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

A. Personal Statement

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, our major research focus is to determine the structural basis for resistance cause by mutations in the ribosome. We are especially interested in mutations that cause resistance by modulating ribosomal dynamics instead of distorting the antibiotics binding site. In a close collaboration with Steven Gregory at the University of Rhode Island, we used X-ray crystallography to study streptomycin resistance and dependence mutations. With the advent of the resolution revolution, I initiated a collaboration with Reza Khayat at the New York City College that produced a new ribosome structure from a human pathogen and several ongoing structural studies. In addition, I study cryo-electron microscopy as an embedded trainee at the NIH National Center for Cryo-EM Access and Training in New York. This combination enables my group to use cryo-EM as the major tool to study antibiotics that block ribosomal motions and novel mutations that allosterically modulate these motions to cause resistance.

The associated ongoing research project I would like to highlight is:

R01 GM094157
Jogl (MPI)
09/15/10 – 08/31/25
Structural robustness of ribosome functional centers

Citations

1. 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. 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. Killeavy EE, **Jogl G**, Gregory ST. Tiamulin-Resistant Mutants of the Thermophilic Bacterium *Thermus thermophilus*. Antibiotics (Basel). 2020;9(6). PMCID: PMC7345174.
4. 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.

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
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. Coenzyme B12. My early work in this field focused on the significance of corrin ring flexing motions for the reactivity of coenzyme B12 in enzyme catalyzed reactions. To address this question, we determined neutron crystal structures of the radical coenzyme B12 species cob(II)alamin with a vacant sixth coordination site at the central cobalt atom. Neutron crystallography required the synthesis of this radical B12 coenzyme and the production of up to 5mm long crystals in an oxygen-free environment. This work was complemented by structural studies of two coenzyme B12-dependent enzymes using X-ray crystallography and EXAFS. Our data showed that corrin ring dynamics contribute less to enzyme catalysis than had been anticipated in the field.

1. Langan P., Lehmann M., Wilkinson C., Jogl G., Kratky C. (1999). Neutron Laue diffraction studies of coenzyme cob(II)alamin. Acta Cryst. D 55, 51-59. PMID: 10089394
2. Reitzer R., Gruber K., Jogl G., Wagner U.G., Bothe H., Buckel W., Kratky C. (1999). Glutamate mutase from *Clostridium cochlearium*: the structure of a coenzyme B_{12}-dependent enzyme provides new mechanistic insights. Structure 7, 891-902. PMID: 10467146
3. Champloy F., Jogl G., Reitzer R., Buckel W., Bothe H., Michalowicz A., Meyer-Klaucke W., Kratky C. (1999). EXAFS data support a short axial cobalt-nitrogen bond of the B_{12} cofactor in the two coenzyme B_{12}-dependent enzymes glutamate mutase and 2-methyleneglutarate mutase. J. Amer. Chem. Soc. 121, 11780-11789. DOI: 10.1021/ja990349q.
4. Jogl G., Wang X., Mason S.A., Kovalevsky A., Mustyakimov M., Fisher Z., Hoffman C., Kratky C., Langan P. (2011). High-resolution neutron crystallographic studies of the hydration of the coenzyme cob(II)alamin. Acta Cryst. D 67, 584-591. PMCID: PMCID 3107055.

2. 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. & L. Tong. (2003) Crystal structure of carnitine acetyltransferase and implications for the catalytic mechanism and fatty acid transport. Cell 112, 113-122. PMID: 12526798.
2. Jogl G. & L. Tong. (2004) Crystal structure of yeast acetyl-coenzyme A synthetase in complex with AMP. Biochemistry 43, 1425-1431. PMID: 14769018.
3. 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.
4. 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.

3. Structural enzymology. Several studies reflect my keen interest in understanding enzymatic function on a molecular and structural level. These publications characterize the structure and function of enzymes important in eukaryotic cell function, in biosynthesis of antibiotic compounds, or in gene engineering.

1. 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.
2. 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.
3. 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.
4. East K.W., Newton J.C., Morzan U.N., Narkhede Y.B., Acharya A., Skeens E., Jogl G., Batista V.S., Palermo G., Lisi G.P. (2020). Allosteric Motions of the CRISPR-Cas9 HNH Nuclease Probed by NMR and Molecular Dynamics. J. Am. Chem. Soc. 142, 1348-1358. PMID:31885264

4. 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., 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
2. 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
3. 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.
4. 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.

Complete List of Published Work in MyBibliography:
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