BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Thomas, Leonard M.

eRA COMMONS USER NAME: lmthomas

POSITION TITLE: Facility Director, Biomolecular Structure Core (Lead Researcher)

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
St. Bonaventure Univ., St. Bonaventure, NY	B.S.	05/1983	Physics
SUNY at Buffalo, Buffalo, NY	M.S.	02/1986	Natural Science (H. Box)
SUNY at Buffalo, Buffalo, NY	Ph.D.	02/1996	Biophysics (N. Ramasubbu)
Iowa State University, Ames, IA	Postdoc	08/1997	Crystallography (R. Jacobson)
Univ. of Missouri-Kansas City, Kansas City, MO	Postdoc	11/2000	Structural Biology (M. Yoder)

A. Personal Statement

In my position as Facility Director of the University of Oklahoma-Norman Biomolecular Structure Core (BSC) I am able to offer my expertise and knowledge of X-ray crystallography, crystallization and X-ray instrumentation to provide core facility services to academic research groups that require access to these types of services. I have been working in or managing both single crystal and non-crystalline X-ray diffraction laboratories for over 35 years. I have assembled a Laue diffraction facility for alignment of crystals for solid state laser research along with powder diffraction for determining laser host material phase information. After that I oversaw the small molecule diffraction facility at Iowa State University. As a postdoctoral associate working on the crystallization and structure determination of pectate lyases with Marilyn Yoder, I oversaw the in-house X-ray diffraction setup at UMKC. For the last 23 years I have been working with instrumentation used for the growth of crystals and the collection of X-ray data primarily from single crystals of macromolecules. I have developed and managed high-throughput macromolecular crystallization facilities at both Caltech and OU and have overseen the upgrades of both institutions in-house X-ray diffraction instrumentation. I have over 20 years experience at collecting X-ray diffraction data at national synchrotron laboratories. My experience in macromolecular data collection and subsequent structure determination allows me to interact with research groups who utilize the facility by providing expertise from initial crystallization experiment to final structure deposition. Furthermore, I am familiar with the problems that can arise with crystallization and X-ray instrumentation in a multi-user environment and can resolve any issues that arise. Over the last 2 years I have developed techniques for Cryo-EM grid preparation for Single Particle Analysis in the BSC-Norman also with developing the computational infrastructure to process Cryo-EM data for structure determination.

Ongoing grant-supported project that I would like to highlight include:

P20 GM103640 and P30 GM145423
Director of the OU-Norman Biomolecular Structure Core Facility
09/06/17- Present
Oklahoma Center of Biomedical Research Excellence (COBRE) in Structural Biology (Phase 2 and Phase 3)

B. Positions, Scientific Appointments, and Honors

2008 – present	Lead Researcher and Adjunct Lecturer, Dept. of Chemistry & Biochemistry, U. of Oklahoma, Norman, OK
2000 – 2008	Research Specialist II, Howard Hughes Med. Inst., California Inst. of Tech., Pasadena, CA
1998 – 2000	Research Associate, School of Biology, U. of Missouri-Kansas City, Kansas City, MO
1997 – 1998	Assistant Professor, Div. of Math and Science, Phillips Univ., Enid, OK
1995 – 1997	Supervisor, Dept. of Chemistry, Iowa State Univ., Ames, IA
1994 – 1995	Postdoctoral Associate, Dept. of Chemistry, Iowa State Univ., Ames, IA
1990 – 1994	Research Affiliate, Dept. of Oral Biology, SUNY at Buffalo, Buffalo, NY
1986 – 1990	Scientist, Fibertek, Inc., Herndon VA
1984 – 1986	Graduate Student, Roswell Park Graduate Div., SUNY at Buffalo, Buffalo, NY
1982 – 1983	Undergraduate Teaching Assistant, Dept. of Physics, St. Bonaventure U, St. Bonaventure, NY

C. Contributions to Science

1) As the director of a core research laboratory, I am able to contribute to a wide variety of projects that require expertise in crystallization and crystallography. One of the primary functions of a university is education and I have trained a large number of undergraduate, graduate and postdoctoral students in structural biology in formal classes, workshops, and one-on-one training sessions. I have trained and supervised the undergraduate students that performed the crystal growth and structure determinations of *Escherichia coli* AdhP (ethanol-inducible dehydrogenase) (Thomas et al. 2013) and the G-U Pair RNA constructs (Gu et al. 2015). My collaborations continued to helped determine structures for the Karr lab group, Hcd1 (Dinh et al. 2023), and by the primary authors in the Richter-Addo lab, nitroreductases (Wang et al. 2018).

    a) D.M. Dinh, **L.M. Thomas** and E.A. Karr, (2023) Crystal structure of a putative 3-hydroxypimelyl-CoA dehydrogenase, Hcd1, at 1.78 Å resolution from *Syntrophus aciditrophicus* strain SB. Acta Cryst F Struct Biol Commun 79(6):151-158. doi: 10.1107/S2053230X23004399. PMCID: PMC10231260
    b) B. Wang, Y. Shi, J. Tejero, S.M. Powell, **L.M. Thomas**, M.T. Gladwin, S. Shiva, Y. Zhang, G.B. Richter-Addo (2018) Nitrosyl myoglobins and their nitrite precursors: Crystal structural and quantum mechanical and molecular mechanics theoretical investigations of preferred Fe–NO ligand orientations in myoglobin distal pockets. *Biochemistry* 57: 4788-4802. PMCID: PMC6474360
    c) X. Gu, B.H. Mooers, **L.M. Thomas**, J. Malone, S. Harris, S.J. Schroeder (2015) Structures and energetics of four adjacent G·U pairs that stabilize an RNA helix. *J Phys Chem B.* 119: 13252-61. PMCID: PMC4830635
    d) **L.M. Thomas,** A.R. Harper, W.A. Miner, H.O. Ajufo, K.M. Branscum, L. Kao, P.A. Sims (2013) Structure of *Escherichia coli* AdhP (ethanol-inducible Dehydrogenase) with bound NAD. *Acta Cryst*. F69: 730-732. PMCID: PMC3702314

2) In my capacity of directing and managing a core facility I have worked on a significant number of different macromolecular systems ranging from a variety of enzymes to metal-containing proteins to larger protein complexes. A number of these projects presented crystallography challenges from significant disorder to low resolution diffraction which I was able to help overcome.

    a) L. Chooback, **L.M. Thomas**, N. Blythe, W. Karsten, (2022) Kinetic and structural studies of the reaction of the *Escherichia coli* dihydrodipicolinate synthase with (S) 2-bromo-propionate. *Acta Cryst D.,*78, 846-852. doi: 10.1107/S2059798322005125
    b) B.P Johnson, V. Kumar, E.M. Scull, **L.M. Thomas,** C.R. Bourne and S. Singh, (2022) Molecular basis for the substrate promiscuity of isopentenyl phosphate kinase from *Candidatus methanomethylophilus alvua*. ACS Chem. Bio., 17, 85-102. doi.org/10.1021/acschembio.1c00655, PubMed PMID: 34905349.
    c) W. Karsten, **L.M. Thomas**, C. Fleming, P. Seabourn, C. Bruxvoort, L.Chooback (2021) Kinetic, spectral, and structural studies of the slow-binding inhibition of the *Escherichia coli* dihydrodipicolinate synthase by 2, 4-oxo-pentanoic acid. *Arch. of Biochem. Biophys.* 702: 108819. doi:10.1016/j.abb.2021.108819. PMID: 33639104

d) P.N. Muddala, J.C. White, B. Nammalwar, I. Pratt, **L.M**. **Thomas,** R.A. Bunce, K.D. Berlin, C.R. Bourne (2020) Inhibitor design to target a unique feature in the folate pocket of *Staphylococcus aureus* dihydrofolate reductase. *Eur. J. Med. Chem.* 200: 112412. PMID: 32502861
e) M.I. Davis, M.J. Bennett, **L.M. Thomas**, P.J. Bjorkman (2005) Crystal Structure of prostate-specific membrane antigen, a tumor marker and peptidase. *Proc. Natl. Acad. Sci*. 102: 5981-5986. PMCID: PMC556220

3) The Richter-Addo group at the University of Oklahoma has been investigating the interaction of nitrogen oxides (NOx) with iron containing proteins such as hemoglobin and myoglobin. I have worked with extensively with this group on the solution and refinement of a number of NOx containing structures. Some of the structures presented a challenge due to a significant amount of disorder based on the interaction of the iron containing moiety with NOx. I contributed significantly to the group's research projects by checking both the macromolecular structure and ligand definitions as well as modeling the observed significant disorder in the structures.

a) S.M. Powell, B. Wang, V.E. Herrera, K.Y. Prather, N.T. Ngyuen, E.G. Abucayon, **L.M. Thomas**, M.K. Safo, and G.B. Richter-Addo, (2023) Crystal structural investigations of heme protein derivatives resulting from reactions of aryl- and alkylhydroxylamines with human hemoglobin. J Inorg Biochem. 246:112304. doi: 10.1016/j.jinorgbio.2023.112304. PMCID: PMC10348690
b) S.M. Powell, K.Y. Prather, N.T. Ngyuen, **L.M. Thomas**, and G.B. Richter-Addo, (2023) Interactions of metronidazole and chloramphenicol with myoglobin crystal structure of a Mb-acetamide product. *J. Porphyrins and Phthalocyanines*. 27(7):1142-1147. doi: 10.1142/S10884246235007. PMCID: PMC10588810
c) V.E. Herrera, T.P. Charles, T.G. Scott, K.Y. Prather, N.T. Nguyen, C.D. Sohl, **L.M. Thomas**, and G.B. Richter-Addo**,** (2023) Insights into nitrosoalkane binding to myoglobin provided by crystallography of wild-type and distal pocket mutant derivatives. *Biochemistry* 62(8):1406-1419. doi: 10.1021/acs.biochem.2c00725. PMCID: PMC10338068
d) S.M. Powell, **L.M. Thomas**, G.B. Richter-Addo (2020) The nitrosoamphetamine metabolite is accommodated in the active site of human hemoglobin: Spectroscopy and crystal structure. *J Inorg Biochem.* 213: 111262. PMCID: PMC7686107

4) The increasing availability of high-speed computers has opened up the field molecular modeling and dynamics. I have worked with a number of computational researchers in determining the structures of designed proteins to either prove or disprove the validity of the overall design.

a) Y. Mou, P.S. Houng, **L.M. Thomas**, S.L. Mayo (2015) Using molecular dynamics simulations as an aid in the prediction of domain swapping of computationally designed protein variants. *J Mol. Biol.* 427: 2697-2706. PMID: 26101839
b) H.K. Privett, G. Kiss, T.M. Lee, R. Blomberg, R.A. Chica, **L.M. Thomas**, D. Hilvert, K.N. Houk, S.L. Mayo (2012) Iterative approach to computational enzyme design. *PNAS* 109: 3790-3795. PMID: 22357762
c) G.K. Hom, J.K. Lassila, **L.M. Thomas**, S.L. Mayo (2005) Dioxane contributes to the altered conformation and oligomerization state of a designed engrailed homeodomain variant. *Protein Sci*. 14: 1115-9. PMID: 15741348.

5) In collaboration with my graduate student advisor Dr. N. Ramasubbu I have worked on the structures of several proteins that are found in human saliva. Some of these proteins, such as salivary α-amylase, are involved in the digestive process. Others are involved in the formation of biofilms in the oral cavity, dispersin B.

a) C. Parthiban, D. Varudharasu, M. Shanmugam, P. Gopal, C. Ragunath, **L.M. Thomas**, M. Nitz, N. Ramasubbu (2017) Structural and functional analysis of de-N-acetylase PgaB from periodontopathogen *Aggregatibacter actinomycetemcomitans*. *Mol Oral Microbiol.* 32: 324-340. PMID:27706922
b) N. Ramasubbu, **L.M. Thomas**, C. Ragunath, J.B. Kaplen (2005) Structural analysis of dispersin B, a biofilm-releasing glycoside hydrolase from the periodontopathogen *Actinobacillus actinomycetemcomitians*. *J. Mol. Biol* 349: 475-486. PMID: 15878175

c) N. Ramasubbu, C. Ragunath, P.J. Mirshra, **L.M. Thomas**, G. Gyemant, L. Kandra (2004) Human salivary α-amylase Trp58 situated at subsite-2 is critical for enzyme activity. *Eur J Biochem* 271: 2517-2529. PMID: 15182367

d) N. Ramasubbu, **L.M. Thomas**, K.K. Bhandary, M.J. Levine (1993) Structural characteristics of human salivary statherin: A model for boundary lubrication at the enamel surface. *Crit. Rev. Oral Biol. Med.* 4: 363-370. PMID: 8373992.

Complete List of Published Work in NCBI (MyBibliography – 52 entries):
https://www.ncbi.nlm.nih.gov/myncbi/1xkfdb43CM25M/bibliography/public/

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. DO NOT EXCEED FIVE PAGES.

NAME: Sabisch, Julian

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

POSITION TITLE: Research Scientist

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)	END DATE MM/YYYY	FIELD OF STUDY
University of California, Berkeley, Berkeley, California	BS	05/2011	Materials Science and Engineering
University of California, Berkeley, Berkeley, California	MS	05/2012	Materials Science and Engineering
University of California, Berkeley, Berkeley, California	PHD	12/2017	Materials Science and Engieering
Sandia National Laboratories, Livermore, California	Other training	06/2020	Postdoctoral Appointee

A. Personal Statement

Assisted in the Oklahoma Microscopy Society outreach program, "The Ugly Bug Contest". This program asks local K-12 schoolchildren to submit their "ugly bug" samples for SEM microscopy investigation, after which the year's "ugliest bug" will be voted on.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2020 - Research Scientist, University of Oklahoma, Office for the Vice President of Research and Partnerships, Samuel Roberts Noble Microscopy Laboratory, Norman, CA

2018 - 2020 Postdoctoral Appointee, Sandia National Laboratories, Livermore, CA

C. Contribution to Science

1. a. Sabisch J, Sugar J, Ronevich J, San Marchi C, Medlin D. Interrogating the Effects of Hydrogen on the Behavior of Planar Deformation Bands in Austenitic Stainless Steel. Metallurgical and Materials Transactions A. 2021 February 27; 52(4):1516-1525. Available from: http://link.springer.com/10.1007/s11661-021-06170-3 DOI: 10.1007/s11661-021-06170-3
   b. Kacher J, Sabisch J, Minor A. Statistical analysis of twin/grain boundary interactions in pure rhenium. Acta Materialia. 2019 July; 173:44-51. Available from: https://linkinghub.elsevier.com/retrieve/pii/S1359645419302538 DOI: 10.1016/j.actamat.2019.04.051
   c. Jiang L, Radmilović V, Sabisch J, Qi L, Minor A, Chrzan D, Asta M. Twin nucleation from a singledislocation in hexagonal close-packed crystals. Acta Materialia. 2021 January; 202:35-41.

Available from: https://linkinghub.elsevier.com/retrieve/pii/S1359645420308363 DOI: 10.1016/j.actamat.2020.10.038

d. Sabisch J, Minor A. Microstructural evolution of rhenium Part I: Compression. Materials Science and Engineering: A. 2018 August; 732:251-258. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0921509318308530 DOI: 10.1016/j.msea.2018.06.057

2. a. Noell P, Sabisch J, Medlin D, Boyce B. Nanoscale conditions for ductile void nucleation in copper: Vacancy condensation and the growth-limited microstructural state. Acta Materialia. 2020 February; 184:211-224. Available from: https://linkinghub.elsevier.com/retrieve/pii/S1359645419307530 DOI: 10.1016/j.actamat.2019.11.022

b. San Marchi C, Ronevich J, Sabisch J, Sugar J, Medlin D, Somerday B. Effect of microstructural and environmental variables on ductility of austenitic stainless steels. International Journal of Hydrogen Energy. 2021 March; 46(23):12338-12347. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0360319920334893 DOI: 10.1016/j.ijhydene.2020.09.069

c. Sabisch J, Anapolsky A, Liu G, Minor A. Evaluation of using pre-lithiated graphite from recycled Li-ion batteries for new LiB anodes. Resources, Conservation and Recycling. 2018 February; 129:129-134. Available from: https://linkinghub.elsevier.com/retrieve/pii/S0921344917303634 DOI: 10.1016/j.resconrec.2017.10.029

d. Wu M, Sabisch J, Song X, Minor A, Battaglia V, Liu G. In Situ Formed Si Nanoparticle Network with Micron-Sized Si Particles for Lithium-Ion Battery Anodes. Nano Letters. 2013 October 02; 13(11):5397-5402. Available from: https://pubs.acs.org/doi/10.1021/nl402953h DOI: 10.1021/nl402953h