BIOGRAPHICAL SKETCH

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NAME: Almo, Steven C.

eRA COMMONS USER NAME (credential, e.g., agency login): STEVENALMO

POSITION TITLE: Professor of Biochemistry

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Massachusetts Institute of Technology, Cambridge, MA	B.S.	1982	Biology
Harvard University, Boston, MA	Ph.D.	1990	Biophysics
Johns Hopkins School of Medicine, Baltimore, MD	Postdoctoral	1992	Cell Bio./Biophysics

A. Personal Statement

For the past two decades, the major scientific focus of my laboratory has been high-throughput structure discovery and functional dissection of cell surface immune receptors. My laboratory has been directly involved in a number of large-scale programs involved in technology development and high-throughput applications. I am the Director of the Einstein Macromolecular Therapeutics Development Facility, which provides a wide array of proteins services to the Einstein community, and served as PI of the New York Structural Genomics Research Consortium (NYSGRC), one of the four large-scale high-throughput structure discovery centers supported by the NIGMS Protein Structure Initiative. I served as Director of the Protein Expression Core for the Northeast Biodefense Center (one of the NIAID-funded Regional Centers of Excellence) and was a major participant in the Immune Function Network, an NIGMS-funded program on the mechanistic dissection of innate and adaptive immunity. I also served as co-PI of the Enzyme Function Initiative, an NIGMS-supported Glue Grant focused on the development, implementation and dissemination of strategies for the large scale annotation of enzyme function. My laboratory has made extensive contributions to the structural, functional and mechanistic analysis of numerous challenging mammalian proteins, including protein tyrosine phosphatases, DNA and RNA binding proteins, some in complex with duplex DNA or RNA ligands, and the cell surface and secreted proteins that modulate adaptive and innate immunity (including structures of the CTLA-4:B7, PD-1:PD-L, CTLA-4:ipilimumab, LIGHT:DcR3, TL1A:DcR3, FasL:DcR3 and CD160:HVEM complexes), and we have developed a series of platforms for the high-throughput evaluation of protein interactions and their functional implications. Based on my experience protein expression/purification and biochemical, biophysical, structural, functional and mechanistic analysis of signaling molecules and enzymes, I am well qualified to contribute to the proposed work.

B. Positions and Honors

Employment and Awards

- Teaching Assistant, Stanford University Medical School, Dept. of Biochemistry, September 1982
- Teaching Assistant, Harvard University, Dept. of Biochemistry and Molecular Biology, Sept. 1983-1985
- Recipient, Institute for Biological Recognition and Catalysis, Inc., Travel Grant, March 1988
- Recipient, Institute for Biological Recognition and Catalysis, Inc., Travel Grant, November 1988
- Instructor in Molecular Graphics Course, MIT, Department of Chemistry, 1988-1989

- Instructor, Woods Hole Marine Biology Laboratories, Physiology Summer Course, 1990
- Assistant Professor of Biochemistry, Albert Einstein College of Medicine, Dept. of Biochemistry, 1992-1997
- Member, Albert Einstein Cancer Center, 1996-present
- Associate Professor of Biochemistry, Albert Einstein College of Medicine, Dept. of Biochemistry, 1997-2001
- Professor of Biochemistry, Albert Einstein College of Medicine, Dept. of Biochemistry, 2001-present
- Associate Director for Crystallography, Center for Synchrotron Biosciences, 1997-2006
- Irma T. Hirschl/Monique Weill-Caulier Career Development Award, 2000-2004
- Professor of Physiology & Biophysics, Albert Einstein College of Medicine, Dept of Physiology & Biophysics, 2003-Present
- AMGEN Award, American Society for Biochemistry and Molecular Biology, 2004
- The LaDonne Schulman Faculty Recognition Award for Graduate Teaching at the Albert Einstein College of Medicine, 2005
- Director of Structural Proteomics, New York Structural Biology Center, 2006-present
- Director, Albert Einstein Macromolecular Therapeutic Development Facility (MTDF), 2007-present
- Director, Eukaryotic Expression Core for the Northeast Biodefense Center, 2009-2014
- Wollowick Family Foundation Chair in Multiple Sclerosis and Immunology, 2012-present
- Chairman, Department of Biochemistry, Albert Einstein College of Medicine, September 2015-present
- President, Institute for Protein Innovation, July 2017-July 2019; Board member 2017-present

Academic Service

- Faculty Senate, 1993-1995, 1998-2007, 2014-present
- Sue Golding Graduate Admissions Committee, 1993-1996
- Medical Scientist Training Program (MSTP) Steering Committee, 1996-present
- Molecular Biophysics Training Grant Steering Committee, 1997-2010
- Associate Professor Promotion Committee, 1997-2000
- Advisory Committee, Analytical Imaging Facility, 2000-present
- Professor Promotion Committee, 2002-2004
- Tenure Committee, 2005-present
- Chair, Strategic Planning Committee on Structural Biology and Proteomics, 2007
- Science Council, 2010-present
- Senate Council 2015-2016

National Service

- Special NCI Study Section for Program Project Review, 4/97
- American Cancer Society, Peer Review Committee on Cancer Drug Development, 1/98-12/01
- National Center for Research Resources Special Emphasis Panel ZRR1 BRT-1, 4/98
- Special NCI Study Section for Program Project Review, 5/98
- NIH BBCB Study Section, Ad hoc, 7/98
- NIH Physical Biochemistry Study Section, Ad hoc, 6/00
- Editorial Board, International Archives of Allergy and Immunology, 1/98-12/00
- Proposal Study Panel, Brookhaven National Laboratory (BNL), 99-present
- User Executive Committee, National Synchrotron Light Source, BNL, 2001-2003, 2005-2007
- National Center for Research Resources Review Panel ZRG1 BBCA, 10/01
- Reviewer for J. Biol. Chem., Biochemistry, Science, Nat. Struct. Biol., Biophys. J., Structure, Acta. Cryst, Chemistry & Biology, Nature, Proc. Natl. Acad. Sci., J. Cell Biol., Protein Science, Proteins
- Faculty of 1000, Electronic Reviews, Biology Reports Ltd.
- NIH CDF-4 Study Section, Ad hoc, 2/02
- NIH CSF (formerly CDF-4) Study Section, 10/02-10/06
- NIH Scientific Advisory Board, Epitope Discovery Working Group, NIAID, 9/04-12/05
- NIH Administrative Chairman of Division of Molecular and Cellular Mechanisms Special Emphasis Panel, 7/04-6/06
- NIH ZRG1-SBMI Review Panel, Ad hoc, 3/05
- Chairman**,** NIH ZRG1 CB-B 02 S, Review Panel (Bioengineering Research Partnership), 6/05
- NIH IDM-G (2) Review Panel, Ad hoc, 3/05
- NIH ZRG1 IDM-G (02) Drug Development 8/06

- NIH ZRG1 BST-D (50) Technology Centers for Networks and Pathways, 3/09
- NIH CSF Study Section, Ad hoc, 6/09
- ZRG1 BCMB-B (99) R Review Panel, 7/09
- Beamline Advisory Team, Advanced Beamlines for Biological Investigations with X-rays (ABBIX) Project for the National Synchrotron Light Source (NSLS)-II facility at Brookhaven National Laboratory (BNL), 2009-present; Chair 2013-present
- Scientific Advisory Committee, HIVRAD (Michael Cho, PI; Iowa State) 2009-2012
- Scientific Advisory Committee, Case Center for Synchrotron Biosciences (Mark Chance, PI; Case Western Reserve) 2009-present
- Scientific Advisory Committee, PXRR (Robert Sweet, PI; Brookhaven National Laboratory) 2009-present; Chair 2011-present
- College of CSR Reviewers, 2010
- Organizer, 2012 Keystone Meeting "Structural Biology of Cellular Processes: From Atoms to Cells"
- Linac Coherent Light Source (LCLS) Proposal Review Panel (PRP); SLAC National Accelerator Laboratory May 2014-2016
- Scientific Advisory Board, Institute for Bioscience and Biotechnology Research, University of Maryland, October 2014-present
- Board of Directors, New York Structural Biology Center, 2016-present
- Scientific Advisory Committee, Advanced Photon Source, Argonne National Laboratory, 2017-present

C. Contributions to Science

I. Strategies for Functional Annotation and Metabolism Discovery. The number of newly reported protein sequences inferred from genome sequencing continues to grow at a rate that severely outpaces the assignment of function through comparative genomics or direct biochemical analysis. This situation results in a large proportion of unannotated and misannotated protein sequences precluding the discovery of novel enzymes, activities, and metabolic pathways important to (1) understanding the contributions of the gut microbiome to human health, (2) the realization of new chemical processes for industry, and (3) our understanding of critical environmental issues, including global nutrient cycles and the evolution of complex microbial communities. To address these challenges our laboratory is devising experimental strategies based on the solute binding protein (SBP) components of small molecule transport systems, since the first step in a catabolic pathway is frequently the passage of a metabolite across the cellular membrane by SBP-dependent transport machinery. The ability to identify the initial reactant (or a closely related molecule) for a catabolic pathway provides an immediate toe-hold by placing significant constraints on the regions of chemical space that need to be considered and, in conjunction with knowledge of colocalized and coregulated genes, begins to define details of the *in vivo* biochemical transformations operating within the metabolic pathway. Using our high-throughput infrastructure we produced and screened 158 TRAP SBPs against a small molecule library by differential scanning fluorimetry (DSF). These efforts led to the identification of 40 new TRAP SBP ligands, the generation of experiment-based annotations for 2084 individual SBPs in 71 isofunctional clusters, and the definition of numerous metabolic pathways, including novel catabolic pathways for the utilization of ethanolamine as sole nitrogen source and the use of D-Ala-D-Ala as sole carbon source[1]. Other comparable large scale functional annotation studies were performed for the Isoprenoid Synthase[2] and Haloacid Dehalogenase[3] Superfamilies.

1. Vetting MW, Al-Obaidi N, Zhao S, San Francisco B, Kim J, Wichelecki DJ, Bouvier JT, Solbiati JO, Vu H, Zhang X, Rodionov DA, Love JD, Hillerich BS, Seidel RD, Quinn RJ, Osterman AL, Cronan JE, Jacobson MP, Gerlt JA, Almo SC. (2015) "Experimental strategies for functional annotation and metabolism discovery: targeted screening of solute binding proteins and unbiased panning of metabolomes." Biochemistry. 54(3):909-31.
2. Wallrapp FH, Pan JJ, Ramamoorthy G, Almonacid DE, Hillerich BS, Seidel R, Patskovsky Y, Babbitt PC, Almo SC, Jacobson MP, Poulter CD. (2013) Prediction of function for the polyprenyl transferase subgroup in the isoprenoid synthase superfamily. Proc Natl Acad Sci U S A. 110(13):196-202.
3. Huang H, Pandya C, Liu C, Al-Obaidi NF, Wang M, Zheng L, Toews Keating S, Aono M, Love JD, Evans B, Seidel RD, Hillerich BS, Garforth SJ, Almo SC, Mariano PS, Dunaway-Mariano D, Allen KN, Farelli JD. (2015) Panoramic view of a superfamily of phosphatases through substrate profiling. Proc Natl Acad Sci U S A. 112(16):74-83.

II. High-throughput Protein Production Infrastructure. Despite a multitude of recent technical breakthroughs speeding high-resolution structural and functional analysis of biological macromolecules, production of sufficient quantities of well-behaved, active protein continues to represent the rate-limiting step in many structure discovery and functional annotation efforts. These challenges are amplified when considered in the context of ongoing

large scale efforts to systematically define structure, function and mechanism of a wide range of macromolecules including multi-domain eukaryotic proteins, secreted proteins, and ever larger macromolecular assemblies. As part of our programs at Einstein, we have established robust bacterial expression platforms for the high-throughput discovery of new metabolism. Unique to the Almo group is the world's first integrated system for high-throughput functional and structural biology of oxygen sensitive proteins. This resource has allowed for the recapitulation of the entire high-throughput protein production and crystallization pipeline within an oxygen-free environment (see http://www.nysgrc.org/psi3/anaerobic.html). We have also established high-throughput eukaryotic expression platforms, including insect and mammalian-based systems, which represents a unique resource in academics. We have extensively described the capabilities of our protein production platforms in the literature[4]. These capabilities are being leveraged to realize a wide range of cutting-edge platform technologies, including receptor-ligand deorphaning, epitope discovery, the generation of novel biologics and the development of new clonal-specific T cell strategies for the treatment of malignancies and autoimmunity[5].

4. Almo SC, Garforth SJ, Hillerich BS, Love JD, Seidel RD, Burley SK. (2013) Protein production from the structural genomics perspective: achievements and future needs. Curr Opin Struct Biol. 23(3):335-44.

5. Samanta D, Mukherjee G, Ramagopal UA, Chaparro RJ, Nathenson SG, DiLorenzo TP, Almo SC. (2011) Structural and functional characterization of a single-chain peptide-MHC molecule that modulates both naive and activated CD8+ T cells. Proc Natl Acad Sci U S A. 108(33):13682-7.

III. Structural, functional and mechanistic analysis of the cell surface and secreted proteins that modulate adaptive and innate immunity. Cell surface receptors and adhesion molecules are the gatekeepers of cellular function, and are responsible for the detection of signals arising from developmental, morphogenetic and environmental cues central to normal physiology and pathology. Notably, these receptors and ligands are not only therapeutic targets, but soluble versions of these molecules are themselves widely exploited therapeutics for the treatment of autoimmune diseases, infectious diseases and malignancies. High resolution structural characterization and biochemical analyses of these complexes are mechanistically invaluable as they define the chemical and physical determinants underlying receptor:ligand specificity, affinity, oligomeric state, and valency. We have made significant contributions in these areas, including the structures of complexes of CTLA-4:B7-2[6], PD-1:PD-L2[7], DcR3:TL1A[8], DcR3:LIGHT, DcR3:FasL and HVEM:LIGHT, as well as B7-H3, B7-H4[9], TIM-3, NTB-A, CD84, GITRL, TIGIT, CRTAM, nectins and CD160, all of which are potential/proven targets for immunotherapy. These structures defined the determinants responsible for receptor:ligand recognition, which are being leveraged to generate a wide range of variants with altered biochemical properties (e.g., affinities, selectivities) to probe mechanism and provide new functional/therapeutic insights. A major challenge in these efforts is the fact that many, if not most, receptor:ligand pairs remain undefined and thus cannot be structurally characterized or exploited for immunotherapy. To address this bottleneck, we are developing experimental platform technologies for the rapid, systematic and affordable identification of cell surface protein-protein interacting partners and the mapping of protein interaction interfaces. This same platform provides powerful approaches to generate costimulatory receptors and ligands with a wide range of affinities and selectivities, which can be leveraged for the design of "tunable" immune modulators.

6. Schwartz J-C, Zhang X, Fedorov AA, Nathenson SG & **Almo SC** (2001) Structural Basis for Costimulation by the Human CTLA-4/B7-2 Complex. *Nature* **410**, 604-608.

7. Lázár-Molnár E, Yan Q, Cao E, Ramagopal U, Nathenson SG & **Almo SC** (2008) Crystal structure of the complex between programmed death-1 (PD-1) and its ligand PD-L2. *Proc Natl Acad Sci* U S A. **105**:10483-8.

8. Zhan C, Patskovsky Y, Yan Q, Li Z, Ramagopal U, Cheng H, Brenowitz M, Hui X , Nathenson SG, **Almo SC** (2011) Decoy Strategies: The Structure of TL1A-DcR3 Complex. *Structure* **19**:162-71.

9. Jeon H, Vigdorovich V, Garrett-Thomson SC, Janakiram M, Ramagopal UA, Abadi YM, Lee JS, Scandiuzzi L, Ohaegbulam KC, Chinai JM, Zhao R, Yao Y, Mao Y, Sparano JA, **Almo SC** & Zang X (2014) Structure and cancer immunotherapy of the B7 family member B7x. *Cell Rep* **9**, 1089-98.

MyBibliography: 358 entries; http://www.ncbi.nlm.nih.gov/sites/myncbi/1-CTfoJ579o5l/bibliography/45940359/public/?sort=date&direction=ascending

D. Additional Information: Research Support and/or Scholastic Performance

ACTIVE

P30 CA013330 (Goldman, PI)	07/01/07 – 06/30/22	1.0 cal mos
NIH/NCI	$71,408 TDC	

"Einstein Cancer Center: Structural Biology Facility"

This work provides structural biology facility support to the Einstein Cancer Center.

R01 CA198095-02 (Almo, PI)	06/01/16 – 05/31/21	2.4 cal mos
NIH/NCI	$311,715 Direct	

“Novel Strategies for Precision T-Cell Therapies”
This research focuses on the development and application of clonal-specific T cell immunotherapies.

R01 GM118709-02 (Fiser, PI; Almo, Co-PI) 06/01/16 – 04/30/20 0.6 cal mos
NIH/NIGMS $99,096 Direct
“Molecular Basis of Receptor-Ligand Recognition in the Immunological Synapse”
This grant concerns the development of computational methods for classifying the function of cell surface proteins.

P01 GM118303-02 (Gerlt, PI; Almo, Co-PI) 06/15/16 – 04/30/21 1.2 cal mos
NIH/NIGMS $610,420 Direct
“Novel Strategies for the Discovery of Microbial Metabolic Pathways”
Aims to develop and apply novel computational and experimental strategies to discover metabolic pathways in microbial species for which complete genome sequences are available.

R01 GM115972-01A1 (Hanein, Almo MPIs) 08/01/16 – 07/31/20 0.24 cal mos
NIH/NIGMS $35,262 TDC
“Structural Basis of Allostery and Mechanical Properties of F-Actin”
Studies on the application of experimental approaches to provide structures of actin filaments (F-actin) in different functional states.

R01 GM120238-01 (Wu, PI) 09/01/16 – 07/31/21 0.6 cal mos
NIH/NIGMS $17,575
“A Multiscale Model for Binding Kinetics of Membrane Receptors on Cell Surfaces”
The long-term goal is to design multivalent ligands for specific membrane receptors to artificially modulate cell signaling to shed light on mechanisms of ligand-receptor interactions and design of new drug candidates.

P41 GM118302-01 (Palmer, PI) 07/01/17- 05/31/22 0.24 cal mos
NIH/NIGMS $71,000
“Center on Macromolecular Dynamics by NMR Spectroscopy”
The focus is development and application of NMR methods for characterizing protein and nucleic acid conformational dynamics in biological processes including ligand recognition, allosterism, catalysis, and folding.

R01 AI132633-01 (Chandran, PI) 07/01/17- 06/30/22 0.24 cal mos
NIH/NIAID $72,117
“Dissecting the receptor-mediated infection mechanisms of hantaviruses”
The overall goals are to define the molecular mechanism by which PCDH1 mediates hantavirus entry and infection of endothelial cells and determine its utility as a target for the development of antiviral therapeutics

R01 AI123730-01A1 (DiLorenzo, Almo MPIs) 02/08/19- 01/31/23 1.2 cal mos
NIH/NIAID $146,371
“Structural, functional, and mechanistic analysis of autoreactive CD8 T cells”
Aims 1) Define the in vivo peptide presentation of human class I MHC alleles associated type 1 diabetes.

5R01GM122804-02 (Wu, PI; Almo, Co-PI) 09/20/17 – 07/31/21 0.6 cal mos
NIH/NIGMS $25,220
“Computational models for the signaling of tumor necrosis factor receptor on cell surfaces”

R01 DK120420-01 (DiLorenzo, PI; Almo, Co-PI) 09/01/18 – 07/31/21 1.2 cal mos
NIH/NIDDK $118,741
“An immunotherapeutic strategy for the induction and stabilization of remission in type 1 diabetes”

COMPLETED

U54 GM093342 (Gerlt, PI; Almo, Co-PI) 05/20/10 – 04/30/17
NIH/NIGMS “A Collaborative Center for an Enzyme Function Initiative”

R21 AI133329 (Almo, Grove MPIs) 06/26/17 – 05/31/19
NIH/NIAID “Function and Mechanism of Viperin, a Radical SAM Antiviral Protein”

R01 HG008325-03 (Almo, PI) 09/24/15 – 06/30/19
NIH/NHGRI “Technologies for Mapping the Extracellular Interactome”

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
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NAME: Bonanno, Jeffrey B.

eRA COMMONS USER NAME (credential, e.g., agency login): JBBONANNO

POSITION TITLE: Research Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Alfred University, Alfred, New York	B.A.	1990	Chemistry
Cornell University, Ithaca, New York	Ph.D.	1995	Chemistry
Columbia University, New York, New York	Postdoctoral	1996	Chemistry

A. Personal Statement

The focus of my research efforts has, for the last 20 years, been combining chemical and biochemical observations with structural analysis to more fully understand the structure/function relationship which controls the activities of biological macromolecules. The bulk of this work was with the NYSGRC supported by the Protein Structure Initiative (PSI), in which I served as crystallographer, program manager, and principle investigator (2001-2002). This allowed me to both address a broad range of problems from the perspective of three dimensional protein structure and also gain experience in development, operation and management of multi-investigator programs. I have also collaborated closely with the enzymologists, protein chemists and structural biologists engaged in the Enzyme Function Initiative (EFI) project. Following the PSI project, my focus has shifted to advancing high-impact collaborative projects which benefit strongly from HTP biophysical methods employed at Einstein. Given my experiences with the programs described above, and my position at Einstein as co-Director of the Crystallographic Core Shared Resource, I will be able to meaningfully serve this project.

B. Positions

Employment

09/90 – 05/92 Teaching Assistant, Cornell University, Ithaca
09/95 – 08/96 Postdoctoral Research Associate, Columbia University, New York
09/96 – 04/02 Research Specialist, Howard Hughes Medical Institute, New York
09/96 – 10/01 Research Associate, Rockefeller University, New York
11/01 – 12/02 Research Assistant Professor, Rockefeller University, New York
01/03 – 04/05 Senior Scientist, Structural GenomiX, Inc., San Diego
09/05 – 08/06 Deputy Director NYCOMPS, New York Structural Biology Center, New York
09/05 – 08/06 Regional Coordinator NYSGXRC, Columbia University Medical Center, New York
09/06 – 09/15 Associate, Albert Einstein College of Medicine, New York
09/15 – present Research Assistant Professor, Albert Einstein College of Medicine, New York

C. Contributions to Science

High-throughput Protein Expression and Structure Determination. As a direct result of many of the high-impact contributions of the Protein Structure Initiative (for which I played a variety of roles over 15 years), we now possess the ability to rapidly prosecute targets for gene-to-structure-to-function via bioinformatics target selection, orthologue expansion, domain and construct design, expression, purification, structure determination and biophysical analysis for functional annotation and inhibitor design. These achievements have expanded the approaches researchers will consider in experimental design to address biophysical research problems. The PSI, the EFI, and other structural genomics programs in the US and worldwide have generated an enormous amount of primary data and materials which are now routinely mined in the advancement of ongoing research. Likewise, the methods development which was integral to these projects has resulted in a manifold of accessible techniques for the parallel prosecution of multiple target proteins in structure determination, functional assessment, and inhibitor discovery. This is borne out by the numerous collaborative publications resulting from the support of the biological community by the PSI and EFI investigators and infrastructure (for two examples, see references 1 and 2). Additional studies on biologically focused projects resulted in remarkable discoveries (see references 3 and 4, for example). Finally, a large number of contributions arising from the PSI, EFI and other efforts, detailing powerful methods advancements have been published (see references 5 and 6, for example). See the full list of publications for many more examples in each category.

1. Sampathkumar P, Kim SJ, Upla P, Rice WJ, Phillips J, Timney BL, Pieper U, Bonanno JB, Fernandez-Martinez J, Hakhverdyan Z, Ketaren NE, Matsui T, Weiss TM, Stokes DL, Sauder JM, Burley SK, Sali A, Rout MP, Almo SC. (2013) Structure, dynamics, evolution, and function of a major scaffold component in the nuclear pore complex. *Structure* 21(4), 560-571.
2. Ho MC, Wilczek C, Bonanno JB, Xing L, Seznec J, Matsui T, Carter LG, Onikubo T, Kumar PR, Chan MK, Brenowitz M, Cheng RH, Reimer U, Almo SC, Shechter D. (2013) Structure of the arginine methyltransferase PRMT5-MEP50 reveals a mechanism for substrate specificity. *PLoS One* 8(2):e57008.
3. Kim J, Xiao H, Bonanno JB, Kalyanaraman C, Brown S, Tang X, Al-Obaidi NF, Patskovsky Y, Babbitt PC, Jacobson MP, Lee YS, Almo SC. (2013) Structure-guided discovery of the metabolite carboxy-SAM that modulates tRNA function. *Nature* 498(7452), 123-126.
4. Vladimirova A, Patskovsky Y, Fedorov AA, Bonanno JB, Fedorov EV, Toro R, Hillerich B, Seidel RD, Richards NG, Almo SC, Raushel FM. (2015) Substrate distortion and the catalytic reaction mechanism of 5-carboxyvanillate decarboxylase *J. Am. Chem. Soc.* Dec 30. Epub ahead of print, PMID: 26714575
5. Liu W, Vigdorovich V, Zhan C, Patskovsky Y, Bonanno JB, Nathenson SG, Almo SC. (2015) Increased Heterologous Protein Expression in Drosophila S2 Cells for Massive Production of Immune Ligands/Receptors and Structural Analysis of Human HVEM. *Molecular Biotechnology* 57(10), 914-922.
6. Zhao S, Kumar R, Sakai A, Vetting MW, Wood BM, Brown S, Bonanno JB, Hillerich BS, Seidel RD, Babbitt PC, Almo SC, Sweedler JV, Gerlt JA, Cronan JE, Jacobson MP. (2015) Discovery of new enzymes and metabolic pathways by using structure and genome context. *Nature* 502(7473), 698-702.

D. Additional Information: Research Support and/or Scholastic Performance

Research Support

N/A

NCBI Bibliography (81 entries):

https://www.ncbi.nlm.nih.gov/myncbi/1-9HrxzLoDrcNK/bibliography/public/