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Massachusetts Institute of Technology/Howard Hughes Medical Institute	Phone: (617) 253-3594
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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
Department Head	2012-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

Named Lectureships

NIH Directors Lecture, NIH Bethesda, MD	Fall, 2005
Joan Wood Lecture, Dept. Biology, Indiana University	Spring, 2008
Gavin Borden Visiting Fellow, Cold Spring Harbor Laboratory	Spring, 2008
Storer Endowment "Major Issues in Modern Biology Lecture", UC Davis	Fall, 2010
Gerhard Schmidt Memorial Lecture, Tufts University	Spring 2011

SERVICE:

Massachusetts Institute of Technology

Department Head, Biology	2012-2014
Associate Department Head, Biology	1999-2004
Co-Director, Biology Graduate Program	2008-present
Graduate Program Steering Committee	1994-present
Chair, "Target of Opportunity" Faculty Search Committee	2006-present
Biochemistry/Molecular Mechanism Faculty Search Committee (Chaired 3 years)	7 years
Dean of Science Search Committee	2007
School of Science Committee Overseeing Institute Communications Requirement (Co-Chair/Chair 3 years)	2004-2008
Gender Equity Committee	2007-present
Gender Equity Chairs Committee	2008-present
Steering Committee for the Chemistry/Biology Interface Training Program	2008-present
Institute-wide Planning Task Force	2009
Provost's Committee for Design of the Faculty Housing Benefit	2003
Organized/Taught "Responsible Research Conduct" for Biology PhD Students	2005-2008
Dean's Committee of to recommend Biology Department Head	1998
Co-organizer of the MIT Scientific Retreat for Junior Faculty in the School of Science	1998
Subcommittee to Design Biology Graduate Lab Rotations	1997

Other Service

CSHL Academic Affairs Committee	
CSHL Board of Trustees	
NIGMS Council: Ad Hoc Member	May 2010
NIH Study Section Member (PCMB)	2006-2009
Ad Hoc Reviewer for: NIH Microbial Physiology and Genetics	
Ad Hoc Reviewer for NCI	
National Academy of Science Section 21 Canvassing Panel	2007-present
ASM Promega Biotechnology Research Award Panel (current Chair)	2007-present
Protein Society Nominating Committee	2006, 2009

Editorial Boards (current and former): <i>Molecular Microbiology, Molecular Cell, Genes & Development, Annual Review of Biochemistry</i>	
Member, Nat L. Sternberg Thesis Prize Committee	2002-2004
Co-organizer, Keystone Symposium on Transposition and Other Genome Rearrangements, Santa Fe, NM	2003
Co-organizer, Molecular Genetics of Bacteria and Phages Annual Meeting (U. Wisconsin, Madison and Cold Spring Harbor Labs)	1999, 2000, 2001
Co-organizer, Keystone Symposium on Transposition and DNA Rearrangements, Santa Fe, NM	2000
Keystone Symposia of Molecular and Cellular Biology Scientific Advisory Board for Molecular Biology	2002-2006
Chair, Review Committee for the Department of Biochemistry and Molecular Biology, USC Keck School of Medicine	2007

TEACHING:

<i>Experimental Biology</i> (undergraduate lab)	1993-1995
<i>Method and Logic in Molecular Biology</i> (for graduate students)	1995-1997
<i>Molecular Biology</i> (joint undergraduate/graduate subject)	1997-present
<i>Principles of Biochemical Analysis</i> (for graduate students)	1999-2007

PUBLICATIONS:

- Olivares AO, Nager AR, Yosefson O, Sauer RT, Baker TA (2014) Mechanochemical basis of protein degradation by a double-ring AAA+ machine. *Nat. Struct. Mol. Biol.* (in press).
- Cordova JC, Olivares AO, Shin Y, Stinson BM, Calmat S, Schmitz KR, Aubin-Tam ME, Baker TA, Lang MJ, Sauer RT (2014) Stochastic but Highly Coordinated Protein Unfolding and Translocation by the ClpXP Proteolytic Machine. *Cell*. 158(3):647-58.
- Barthelme D, Chen JZ, Grabenstatter J, Baker TA, Sauer RT (2014) Architecture and assembly of the archaeal Cdc48*20S proteasome. *Proc Natl Acad Sci*. [Epub ahead of print].
- Vieux EF, Wohlever ML, Chen JZ, Sauer RT, Baker TA (2013) Distinct quaternary structures of the AAA+ Lon protease control substrate degradation. *Proc Natl Acad Sci U S A*. 110(22):E2002-8.
- Wohlever ML, Baker TA, Sauer, RT (2013) Roles of the N domain of the AAA+ Lon protease in substrate recognition, allosteric regulation and chaperone activity. *Mol Microbiol*. 91(1):66-78.
- Wohlever ML, Baker TA, Sauer RT (2013) A mutation in the N domain of the *Escherichia coli* lon stabilizes dodecamers and selectively alters degradation of model substrates. *J Bacteriol*. 195(24):5622-8.
- Wohlever ML, Nager AR, Baker TA, Sauer RT (2013) Engineering fluorescent protein substrates for the AAA+ Lon protease. *Protein Eng Des Sel*. [Epub ahead of print]
- Stinson BM, Nager AR, Glynn SE, Schmitz KR, Baker TA, Sauer RT (2013) Nucleotide binding and conformational switching in the hexameric ring of AAA+ machine. *Cell*. 153(3):628-39.
- Glynn SE, Nager AR, Baker TA, Sauer RT (2012) Dynamic and static components power unfolding in topologically closed rings of a AAA+ proteolytic machine. *Nat Struct Mol Biol*. 19(6):616-22.
- Peterson CN, Levchenko I, Rabinowitz JD, Baker TA, Silhavy TJ (2012) RpoS proteolysis is controlled directly by ATP levels in *Escherichia Coli*. *Genes Dev*. 26(6):548-53.
- Landgraf D, Okumus B, Chien P, Baker TA, Paulsson J (2012) Segregation of molecules at bacterial cell division reveals native protein localization. *Nature Methods* 9(5):480-2.
- Sundar S, Baker TA, Sauer RT (2012) The I domain of the AAA+ HslUV protease coordinates substrate binding, ATP hydrolysis, and protein degradation. *Protein Sci*. 21(2):188-98.
- Davis JH, Baker TA, Sauer RT (2011) Small-molecule control of protein degradation using split adaptors. *ACS Chem Biol*. 6(11):1205-13.

- Abel S, Chien P, Wassmann P, Schirmer T, Kaefer V, Laub MT, Baker TA, Jenal U (2011) Regulatory cohesion of cell cycle and cell differentiation through interlinked phosphorylation and second messenger networks. *Mol Cell*. 43(4):550-60.
- Nager AR, Baker TA, Sauer RT (2011) Stepwise Unfolding of a β Barrel Protein by the AAA+ ClpXP Protease. *J Mol Biol*. 413(1):4-16.
- 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-degradation machine. *Biochim Biophys Acta* 1823(1):15-28
- 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
- Chien P, Grant RA, Sauer RT, and Baker TA (2007) Structure and substrate specificity of a SspB ortholog: design implications for AAA+ adaptors. *Structure* 15: 1296-1305
- 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.
- Chien P, Perchuk BS, Laub MT, Sauer RT and Baker TA (2007) Direct and adaptor-mediated substrate recognition by an essential AAA+ protease. *Proc. Natl. Acad. Sci. USA* 104: 6590-5.
- McGinness KE, Bolon DN, Kaganovich M, Baker TA and Sauer RT (2007) Altered tethering of the SspB adaptor to the ClpXP protease causes changes in substrate delivery. *J Biol Chem*. 282: 11465-73.
- Pruteanu M, Neher SB and Baker TA (2007) Ligand-controlled proteolysis of the *Escherichia coli* transcriptional regulator ZntR. *J Bacteriol*. 189: 3017-25.
- Wang KH, Sauer RT and Baker TA (2007) ClpS modulates but is not essential for bacterial N-end rule degradation. *Genes Dev*. 21: 403-8.
- Farrell CM, Baker TA and Sauer RT (2007) Altered specificity of a AAA+ protease. *Mol Cell*. 25: 161-6.
- Chaba R, Grigorova IL, Flynn JM, Baker TA and Gross CA (2007) Design principles of the proteolytic cascade governing the sigmaE-mediated envelope stress response in *Escherichia coli*: keys to graded, buffered, and rapid signal transduction. *Genes Dev*. 21: 124-36.
- Baker TA and Sauer RT (2006) ATP-dependent proteases of bacteria: recognition logic and operating principles. *Trends Biochem Sci*. 31: 647-653.
- McGinness KE, Baker TA and Sauer RT (2006) Engineering Controllable Protein Degradation. *Mol Cell* 22: 701-707.
- Neher SB, Villén J, Oakes EC, Bakalarski CE, Sauer RT, Gygi SP and Baker TA (2006) Proteomic profiling of ClpXP substrates after DNA damage reveals extensive instability within SOS regulon. *Mol Cell* 22: 193-204.
- Martin A, Baker TA and Sauer RT (2005) Rebuilt AAA + motors reveal operating principles for ATP-fuelled machines. *Nature* 437: 1115-20.
- 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.
- Burton BM and Baker TA (2005) Remodeling protein complexes: insights from the AAA+ unfoldase ClpX and Mu transposase. *Protein Sci*. 14: 1945-54.
- Hersch GL, Burton RE, Bolon DN, Baker TA and Sauer RT (2005) Asymmetric interactions of ATP with the AAA+ ClpX6 unfoldase: allosteric control of a protein machine. *Cell* 121: 1017-1027.
- Levchenko I, Grant RA, Flynn JM, Sauer RT and Baker TA (2005) Versatile modes of peptide recognition by the AAA+ adaptor protein SspB. *Nat Struct Mol Biol*. 12: 520-525.
- Kenniston JA, Baker TA, and Sauer RT (2005) Partitioning between unfolding and release of native domains during ClpXP degradation determines substrate selectivity and partial processing. *Proc. Natl. Acad. Sci. USA* 102: 1390-5.
- Burton RE, Baker TA and Sauer RT (2005) Nucleotide-dependent substrate recognition by the AAA+ HslUV protease. *Nat Struct Mol Biol*. 12: 245-51.
- Bolon DN, Grant RA, Baker TA and Sauer RT (2004) Nucleotide-dependent substrate handoff from the SspB adaptor to the AAA+ ClpXP protease. *Mol Cell* 16: 343-50.

- Sauer RT, Bolon DN, Burton BM, Burton RE, Flynn JM, Grant RA, Hersch GL, Joshi SA, Kenniston JA, Levchenko I, Neher SB, Oakes ES, Siddiqui SM, Wah DA, and Baker TA (2004) Sculpting the proteome with AAA(+) proteases and disassembly machines. *Cell* 119: 9-18.
- Flynn JM, Levchenko I, Sauer RT and Baker TA (2004) Modulating substrate choice: the SspB adaptor delivers a regulator of the extracytoplasmic-stress response to the AAA+ protease ClpXP for degradation. *Genes Dev.* 18: 2292-2301.
- Hersch GL, Baker TA and Sauer RT (2004) SspB delivery of substrates for ClpXP proteolysis probed by the design of improved degradation tags. *Proc. Natl. Acad. Sci. USA* 101: 12136-12141.
- Siddiqui SM, Sauer RT and Baker TA (2004) Role of the protein-processing pore of ClpX, an AAA+ ATPase, in recognition and engagement of specific protein substrates. *Genes Dev.* 18: 369-74.
- Joshi SA, Hersch GL, Baker TA and Sauer RT (2004) Communication between ClpX and ClpP during substrate processing and degradation. *Nat Struct Mol Biol.* 11: 404-11.
- Kenniston JA, Burton RE, Siddiqui SM, Baker TA and Sauer RT (2004) Effects of local protein stability and the geometric position of the substrate degradation tag on the efficiency of ClpXP denaturation and degradation. *J Struct Biol.* 146: 130-40.
- Bolon DN, Wah DA, Hersch GL, Baker TA and Sauer RT (2004) Bivalent tethering of SspB to ClpXP is required for efficient substrate delivery: a protein-design study. *Mol Cell.* 13: 443-9.
- Williams, TL and Baker TA (2004) Reorganization of the Mu transpososome active sites during a cooperative transition between DNA cleavage and joining. *J Biol Chem.* 279: 5135-45.
- Spector S, Flynn JM, Tidor B, Baker TA and Sauer RT (2003) Expression of N-formylated proteins in *Escherichia coli*. *Protein Expr. Purif.* 32: 317-322.
- Goldhaber-Gordon I, Early MH and Baker TA. (2003) MuA transposase separates DNA sequence recognition from catalysis. *Biochem.* 42: 14633-42.
- Neher SB, Sauer RT and Baker TA (2003) Distinct peptide signals in the UmuD and UmuD' subunits of the UmuD/D' heterodimer mediate tethering and substrate-processing by the ClpXP protease. *Proc. Natl. Acad. Sci. USA* 100: 13219-24.
- Wah DA, Levchenko I, Rieckhof GE, Bolon DN, Baker TA and Sauer RT (2003) Flexible linkers leash the substrate binding domain of SspB to a peptide module that stabilizes delivery complexes with the AAA+ ClpXP protease. *Mol. Cell* 12: 355-363.
- Levchenko I, Grant RA, Wah DA, Sauer RT and Baker TA (2003) Structure of a delivery protein for an AAA+ protease in complex with a peptide degradation tag. *Mol. Cell* 12: 365-372.
- Coros CJ, Sekino Y, Baker TA and Chaconas G (2003) Effect of mutations in the C-terminal domain of Mu B on DNA binding and interactions with Mu A transposase. *J Biol Chem.* 278: 31210-7.
- Kenniston JA, Baker TA, Fernandez JM and Sauer RT (2003) Linkage between ATP consumption and mechanical unfolding during the protein processing reactions of an AAA+ degradation machine. *Cell* 114: 511-20.
- Goldhaber-Gordon I, Early MH and Baker TA (2003) The terminal nucleotide of the Mu genome controls catalysis of DNA strand transfer. *Proc. Natl. Acad. Sci. USA* 100:7509-14.
- Burton RE, Baker TA and Sauer RT (2003) Energy-dependent degradation: linkage between ClpX-catalyzed nucleotide hydrolysis and protein-substrate processing. *Protein Science* 12: 893 - 902.
- Burton BM and Baker TA (2003) Mu transpososome architecture ensures that unfolding by ClpX or proteolysis by ClpXP remodels but does not destroy the complex. *Chem Biol.* 10:463-72.
- Joshi SA, Baker TA and Sauer RT. (2003) C-terminal domain mutations in ClpX uncouple substrate binding from an engagement step required for unfolding. *Mol Microbiol.* 48: 67-76.
- Neher SB, Flynn JM, Sauer RT and Baker TA (2003) Latent ClpX-recognition signals ensure LexA destruction after DNA damage. *Genes and Development* 17: 1084-1089.
- Sokolsky TD and Baker TA (2003) DNA gyrase requirements distinguish the alternate pathways of Mu transposition. *Mol Microbiol.* 47:397-409
- Flynn JM, Neher SB, Kim YI, Sauer RT and Baker TA (2003) Proteomic discovery of cellular substrates of the ClpXP protease reveals five classes of ClpX-recognition signals. *Mol Cell.* 11: 671-83.

- Wah DA, Levchenko I, Baker TA and Sauer RT (2002) Characterization of a specificity factor for an AAA+ ATPase: Assembly of SspB Dimers with ssrA-Tagged Proteins and the ClpX Hexamer. *Chem Biol* 9: 1237-1245.
- Goldhaber-Gordon I, Early MH, Gray MK, and Baker TA (2002) Sequence and positional requirements for DNA sites in a Mu transpososome. *J. Biol. Chem.* 277:7703-7712.
- Goldhaber-Gordon I, Williams TL, and Baker TA (2002) DNA recognition sites activate MuA transposase to perform transposition of non-Mu DNA. *J. Biol. Chem.* 277: 7694-7702.
- Kim Y-I, Levchenko I, Fraczkowska K, Woodruff RV, Sauer RT, and Baker TA (2001) Molecular determinants of complex formation between Clp/Hsp100 ATPases and the ClpP peptidase. *Nature Structural Biology* 8: 230-233.
- Lo JH, Baker TA, and Sauer RT (2001) Characterization of the N-terminal repeat domain of *Escherichia coli* ClpA-A class I Clp/HSP100 ATPase. *Protein Science* 10: 551-559.
- Roldan LAS, and Baker TA (2001) Differential role of the Mu B protein in phage Mu integration versus replication: mechanistic insights into two transposition pathways. *Mol Microbiol* 40: 141-55.
- Burton BM, Williams TL, and Baker TA (2001) ClpX-mediated remodeling of Mu transpososomes: selective unfolding of subunits destabilizes the entire complex. *Mol Cell.* 8: 449-54.
- Flynn JM, Levchenko I, Seidel M, Wickner SH, Sauer RT, and Baker TA (2001) Overlapping recognition determinants within the ssrA degradation tag allow modulation of proteolysis. *Proc Natl Acad Sci USA* 11: 10584-9.
- Burton RE, Siddiqui SM, Kim Y-I, Baker TA, and Sauer RT (2001) Effects of protein stability and structure on substrate processing by the ClpXP unfolding and degradation machine. *EMBO J.* 20: 3092-100.
- Rice PA, and Baker TA (2001) Comparative architecture of transposase and integrase complexes. *Nat Struct Biol.* 8: 302-307.
- Mizuuchi K, and Baker TA (2001) Chemical mechanisms for mobilizing DNA. In *Mobile DNA II* (NL Craig et al., ed.), American Society of Microbiology, Washington, D.C., pp. 12-23.
- Kim Y-I, Burton RE, Burton BM, Sauer RT, and Baker TA (2000) Dynamics of substrate denaturation and translocation by the ClpXP degradation machine. *Molecular Cell* 5: 639-648.
- Levchenko I, Seidel M, Sauer RT, and Baker TA (2000) A specificity-enhancing factor for the ClpXP degradation machine. *Science* 289: 2354-6.
- Williams TL, and Baker TA (2000) Transposase team puts a headlock on DNA. *Science* 289: 73-4.
- Goldhaber-Gordon IM, and Baker TA (2000) Non-homologous recombination: simplicity in complexity. Keystone Symposium on Transposition and Other Genome Rearrangements, Santa Fe, NM, USA, 27 January - 2 February. *Trends in Genetics* 16:201-202
- Smith CK, Baker TA, and Sauer RT (1999) Lon and Clp family proteases and chaperones share homologous substrate-recognition domains. *Proc. Natl. Acad. Sci. USA* 96: 6678-6682.
- Williams TL, Jackson EL, Carritte A, and Baker TA (1999) Organization and dynamics of the Mu transpososome: recombination by communication between two active sites. *Genes Dev* 13: 2725-2737.
- Baker TA (1999) Protein unfolding. Trapped in the act *Nature* 401: 29-30.
- Levchenko I, Smith CK, Walsh NP, Sauer RT, and Baker TA (1998) PDZ-like domains mediate binding specificity in the Clp/Hsp100 family of chaperones and protease regulatory subunits. *Cell* 91: 939-947.
- Krementsova E, Giffin MJ, Pincus D, and Baker TA (1998) Mutational analysis of the Mu transposase. *J. Biol. Chem.* 273: 31358-31365.
- Yamauchi M, and Baker TA (1998) An ATP-ADP switch in MuB controls progression of the Mu transposition pathway. *EMBO J* 17: 5509-5518.
- Baker TA, and Bell SP (1998) Polymerases and the replisome: machines within machines. *Cell* 92: 295-305.
- Levchenko I, Yamauchi M, and Baker TA (1997) ClpX and MuB interact with overlapping regions of Mu transposase: implications for control of the transposition pathway. *Genes and Development* 11: 1561-1572.

- Aldaz H, Schuster E, and Baker TA (1996) The interwoven architecture of the Mu transposase couples DNA synapsis to catalysis. *Cell* 85: 257-269.
- Levchenko I, Luo L, and Baker TA (1995) Disassembly of the Mu transposase tetramer by the ClpX chaperone. *Genes and Development* 9: 2399-2408.
- Mizuuchi M, Baker TA, and Mizuuchi K (1995) Assembly of Phage Mu transpososomes: cooperative transitions assisted by protein and DNA sequence cofactors as scaffolds. *Cell* 83: 375-385.
- Baker TA (1995) Replication arrest. *Cell* 80: 521-524.
- Baker TA (1995) Bacteriophage Mu: a transposing phage that integrates like retroviruses. *Seminars in Virology* 6: 53-63.
- Baker TA, and Luo L (1994) Identification of residues in the Mu transposase essential for catalysis. *Proc. Natl. Acad. Sci. USA* 91: 6654-6658.
- Baker TA, Krementsova E, and Luo L (1994) Complete transposition requires four active monomers in the Mu transposase tetramer. *Genes and Development* 8: 2416-2428.
- Baker TA (1994) Replication initiation: a new controller in *Escherichia coli*. *Current Biology* 4: 945-946.
- Baker TA, Mizuuchi M, Savilahti H, and Mizuuchi K (1993) Division of labor among monomers within the Mu transposase tetramer. *Cell* 74: 723-733.
- Baker TA (1993) Untangling the steps in chromosome segregation. *Current Biology* 3: 94-96.
- Baker TA (1993) Protein-DNA assemblies controlling lytic development of bacteriophage Mu. *Current Opinion in Genetics and Development* 3.
- Mizuuchi M, Baker TA, and Mizuuchi K (1992) Assembly of the active form of the transposase-Mu DNA complex: a critical control point in Mu transposition. *Cell* 70: 303-311.
- Baker TA, and Mizuuchi K (1992) DNA-promoted assembly of the active tetramer of the Mu transposase. *Genes and Development* 6: 2221-2232.
- Baker TA, and Funnell BE (1992) Replication, recombination, and red chili amidst the pueblos. *New Biologist* 4: 482-487.
- Baker TA, and Wickner SH (1992) Genetics and enzymology of DNA replication in *E. coli*. *Ann. Rev. Genetics* 24: 447-477.
- Baker TA, Mizuuchi M, and Mizuuchi K (1991) MuB protein allosterically activates strand transfer by the transposase of phage Mu. *Cell* 65: 1003-1013.
- Mizuuchi M, Baker TA, and Mizuuchi K (1991) DNase footprint analysis of the stable synaptic complexes involved in Mu transposition. *Proc. Natl. Acad. Sci. USA* 88, 9031-9035.
- Baker TA, and Kornberg A (1991) Initiation of chromosomal replication. In: *Nucleic Acids and Molecular Biology, vol 5* (DMJ Lilly ed.) Springer-Verlag.
- Baker TA (1991) "...and then there were two". *Nature* 353: 794-795.
- Skarstad K, Baker TA, and Kornberg A (1990) Strand separation required for initiation of replication at the chromosomal origin of *E. coli* is facilitated by a distant RNA-DNA hybrid. *EMBO J.* 9: 2341-2348.
- Kornberg A, Baker TA, Yung BY-M, and Skarstad K (1990) Early events in the enzymatic replication of plasmids containing the origin of the *E. coli* chromosome. In: *Molecular Mechanisms in DNA Replication and Recombination*, (IR Lehman and CC Richardson, eds.) Alan R. Liss, Inc. pp. 227-236.
- Singer M, Baker TA, Schnitzler G, Deischel SM, Goel M, Dove W, Jaacks KJ, Grossman AD, Erickson JW, and Gross CA (1989) A collection of strains containing genetically linked alternating antibiotic resistance elements for genetic mapping of *Escherichia coli*. *Microbiol. Rev.* 53: 1.
- Baker TA, and Kornberg A (1988) Transcriptional activation of initiation of replication from the *E. coli* chromosomal origin: An RNA-DNA hybrid near *oriC*. *Cell* 55: 113-123.
- Baker TA, Bertsch LL, Bramhill D, Sekimizu K, Wahle E, Yung B, and Kornberg A (1988) Enzymatic replication of plasmids from the origin of the *E. coli* chromosome. In *Cancer Cells, Vol. 6, Eukaryotic DNA Replication* (TJ Kelly and B Stillman, eds.), Cold Spring Harbor Laboratories, Cold Spring Harbor, N.Y.
- Baker TA, Funnell BE, and Kornberg A (1987) Helicase action of dnaB protein during replication from the *Escherichia coli* chromosomal origin in vitro. *J. Biol. Chem.* 262: 6877-6885.

- Funnell BE, Baker TA, and Kornberg A (1987) *In vitro* assembly of a prepriming complex at the origin of the *Escherichia coli* chromosome. *J. Biol. Chem.* 262: 10327-10334.
- Kornberg A, Baker TA, Bertsch LL, Bramhill D, Funnell BE, Lasken RS, Maki H, Maki S, Sekimizu K, and Wahle E (1987) Enzymatic studies of replication of *oriC* plasmids. In *DNA Replication and Recombination* (T Kelly and R McMacken eds.), Alan R. Liss, Inc., New York., pp. 137-149.
- Baker TA, Sekimizu K, Funnell BE, and Kornberg A (1986) Extensive unwinding of the plasmid template during staged enzymatic initiation of DNA replication from the origin of the *Escherichia coli* chromosome. *Cell* 45: 53-64.
- Funnell BE, Baker TA, and Kornberg A (1986) Complete enzymatic replication of plasmids containing the origin of the *Escherichia coli* chromosome. *J. Biol. Chem.* 261: 5616-5624.
- Ogawa T, Baker TA, van der Ende A, and Kornberg A (1985) Initiation of enzymatic replication at the origin of the *Escherichia coli* chromosome: contributions of RNA polymerase and primase. *Proc. Natl. Acad. Sci. USA* 82: 3562-3566.
- van der Ende A, Baker TA, Ogawa T, and Kornberg A (1985) Initiation of enzymatic replication at the origin of the *Escherichia coli* chromosome: primase as the sole priming enzyme. *Proc. Natl. Acad. Sci. USA* 82: 3954-3958.
- Smith DW, Garland AM, Herman G, Enns RE, Baker TA, and Zyskind JW (1985) Importance of state of methylation of *oriC* GATC sites in initiation of DNA replication in *Escherichia coli*. *EMBO J.* 4: 1319-1326.
- Grossman AD, Cowing D, Erickson J, Baker T, Zhou YN, and Gross C (1985) Analysis of the *Escherichia coli* heat shock response. In *Microbiology 1985* (L Leive, ed.), American Society of Microbiology, Washington, D.C., pp. 327-331.
- Baker TA, Grossman AD, and Gross CA (1984) A gene regulating the heat shock response in *E.coli* also causes a defect in proteolysis. *Proc. Natl. Acad. Sci. USA* 81: 6779-6783.
- Baker TA, Howe MM, and Gross CA (1983) MudX, a derivative of Mud1 (*lac Ap^r*) which makes stable *lacZ* fusions at high temperature. *J. Bacteriol.* 156: 970-974.

Books:

- Watson JD, Baker TA, Bell SP, Gann A, Stephen Harrison, Levine M, Losick R (2013) *Molecular Biology of the Gene, 7th Edition* CSHL Press & Benjamin Cummings, San Francisco, CA.
- Watson JD, Baker TA, Bell SP, Gann A, Levine M, Losick R (2007) *Molecular Biology of the Gene, 6th Edition* CSHL Press & Benjamin Cummings, San Francisco, CA.
- Watson JD, Baker TA, Bell SP, Gann A, Levine M, Losick R (2003) *Molecular Biology of the Gene, 5th Edition* Benjamin Cummings, San Francisco, CA.
- Kornberg A, and Baker TA (1992) *DNA Replication, 2nd Edition* WH Freeman and Company, New York, New York. (Republished by University Science Press, 2005)