



SOBRE LOS AUTORES

ABOUT THE AUTHORS

CELERINO ABAD-ZAPATERO, Ph.D. Obtained a Licenciado degree in Physics from the University of Valladolid, Spain, and later a Ph.D. in Biophysics (Macromolecular Crystallography) from the University of Texas at Austin, sponsored by a Fulbright Scholarship. He was part of the team that unveiled the atomic structures of the first viruses (SBMV) in the early 1980's with Michael Rossmann at Purdue University. He worked in the pharmaceutical industry (Abbott Laboratories) for twenty-two years using the methods of Structure-Based Drug Design to expedite the design and optimization of medicinal drugs. He retired from the private industry in 2008 and is currently Adjunct Professor to the Graduate Faculty at the University of Chicago. His research interests are related to the development of more effective and efficient methods to design drugs using the concepts of 'Ligand Efficiency Indices' and 'alternative variables' beyond the dominant affinity between the ligand and the target. He is the author of *Crystals and Life: A Personal Journey* (IUL, 2002) and *Ligand Efficiency Indices for Drug Discovery: Towards an Atlas-Guided Paradigm* (Academic Press, 2013).

PAUL D. ADAMS, Ph.D., is a Senior Scientist at Lawrence Berkeley National Laboratory and an Adjunct Professor in the Department of Bioengineering at UC Berkeley. He also is Vice President for Technology at the Joint BioEnergy Institute, and is Deputy Director of the LBNL Physical Biosciences Division. His research focuses on the development of new algorithms and methods for crystallography, structural studies of large macromolecular machines, and development of cellulosic biofuels. He earned his doctorate in biochemistry at the University of Edinburgh and performed postdoctoral work at Yale University.

PAVEL V. AFONINE, Ph.D., obtained his BS/MS degrees in applied physics and mathematics, biology and biotechnology at the Moscow Institute of Physics and Technology (Russian state university) in 2000. At present, Pavel is a research scientist at Lawrence Berkeley National Laboratory, which he joined in the year 2003 after receiving his PhD degree at the Henri Poincaré University, Nancy, France. His main scientific activities include development of Phenix software for complete automated crystallographic and cryo-EM structure solution where he focuses on both low-level core routines and end-user applications, work on methodological and computational aspects of X-ray and neutron crystallography as well as cryo-EM.

GAVIN CONNOR FOX, Ph.D., is a Beamline Scientist at Synchrotron SOLEIL, Paris, France. He received his M.Sc. in Biomolecular Technology from the UK National Center for Macromolecular Hydrodynamics at Leicester University, and carried out his Doctoral research at the GlaxoSmithKline Medicines Research Centre, Stevenage, UK, and the London Institute of Cancer Research UK. He worked as a Beamline Scientist at the Spanish CRG beamline, BM16, which was established and coordinated by the consortia who initiated the design and construction of the ALBA synchrotron, and at several ESRF macromolecular crystallography (MX) beamlines before being recruited by the CNRS and moving to SOLEIL in 2010. At SOLEIL, Gavin is part of the core team tasked with the design, construction and exploitation of Proxima 2-A (PX2-A). PX2-A is currently one of the most intense microfocus beamlines dedicated to MX available in Europe. Gavin has published widely with research groups from France, Spain and the UK and his research interests are focussed on the next generation of beamline technologies and applications.

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JUAN ANTONIO GARRIDO ARDILA es catedrático de literatura española y de literatura comparada en la Universidad de Edimburgo (Gran Bretaña). Especialista en literatura áurea y contemporánea, ha publicado los libros *Charlotte Temple* (Universidad de Extremadura, 2002), *Sociopragmática y retórica interpersonal* (Edwin Mellen, 2004), *Cervantes en Inglaterra*

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EUGENE KRISSINEL, Ph.D., is CCP4 Core Group Leader in the Research Complex at Harwell, Rutherford-Appleton Laboratory near Oxford, UK. He received PhD diploma from Kazan Physical-Technical Institute, USSR, after completion of post-graduate studies in Novosibirsk State University, USSR. In 1989-94, Dr. Krissinel worked in the Institute for Water and Environmental Problems of Russian Academy of Sciences, studying effects of mercury and radionuclide pollution in the Altai region of South Siberia, close to Semipalatinsk nuclear test area. In 1995-97, he worked as a visiting scientist in Argonne National Laboratory, Chicago, USA, focussing on thermodynamic properties and MD simulations of metallic alloy microclusters. In 1997, he moved as a Humboldt Fellow to the University of Konstanz, Germany, to further advance his PhD studies on magnetic and spin effects in radical reactions, working with Prof. Ulrich Steiner, Konstanz, and Prof. Anatoly Burshtein, Weizmann Institute of Science, Rehovot, Israel. After 2000, Dr. Krissinel works as a senior scientific officer in the European Bioinformatics Institute, Cambridge, UK, where he develops methods and software for protein structure analysis (SSM) and identification of protein oligomeric states from crystal packings (PISA). In 2009, Dr. Krissinel joins the CCP4 Project, assuming a leading position for the CCP4 Core Group, developing and maintaining the world-recognised CCP4 Software Suite for protein crystallography.

MARÍA MERINO BOBILLO es Doctora con Mención Europea por la Universidad de Valladolid, Máster en *Communication Sociale-Journalisme* por la Université Catholique de Louvain-la-Neuve (Bélgica), Licenciada en Geografía e Historia por la UNED y Diplomada Profesor de Enseñanza Básica por la Universidad de Valladolid. En 2004 se incorpora como docente en la

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CLAUDIA MILLÁN is a member of the Crystallographic Methods group at the María de Maeztu Unit of Excellence in Structural Biology in the Molecular Biology Institute of Barcelona. She received a degree in Biotechnology from Pablo de Olavide University in 2011, and a MSc in Crystallography and Crystallization in 2012. She is currently developing computational methods to solve difficult macromolecular structures. She likes to write about science in general and structural biology in particular, and is editor of a Crystallography section in the university science magazine MoleQla.

GUILLERMO MONTOYA, Ph.D., is the Research Director of the Protein Structure & Function NNF-CPR centre at the University of Copenhagen. He obtained his BS degree in Biochemistry at the Universidad del País Vasco in 1990, and his PhD in Chemistry from the Universidad de Zaragoza in 1993. He obtained both a European Molecular Biology Organisation (EMBO) and a Federation of European Biochemical Societies (FEBS) Fellowship and moved to the Max Planck-Institut für Biophysik in Frankfurt am Main (Germany), where he worked on membrane protein crystallisation in the group of the Nobel Laureate H. Michel. Montoya later obtained both an EMBO long-term and a Marie Curie Fellowship and spent nine years at the European Molecular Biology Laboratory (EMBL) in Heidelberg (Germany), working in I. Sinning's Group where he pioneered the study of the structure of the signal recognition particle (SRP), an essential ribonucleoprotein complex involved in protein targeting. In the last years, his main research interests are the structural analysis of macromolecular complexes of the cell cycle such as the mammalian chaperonin CCT complex, and kinase regulators, where he uses the combination of X-ray crystallography and electron microscopy to gain new molecular insights. Dr. Montoya

is also systematically pursuing the structure-function analysis of homing endonucleases also known as meganucleases, which are of great interest because of their potential applications in gene therapy. Many of his papers show an impressive diversity of interdisciplinary methods centered on the structural information provided by X-ray crystallography or electron microscopy, thus allowing a thorough description of structure and function of macromolecular complexes at molecular, supramolecular and cellular level. He is member of international project evaluation panels and also reviews projects for European funding agencies (ERC, EU, SNF, DFG, NWO, Wellcome Trust) and serves as an ad-hoc reviewer for high-profile journals. He has been awarded the National Prize from the *Fundación Mutua Madrileña* (2009) and the V Health Sciences Prize from *Caja Rural de Granada-Ministerio de Sanidad* (2009).

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ENRICO STURA received his DPhil from the University of Oxford in Molecular Biophysics in 1978. Currently he carries out his research in protein crystallization and X-ray crystallography at the Commissariat à l'énergie atomique et aux énergies alternatives in Saclay, France. He has authored over 150 publications. He is well known for crystal growing and crystal manipulation methodology. His special interest is in proteins of the immune system and pathogen derived antigens. Recent studies involve structural studies of human proteases to develop inhibitors for cancer therapy. A second line of research concerns snake venom derived polypeptides that target mammalian channels and receptors.

ALEXANDRE URZHUMTSEV, Ph.D., is a full professor at the Université de Lorraine, Nancy, and a researcher at the IGBMC, Illkirch. After graduating from the Kolmogorov's school-internat and the Faculty of Computational Mathematics at the Moscow State University, he moved to Pushchino (Institute of Mathematical Problems of Biology) where he obtained his PhD in X-ray macromolecular crystallography. His main research interests are the development of computational methods and programs for structure solution, refinement and validation, as well as solution of 'difficult' structures where development and application of original algorithms are required.

ISABEL USÓN, Ph.D., is an ICREA Research Professor at the María de Maeztu Unit of Excellence in Structural Biology, Molecular Biology Institute of Barcelona IBMB-CSIC. She studied Chemistry at the University of Zaragoza, where she completed her Ph.D. She worked as a Product Research Scientist at Procter & Gamble's European Research Center in Brussels. Moving back to academia, she completed an habilitation (German higher doctorate) at the University of Göttingen, receiving the *venia legendi* in Structural Chemistry and starting her own research group. In 2003 she took her present position. She is the author of over 130 research articles in peer reviewed journals and develops the phasing methods implemented in the ARCM-BOLDO software.