N.J. Panopoulos *In silico* analysis reveals multiple putative type VI secretion systems and effector proteins in Pseudomonas syringae pathovars, Mol. Plant Pathol. 11, 795-804 (2010) (*This paper has been selected among the Top 50 Biomedical Articles on P.syringae for the period 2006-2011)*

Organizer/co-organizer of symposia/workshops (selection of recent events):

1) Patenting inventions "From idea to commercialization" (co-organizer in the framework of the InnovCrete project), 28-11-2013, Heraklion, Crete 2) Workshop on **X-FEL Radiation & its Applications**, 18-19/6, 2010, NCSR "Demokritos", Athens, Greece 3) **Targeted Genome Modification** Symposium, 23-24/4, 2009, Groningen, The Netherlands 4) **Protein-Nucleic Acids Interactions** Workshop, 28/6-2/7, 2008, Chania, Greece.

Invited presentations (selection of recent events):

1) European Crystallography Meeting (ECM28) 25-29th August, 2013, Warwick, UK. 2) International Atomic Agency (IAEA) Meeting, University of Patras, 24-27th September 2013 3) 2nd European Workshop, "**Molecular A-Biotic Plant Interactions**" 06 May 2011, Athens, Greece 4) Minisymposium on **Coherent Diffractive imaging**, 14-May-2010, , Uppsala, Sweden 5) "**Methods for the analysis of Macromolecular interactions**", Jacobs University, 21-24 November, 2008, Bremen, Germany 6) Summer school "**Study of Nucleic Acids**" (AsiaLink Human Resources Development), August 24 - 31, 2007, Hangzhou, China 7) Workshop on the **development and directions for power diffraction studies on proteins**, 22-23 June 2007, ESRF, Grenoble, France 8) Summer school "**Study of Nucleic Acids**" (AsiaLink Human Resources Development), Sept. 15-20, 2006, Bangalore, India 9) 1st Intern. Conference on **Clinical Gene Therapy**, 24-26 January, Groningen, Netherlands.

RESEARCH FUNDING 2005-2013

COORDINATION OF EU-FUNDED PROJECTS & CONSORTIA

Development of Highly Specific Enzymes for Genome Manipulation, (Commission of the European Communities, Quality of Life Programme, Contract number QLK3-CT-2001-00448 (2002-2005), **€ 240.000**
Role in the project: Structural studies of programmable endonucleases, coordination of the consortium

MenuG: Meganucleases for Gene Replacement (Commission of the European Communities, NEST/FP6 Programme, Contract number 015509 (2006-2009), **€ 295.000**
Role in the project: Structural studies of meganucleases and engineering of maganucleases with novel DNA specificities, coordination of the consortium

InnovCrete: Unlocking the innovative capacity of multidisciplinary structural biology-driven research in Crete (Commission of the European Communities, FP7 Programme, FP7-REGPOT-2012-2013-1, No. 316223, (2012-2016), **€ 4.003.534**
Role in the project: Coordination of a Research Potential project aiming to support and further develop the innovative capacity of Structural Biology Research at IMBB/FORTH

PARTCIPATION IN EU-FUNDED CONSORTIA

The European Bio-Crystallogenesis Initiative, Commission of the European Communities, Biotechnology Programme (1999-2002), 144.000 ecu
Role in the project: Development of the ionic-strength reducer concept for protein crystallization

Genestream: Massive Genetic Data will become critical Knowledge, Commission of the European Communities, Information Society Programme, Contract number IST-2001-35041, 2002-2004) € 140.000
Role in the project: Data mining from structural databases

Human Resources Development In The Study Of Nucleic Acids, Commission of the European Communities, FP6 ASIA LINK PROGRAMME € 50.000 (2005-2008) ***Role in the project***: Structural studies and DNA binding enzymes

COORDINATOR OF CONSORTIA/GRANTS WITH NATIONAL FUNDING

Development of crystallogenesis tools for biological macromolecules, GSRT PENED Programme, € 169.508 (2002-2005) ***Role in the project***: Development of protein crystallization kits based on the ionic strength reducers concept

Chitin and peptidoglycane deacetylases: Structure function relationships & development of applications, Greek Ministry of Education, Pythagoras I Programme, € 65000 (2004-2006) ***Role in the project***: Determination of enzyme structures

Purification, characterization and crystallographic study of a thermostable gellan lyase, synthesized by a thermophilic aerobic bacterial strain, GSRT-Joint Research and Technology Programmes Greece-Bulgaria, € 11700 (2005-2007) ***Role in the project***: Crystallization studies of the enzyme

Study of bacterial pathogenicity mechanisms and development of computer tools for antimicrobials design, PEP program (Region of Crete, € 170.000, (2006-2008) ***Role in the project***: Structural studies of selected T3SS proteins. Furthermore, collaboration with a software company to develop a computer program for the identification of potential T3SS inhibitors from structural databases of small molecules.

Network To Optimize Use Of The European X-Fel By The Greek Research Community, GSRT, 2010-2011, € 125.000 ***Role in the project***: The European X-FEL will create a basis for the performance of presently impossible and potentially revolutionary experiments. Our role as coordinator of the project is: a) To prepare a feasibility study which will evaluate costs and benefits of a Greek participation in the X-FEL project b) To mobilize and stimulate the Greek community of potential X-FEL users through a workshop, periodic meetings and dissemination of information relevant to X-FEL and c) To coordinate and support at national level preparatory activities and foster national/international research collaborations which will optimize the use of the European X-FEL by the Greek researchers after it becomes fully implemented.

Bacterial Type III Secretion Systems: Study of Supramolecular Structures, GSRT, Joint Research and Technology Programmes Greece-France 2010 – 2011 (EGIDE) ***Role in the project***: Study of *P.syringae* T3SS proteins and their complexes using SAXS (Small angle X-ray scattering)

Engineering of "meganucleases" consisting of a transcription factor like effector (TALE) proteins as the DNA binding module and a site specific nuclease as the DNA cleavage module (2013-2014) IKYDA project (GR-D cooperation in TTD). ***Role in the project***: Coordinator

Attaching Functions to Protein Scaffolds: Development of Artificial Enzymes for Green Chemistry. (2013-2015) SYNERGASIA II programme**,** € 340.000. ***Role in the project***: Coordinator

PARTICIPANT IN CONSORTIA/GRANTS WITH NATIONAL FUNDING

Study of psychrophilic enzymes: Design of enzymatic stability and catalytic properties (GSRT PENED Programme, 2002-2005) € 150.000 (coordinator Prof. V. Bouriotis) ***Role in the project***: *In silico* analysis of properties of psychrophilic enzymes

Development and application of a prototype for internet-based teaching in biological sciences (APHRODITE), e-learning/ GSRT-Information Society Programme (2003-2006), € 42.400 (coordinator Prof. E. Eliopoulos, Agricultural University of Athens) ***Role in the project***: Development of web-based courses on Crystallography and Protein Engineering

Design and structural studies of asymmetric restriction endonucleases, GSRT PENED Programme, (2002-2005) € 150.000 (coordinator Prof. E. Eliopoulos, Agricultural University of Athens) ***Role in the project***: Re-engineering of homodimeric restriction endonucleases and structural/functional analysis of the single-chain enzymes developed.

Pathogenicity proteins and class III chaperones: novel antibacterial targets and applications in the classical genetic improvement of plants Pythagoras II programme, Ministry of education (2005-2008) € 38.760 (coordinator Prof. N. Panopoulos) ***Role in the project***: Structural and biochemical characterization of T3SS chaperone-like proteins

Neural system-specific GDH: Effects of regulatory mutations to the basic activity of the enzyme and crystal structures PENED-2003 programme (2006-2008) € 71.875 (coordinator Prof. A. Plaitakis) ***Role in the project***: Overexpression, crystallization experiments and circular dichroism studies of selected GDH variants.

Chitin deacetylases from *Fusarium graminearum* : purification, biochemical, structural characterization, role in pathogenicity and biotechnological applications, PENED 2003 programme (2006-2008) € 112.500 (coordinator Prof. V. Bouriotis) ***Role in the project***: Purification in mg quantities and crystallization experiments.

Engineering of Enzymes for Genome Modulation, GSRT Greece-China cooperation in RTD (2013-2015) € 150.000. ***Role in the project***: Enzyme engineering, crystallographic work.