CURRICULUM VITAE

ROBERT THOMAS SAUER

Born: 13 July, 1948, Cornwall, New York

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

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)

SERVICE

Chairman, M.I.T. Committee on Graduate Programs (2011-2012)
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)
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-present)
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)

NAMED LECTURESHIPS

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)

PUBLICATIONS:

309. Mauldin, R.V. & Sauer, R.T. (2012) The allosteric energy landscape of DegS, a regulated PDZ protease. (submitted).

308. Lima, S., Guo, M.S., Chaba. R., Gross, C.A. & Sauer, R.T. (2012) An integrated signaling system monitors outer-membrane homeostasis (submitted).

307. Barthelme, D. & Sauer, R.T. (2012) Identification of the Cdc48•20S proteasome as an ancient AAA+ proteolytic machine. *Science* (accepted for publication).

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 Science* **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 Science* **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.

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.* **403**, 420-429.

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., Korkin, 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**, 406-14.

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.

273. Wang, K.H., Oakes, E.S.C., Sauer, R.T. & Baker, T.A. (2008) Tuning the strength of a bacterial N-end rule degradation signal. *J. Biol. Chem.* **283**, 24600-24607.

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.

257. Farrell, C.M., Baker, T.A. & Sauer, R.T. (2007) Altered specificity of a AAA+ protease. *Mol. Cell* **25**, 161-166.

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.

254. Neher, S.B., Villen, J., Oakes, E., Bakalarski, C. Sauer, R.T., Gygi, S.P. & Baker, T.A. (2006) Proteomic profiling of ClpXP substrates following DNA damage reveals extensive instability within SOS regulon. *Mol. Cell* **22**, 193-204.

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.

252. Bolon, D.N., Grant, R.A., Baker, T.A. & Sauer, R.T. (2005) Specificity versus stability in computational protein design. *Proc. Natl. Acad. Sci. USA* **102**, 12724-12729.

251. Moore, S.D. & Sauer, R.T. (2005) Ribosome rescue: tmRNA tagging activity and capacity in *Escherichia coli*. *Mol. Micro.* **58**, 456-466.

250. Martin, A., Baker, T.A. & Sauer, R.T. (2005) Rebuilt AAA+ motors reveal operating principles for ATP-fueled machines. *Nature* **437**, 1115-1120.

249. Farrell, C.M., Grossman, A.D. & Sauer, R.T. (2005) Cytoplasmic degradation of ssrA-tagged proteins. *Mol. Micro.* **57**, 1750-1761.

248. Hersch, G.L., Burton, R.E., Bolon, D.N., Baker, T.A. & Sauer, R.T. (2005) Asymmetric interactions of ATP with the AAA+ $ClpX_6$ unfoldase: allosteric control of a protein machine. *Cell* **121**, 1017-1027.

247. Levchenko, I., Grant, R.A., Flynn, J.M., Sauer, R.T. & Baker, T.A. (2005) Versatile modes of peptide recognition by the AAA+ adaptor protein SspB. *Nat. Struct. Mol. Biol.* **12**, 520-525.

246. Tabtiang, R.K., Cezairliyan, B.O., Grant, R.A, Cochrane, J.C. & Sauer, R.T. (2005) Consolidating critical binding determinants by non-cyclic rearrangement of protein secondary structure. *Proc. Natl. Acad. Sci. USA* **102**, 2305-2309.

245. Kenniston, J.A., Baker, T.A. & Sauer, R.T. (2005) Partitioning between unfolding and release of native domains during ClpXP degradation determines substrate selectivity and partial processing. *Proc. Natl. Acad. Sci. USA* **102**, 1390-1395.

244. Burton, R.E., Baker, T.A. & Sauer, R.T. (2005) Nucleotide-dependent substrate recognition by the AAA+ HslUV protease. *Nat. Struct. Mol. Biol.* **12**, 245-251.

243. Sauer, R.T., Bolon, D.N., Burton, B.M., Burton, R.E., Flynn, J.M., Grant, R.A., Hersch, G.L., Joshi, S.A., Kenniston, J.A., Levchenko, I., Neher, S.B., Oakes, E.S.C., Siddiqui, S.M., Wah, D.A. & Baker**,** T.A. (2004) Sculpting the proteome with AAA+ proteases and disassembly machines. *Cell* **119**, 9-18.

242. Kenniston, J.A. & Sauer, R.T. (2004) Signaling degradation. *Nat. Struct. Mol. Biol.* **11,** 800-802.

241. McGinness, K.E. & Sauer, R.T. (2004) Ribosomal protein S1 binds tmRNA and mRNA similarly but plays distinct roles in translating these molecules. *Proc. Natl. Acad. Sci. USA* **101**, 13454-13459.

240. Flynn, J.F., Levchenko, I., Sauer, R.T. & Baker, T.A. (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.

239. Bolon, D.N., Grant, R.A., Baker, T.A. & Sauer, R.T. (2004) Nucleotide-dependent substrate handoff from the SspB adaptor to the AAA+ ClpXP protease. *Mol. Cell* **16**, 343-350.

238. Hersch, G.L., Baker, T.A. & Sauer, R.T. (2004) SspB delivery of substrates for ClpXP proteolysis probed by the design of improved degradation tags. *Proc. Natl. Acad. Sci. USA* **101**, 12136-12141.

237. Spector, S., Sauer, R.T. & Tidor, B. (2004) Computational and experimental probes of symmetry mismatches in the Arc repressor-DNA complex. *J. Mol. Biol.* **340**, 253-261.

236. Joshi, S.A., Hersch, G.L., Baker, T.A. & Sauer, R.T. (2004) Communication between ClpX and ClpP during substrate processing and degradation. *Nat. Struct. Mol. Biol.* **11**, 404-411.

235. Siddiqui, S.M., Sauer, R.T. & Baker, T.A. (2004) Role of the protein-processing pore of ClpX, an AAA+ ATPase, in recognition and engagement of specific protein substrates. *Genes Dev.* **18**, 369-374.

234. Bolon, D.N., Wah, D.A., Hersch, G.L., Baker, T.A. & Sauer, R.T. (2004) Bivalent tethering of SspB to ClpXP is required for efficient substrate delivery: a protein-design study. *Mol. Cell* **13**, 443-449.

233. Kenniston, J.A., Burton, R.E., Siddiqui, S.M., Baker, T.A. & Sauer, R.T. (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**, 130-140.

232. Neher, S.B., Sauer, R.T. & Baker, T.A. (2003) Distinct Peptide Signals in the UmuD and UmuD´ Subunits of UmuD/D´ Mediate Tethering and Substrate-Processing by the ClpXP Protease. *Proc. Natl. Acad. Sci. USA* **100**, 13219-13224.

231. Spector, S., Flynn, J.M., Tidor, B., Baker, T.A. & Sauer, R.T. (2003) Expression of N-formylated proteins in *Escherichia coli*. *Protein Expr. Purif.* **32**, 317-322.

230. Hayes, C.S. & Sauer, R.T. (2003) Cleavage of the A-site mRNA codon during ribosome pausing provides a mechanism for translational quality control. *Mol. Cell* **12**, 903-911.

229. Schreiter, E.R., Sintchak, M.D., Yayi Guo, Y., Chivers, P.C, Sauer, R.T. & Drennan, C.L. (2003) Crystal structure of the nickel-responsive transcription factor NikR. *Nat. Struct. Biol.* **10**, 794-799.

228. Kenniston, J.A., Baker, T.A., Fernandez, J.M. & Sauer, R.T. (2003) Linkage between ATP consumption and mechanical unfolding during the protein processing reactions of an AAA+ degradation machine. *Cell* **114**, 511-520.

227. Levchenko, I. Grant, R.A., Wah, D.A., Sauer, R.T. & Baker, T.A. (2003) Structure of a delivery protein for a AAA+ protease in complex with a peptide degradation tag. *Mol. Cell* **12**, 365-372.

226. Wah, D.A., Levchenko, I., Rieckhof, G.E., Bolon, D.N., Baker, T.A. & Sauer, R.T. (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.

225. Moore, S.D., McGinness, K.E. & Sauer, R.T. (2003) A glimpse into tmRNA-mediated ribosome rescue. *Science* **300**, 72-73.

224. Anderson, T.A. & Sauer, R.T. (2003) Role of an N_{cap} residue in determining the stability and operator-binding affinity of Arc repressor. *Biophys.Chem.* **100**, 341-350.

223. Neher, S.B., Flynn, J.M., Sauer, R.T. & Baker, T.A. (2003) Latent ClpX-recognition signals ensure LexA destruction after DNA damage. *Genes Dev.* **17**, 1084-1089.

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221. Cordes, M.H., Walsh, N.P., McKnight, C.J., & Sauer, R.T. (2003) Solution structure of switch Arc, a mutant with 3_{10} helices replacing a wild-type beta-ribbon. *J. Mol. Biol.* ***326***, 899-909.

220. Hayes, C.S., Sauer, R.T. (2003) Toxin-antitoxin pairs in bacteria. Killers or stress regulators? *Cell* **112**, 2-4.

219. Flynn, J.M., Neher, S.B., Kim, Y.I., Sauer, R.T. & Baker, T.A. (2003) Proteomic discovery of cellular substrates of the ClpXP protease reveals five classes of ClpX-recognition signals. *Mol. Cell* **11**, 671-683.

218. Burton, R.E., Baker, T.A. & Sauer, R.T. (2003) Energy-dependent degradation: Linkage between ClpXP-catalyzed nucleotide hydrolysis and protein-substrate processing. *Protein Science* **12**, 893-902.

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