BIOGRAPHICAL SKETCH

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NAME: Jogl, Gerwald

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

POSITION TITLE: Associate Professor of Biology

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
Columbia University, New York	Post-Doc	08/2004	Structural Biology
Karl Franzens Universität Graz, Austria	Dr. rer. nat.	12/1999	Chemistry/Protein Crystallography
Karl Franzens Universität Graz, Austria	Mag. rer. nat.	05/1994	Chemistry/Crystallography

A. Personal Statement

My undergraduate research in chemistry and small molecule crystallography focused on the structure of cob(II)alamin, the radical species of coenzyme B12. My graduate research extended this work to structure-function studies of coenzyme B12 binding enzymes. During my postdoctoral training, I contributed to the structural biology of enzymes in fatty acid metabolism that are potential drug targets for the treatment of obesity (carnitine acetyl transferase, acetyl Co-A synthetase, carnitine palmitoyl transferase). With these studies, I acquired extensive expertise in X-ray and neutron crystallography. Current research in my group focuses on the structural biology of ribonucleoprotein complexes. In the first project, we use cryo-electron microscopy to study antibiotic resistance in bacterial ribosomes. Here, we focus on antibiotics that block ribosomal intersubunit and interdomain motions and on novel mutations that allosterically modulate these motions to cause resistance. The second project focuses on the structure and function of the human LINE-1 retrotransposon. We recently discovered small-molecule inhibitors against the endonuclease domain of the LINE-1 ORF2 protein and characterized their activity biochemically and in cell culture (in collaboration with Dr. John Sedivy). We also discovered that the LINE-1 ORF1 protein serves as RNA chaperone and is capable of phase separation. The third project, in collaboration with Dr. George Lisi, focuses on the structural dynamics and allosteric regulation of CRISPR-Cas9.

1. Murphy EL, Singh KV, Avila B, Kleffmann T, Gregory ST, Murray BE, Krause KL, Khayat R, Jogl G; Cryo-electron microscopy structure of the 70S ribosome from *Enterococcus faecalis*. Sci Rep 2020;10(1):16301. PMCID: PMC7530986.
2. Newton JC, Naik MT, Li GY, Murphy EL, Fawzi NL, Sedivy JM, Jogl, G; Phase separation of the LINE-1 ORF1 protein is mediated by the N-terminus and coiled-coil domain. Biophys J, 2021; 120(11): 2181-2191. PMCID: PMC8390800.
3. D'Ordine AM, Jogl G, Sedivy JM; Identification and characterization of small molecule inhibitors of the LINE-1 retrotransposon endonuclease. Nat Commun 2024; 15(1):3883. PMCID: PMC11078990
4. Skeens E, Sinha S, Ahsan M, D'Ordine AM, Jogl G, Palermo G, Lisi GP**;** High-fidelity, hyper-accurate, and evolved mutants rewire atomic-level communication in CRISPR-Cas9. Sci Adv 2024; 10(10):eadl1045. PMCID: PMC10917355.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2011 – present	Associate Professor of Biology, Brown University.
2004 – 2011	Assistant Professor of Biology, Brown University.
2020 – present	Instructor, Epiphany Education Limited, Hong Kong

2024	NIH ad-hoc reviewer study section ZRG1 F04-S.
2022	NIH ad-hoc reviewer study section Macromolecular Structure and Function B.
2019	NIH ad-hoc reviewer study section Macromolecular Structure and Function B.
2018	NIH ad-hoc reviewer panel ZRG1 IMST H02.
2017	NIH ad-hoc reviewer study section Macromolecular Structure and Function B. NIH mail-in reviewer panel ZRG1 RPHB-W.
2016	NIH ad-hoc reviewer study section Macromolecular Structure and Function B.
2015	NIH ad-hoc reviewer study section Macromolecular Structure and Function C.
2014	NIH ad hoc reviewer panel ZRG1 IDM S02.
2012 - 2015	Lecturer for the RapiData data collection and structure solving course at the NSLS I.
2012 - 2015	Ad hoc grant proposal reviewer for the Biotechnology and Biological Sciences Research Council, UK, the Czech Science Foundation, the Universities of Vienna and of Graz, Austria
2010	National Science Foundation major research instrumentation review panelist
2008 – present	Member, RNA Society
2006 – present	Member, American Society for Biochemistry and Molecular Biology
2004 – present	Member, American Crystallographic Association

Honors

2018	Brown University Elizabeth Leduc Award of Excellence in Teaching in the Life Sciences
1994	M.Sc. Thesis Award, Austrian Chemical Society.
1992	Erasmus, EU Student Research Scholarship with the Glaxo-Wellcome Protein Structure Group, London, UK

C. Contributions to Science

1. Antibiotic resistance in bacterial ribosomes. The rise of antibiotic-resistant pathogens presents a continuous threat to human health. Given that the bacterial ribosome is the target for many antibiotic compounds, a major research focus is to determine the structural basis for resistance caused by mutations in the ribosome. In close collaboration with Drs. Steven Gregory (University of Rhode Island) and Reza Khayat (New York City College), we study ribosomes from pathogenic bacteria and the mechanism of antibiotic resistance due to mutations in ribosomal RNA.

1. Killeavy EE, Jogl G, Gregory ST. Tiamulin-Resistant Mutants of the Thermophilic Bacterium *Thermus thermophilus*. Antibiotics (Basel). 2020;9(6). PMCID: PMC7345174.
2. Demirci H, Murphy FVt, Murphy EL, Connetti JL, Dahlberg AE, Jogl G, Gregory ST. Structural analysis of base substitutions in *Thermus thermophilus* 16S rRNA conferring streptomycin resistance. Antimicrobial agents and chemotherapy. 2014;58(8):4308-17. PMCID: PMC4136021.
3. Demirci H, Murphy Ft, Murphy E, Gregory ST, Dahlberg AE, Jogl G. A structural basis for streptomycin-induced misreading of the genetic code. Nature communications. 2013;4:1355. PMCID: PMC3552334.

2. Post synthesis ribosome modification. Both ribosomal RNA and ribosomal proteins are post-transcriptionally and post-translationally modified on sites that are conserved from bacteria to humans. In contrast to tRNA modifications, the function of ribosomal modifications remains poorly understood. In collaboration with Steven Gregory, we studied a considerable number of ribosome methyltransferases. This work defined substrate recognition mechanisms of bacterial methyltransferases and contributed to understanding the significance of these modifications for ribosome function.

1. Demirci H., Murphy IV F.V., Belardinelli R., Kelley A.C., Ramakrishnan V., Gregory S.T., Dahlberg A.E., Jogl G. (2010). Modification of 16S ribosomal RNA by the KsgA methyltransferase restructures the 30S subunit to optimize ribosome function. RNA 16, 2319-2324. PMCID: PMC2995393.
2. Demirci H., Larsen H.G.L., Hansen T., Rasmussen A., Cadambi A., Gregory S.T., Kirpekar F., Jogl G. (2010). Multi-site specific 16S rRNA methyltransferase RsmF from *Thermus thermophilus*. RNA 16, 1584-1596. PMCID: PMC2905757.
3. Demirci H., Belardinelli R., Seri E., Gregory S.T., Gualerzi C., Dahlberg A.E., Jogl G. (2009). Structural rearrangements in the active site of the *Thermus thermophilus* 16S rRNA methyltransferase KsgA in a binary complex with 5'-methylthioadenosine. J. Mol. Biol. 388, 271-282. PMCID: PMC2679894
4. Demirci H., Gregory S.T., Dahlberg A.E., Jogl G. (2007). Recognition of ribosomal protein L11 by the protein trimethyltransferase PrmA. EMBO J. 26, 567-577. PMCID: PMC1783454

3. Protein structure and function. We continue to characterize the structure and function of enzymes important in eukaryotic cell function, in biosynthesis of antibiotic compounds, or in gene engineering.

1. Newton J.C., Naik M.T., Li G.Y., Murphy E.L., Fawzi N.L., Sedivy J.M., Jogl G. (2021) Phase separation of the LINE-1 ORF1 protein is mediated by the N-terminus and coiled-coil domain. Biophys J, 120(11):2181-2191. PMCID: PMC8390800.
2. Li H. & Jogl G. (2009). Structural and biochemical studies of TIGAR (*TP53*-Induced Glycolysis and Apoptosis Regulator). J. Biol. Chem. 284, 1748-1754. PMCID: PMC2615519.
3. You Z., Omura S., Ikeda H., Cane D.E., Jogl G. (2007). Crystal structure of the non-heme iron dioxygenase PtlH in pentalenolactone biosynthesis. J. Biol. Chem. 282, 36552-36560. PMCID: PMC3010413.
4. Holmes W. & Jogl G. (2006). Crystal structure of inositol phosphate multikinase 2 and implications for substrate specificity. J. Biol. Chem. 281, 38109-38116. PMID: 17050532.

4. Fatty Acid metabolism. My work in this field defined for the first time the structural biology of fatty acid transfer onto carnitine, a fundamental step in fatty acid catabolism. Structural and biochemical studies of four carnitine acyltransferases, crucial enzymes in fatty acid metabolism, explored the potential of these enzymes as drug targets for the treatment of obesity.

1. Jogl G., Hsiao Y., Tong L. (2005). Crystal structure of mouse carnitine octanoyltransferase and molecular determinants of substrate selectivity. J. Biol. Chem. 280, 738-744. PMID: 15492013.
2. Hsiao Y., Jogl G.**,** Tong L. (2004). Structural and biochemical studies of the substrate selectivity of carnitine acetyltransferase. J. Biol. Chem. 279, 31584-31589 (2004). PMID: 15155726.
3. Jogl G. & L. Tong. (2004) Crystal structure of yeast acetyl-coenzyme A synthetase in complex with AMP. Biochemistry 43, 1425-1431. PMID: 14769018.
4. Jogl G. & L. Tong. (2003) Crystal structure of carnitine acetyltransferase and implications for the catalytic mechanism and fatty acid transport. Cell 112, 113-122. PMID: 12526798.

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/myncbi/gerwald.jogl.1/bibliography/public/