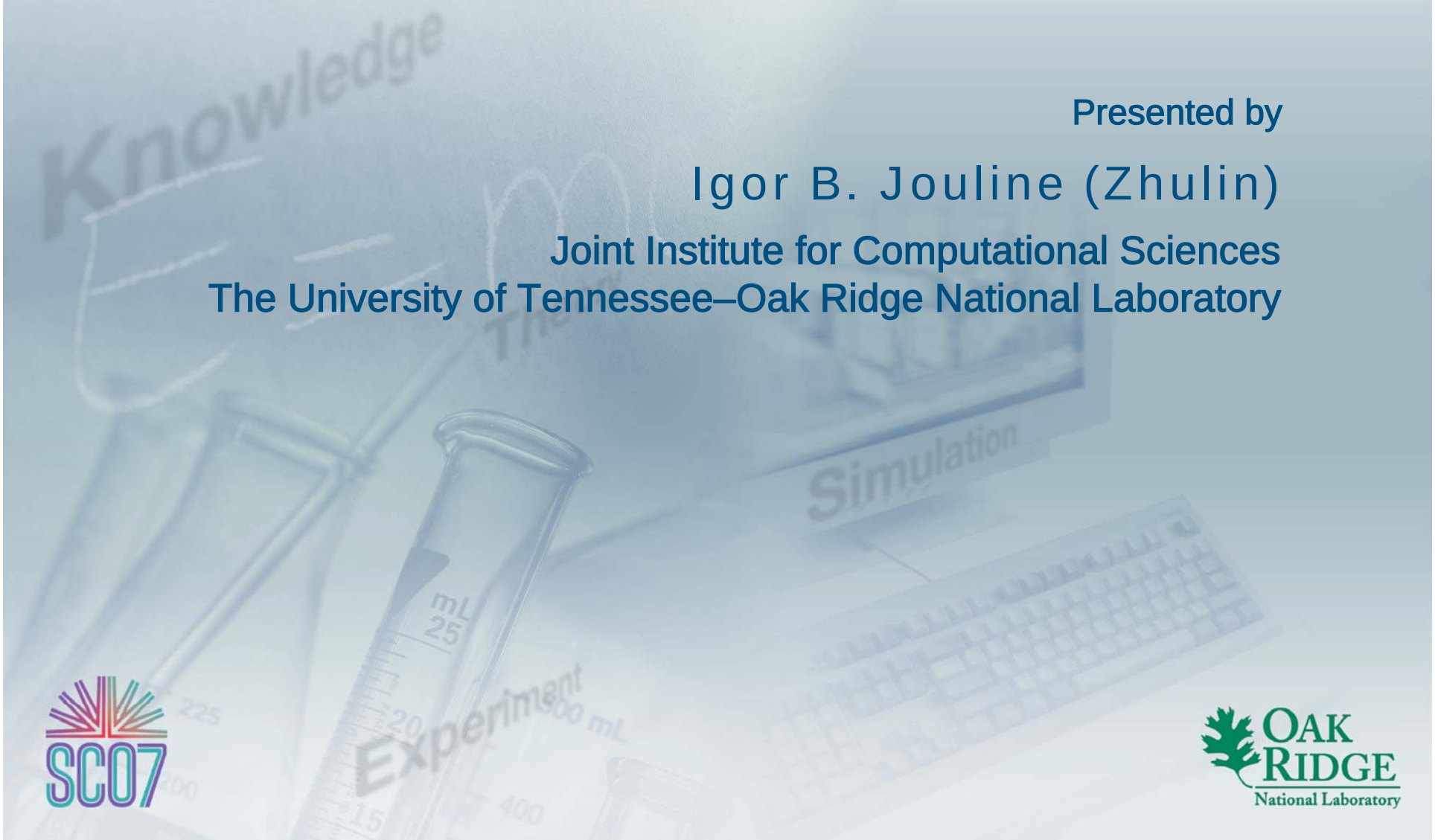
ORNL–University Partnerships in Computational Biology



Presented by

Igor B. Jouline (Zhulin)

Joint Institute for Computational Sciences
The University of Tennessee–Oak Ridge National Laboratory

SC07

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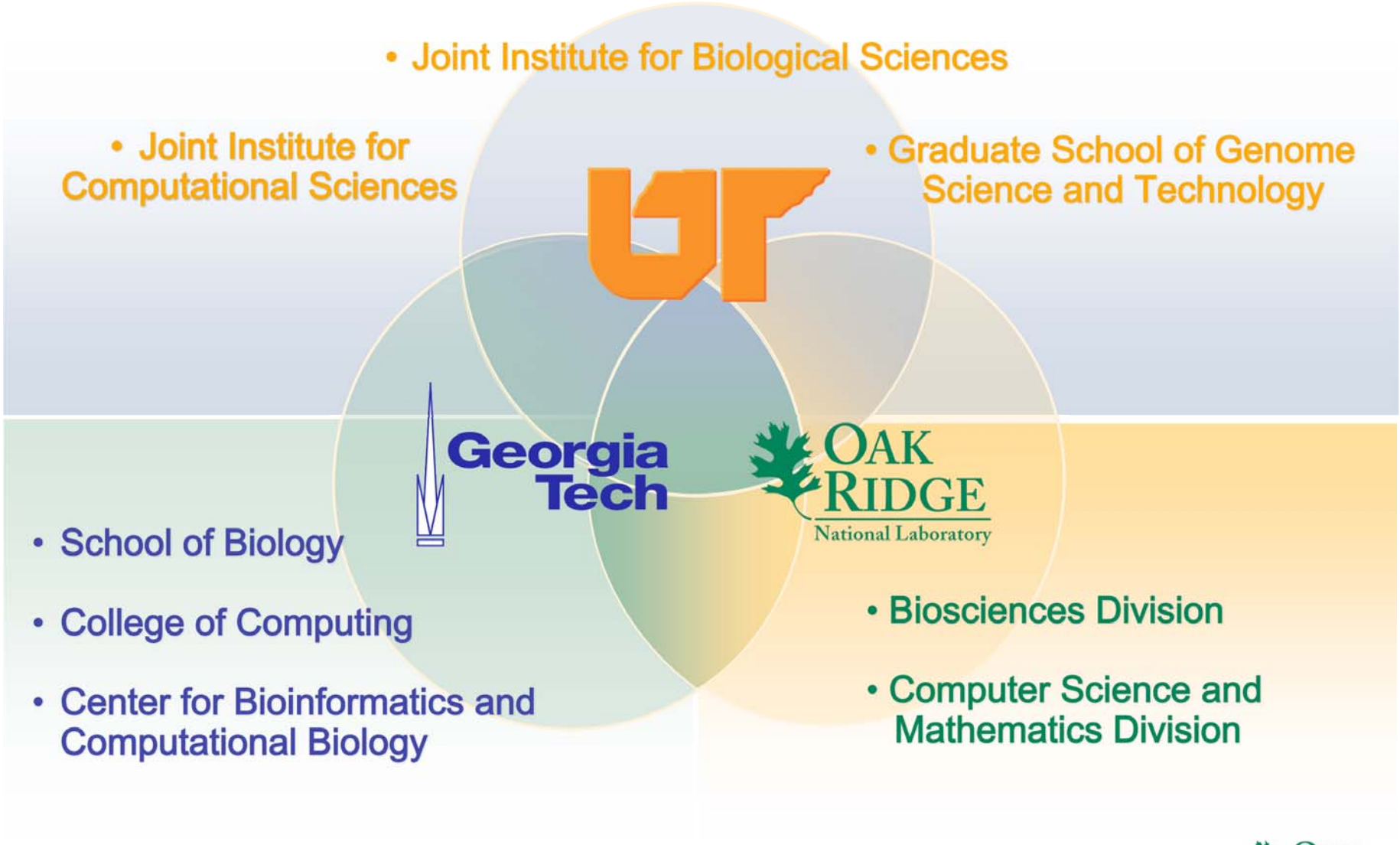
ORNL–University partnerships in computational biology



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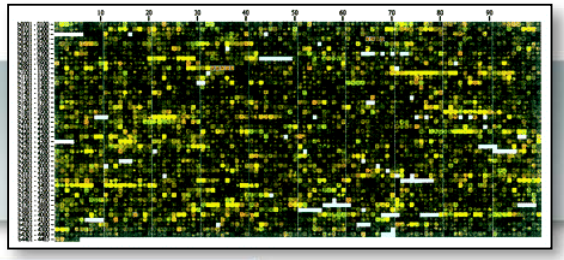
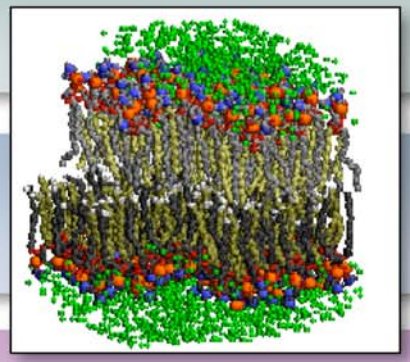
Genome Science & Technology

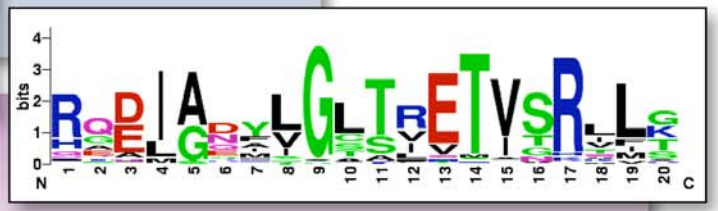
UT

Areas of research and education:

- Genetics and genomics
- Structural biology and proteomics
- Computational biology and bioinformatics







http://gst.ornl.gov

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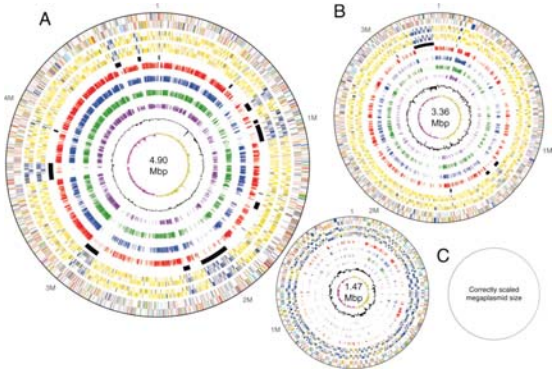
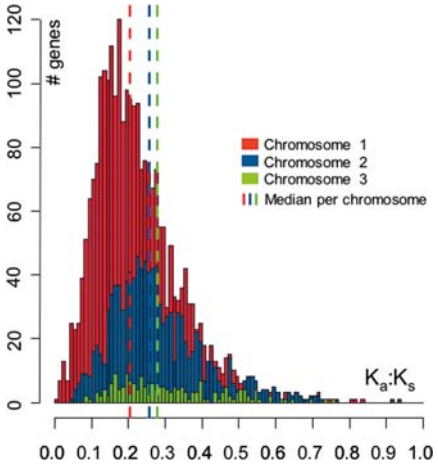
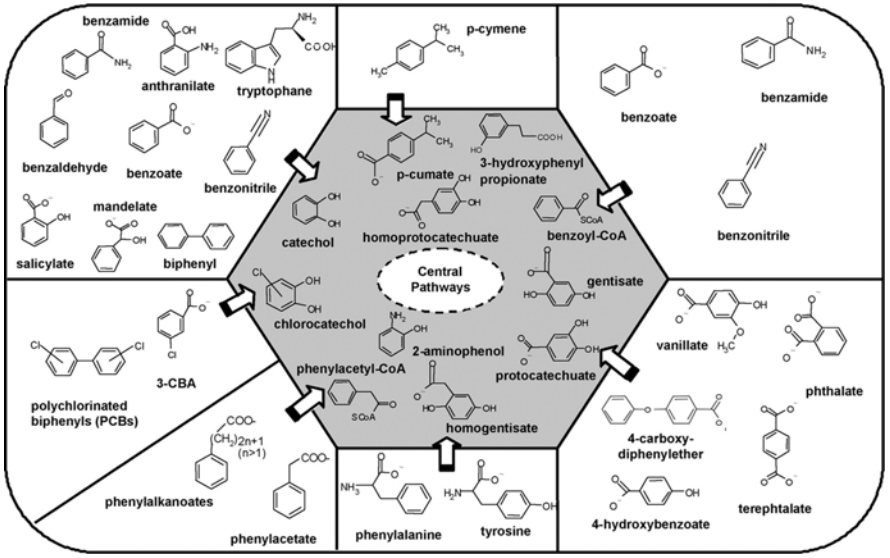
Novel microbial genome reveals extraordinary metabolic versatility

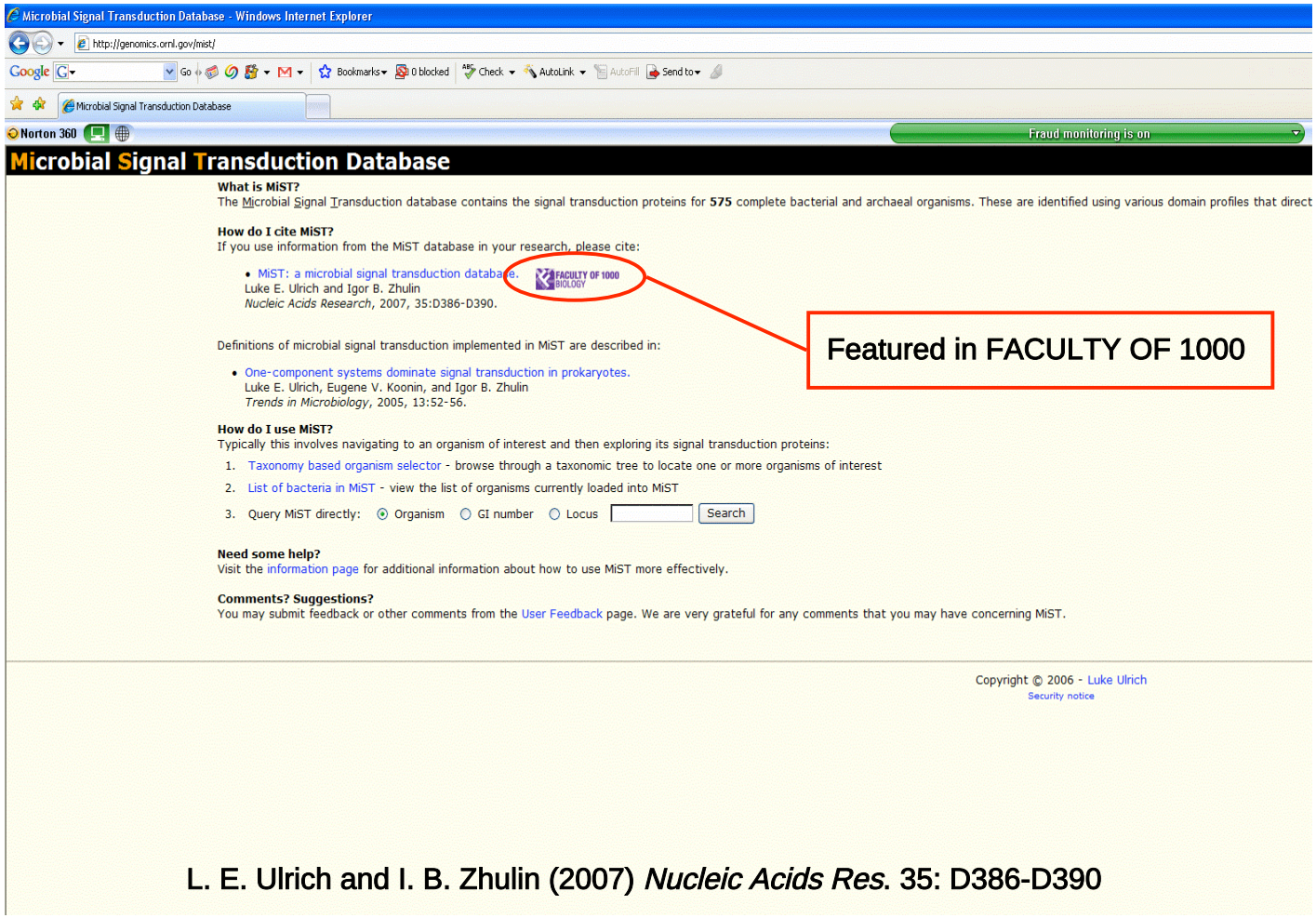






P. S. G. Chain, et al. (2006) *Proc. Natl. Acad. Sci. USA* 103: 15280-15287

MiST: Microbial Signal Transduction Database



L. E. Ulrich and I. B. Zhulin (2007) *Nucleic Acids Res.* 35: D386-D390

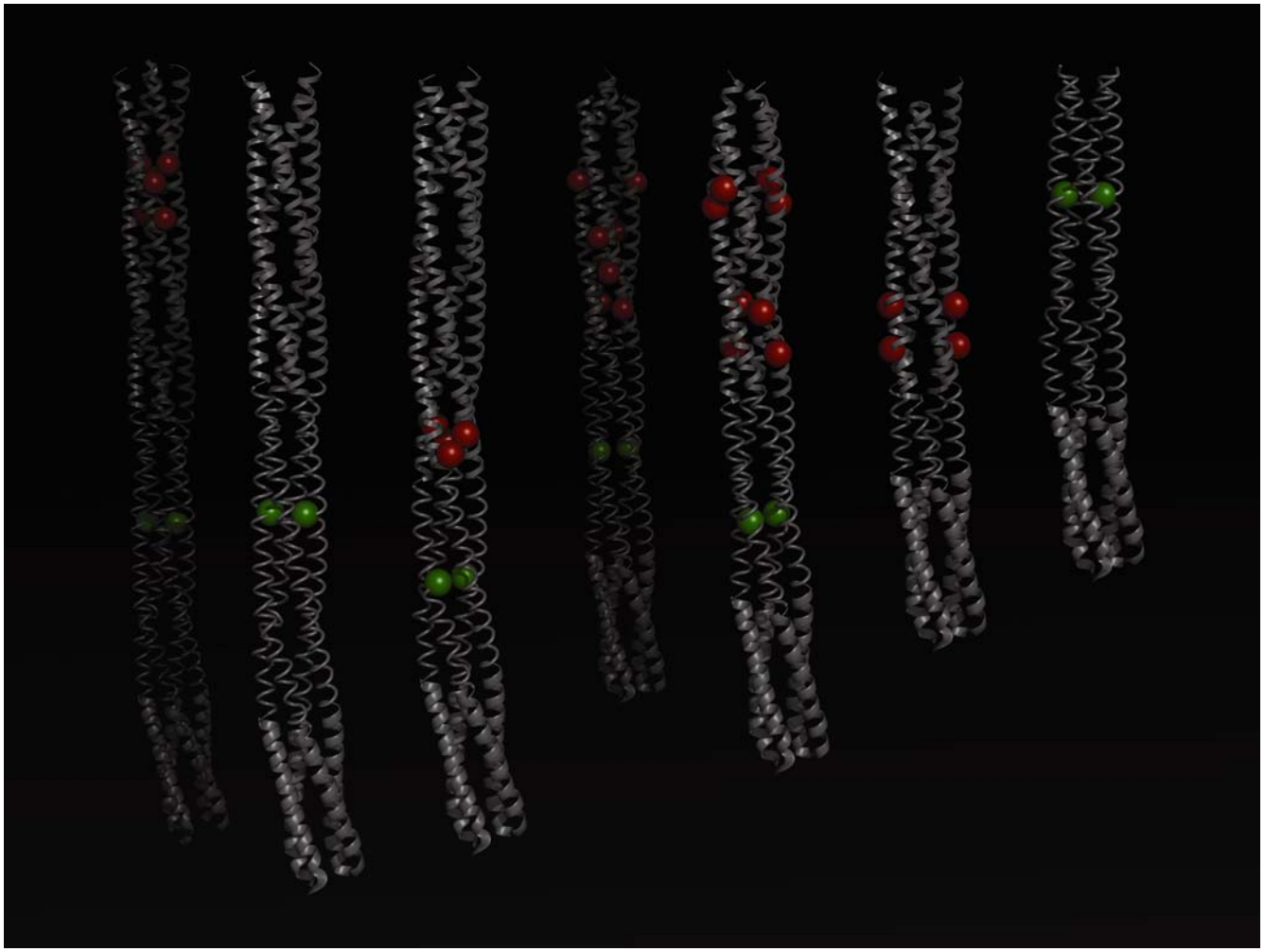
http://genomics.ornl.gov/mist

New computational study reveals novel conserved features in chemoreceptors

From the cover:
Evolutionary genomics reveals conserved structural determinants of signaling and adaptation in microbial chemoreceptors.

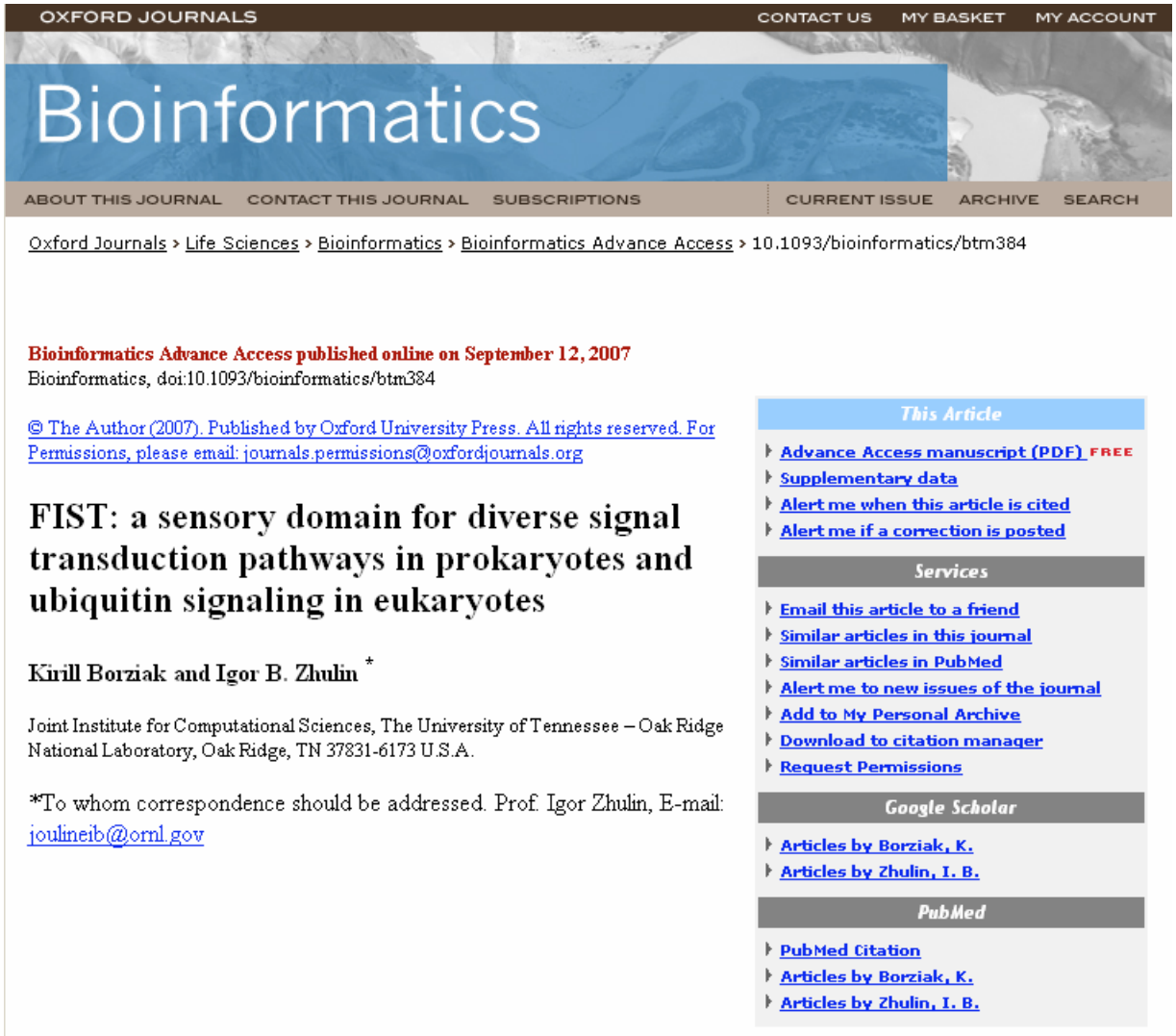
R. P. Alexander and I. B. Zhulin (2007) *Proc. Natl. Acad. Sci. USA* 104: 2885-2890

New computational study reveals novel conserved features in chemoreceptors



R. P. Alexander and I. B. Zhulin (2007) *Proc. Natl. Acad. Sci. USA* 104: 2885-2890

Computational prediction of a novel sensor in all domains of life



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Bioinformatics Advance Access published online on September 12, 2007
Bioinformatics, doi:10.1093/bioinformatics/btm384

FIST: a sensory domain for diverse signal transduction pathways in prokaryotes and ubiquitin signaling in eukaryotes

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