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EDUCATION AND TRAINING:

University of Wisconsin, Madison
B.S. Biochemistry, with distinction, 1983

Stanford University Medical School
Ph.D. Biochemistry, 1988
Advisor: Professor Arthur Kornberg

Stanford University Medical School, Department of Biochemistry
Postdoctoral Fellow, 1988-89
Advisor: Professor Arthur Kornberg

National Institute of Diabetes and Digestive and Kidney Disease,
National Institutes of Health
Postdoctoral Fellow, 1989-1992
Advisor: Kiyoshi Mizuuchi

POSITIONS HELD:

Massachusetts Institute of Technology - Department of Biology

Assistant Professor	1992-1997
Associate Professor	1997-2002
Associate Department Head	1999-2004
E. C. Whitehead Professor	2002-present
Co-Director, Biology Graduate Program	2008-present

Howard Hughes Medical Institute

Assistant Investigator	1994-1997
Associate Investigator	1997-2002
Investigator	2002-present

HONORS:

2008	MacVicar Faculty Fellow for Innovation & Dedication to Undergraduate Education
2007	Elected Member of the National Academy of Sciences
2005	Elected Fellow of the American Association for the Advancement of Science
2004	Elected Fellow of the American Academy of Arts and Sciences
2002	Elected Fellow of the American Society for Microbiology
2002	E. C. Whitehead Professor of Biology
2001	Eli Lilly and Co. Research Award from the American Society for Microbiology
2000	MIT School of Science Teaching Prize for Excellence in Undergraduate Education
1999	Harold E. Edgerton Award for Distinction in Teaching, Research, and Service to MIT
1998	ASBMB Schering-Plough Research Institute Award
1993	NSF Young Investigator Award
1992-94	Robert A. Swanson Career Development Professorship in the Life Sciences
1992-93	Surdna Foundation Research Award for Support of Junior Faculty in Life Sciences

1989-92 Helen Hay Whitney Foundation Fellowship for Postdoctoral Research
1982-83 Mary Shine Peterson Fellowship for Undergraduate Research
1982 Undergraduate Summer Research Fellowship to Cold Spring Harbor Laboratory

PUBLICATIONS:

Nager AR, Baker TA, Sauer RT (2011) Stepwise Unfolding of a β Barrel Protein by the AAA+ ClpXP Protease. *J Mol Biol.* [Epub ahead of print]

Román-Hernández G, Hou JY, Grant RA, Sauer RT, Baker TA (2011) The ClpS Adaptor Mediates Staged Delivery of N-End Rule Substrates to the AAA+ ClpAP Protease. *Mol Cell* 43(2):217-28.

Baker TA, Sauer RT (2011) ClpXP, an ATP-powered unfolding and protein-degradationmachine. *Biochim Biophys Acta* [Epub ahead of print]

Aubin-Tam ME, Olivares AO, Sauer RT, Baker TA, Lang MJ (2011) Single-molecule protein unfolding and translocation by an ATP-fueled proteolytic machine. *Cell* 145(2):257-67.

Sauer RT, Baker TA (2011) AAA+ proteases: ATP-fueled machines of protein destruction. *Annu Rev Biochem* 7;80:587-612.

Sundar S, McGinness KE, Baker TA, Sauer RT (2010) Multiple sequence signals direct recognition and degradation of protein substrates by the AAA+ protease HslUV. 403(3):420-9.

Lee Me, Baker TA, Sauer RT (2010) Control of Substrate Gating and Translocation into ClpP by Channel Residues and ClpX Binding. *J Mol Biol.* 399(5):707-18.

Bissonnette SA, Rivera-Rivera I, Sauer RT, Baker TA (2010) The IbpA and IbpB small heat-shock proteins are substrates of the AAA+ Lon protease. *Mol Microbiol.* 5(6):1539-49.

Abdelhakim AH, Sauer RT, and Baker TA (2010) The AAA+ ClpX machine unfolds a keystone subunit to remodel the Mu transpososome. *Proc Natl Acad Sci U S A* (6):2437-42.

Chowdhury T, Ebrahim S, Chien P, Sauer RT, and Baker TA (2010) Versatile modes of peptide recognition by the ClpX N domain mediate alternative adaptor-binding specificities in different bacterial species. *Protein Sci.* 219(2):242-54.

Glynn SE, Baker TA, and Sauer RT (2009) Crystal structures of asymmetric ClpX hexamers reveal nucleotide-dependent motions in a AAA+ protein-unfolding machine. *Cell* 139(4):744-56.

Shin Y, Davis JH, Brau RR, Martin A, Kenniston JA, Baker TA, Sauer RT, Lang MJ. (2010) Single-molecule denaturation and degradation of proteins by the AAA+ ClpXP protease. *Proc Natl Acad Sci U S A* 106(46):19340-5.

Pruteanu M, Baker TA (2009). Proteolysis in the SOS response and metal homeostasis in *Escherichia coli*. *Res Microbiol.* 160(9):677-83.

Davis JH, Baker TA, and Sauer RT (2009). Engineering synthetic adaptors and substrates for controlled ClpXP degradation. *J Biol Chem*. 284(33):21848-55

Barkow SR, Levchenko I, Baker TA, and Sauer RT (2009). Polypeptide translocation by the AAA+ ClpXP protease machine. *Chem Biol.* 16(6):605-12

Román-Hernández G, Grant RA, Sauer RT, and Baker TA (2009) Molecular basis of substrate selection by the N-end rule adaptor protein ClpS. *Proc Natl Acad Sci U S A*. 106(22):8888-93.

Pruteanu M, and Baker TA (2009) Controlled degradation by ClpXP protease tunes the levels of the excision repair protein UvrA to the extent of DNA damage. *Mol Microbiol*. 71(4):912-24.

Wang KH, Roman-Hernandez G, Grant RA, Sauer RT, and Baker TA (2008) The molecular basis of N-end rule recognition. *Mol Cell* 32: 406-14

Martin A, Baker TA, and Sauer RT (2008) Pore loops of the AAA+ ClpX machine grip substrates to drive translocation and unfolding. *Nat Struct Mol Biol.* 15: 1147-51

Schweidenback CT & Baker TA (2008) Dissecting the roles of MuB in Mu transposition: ATP regulation of DNA binding is not essential for target delivery. *Proc Natl Acad Sci USA* 105: 12101-7.

Moore SD, Baker TA and Sauer RT (2008) Forced extraction of targeted components from complex macromolecular assemblies. *Proc Natl Acad Sci USA* 105: 11685-90.

Yakamavich JA, Baker TA, and Sauer RT (2008) Asymmetric Nucleotide Transactions of the HslUV Protease. *J Mol Biol.* 380: 946-57.

Wang KH, Oakes ES, Sauer RT, and Baker TA (2008) Tuning the strength of a bacterial N-end rule degradation signal. *J Biol Chem.* 283: 24600-7.

Martin A, Baker TA, and Sauer RT (2008) Diverse pore loops of the AAA+ ClpX machine mediate unassisted and adaptor-dependent recognition of ssrA-tagged substrates. *Mol. Cell* 29: 441-50.

Abdelhakim A, Oakes EC, Sauer RT, and Baker TA (2008) Unique contacts direct high-priority recognition of the tetrameric Mu transposase-DNA complex by the AAA+ unfoldase ClpX. *Mol. Cell* 30: 39-50.

Hou JY, Sauer RT, and Baker TA (2008) Distinct structural elements of the adaptor proteins ClpS are required for activation and inhibition of degradation by AAA+ protease ClpAP. *Nat Struct Mol. Biol* 15: 288-94.

Martin A, Baker TA, and Sauer RT (2008) Protein unfolding by AAA+ protease: critical dependence on ATP-hydrolysis rates, energy landscapes, and substrate engagement. *Nat Struct Mol Biol.* 15: 139-145.

Lemberg KM, Schweidenback CTH and Baker TA (2007) The dynamic Mu transpososome: MuB activation prevents disintegration. *J. Mol. Biol*. 374: 1158-1171

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Martin A, Baker TA and Sauer RT (2007) Distinct static and dynamic interactions control ATPase-peptidase communication in a AAA+ protease. *Mol Cell* 27: 41-52.

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Bolon DN, Grant RA, Baker TA and Sauer RT (2005) Specificity versus stability in computational protein design. *Proc. Natl. Acad. Sci. USA* 102: 12724-9.

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Books:

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