

Curriculum Vitae

Robert T. Sauer

Education

Amherst College	B.A.	1972	Biophysics
Harvard University	Ph.D.	1979	Biochemistry & Molecular Biology

Professional

Professor, Dept. of Biology, M.I.T. (1987-present)
 Associate Professor, M.I.T. (1982-1987)
 Assistant Professor, M.I.T. (1978-1982)
 Scientific Advisory Board, Phylos, Inc. (1998-2003)
 Scientific Advisory Board, Anadys, Inc. (2000-2002)
 Scientific Advisory Board, Scriptgen, Inc. (1993-2000)
 Consultant, Genentech, Inc. (1988-1995)
 Consultant, Collaborative Research (1981-1988)
 Consultant, Merck (1978-1980)
 Research Technician, Massachusetts General Hospital (1968-1970; 1972-1973)

Honors

Stein and Moore Award (2013)
 Hans Neurath Award (2007)
 Amgen Award of the Protein Society (2001)
 Salvador E. Luria Professorship (1999-present)
 MIT School of Science Prize for Excellence in Graduate Teaching (1998)
 National Academy of Sciences (elected 1996)
 American Academy of Microbiology (elected 1996)
 American Academy of Arts and Sciences (elected 1993)
 Edwin C. Whitehead Professorship (1991-1999)

Named Lectures

Frederick M. Richards Lecture, Yale (2015)
 Michael Smith Lecture, University of British Columbia (2014)
 Axelrod Lectures, Purdue University (2010)
 Philip Handler Lecturer, Duke University (2009)
 Cecile Pickardt Lecturer, Johns Hopkins University (2008)
 Ernest C. Pollard Lecturer, Pennsylvania State University (2006)
 Helen Riaboff Whiteley Lecture in Regulatory Biology, U. Washington (1998)
 J.W. Pace Memorial Lecturer, University of Utah (1996)
 Everett H. Pryde Memorial Lecturer, Amherst College (1996)
 Jeanette Piperno Memorial Lecturer, Temple University (1992)
 Cynthia Ann Chan Memorial Lecturer, U.C. Berkeley (1992)

Service

Member, NIH Macromolecular Structure and Function B Study Section (2014-2020)
 Member, Brandeis Department of Biochemistry Visiting Committee (2014)
 Member, U. Texas (Austin) Department of Chemistry Visiting Committee (2013)
 Chairman, M.I.T. Committee on Graduate Programs (2011-2013)
 Member, Scientific Advisory Committee, Children's Hospital, Boston (2011)
 Chairman, M.I.T. Graduate Program in Biology (2011-2012)
 Co-organizer, Keystone Meeting on AAA+ and Related ATP-Driven Protein Machines: Structure, Function and Mechanism (Tahoe, 2011)
 Member, M.I.T. Committee on Graduate Programs (2010-2011)
 Member, Editorial Board, *Structure* (2006-present)
 Chairman, N.I.H. Special Emphasis Study Section ZRG1 BST-N(03) Bioengineering Sciences and Technologies (2010)
 Member, M.I.T. Tenure Review Committee (2009)
 Chairman, NIH Special Emphasis Study Section ZRG1 IDM-S Topics in Microbiology (2009)
 Member, MIT Faculty Committee on Open Access Publication (2008-2009)
 Chairman, Biochemistry Section, National Academy of Sciences (2008-2011)
 Member, Editorial Board, *Molecular Microbiology* (2007-2009)
 Member, Edgerton Award Committee, M.I.T. (2006)
 Member, Visiting Committee, U. Pennsylvania Dept of Biochemistry & Biophysics (2006)
 Chairman, M.I.T. Computational and Systems Biology Initiative Executive Committee (2004-2005)
 Member, Review Committee for the Department of Biochemistry and Molecular Pharmacology, Harvard Medical School (2004)
 Head, M.I.T. Dept. of Biology (1999-2004)
 Member, NE-CAT Executive Committee (2002-2012)
 Member, Scientific Review Board, Structural Biology, Howard Hughes Medical Institute (1998-present)
 Member-at-large, NAS Class Membership Committee (2002-2004)
 Chairman, Argonne National Labs Biosciences Division Review (2002)
 Member, NAS Nominating Committee (2001)
 Member, Whitehead Director Search Committee (2001)
 Member, NAS Molecular Biology Award Committee (2000)
 President, Protein Society (1997-1999)
 Member, Visiting Committee, Stanford University Dept. of Biological Sciences (1997)
 Member, Visiting Committee, Vanderbilt University Dept. of Molecular Biology (1997)
 Chairman, M.I.T. Outside Professional Activities Committee (1996-1998)
 Member, Editorial Board, *Folding and Design* (1995-2000)
 Member, Eli Lilly Award Microbiology & Immunology Selection Committee (1995-1998)
 Member, Editorial Board, *Protein Science* (1992-1998; 2007-present)
 Chairman, Board of Scientific Counselors, National Center for Biotechnology Information, National Library of Medicine (1990-1996)
 Associate Head, M.I.T. Dept. of Biology (1989-1998)
 Chairman, M.I.T. Graduate Program in Biology (1987-1991)

Member, Protein Society Nominating Committee (1987-1990)
 Member, Editorial Board, *Proteins: Structure, Function, and Genetics* (1986-1999)
 Member, Editorial Board, *Protein Engineering* (1986-present)
 Member, Editorial Board, *Current Opinions in Structural Biology* (1990-1998)
 Organizer, Protein Society Meeting (Seattle; 1989)
 Co-chairman, Nucleic Acids Gordon Conference (1987)
 Member, NAS Research Briefing Panel on Protein Structure & Function (1986)
 Organizer, Banbury Meeting on Protein Structure and Stability (1983)

Publications

341. Alvaro, A.J., Schmitz, K.R., Sello, J.K., Baker, T.A. & Sauer, R.T. (2016) Highly dynamic interactions maintain kinetic stability of the ClpXP protease during the ATP-fueled mechanical cycle. *ACS Chem. Biol.* (submitted).
340. Stein, B.J., Grant, R.A., Sauer, R.T., & Baker, T.A. (2016) Structural basis of an N-degron adaptor with more stringent specificity. *Structure* **2**, 232–242.
339. Barthelme, D. & Sauer, R.T. (2016) Origin and functional evolution of the Cdc48/p97/VCP AAA+ protein unfolding and remodeling machine. *J. Mol. Biol.* (in press).
338. Olivares, A.O., Baker, T.A. & Sauer, R.T. (2016) Structural and mechanistic insights into bacterial AAA+ proteases and protein-remodeling machines. *Nat. Rev. Microbiol.* **14**, 33–44.
337. Totaro, K.A., Barthelme, D., Simpson, P.T., Sauer, R.T. & Sello, J.K. (2015) Substrate-guided optimization of the syringolins yields potent proteasome inhibitors with activity against leukemia cell lines. *Bioorg. Med. Chem.* **23**, 6218–6222.
336. Carney, D.W., Schmitz, K.R., Scrusse, A., Sauer, R.T. & Sello, J.K. (2015) Examination of a structural model of peptidomimicry by cyclic acyldepsipeptides antibiotics in their interaction with the ClpP peptidase. *ChemBioChem* **16**, 1875–1879.
335. Iosefson, O., Olivares, A.O., Baker, T.A. & Sauer, R.T. (2015) Dissection of axial-pore loop function during unfolding and translocation by a AAA+ proteolytic machine. *Cell Reports* **12**, 1032–1041.
334. Barthelme, D., Jauregui, R. & Sauer, R.T. (2015) An ALS disease mutation in Cdc48/p97 impairs 20S proteasome binding and proteolytic communication. *Protein Sci.* **24**, 1521–1527.
333. Baytshtok, V., Baker, T.A. & Sauer, R.T. (2015) Assaying the kinetics of protein denaturation catalyzed by AAA+ unfolding machines and proteases. *Proc. Natl. Acad. Sci. USA* **112**, 5377–5382.

332. Ling, L., Montañño, S.P., Sauer, R.T., Rice, P.A., & Baker, T.A. (2015) Deciphering the roles of multi-component recognition signals by the AAA+ unfoldase, ClpX. *J. Mol. Biol.* **427**, 2966–2982.
331. Stinson, B.M., Baytshtok, V., Schmitz, K.R., Baker, T.A. & Sauer, R.T. (2015) Subunit asymmetry and roles of conformational switching in the hexameric AAA+ ring of ClpX. *Nat. Struct. Mol. Biol.* **22**, 411–416.
330. de Regt, A.K., Baker, T.A. & Sauer, R.T. (2015) Steric clashes with bound OMP peptides activate the DegS stress-response protease. *Proc. Natl. Acad. Sci. USA* **112**, 3326–3331.
329. de Regt, A.K., Kim, S., Sohn, J., Grant, R.A., Baker, T.A. & Sauer, R.T. (2015) A conserved activation cluster is required for allosteric communication in HtrA-family proteases. *Structure* **23**, 517–526.
328. Iosefson, O., Nager, A.R., Baker, T.A. & Sauer, R.T. (2015) Coordinated gripping of substrate by subunits of a AAA+ proteolytic machine *Nat. Chem. Biol.* **11**, 201–206.
327. Schmitz, K.R., Carney, D.W., Sello, J.K. & Sauer, R.T. (2014) The crystal structure of *M. tuberculosis* ClpP1P2 suggests a model for peptidase activation by AAA+ partner binding and substrate delivery. *Proc. Natl. Acad. Sci. USA* **111**, E4587–4595.
326. Rivera-Rivera, I., Román-Hernández, G., Sauer, R.T. & Baker, T.A. (2014). Remodeling of a delivery complex allows ClpS-mediated degradation of N-degron substrates. *Proc. Natl. Acad. Sci. USA* **111**, E3853–3859.
325. Olivares, A.O., Nager, A.R., Yosefson, O., Sauer, R.T. & Baker, T.A. (2014) Mechanochemical basis of protein degradation by a double-ring AAA+ machine. *Nat. Struct. Mol. Biol.* **21**, 871–875.
324. Carney, D.W., Compton, C.L., Schmitz, K.R., Stevens, J.P., Sauer, R.T. & Jason K. Sello (2014) A simple fragment of the acyldepsipeptide antibacterial agents is necessary and sufficient for ClpP activation and antibacterial activity. *Chembiochem.* **15**, 2216-2220.
323. Schmitz, K.R. & Sauer, R.T. (2014) Substrate delivery by the AAA+ ClpX and ClpC1 unfoldases activates the mycobacterial ClpP1P2 peptidase. *Mol. Micro.* **93**, 617–628.
322. de Regt, A.K., Yin, Y., Withers, T.R., Wang, X., Baker, T.A., Sauer, R.T. & Yu, H.D. (2014) Overexpression of CupB5 activates alginate overproduction in *Pseudomonas aeruginosa* by a novel AlgW-dependent mechanism. *Mol. Micro.* **93**, 415–425.
321. Cordova, J.C, Olivares, A.O., Shin, Y., Stinson, B.M., Calmat, S., Schmitz, K.R., Aubin-Tam, M-E. Baker, T.A., Lang, M.J., and Sauer R.T. (2014) Stochastic but highly coordinated protein unfolding and translocation by the ClpXP proteolytic machine. *Cell* **158**, 647–658.

320. Barthelme, D., Chen, J.Z., Grabenstatter, J., Baker, T.A. & Sauer, R.T. (2014) Architecture and assembly of the archaeal Cdc48•20S proteasome. *Proc. Natl. Acad. Sci. USA* **111**, E1687–1694.
319. Kim, S. & Sauer, R.T. (2014) Distinct regulatory mechanisms balance DegP proteolysis to maintain cellular fitness during heat stress. *Genes Dev.* **28**, 902–911.
318. Carney, D., Schmitz, K.R., Truong, J., Sauer, R.T. & Sello, J.K. (2014) Restriction of the conformational dynamics of the cyclic acyldepsipeptide macrocycle improves antibacterial activity by enhancing both ClpP peptidase binding and activation. *J. Amer. Chem. Soc.* **136**, 1922–1929.
317. Wohlever, M.L., Baker, T.A. & Sauer, R.T. (2014) Roles of the N domain of the AAA+ Lon protease in substrate recognition, allosteric regulation, and chaperone activity. *Mol. Microbiol.* **91**, 66–78.
316. Wohlever, M.L., Baker, T.A. & Sauer, R.T. (2013) A mutation in the N domain of *E. coli* Lon stabilizes dodecamers and selectively alters degradation of model substrates. *J. Bacteriology* **195**, 5622–5628.
315. Compton, C.L., Schmitz, K.R., Sauer, R.T. & Sello, J.K. (2013) Antibacterial activity of and resistance to small molecule inhibitors of the ClpP peptidase. *ACS Chem. Biol.* **8**, 2669–2677.
314. Sauer, R.T. (2013) Mutagenic dissection of the sequence determinants of protein folding, recognition, and machine function. *Protein Sci.* **22**, 1675–1687.
313. Vieux, E.F., Wohlever, M.L., Chen, J.Z., Sauer, R.T. & Baker, T.A. (2013) Distinct quaternary structures of the AAA+ Lon protease control substrate degradation. *Proc. Natl. Acad. Sci. USA* **110**, 2002–2008.
312. Lima, S., Guo, M.S., Chaba, R., Gross, C.A. & Sauer, R.T. (2013) Dual molecular signals mediate the bacterial response to outer-membrane stress. *Science* **340**, 837–841.
311. Stinson, B.M., Nager, A.R., Glynn, S.E., Schmitz, K.R., Baker, T.A. & Sauer, R.T. (2013) Nucleotide binding and conformational switching in the hexameric ring of a AAA+ machine. *Cell* **153**, 628–639.
310. Barthelme, D. & Sauer, R.T. (2013) Bipartite determinants mediate an evolutionarily conserved interaction between Cdc48 and the 20S peptidase. *Proc. Natl. Acad. Sci. USA* **110**, 3327–3332.
309. Wohlever, M.L., Nager, A.R., Baker, T.A. & Sauer, R.T. (2013) Engineering fluorescent protein substrates for the AAA+ Lon protease. *Protein Eng. Des. Sel.* **26**, 299–305.
308. Mauldin, R.V. & Sauer, R.T. (2013) Allosteric regulation of DegS protease subunits through a shared energy landscape. *Nat. Chem. Biol.* **9**, 90–96.

307. Barthelme, D. & Sauer, R.T. (2012) Identification of the Cdc48•20S proteasome as an ancient AAA+ proteolytic machine. *Science* **337**, 843–846.
306. Kim, S. & Sauer, R.T. (2012) Cage assembly of DegP protease is not required for substrate-dependent regulation of proteolytic activity or high-temperature cell survival. *Proc. Natl. Acad. Sci. USA* **109**, 7263–7268.
305. Glynn, S.E., Nager, A.R., Baker, T.A. & Sauer, R.T. (2012) Dynamic and static components power unfolding in topologically closed rings of a AAA+ proteolytic machine. *Nat. Struct. Mol. Biol.* **19**, 616–622.
304. Baker, T.A. & Sauer, R.T. (2012) ClpXP, an ATP-powered unfolding and protein-degradation machine. *Biochim. Biophys. Acta* **1823**, 15–28.
303. Gur, E., Vishkautsan, M. & Sauer, R.T. (2012) Protein unfolding and degradation by the AAA+ Lon protease. *Protein Sci.* **21**, 268–278.
302. Sundar, S., Baker, T.A. & Sauer, R.T. (2012) The I domain of the AAA+ HslUV protease coordinates substrate binding, ATP hydrolysis, and protein degradation. *Protein Sci.* **21**, 188–198.
301. Nager, A.R., Baker, T.A. & Sauer, R.T. (2011) Stepwise unfolding of a β -barrel protein by the AAA+ ClpXP protease. *J. Mol. Biol.* **413**, 4–16. Erratum *J. Mol. Biol.* **425**, 1241–1243.
300. Davis, J.H., Baker, T.A. & Sauer, R.T. (2011) Small-molecule control of protein degradation using split adaptors. *ACS Chem. Biol.* **6**, 1205–1213.
299. Román-Hernández, G., Hou, J.Y., Grant, R.A., Sauer, R.T. & Baker, T.A. (2011) The ClpS adaptor mediates staged delivery of N-end-rule substrates to the AAA+ ClpAP protease. *Mol. Cell* **43**, 217–228.
298. Sauer, R.T. & Baker, T.A. (2011) AAA+ proteases: ATP-fueled machines of destruction. *Ann. Rev. Biochem.* **80**, 587–612.
297. Aubin-Tam, M.E., Olivares, A.O., Sauer, R.T., Baker, T.A. & Lang, M.J. (2011) Single-molecule protein unfolding and translocation by an ATP-fueled proteolytic machine. *Cell* **145**, 257–267.
296. Kim, S., Grant, R.A. & Sauer, R.T. (2011) Covalent linkage of distinct substrate degrons controls assembly and disassembly of DegP proteolytic cages. *Cell* **145**, 67–78.
295. Chaba, R., Alba, B.M., Guo, M., Sohn, J., Sauer, R.T. & Gross, C.A. (2011) Signal integration by DegS and RseB governs the σ^E -mediated envelope stress response in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **108**, 2106–2111.
294. Davis, J.H., Rubin, A.J. & Sauer, R.T. (2011) Design, construction, and characterization of a set of insulated bacterial promoters. *Nucleic Acids Res.* **39**, 1131–1141.

293. Sundar, S., McGinness, K.E., Baker, T.A. & Sauer, R.T. (2010) Multiple sequence signals direct recognition and degradation of protein substrates by the AAA+ protease HslUV. *J. Mol. Biol.* **403**, 420–429.
292. Sohn, J., Grant, R.A. & Sauer, R.T. (2010) Allostery is an intrinsic property of the protease domain of DegS: implications for enzyme function and evolution. *J. Biol. Chem.* **285**, 34039–34047.
291. Lee, M.E., Baker, T.A. & Sauer, R.T. (2010) Control of substrate gating and translocation into ClpP by channel residues and ClpX binding. *J. Mol. Biol.* **399**, 707–718.
290. Bissonnette, S.A., Rivera-Rivera, I., Sauer, R.T. & Baker, T.A. (2010) The IbpA and IbpB small heat-shock proteins are substrates of the AAA+ Lon protease. *Mol. Micro.* **75**, 1539–1549.
289. Abdelhakim, A., Sauer, R.T., & Baker, T.A. (2010) The AAA+ ClpX machine unfolds a keystone subunit to remodel the Mu transpososome. *Proc. Natl. Acad. Sci. USA* **107**, 2437–2442.
288. Chowdhury, T., Chien, P. Ebrahim, S., Sauer, R.T. & Baker, T.A. (2010) Versatile modes of peptide recognition by the ClpX N domain mediate alternative adaptor-binding specificities in different bacterial species. *Protein Sci.* **19**, 242–254.
287. Shin, Y., Davis, J.H., Brau, R.R., Martin, A., Kenniston, J.A., Baker, T.A., Sauer, R.T. & Lang, M.J. (2009) Single-molecule denaturation and degradation of proteins by the AAA+ ClpXP protease. *Proc. Natl. Acad. Sci. USA* **106**, 19340–19345.
286. Gur, E. & Sauer, R.T. (2009) Degrons in protein substrates program the speed and operating efficiency of the AAA+ Lon proteolytic machine. *Proc. Natl. Acad. Sci. USA* **106**, 18503–18508.
285. Glynn, S.E., Martin, A., Nager, A.R., Baker, T.A. & Sauer, R.T. (2009) Crystal structures of asymmetric ClpX hexamers reveal nucleotide-dependent motions in a AAA+ protein-unfolding machine. *Cell* **139**, 744–756.
284. Sohn, J., Grant, R.A. & Sauer, R.T. (2009) OMP peptides activate the DegS stress-sensor protease by a relief of inhibition mechanism. *Structure* **17**, 1411–1421.
283. Davis, J.H., Baker, T.A. & Sauer, R.T. (2009) Engineering synthetic adaptors and substrates for controlled ClpXP degradation. *J. Biol. Chem.* **14**, 21848–21855.
282. Román-Hernández, G., Grant, R.A., Sauer, R.T. & Baker, T.A. (2009) Molecular basis of substrate selection by the N-end rule adaptor protein ClpS. *Proc. Natl. Acad. Sci USA* **106**, 8888–8893.
281. Barkow, S.R., Levchenko, I., Baker, T.A. & Sauer, R.T. (2009) Polypeptide translocation by the AAA+ ClpXP protease machine. *Chem. Biol.* **16**, 605–612.

280. Cezairliyan, B.O. & Sauer, R.T. (2009) Control of *P. aeruginosa* AlgW protease cleavage of MucA by peptide signals and MucB. *Mol. Micro.* **72**, 368–379.
279. Ahuja, N., Korkein, D., Chaba, R., Cezairliyan, B.O., Sauer, R.T., Kim, K.K. and Gross, C.A. (2009) Analyzing the interaction of RseA and RseB, the two negative regulators of the σ^E envelope stress response, using a combined bioinformatic and experimental strategy. *J. Biol. Chem.* **284**, 5403–5413.
278. Sohn, J. & Sauer, R.T. (2009) OMP peptides modulate the activity of DegS protease by differential binding to active and inactive conformations. *Mol. Cell* **33**, 64–74.
277. Moore, S.D. & Sauer, R.T. (2008) Revisiting the mechanism of macrolide-antibiotic resistance mediated by ribosomal protein L22. *Proc. Natl. Acad. Sci. USA* **105**, 18261–18266.
276. Gur, E. & Sauer, R.T. (2008) Evolution of the *ssrA* degradation tag in *Mycoplasma*: specificity switch to a different protease. *Proc. Natl. Acad. Sci. USA* **105**, 16113–16118.
275. Wang, K.H., Román-Hernández, G., Grant, R.A., Sauer, R.T. & Baker, T.A. (2008) The molecular basis of N-end rule recognition. *Mol. Cell* **32**, 406–414.
274. Moore, S.D., Baker, T.A. & Sauer, R.T. (2008) Forced extraction of targeted components from complex macromolecular assemblies. *Proc. Natl. Acad. Sci. USA* **105**, 11685–11690.
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272. Yakamavich, J.A., Baker, T.A. & Sauer, R.T. (2008) Asymmetric nucleotide transactions of the HslUV protease. *J. Mol. Biol.* **380**, 946–957.
271. Martin, A., Baker, T.A. & Sauer, R.T. (2008) Pore loops of the AAA+ ClpX machine grip substrates to drive translocation and unfolding. *Nat. Struct. Mol. Biol.* **15**, 1147–1151.
270. Gur, E. & Sauer, R.T. (2008) Recognition of misfolded proteins by Lon, a AAA+ protease. *Genes Dev.* **22**, 2267–2277.
269. Martin, A., Baker, T.A. & Sauer, R.T. (2008) Diverse pore loops of the AAA+ ClpX machine mediate unassisted and adaptor-dependent recognition of *ssrA*-tagged substrates. *Mol. Cell* **29**, 441–450.
268. Abdelhakim, A.H., Oakes, E.S.C. Sauer, R.T., & Baker T.A. (2008) Unique contacts direct high-priority recognition of the tetrameric transposase-DNA complex by the AAA+ unfoldase ClpX. *Mol. Cell* **11**, 39–50.
267. Hou, J.Y., Sauer, R.T. & Baker, T.A. (2008) Distinct structural elements of the adaptor protein ClpS are required for activation and inhibition of degradation by the AAA+ protease ClpAP. *Nat. Struct. Mol. Biol.* **15**, 288–294.

266. Martin, A., Baker, T.A. & Sauer, R.T. (2008) Protein unfolding by a AAA+ protease: critical dependence on ATP-hydrolysis rates and energy landscapes. *Nat. Struct. Mol. Biol.* **15**, 139–145.
265. Sohn, J., Grant, R.A. & Sauer, R.T. (2007) Allosteric activation of DegS, a stress sensor PDZ-protease. *Cell* **131**, 572–583.
264. Chien, P., Grant, R.A., Sauer, R.T. & Baker, T.A. (2007) Structure and substrate specificity of an SspB ortholog: design implications for AAA+ adaptors. *Structure* **15**, 1296–1305.
263. Martin, A., Baker, T.A. & Sauer, R.T. (2007) Distinct static and dynamic interactions control ATPase-peptidase communication in a AAA+ protease. *Mol. Cell* **27**, 41–52.
262. Chien, P., Perchuk, B.S., Laub, M.T., Sauer, R.T. & Baker, T.A. (2007) Direct and adaptor-mediated substrate recognition by an essential AAA+ protease. *Proc. Natl. Acad. Sci USA* **104**, 6590–6595.
261. McGinness, K.E., Bolon, D.N., Kaganovich, M., Baker, T.A. & Sauer, R.T. (2007) Altered tethering of the SspB adaptor to the ClpXP protease causes changes in substrate delivery. *J. Biol. Chem.* **282**, 11465–11473.
260. Moore, S.E. & Sauer, R.T. (2007) The tmRNA system for translational surveillance and ribosome rescue. *Annu. Rev. Biochem.* **76**, 101–124.
259. Cezairliyan, B.O. & Sauer, R.T. (2007) Inhibition of regulated proteolysis by RseB. *Proc. Natl. Acad. Sci. USA* **10**, 3771–3776.
258. Wang, K.H., Sauer, R.T. & Baker, T.A. (2007) ClpS modulates but is not essential for bacterial N-end rule degradation. *Genes Dev.* **21**, 403–408.
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256. Baker, T.A. & Sauer, R.T. (2006) ATP-dependent proteases: recognition logic and operating principles. *Trends Biochem. Sci.* **31**, 647–653.
255. McGinness, K.E., Baker, T.A. & Sauer, R.T. (2006) Engineering controllable protein degradation. *Mol. Cell* **22**, 701–707.
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253. Anderson, T.A., Cordes, M.H.J. & Sauer, R.T. (2005) Sequence determinants of a conformational switch in a protein structure. *Proc. Natl. Acad. Sci. USA* **102**, 18344–18349.

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251. Moore, S.D. & Sauer, R.T. (2005) Ribosome rescue: tmRNA tagging activity and capacity in *Escherichia coli*. *Mol. Micro.* **58**, 456–466.
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249. Farrell, C.M., Grossman, A.D. & Sauer, R.T. (2005) Cytoplasmic degradation of ssrA-tagged proteins. *Mol. Micro.* **57**, 1750–1761.
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