



## Dr. Susan De Long

- Associate Professor of Civil and Environmental Engineering, Colorado State University
- Joint faculty in Chemical and Biological Engineering
- Associate faculty in the School of Biomedical Engineering

Dr. Susan De Long is an Associate Professor in the Department of Civil and Environmental Engineering at Colorado State University. She has Bachelor's degrees in Environmental Science and Molecular and Cell Biology from the University of California, Berkeley and an M.S. and Ph.D. in Environmental Engineering from The University of Texas, Austin. She has over 15 years of experience working in the fields of environmental engineering, microbiology and applied molecular biology.

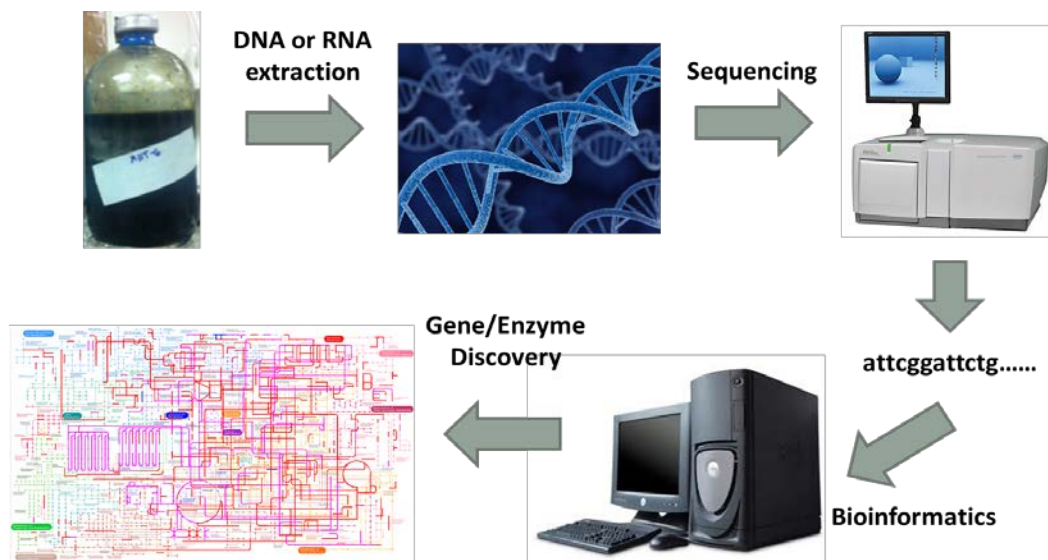
Her on-going research thrusts include:

- LNAPL bioremediation
- Enhanced natural source zone depletion
- Leveraging RNA methods for documenting biodegradation activity
- Cryocore analysis
- Application of next-generation gene sequencing methods, including metagenomics and metatranscriptomics, to site remediation and contaminant treatment
- Development of novel biomarkers for biodegradation
- Molecular assay development.
- Biodegradation of emerging contaminants, including pharmaceuticals and personal care products
- Bioenergy and biomaterial generation from waste
- Wastewater treatment for reuse.



*Processing cryocore*

*biomarker discovery using next generation gene sequencing workflow*



# Papers and Theses

## Selected publications

Chignell J.F., De Long SK, Reardon KF. (2018). Meta-proteomic analysis of protein expression distinctive to electricity-generating biofilm communities in air-cathode microbial fuel cells. *Biotechnology for Biofuels* 11. Epub ahead of print.

Kim, S., Rossmassler, K., Broeckling, C.D., \*Galloway, S., Prenni, J. and De Long, S.K. (2017) Impact of inoculum sources on biotransformation of pharmaceuticals and personal care products. *Water Res.*125: 227-236.

Chignell, J.F., Park, S., Lacerda, C.M.R., De Long, S.K., Reardon, K.F. (2017) Label-free proteomics of a defined, binary co-culture reveals diversity of competitive responses between members of a model soil microbial system. *Microbial Ecol.* 75:701-719. doi: 10.1007/s00248-017-1072-1.

Wilson, L.P., Sharvelle, S.E., De Long, S.K. 2016. Enhanced anaerobic digestion performance via combined solids- and leachate-based hydrolysis reactor inoculation. *Bioresour. Technol.*, 220, 94-103.

Irianni-Renno, M., Akhbari, D., Olson, M.R., Byrne, A.P., Lefevre, E., Zimbron, J., Lyverse, M., Sale, T.C., De Long, S.K. (2016) Comparison of bacterial and archaeal communities in depth-resolved zones in an LNAPL body. *Appl. Microbiol. Biotechnol.* 100(7):3347-60.

Zeman, N.R., Irianni Renno, M., Olson, M.R., Wilson, L.P., Sale, T.C., De Long, S.K. (2014) Temperature impacts on anaerobic biotransformation of LNAPL and concurrent shifts in microbial community structure. *Biodegradation.*25, 569-585.

Wilson, L.P., Loetscher, L.H., Sharvelle, S.E., De Long, S.K. (2013) Microbial community acclimation enhances waste hydrolysis rates under elevated ammonia and salinity conditions. *Bioresour. Technol.* 146, 15-22.

Lefèvre, E., Pereyra, L.P., Hiibel, S.R., Perrault, E.M., De Long, S.K., Reardon, K.F., Pruden, A. (2013) Molecular assessment of the sensitivity of sulfate-reducing microbial communities remediating mine drainage to aerobic stress. *Water Res.* 47, 5316-25.

Ledeker, B.M., De Long, S.K. (2013) The effect of multiple primer-template mismatches on quantitative PCR accuracy and development of a multi-primer set assay for accurate quantification of *pcrA* sequence variants. *J. Microbiol. Methods.* 3, 224-31.

De Long, S.K., Li, X., Bae, S., Brown, J.C., Raskin, L., Kinney, K.A., Kirisits, M.J. (2012) Quantification of genes and gene transcripts for microbial perchlorate reduction in fixed-bed bioreactors. *J. Appl. Microbiol.* 112, 579-592.

London, M.R., De Long, S.K., Strahota, M.D., Katz, L.E. and Speitel, G.E. (2011) Autohydrogenotrophic perchlorate reduction kinetics of a microbial consortium in the presence and absence of nitrate. *Water Res* 45, 6593-6601.

De Long, S.K., Kinney, K.A., Kirisits, M.J. (2010) qPCR assays to quantify genes and gene expression associated with microbial perchlorate reduction. *J. Microbiol. Methods* 83,270-4.

De Long, S.K., Kinney, K.A., Kirisits, M.J. (2008) A targeted method to sequence prokaryotic biodegradation genes: prokaryotic SSH PCR cDNA subtraction. *Appl. Environ. Microbiol.* 74(1):225-232.

## Technical Reports

M. Olson, W. Clayton, T. Sale, R. Johnson, S.K. De Long, M. Irianni-Renno, and R. Rogers. (2017) Evaluating Long-Term Impacts of Soil Mixing Source-Zone Treatment using Cryogenic Core Collection. ESTCP. Report no.: ER-201587.

Kirisits, M., Kinney, K., Bae, S. and De Long, S.K. (2013) Prokaryotic cDNA Subtraction: A Method to Rapidly Identify Functional Gene Biomarkers. SERDP Project ER-1563.

## Theses

Emerson, E.D. Biotic Control of LNAPL Longevity-laboratory and field-scale studies. Master's Thesis, Colorado State University, 2016.

Irianni-Renno, M. Biogeochemical characterization of a LNAPL body in support of STELA. Master's Thesis, Colorado State University, 2013.