

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 (MSFB) 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

347. Amberg-Johnson, K., Hari, S.B., Ganesan, S.M., Lorenzi, H.A., Sauer, R.T., Niles, J.C. & Yeh, E. (2017) Small molecule inhibition of apicomplexan FtsH1 disrupts plastid biogenesis in human pathogens. *eLife* doi: 10.7554/eLife.29865..
346. Olivares, A.O., Kotamarthi, H.C., Stein, B.J., Sauer, R.T. & Baker, T.A. (2017) Effect of directional pulling on mechanical protein degradation by ATP-dependent proteolytic machines. *Proc. Natl. Acad. Sci. USA* doi: 10.1073/pnas.1707794114.
345. Baytshtok, V., Chen, J., Glynn, S.E., Nager, A.R., Grant, R.A, Baker, T.A. & Sauer, R.T. (2017) Covalently linked HslU hexamers support a probabilistic mechanism that links ATP hydrolysis to protein unfolding and translocation. *J. Biol. Chem.* **292**, 5695–5704.
344. Totaro, K.A., Barthelme, D., Simpson, P.T., Jiang, X., Lin, G. Nathan, C.F., Sauer, R.T., & Sello, J.K. (2016) Rational design of selective and bioactive inhibitors of the *Mycobacterium tuberculosis* proteasome. *ACS Infectious Diseases* **3**, 176–181.
343. Hari, S. & Sauer, R.T. (2016) The AAA+ FtsH protease degrades an ssrA-tagged model protein in the inner membrane of *E. coli*. *Biochemistry* **55**, 5649–5652.
342. Baytshtok, V., Fei, X., Grant, R.A., Baker, T.A. & Sauer, R.T. (2016) A structurally dynamic region of the HslU intermediate domain controls protein degradation and ATP hydrolysis. *Structure* **24**, 1766–1777.
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.* **11**, 1552–1560.
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.* **428**, 1861–1869.
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., Scruse, 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., Montañó, 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.
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+ ClpX₆ 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.
222. Walsh, N.P., Alba, B.M., Bose, B., Gross, C.A. & Sauer, R.T. (2003) OMP peptide signals initiate the envelope-stress response by activating DegS protease through relief of inhibitory interactions mediated by its PDZ domain. *Cell* **113**, 61–71.
221. Cordes, M.H., Walsh, N.P., McKnight, C.J. & Sauer, R.T. (2003) Solution structure of switch Arc, a mutant with 3₁₀ 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 Sci.* **12**, 893–902.
217. Joshi, S.A., Baker, T.A. & Sauer, R.T. (2003) C-terminal domain mutations in ClpX uncouple substrate binding from an engagement step required for unfolding. *Mol. Micro.* **48**, 67–76.
216. Al-Mjeni, F., Chivers, P.T., Carrington, P.E., Sauer, R.T. & Maroney, M.J. (2003) Nickel coordination is regulated by the DNA-bound state of NikR. *Nat. Struct. Biol.* **10**, 126–130.
215. Wah, D.A., Levchenko, I., Baker, T.A. & Sauer, R.T. (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.
214. Chivers, P.T. & Sauer, R.T. (2002) NikR repressor: high-affinity nickel binding to the C-terminal domain regulates binding to operator DNA. *Chem. Biol.* **9**, 1141–1148.
213. Krantz, B.A., Srivastava, A.K., Nauli, S., Baker, D., Sauer, R.T. & Sosnick, T.R. (2002) Understanding protein hydrogen-bond formation with kinetic H/D amide isotope effects. *Nat. Struct. Biol.* **9**, 458–463.
212. Hayes, C.S., Bose, B. & Sauer, R.T. (2002) Proline residues at the C-terminus of nascent chains induce SsrA tagging during translation termination. *J. Biol. Chem.* **277**, 33825–33832.
211. Srivastava, A.K., & Sauer, R.T. (2002) Mutational studies of protein stability and folding of the hyperstable MYL Arc repressor variant. *Biophys. Chem.* **101-102**, 35–42.
210. Hayes, C.S., Bose, B. & Sauer, R.T. (2002) Stop codons preceded by rare arginine codons are efficient determinants of SsrA-tagging in *Escherichia coli*. *Proc. Natl. Acad. Sci. USA* **99**, 344–3445.
209. Smith, C.K., Wohnert, J., Sauer, R.T. & Schwalbe, H. (2001) Assignments of the ^1H , ^{13}C , and ^{15}N resonances of the substrate-binding SSD domain from Lon protease. *J. Biomol. NMR* **21**, 387–388.
208. Barends, S., Karzai, A.W., Sauer, R.T., Wower, J. & Kraal, B. (2001) Simultaneous and functional binding of SmpB and EF-TU to the alanyl acceptor arm of tmRNA. *J. Mol. Biol.* **314**, 9–21.
207. Flynn, J.M., Levchenko, I., Seidel, M., Wickner, S.H., Sauer, R.T. & Baker, T.A. (2001) Overlapping recognition determinants within the *ssrA* degradation tag allow modulation of proteolysis. *Proc. Natl. Acad. Sci. USA* **11**, 10584–10589.
206. Keiler, K. & Sauer, R.T. (2002) Tsp and related C-terminal processing proteases. in *The Enzymes, Vol. 22 Co- and Posttranslational Proteolysis of Proteins* (Ross E. Dalbey, David S. Sigman eds.) Third Edition, Academic Press, 373–386.

205. Roche, E.D. & Sauer, R.T. (2001) Identification of endogenous SsrA-tagged proteins reveals tagging at positions corresponding to stop codons. *J. Biol. Chem.* **276**, 28509–28515.
204. Burton, R.E., Siddiqui, S.M., Kim, Y.I., Baker, T.A. & Sauer, R.T. (2001) Effects of protein stability and structure on substrate processing by the ClpXP unfolding and degradation machine. *EMBO J.* **20**, 3092–3100.
203. Karzai, A.W. & Sauer, R.T. (2001) Protein factors associated with the SsrA•SmpB tagging and ribosome rescue complex. *Proc. Natl. Acad. Sci. USA* **98**, 3040–3044.
202. Nohaile, M.J., Hendsch, Z.S., Tidor, B. & Sauer, R.T. (2001) Altering dimerization specificity by changes in surface electrostatics. *Proc. Natl. Acad. Sci. USA* **98**, 3109–3114.
201. Berggrun, A. & Sauer, R.T. (2001) Contributions of distinct quaternary contacts to cooperative operator binding by Mnt repressor. *Proc. Natl. Acad. Sci. USA* **98**, 2301–2305.
200. Kim, Y.I., Levchenko, I., Fraczkowska, K., Woodruff, R.V., Sauer, R.T. & Baker, T.A. (2001) Molecular determinants of complex formation between Clp/Hsp100 ATPases and the ClpP peptidase. *Nat. Struct. Biol.* **8**, 230–233.
199. Hendsch, Z.S., Nohaile, M.J., Sauer, R.T. & Tidor, B. (2001) Preferential heterodimer formation via undercompensated electrostatic interactions. *J. Amer. Chem. Soc.* **123**, 1264–1265.
198. Lo, J., Baker, T.A. & Sauer, R.T. (2001) Characterization of the N-terminal repeat domain of *E. coli* ClpA—a class I Clp/Hsp100 ATPase. *Protein Sci.* **10**, 551–559.
197. Nooren, I.M.A., Folkers, G.E., Kaptein, R., Sauer, R.T. & Boelens, R. (2000) Structure and Dynamics of the Tetrameric Mnt Repressor and a Model for its DNA complex. *J. Biomol. Struct. Dynam.* **11**, 113–122.
196. Levchenko, I., Seidel, M., Sauer, R.T. & Baker, T.A. (2000) A specificity-enhancing factor for the ClpXP degradation machine. *Science* **289**, 2354–2356.
195. Robinson, C.R. & Sauer, R.T. (2000) Striking stabilization of Arc repressor by an engineered disulfide bond. *Biochemistry* **39**, 12494–12502.
194. Cordes, M.H.J., Burton, R.E., Walsh, N.P., McKnight, C.J. & Sauer, R.T. (2000) An evolutionary bridge to a new protein fold. *Nat. Struct. Biol.* **7**, 1129–1132.
193. Berggrun, A. & Sauer, R.T. (2000) Interaction of Arg2 in Mnt's N-terminal arm with the central and flanking regions of the *mnt* operator. *J. Mol. Biol.* **301**, 959–973.
192. Srivastava, A.K. & Sauer, R.T. (2000) Evidence for partial secondary structure formation in the transition state for Arc repressor refolding and dimerization. *Biochemistry* **39**, 8308–8314.

191. Chivers, P.T. & Sauer, R.T. (2000) Regulation of high-affinity nickel uptake in bacteria: Ni²⁺-dependent interaction of NikR with wild-type and mutant operator sites. *J. Biol. Chem.* **275**, 19735–19741.
190. Karzai, A.W., Roche, E.D. & Sauer, R.T. (2000) The SsrA-SmpB system for protein tagging, directed degradation, and ribosome rescue. *Nat. Struct. Biol.* **7**, 449–455.
189. Kim, Y.I., Burton, R.E., Burton, B.M., Sauer, R.T. & Baker, T.A. (2000) Dynamics of substrate denaturation and translocation by the ClpXP degradation machine. *Mol. Cell* **5**, 639–648.
188. Lin, H., Abida, W.A., Sauer, R.T. & Cornish, V.W. (2000) Dexamethasone-methotrexate: an efficient chemical inducer of protein dimerization *in vivo*. *J. Amer. Chem. Soc.* **122**, 4247–4248.
187. Chivers, P.T. & Sauer, R.T. (1999) NikR is a ribbon-helix-helix DNA-binding protein. *Protein Sci.* **8**, 2494–2500.
186. Gazit, E. & Sauer, R.T. (1999) The Doc toxin and Phd antidote proteins of the bacteriophage P1 plasmid addiction system form a heterotrimeric complex. *J. Biol. Chem.* **274**, 16813–16818.
185. Roche, E.D. & Sauer, R.T. (1999) SsrA-mediated tagging caused by rare codons and tRNA scarcity. *EMBO J.* **18**, 4579–4589.
184. Karzai, A.W., Susskind, M.M. & Sauer, R.T. (1999) SmpB, a unique RNA-binding protein essential for the peptide-tagging activity of SsrA (tmRNA) *EMBO J.* **18**, 3793–3799.
183. Smith, C.K., Baker, T.A. & Sauer, R.T. (1999) Lon and Clp family proteases and chaperones share homologous substrate-recognition domains. *Proc. Natl. Acad. Sci. USA* **96**, 6678–6682.
182. Nooren, I.M.A., George, A.V.E., Kaptein, R., Sauer, R.T. & Boelens, R. (1999) The structure of the tetramerization domain of the Mnt repressor reveals a four-helix bundle with an asymmetric subunit assembly. *J. Biomol. NMR* **15**, 39–53.
181. Nooren, I.M.A., Kaptein, R., Sauer, R.T. & Boelens, R. (1999) The tetramerization domain of the Mnt repressor consists of two right-handed coiled coils. *Nat. Struct. Biol.* **6**, 755–759.
180. Brown, B.M. & Sauer, R.T. (1999) Tolerance of Arc repressor to multiple alanine substitutions. *Proc. Natl. Acad. Sci. USA* **96**, 1983–1988.
179. Nooren, I.M.A., Rietveld, A.W.M., Melacini, G., Sauer, R.T., Kaptein, R. & Boelens, R. (1999) The solution structure and dynamics of an Arc repressor mutant reveal premelting conformational changes related to DNA binding. *Biochemistry* **38**, 6035–6042.

178. Rentzeperis, D., Jonsson, T., & Sauer, R.T. (1999) Acceleration of the refolding of Arc repressor by nucleic acids and other polyanions. *Nat. Struct. Biol.* **6**, 569–573.
177. Cordes, M.J., Walsh, N., McKnight, J. & Sauer, R.T. (1999) Evolution of a protein fold *in vitro*. *Science* **284**, 325–327.
176. Cordes, M.J. & Sauer, R.T. (1999) Tolerance of a protein to multiple hydrophobic to polar surface substitutions. *Protein Sci.* **8**, 318–325.
175. Schildbach, J.F., Karzai, A.W., Raumann, B.E. & Sauer, R.T. (1999) Origins of DNA-binding specificity: role of protein contacts with the DNA backbone. *Proc. Nat. Acad. Sci. USA* **96**, 811–817.
174. Gazit, E. & Sauer, R.T. (1999) Stability and DNA binding of the Phd protein of the phage-P1 plasmid addiction system. *J. Biol. Chem.* **274**, 2652–2657.
173. Robinson, C.R. & Sauer, R.T. (1998) Optimizing the stability of single-chain proteins by linker length and composition mutagenesis. *Proc. Natl. Acad. Sci. USA* **95**, 5929–5934.
172. Gregoret, L.M. & Sauer, R.T. (1998) Tolerance of a protein helix to multiple alanine and valine substitutions. *Fold. Des.* **3**, 119–126.
171. Gottesman, S., Roche, E., Zhou, Y.N., & Sauer, R.T. (1998) The ClpXP and ClpAP proteases degrade proteins with C-terminal peptide tails added by the SsrA tagging system. *Genes Dev.* **12**, 1338–1347.
170. Schildbach, J.F., Robinson, C.R. & Sauer, R.T. (1998) Biophysical characterization of the TraY protein of *Escherichia coli* F factor. *J. Biol. Chem.* **273**, 1329–1333.
169. Keiler, K C. & Sauer, R.T. (1998) Tail-specific protease. in *Handbook of Proteolytic Enzymes* (Woessner, F, Barrett, A.J., Rawlings, N.D., eds.). Academic Press, Orlando, FL.
168. Levchenko, I., Smith, C.K., Walsh, N.P., Sauer, R.T. & Baker, T.A. (1997) PDZ-like domains mediate binding specificity in the Clp/Hsp100 Family of chaperones and protease regulatory subunits. *Cell* **91**, 939–947.
167. Tucker-Kellogg, L., Rould, M.A., Chambers, K.A., Ades, S.E., Sauer, R.T. & Pabo, C.O. (1997) Engrailed (Gln50→Lys) homeodomain-DNA complex at 1.9 Å resolution: structural basis for enhanced affinity and altered specificity. *Structure* **5**, 1047–1054.
166. Robinson, C.R., Rentzeperis, D., Silva, J.R., & Sauer, R.T. (1997) Formation of a denatured dimer limits the thermal stability of Arc repressor. *J. Mol. Biol.* **273**, 692–700.
165. Kolmar, H., Waller, P.R.H. & Sauer, R.T. (1996) The DegP and DegQ periplasmic endoproteases of *Escherichia coli*: specificity for cleavage sites and substrate conformation. *J. Bact.* **178**, 5925–5929.

164. Waldburger, C.D. & Sauer, R.T. (1996) Signal detection by the PhoQ sensor-transmitter: characterization of the sensor domain and a response-impaired mutant that identifies ligand-binding determinants. *J. Biol. Chem.* **271**, 26630–26636.
163. Robinson, C.R. & Sauer, R.T. (1996) Equilibrium stability and sub-millisecond refolding of a designed single-chain Arc repressor. *Biochemistry* **35**, 13878–13884.
162. Smith, T.L. & Sauer, R.T. (1996) Role of operator subsites in Arc repression. *J. Mol. Biol.* **264**, 233–242.
161. Sauer, R.T. (1996) Protein folding from a combinatorial perspective. *Fold. Des.* **1**, 27–30.
160. Smith, T.L. & Sauer, R.T. (1996) Dual regulation of open-complex formation and promoter clearance by Arc explains a novel repressor to activator switch. *Proc. Nat. Acad. Sci. USA* **93**, 8868–8872.
159. Hendsch, Z.S., Jonsson, T., Sauer, R.T. & Tidor, B. (1996) Protein stabilization by removal of unsatisfied polar groups: computational approaches and experimental tests. *Biochemistry* **35**, 7621–7625.
158. Jonsson, T., Waldburger, C.D. & Sauer, R.T. (1996) Nonlinear free-energy relationships in Arc repressor unfolding imply existence of unstable, native-like folding intermediates. *Biochemistry* **35**, 4795–4802.
157. Sauer, R.T. & Harrison, S.C. (1996) Interactions of proteins with RNA and DNA. *Curr. Opin. Struct. Biol.* **6**, 51–52.
156. Sauer, R.T. (1996) Lac repressor at last. *Structure* **4**, 219–222.
155. Keiler, K.C., Waller, P.R.H. & Sauer, R.T. (1996) Role of a peptide-tagging system in degradation of proteins translated from damaged mRNA. *Science* **271**, 990–993.
154. Waldburger, C.D., Jonsson, T. & Sauer, R.T. (1996) Barriers to protein folding: formation of buried polar interactions is a slow step in acquisition of structure. *Proc. Natl. Acad. Sci USA* **93**, 2629–2634.
153. Keiler, K C. & Sauer, R.T. (1996) Sequence determinants of C-terminal substrate recognition by the Tsp Protease. *J. Biol. Chem.* **271**, 2589–2593.
152. Cordes, M.H.J., Davidson, A.R. & Sauer, R.T. (1996) Sequence space, folding, and protein design. *Curr. Opin. Struct. Biol.* **6**, 3–10.
151. Sauer, R.T., Milla, M.E., Waldburger, C.D., Brown, B.M. & Schildbach, J.F. (1996) Sequence determinants of folding and stability for the P22 Arc repressor dimer. *FASEB J.* **10**, 42–48.
150. Waller, P.R.H. & Sauer, R.T. (1996) Characterization of *degQ* and *degS*, *Escherichia coli* genes encoding homologs of the DegP protease. *J. Bact.* **178**, 1146–1153.

149. Robinson, C.R. & Sauer, R.T. (1996) Covalent attachment of Arc repressor subunits by a peptide linker enhances affinity for operator DNA. *Biochemistry* **35**, 109–116.
148. Keiler, K. C. & Sauer, R.T. (1995) Identification of active-site residues of the Tsp protease *J. Biol. Chem.* **270**, 28864–28868.
147. Raumann, B.E., Knight, K.L. & Sauer, R.T. (1995) Dramatic changes in DNA-binding specificity caused by single-residue substitutions in an Arc/Mnt Hybrid repressor. *Nat. Struct. Biol.* **2**, 1115–1122.
146. Ades, S.E. & Sauer, R.T. (1995) Specificity of minor-groove and major-groove interactions in a homeodomain-DNA complex *Biochemistry* **34**, 14601–14608.
145. Milla, M.E., Brown, B.M., Waldburger, C.D. & Sauer, R.T. (1995) P22 Arc repressor: transition-state properties inferred from mutational effects on the rates of protein unfolding and refolding. *Biochemistry* **34**, 13914–13919.
144. Waldburger, C.D. & Sauer, R.T. (1995) Domains of Mnt repressor: roles in tetramer formation, protein stability, and operator-DNA binding. *Biochemistry* **34**, 13109–13116.
143. Davidson, A.R., Lumb, K.J. & Sauer, R.T. (1995) Cooperatively folded proteins in random sequence libraries. *Nat. Struct. Biol.* **2**, 856–863.
142. Sauer, R.T. (1995) Minor groove DNA recognition by α -helices. *Nat. Struct. Biol.* **2**, 7–9.
141. Keiler, K.C., Silber, K.R., Downard, K.M., Papayannopoulos, I.A., Biemann, K. & Sauer, R.T. (1995) C-terminal specific protein degradation: activity and substrate specificity of the Tsp protease. *Protein Sci.* **4**, 1507–1515.
140. Smith, T.L. & Sauer, R.T. (1995) P22 Arc repressor: role of cooperativity in repression and binding to operators with altered half-site spacing. *J. Mol. Biol.* **249**, 729–742.
139. Schildbach, J.F., Milla, M.E., Jeffrey, P.D., Raumann, B.E., & Sauer, R.T. (1995) Crystal structure, folding, and operator binding of the hyperstable Arc repressor mutant PL8. *Biochemistry* **34**, 1405–1412.
138. Milla, M.E. & Sauer, R.T. (1995) Critical side-chain interactions at a subunit interface in the Arc repressor dimer *Biochemistry* **34**, 3344–3351.
137. Waldburger, C.D., Schildbach, J.F. & Sauer, R.T. (1995) Are buried salt bridges important for protein stability and conformational specificity. *Nat. Struct. Biol.* **2**, 122–128.
136. Burgering, M.J., Boelens, R., Gilberyt, D.E., Breg, J.N., Knight, K.L., Sauer, R.T. & Kaptein, R. (1994) Solution structure of dimeric Mnt repressor (1-76). *Biochemistry* **33**, 15036–15045.
135. Ades, S.E. & Sauer, R.T. (1994) Differential DNA-binding specificity of the engrailed homeodomain: the role of residue 50. *Biochemistry* **33**, 9187–9194.

134. Milla, M.E., Brown, B.M. & Sauer, R.T. (1994) Protein stability effects of a complete set of alanine substitutions in Arc repressor. *Nat. Struct. Biol.* **1**, 518–523.
133. Marqusee, S. & Sauer, R.T. (1994) Dissection of protein stability: the relative contributions of secondary and tertiary interactions involving a salt bridge-hydrogen bond network in the N-terminal domain of λ repressor. *Protein Sci.* **3**, 2217–2225.
132. Waugh, D.S. & Sauer, R.T. (1994) A novel class of *Fok* I restriction endonuclease mutants that cleave hemi-methylated substrates. *J. Biol. Chem.* **269**, 12298–12303.
131. Raumann, B.E., Rould, M.A., Pabo, C.O. & Sauer, R.T. (1994) DNA recognition by β -sheets in the Arc repressor-operator crystal structure. *Nature* **367**, 754–757.
130. Brown, B.M., Milla, M.E., Smith, T.L. & Sauer, R.T. (1994) Scanning mutagenesis of Arc repressor as a functional probe of operator recognition. *Nat. Struct. Biol.* **1**, 164–168.
129. Davidson, A.R. & Sauer, R.T. (1994) Folded proteins occur frequently in libraries of random amino acid sequences. *Proc. Natl. Acad. Sci. USA* **91**, 2146–2150.
128. Raumann, B.E., Brown, B.M. & Sauer, R.T. (1994) Major groove DNA recognition by β -sheets: the ribbon-helix-helix family of gene regulatory proteins. *Curr. Opin. Struct. Biol.* **4**, 36–43.
127. Silber, K.R. & Sauer, R.T. (1994) Deletion of the *prc* (*tsp*) gene provides evidence for additional tail-specific proteolytic activity in *Escherichia coli* K12. *Mol. Gen. Genet.* **242**, 237–240.
126. Lim, W.A., Hodel, A., Sauer, R.T. & Richards, F.M. (1994) The crystal structure of a mutant protein with altered but improved hydrophobic-core packing. *Proc. Natl. Acad. Sci. USA* **91**, 423–427.
125. Milla, M.E. & Sauer, R.T. (1994) P22 Arc repressor: folding kinetics of a single-domain dimeric protein. *Biochemistry* **33**, 1125–1133.
124. Harrison, S.C. & Sauer, R.T. (1994) Protein-nucleic acid interactions: editorial overview. *Curr. Opin. Struct. Biol.* **4**, 1–2.
123. Milla, M.E., Brown, B.M., and Sauer, R.T. (1993) P22 Arc repressor: enhanced expression of unstable mutants by addition of polar C-terminal sequences. *Protein Sci.* **2**, 2198–2205.
122. Hu, J.C., Newell, N.E., Tidor, B. and Sauer, R.T. (1993) Probing the roles of residues at the **e** and **g** positions of the GCN4 leucine zipper by combinatorial mutagenesis. *Protein Sci.* **2**, 1072–1084.
121. Gregoret, L. and Sauer, R.T. (1993) Additivity of mutant effects assessed by binomial mutagenesis. *Proc. Nat. Acad. Sci. USA* **90**, 4246–4250.

120. Beckett, D., Burz, D.S., Ackers, G.K. & Sauer, R.T. (1993) Isolation of λ repressor mutants with defects in cooperative operator binding. *Biochemistry* **32**, 9073–9079.
119. Waugh, D.S. & Sauer, R.T. (1993) Single amino-acid substitutions uncouple the sequence specific DNA binding and strand scission activities of *Fok I* endonuclease. *Proc. Natl. Acad. Sci. USA* **90**, 9596–9600.
118. Brown, B.M. & Sauer, R.T. (1993) Assembly of the Arc repressor-operator complex: cooperative interactions between DNA-bound dimers. *Biochemistry* **32**, 1354–1363.
117. Sauer, R.T. & Lim, W.A. (1992) Mutational analysis of protein stability. *Curr. Opin. Struct. Biol.* **2**, 46–51.
116. Pabo, C.O. & Sauer, R.T. (1992) Transcription factors: structural families and principles of DNA recognition. *Ann. Rev. Biochem.* **6**, 1053–1095.
115. Lim, W.A., Farruggio, D.C. & Sauer, R.T. (1992) The structural and energetic consequences of disruptive mutations in a protein core. *Biochemistry* **31**, 4324–4333.
114. Silber, K.R., Keiler, K.C. & Sauer, R.T. (1992) Tsp; a tail-specific protease that selectively degrades proteins with non-polar C-termini. *Proc. Natl. Acad. Sci. USA* **89**, 295–299.
113. Knight, K.L. & Sauer, R.T. (1992) Biochemical and genetic analysis of operator contacts made by residues within the β -sheet DNA-binding motif of Mnt repressor *EMBO J.* **11**, 215–223.
112. Hu, J.C. & Sauer, R.T. (1992) The basic-region leucine-zipper family of DNA binding proteins. in *Nucleic Acids and Molecular Biology* vol VI (Eckstein, F. and Lilley, D.M.J., eds.) Springer-Verlag, Berlin, pps. 82–101.
111. Lim, W.A., Sauer, R.T. & Lander, A.D. (1991) Analysis of DNA-protein interactions by affinity co-electrophoresis. *Methods Enz.* **208**, 196–210.
110. Mossing, M.C., Bowie, J.U. & Sauer, R.T. (1991) A streptomycin selection for DNA binding activity. *Methods Enz.* **208**, 604–619.
109. Reidhaar-Olson, J.F., Bowie, J.U., Breyer, R.M., Hu, J.C., Knight, K.L., Lim, W.A., Mossing, M.C., Parsell, D.A., Shoemaker, K.R. & Sauer, R.T. (1991) Random mutagenesis of protein sequences using oligonucleotide cassettes. *Methods Enz.* **208**, 564–586.
108. Lim, W.A. & Sauer, R.T. (1991) The role of internal packing interactions in determining the structure and stability of a protein. *J. Mol. Biol.* **219**, 359–376.
107. Doig, A.J., Williams, D.H. & Sauer, R.T. (1990) Surface areas of unfolded proteins. *Nature* **348**, 397.
106. Sauer, R.T. (1990) Scissors and helical forks. *Nature* **347**, 514–515.

105. Mossing, M.C. & Sauer, R.T. (1990) Stable, monomeric variants of λ Cro obtained by insertion of a designed β -hairpin sequence. *Science* **250**, 1712–1715.
104. Hu, J.C., O’Shea, E.K., Kim, P.S. & Sauer, R.T. (1990) Sequence requirements for coiled-coil interactions: analysis using λ repressor-GCN4 leucine zipper fusions. *Science* **250**, 1400–1403.
103. Brown, B.M., Bowie, J.U. & Sauer, R.T. (1990) Arc repressor is tetrameric when bound to operator DNA. *Biochemistry* **29**, 11189–11195.
102. Reidhaar-Olson, J.F., Parsell, D.A. & Sauer, R.T. (1990) An essential proline in λ repressor is required for resistance to intracellular proteolysis. *Biochemistry* **29**, 7563–7571.
101. Reidhaar-Olson, J.F. & Sauer, R.T. (1990) Functionally acceptable substitutions in two α -helical regions of λ repressor. *Proteins* **7**, 306–316.
100. Bowie, J.U., Clarke, N.D, Pabo, C.O. & Sauer, R.T. (1990) Identification of protein folds: matching hydrophobicity patterns of sequence sets with solvent accessibility patterns of known structures. *Proteins* **7**, 257–264.
99. Pakula, A.A. & Sauer, R.T. (1990) Reverse hydrophobic effects relieved by amino-acid substitutions at a protein surface. *Nature* **344**, 363–364.
98. Bowie, J.U. & Sauer, R.T. (1990) TraY proteins of F and related episomes are members of the Arc and Mnt repressor family. *J. Mol. Biol.* **211**, 5–6.
97. Bowie, J.U., Reidhaar-Olson, J.F., Lim, W.A. & Sauer, R.T. (1990) Deciphering the message in protein sequences: tolerance to amino acid substitutions. *Science* **247**, 1306–1310.
96. Parsell, D.A., Silber, K.R. & Sauer, R.T. (1990) C-terminal determinants of intracellular protein degradation. *Genes Dev.* **4**, 277–286.
95. Sauer, R.T., Jordan, S.R. & Pabo, C.O. (1990) λ repressor: a model system for understanding protein-DNA interactions and protein stability. *Adv. Prot. Chem.* **40**, 1–61.
94. Zagorski, M.G., Bowie, J.U., Vershon, A.K., Sauer, R.T. & Patel, D.J. (1989) NMR studies of the Arc repressor mutant PL8: resonance assignments, secondary structure and long range contacts. *Biochemistry* **28**, 9813–9825.
93. Bowie, J.U. & Sauer, R.T. (1989) Equilibrium dissociation and unfolding of the Arc repressor dimer. *Biochemistry* **28**, 7139–7143.
92. Parsell, D.A. & Sauer, R.T. (1989) Induction of a heat shock-like response by unfolded protein in *E. coli*: dependence on protein level not protein degradation. *Genes Dev.* **3**, 1226–1232.

91. Pakula, A.A. & Sauer, R.T. (1989) Genetic analysis of protein stability and function. *Ann. Rev. Genetics* **23**, 289–310.
90. Lim, W.A. & Sauer, R.T. (1989) Alternative packing arrangements in the hydrophobic core of λ repressor. *Nature* **339**, 31–36.
89. Bowie, J.U. & Sauer, R.T. (1989) Identification of C-terminal extensions that protect proteins from intracellular proteolysis. *J. Biol. Chem.* **264**, 7596–7602.
88. Parsell, D.A. & Sauer, R.T. (1989) The structural stability of a protein is an important determinant of its proteolytic susceptibility in *E. coli*. *J. Biol. Chem.* **264**, 7590–7595.
87. Breyer, R.M. & Sauer, R.T. (1989) Mutational analysis of the fine specificity of binding of monoclonal antibody 51F to λ repressor. *J. Biol. Chem.* **264**, 13355–13360.
86. Breyer, R.M. & Sauer, R.T. (1989) Production and characterization of monoclonal antibodies to the N-terminal domain of λ repressor. *J. Biol. Chem.* **264**, 13348–13354.
85. Knight, K.L., Bowie, J.U., Vershon, A.K., Kelley, R.D. & Sauer, R.T. (1989) The Arc and Mnt repressors: a new class of sequence specific DNA-binding protein. *J. Biol. Chem.* **264**, 3639–3642.
84. Knight, K.L. & Sauer, R.T. (1989) Identification of functionally important residues in the DNA-binding region of the Mnt repressor. *J. Biol. Chem.* **264**, 13706–13710.
83. Bowie, J.U. & Sauer, R.T. (1989) Identifying determinants of folding and activity for a protein of unknown structure. *Proc. Natl. Acad. Sci. USA* **86**, 2152–2156.
82. Pakula, A.A. & Sauer, R.T. (1989) Amino acid substitutions that increase the thermal stability of the λ Cro protein. *Proteins* **5**, 202–210.
81. Vershon, A.K., Kelley, R.D. & Sauer, R.T. (1989) Sequence-specific binding of Arc repressor to DNA: effects of operator mutations and modifications. *J. Biol. Chem.* **264**, 3267–3273.
80. Knight, K.L. & Sauer, R.T. (1989) DNA binding specificity of the Arc and Mnt repressors is determined by a short region of N-terminal residues. *Proc. Natl. Acad. Sci. USA* **86**, 797–801.
79. Gimble, F.S. & Sauer, R.T. (1989) λ repressor mutants that are better substrates for RecA-mediated cleavage. *J. Mol. Biol.* **206**, 29–39.
78. Sauer, R.T., Smith, D.L. & Johnson, A.D. (1988) Flexibility of the yeast $\alpha 2$ repressor enables it to occupy the ends of its operator, leaving the center free. *Genes Dev.* **2**, 807–816.
77. Reidhaar-Olson, J.F. & Sauer, R.T. (1988) Combinatorial cassette mutagenesis as a probe of the informational content of protein sequences. *Science* **241**, 53–57.

76. Knight, K.L. & Sauer, R.T. (1988) The Mnt repressor of bacteriophage P22: role of C-terminal residues in operator binding and tetramer formation. *Biochemistry* **27**, 2088–2094.
75. Weiss, M.A., Karplus, M. & Sauer, R.T. (1987) Quaternary structure and function in phage λ repressor: $^1\text{H-NMR}$ studies of genetically altered proteins. *J. Biomol. Struct. Dynam.* **5**, 539–556.
74. Vershon, A.K., Liao, S-M., McClure, W.R. & Sauer, R.T. (1987) Bacteriophage P22 Mnt repressor: DNA binding and effects on transcription *in vitro*. *J. Mol. Biol.* **195**, 311–322.
73. Vershon, A.K., Liao, S-M., McClure, W.R. & Sauer, R.T. (1987) Interaction of the bacteriophage P22 Arc repressor with operator DNA. *J. Mol. Biol.* **195**, 323–331.
72. Weiss, M.A., Karplus, M. & Sauer, R.T. (1987) The $^1\text{H-NMR}$ aromatic spectrum of the operator-binding domain of the λ repressor: resonance assignment with application to structure and dynamics. *Biochemistry* **26**, 890–897.
71. Weiss, M.A., Pabo, C.O., Karplus, M. & Sauer, R.T. (1987) Dimerization of the operator-binding domain of phage λ repressor. *Biochemistry* **26**, 897–904.
70. Sauer, R.T., Hecht, M.H., Nelson, H.C.M. & Pakula, A. (1987) Identifying the determinants of protein function and stability. in *New Frontiers in the Study of Gene Functions* (G. Poste and S. Crooke, eds.), Plenum, pps. 177–198.
69. Weiss, M.A., Stearman, R., Jeitler-Nilsson, A., Karplus, M & Sauer, R.T. (1986) Protein-protein interactions in DNA recognition. Proton nuclear magnetic resonance studies of λ *cl* repressors genetically altered by site-directed mutagenesis. *Biophys. J.* **49**, 29–33.
68. Weiss, M.A., Jeitler-Nilsson, A., Fischbein, N.J., Karplus, M & Sauer, R.T. (1986) Genetic methods in high-resolution NMR studies of proteins. *NATO ASI Ser.* **107**, 37–48.
67. Vershon, A.K., Bowie, J.U., Karplus, T.M. & Sauer, R.T. (1986) Isolation and analysis of Arc repressor mutants: evidence for an unusual mechanism of DNA binding. *Proteins* **1**, 302–311.
66. Hecht, M.H., Sturtevant, J.M. & Sauer, R.T. (1986) Stabilization of λ repressor against thermal denaturation by site-directed Gly \rightarrow Ala changes in α -helix three. *Proteins* **1**, 43–46.
65. Sauer, R.T., Hehir, K., Stearman, R.S., Weiss, M.A., Jeitler-Nilsson, A., Suchanek, E.G. & Pabo, C.O. (1986) An engineered intersubunit disulfide enhances the stability and DNA binding of the N-terminal domain of λ repressor. *Biochemistry* **25**, 5992–5998.
64. Gimble, F.S. & Sauer, R.T. (1986) λ repressor inactivation: properties of purified *ind*-proteins in the autodigestion and RecA-mediated cleavage reactions. *J. Mol. Biol.* **192**, 39–47.

63. Nelson, H.C.M. & Sauer, R.T. (1986) Interaction of mutant λ repressors with operator and non-operator DNA. *J. Mol. Biol.* **192**, 27–38.
62. Pakula, A., Young, V. & Sauer, R.T. (1986) λ Cro mutations: effects on activity and intracellular degradation. *Proc. Nat. Acad. Sci. USA* **83**, 8829–8833.
61. Vershon, A.K., Blackmer, K. & Sauer, R.T. (1986) Mutagenesis of the Arc repressor using synthetic primers with random nucleotide substitutions. in *Protein Engineering* (M. Inouye and R. Sarma, eds.), Academic Press, Orlando, Florida, pps. 243–256.
60. Poteete, A.R., Hehir, K. & Sauer, R.T. (1986) Bacteriophage P22 Cro protein: sequence, purification, and properties. *Biochemistry* **25**, 251–256.
59. Jordan, S.R., Pabo, C.O., Vershon, A.K. & Sauer, R.T. (1985) Crystallization of the Arc repressor. *J. Mol. Biol.* **185**, 445–446.
58. Nelson, H.C.M. & Sauer, R.T. (1985) λ repressor mutations that increase the affinity and specificity of operator binding. *Cell* **42**, 549–558.
57. Vershon, A.K., Youderian, P., Weiss, M.A., Susskind, M.M. & Sauer, R.T. (1985) Mnt repressor-operator interactions: altered specificity requires N⁶ methylation of operator DNA. in *Specificity in Transcription and Translation* (R. Calendar and L. Gold, eds.), Alan Liss, Inc., New York, NY, pps. 209–218.
56. Vershon, A.K., Youderian, P., Susskind, M.M. & Sauer, R.T. (1985) The bacteriophage P22 Arc and Mnt repressors: overproduction, purification, and properties. *J. Biol. Chem.* **260**, 12124–12129.
55. Hecht, M.H., Hehir, K.M., Nelson, H.C.M., Sturtevant, J.M. & Sauer, R.T. (1985) Increasing and decreasing protein stability: effects of revertant substitutions on the thermal denaturation of phage λ repressor. *J. Cell. Biochem.* **29**, 217–224.
54. Hecht, M.H. & Sauer, R.T. (1985) Phage λ repressor revertants: amino acid substitutions that restore activity to mutant proteins. *J. Mol. Biol.* **186**, 53–63.
53. Gimble, F.S. & Sauer, R.T. (1985) Mutations in bacteriophage λ repressor that prevent RecA-mediated cleavage. *J. Bacteriol.* **162**, 147–154.
52. Sauer, R.T. & Pabo, C.O. (1984) How λ repressor binds operator DNA. in *Microbiology* (D. Schlessinger, ed.) ASM Press, Washington, D.C.
51. Weiss, M.A., Patel, D.J., Sauer, R.T. & Karplus, M. (1984) NMR characterization of DNA: assignment of major groove sugar protons of the λ -phage operator site O_L1 by 2D-NOE and J-correlated spectra. *J. Amer. Chem. Soc.* **106**, 4269–4270.
50. Hecht, M.H., Sturtevant, J.M. & Sauer, R.T. (1984) Effect of single amino acid replacements on the thermal stability of the NH₂-terminal domain of phage λ repressor. *Proc. Nat. Acad. Sci. USA* **81**, 5685–5689.

49. Weiss, M.A., Sauer, R.T., Patel, D.J. & Karplus, M. (1984) Amino-terminal arm of the λ repressor: a $^1\text{H-NMR}$ study. *Biochemistry* **23**, 5090–5095.
48. Hopper, P., Harrison, S.C. & Sauer, R.T. (1984) Structure of tomato bushy stunt virus; V: coat-protein sequence determination and its structural implications. *J. Mol. Biol.* **177**, 701–713.
47. Pabo, C.O. & Sauer, R.T. (1984) Protein-DNA recognition. *Ann. Rev. Biochemistry* **53**, 293–321.
46. Weiss, M.A., Patel, D.J., Sauer, R.T. & Karplus, M. (1984) $^1\text{H-NMR}$ study of the λ operator site O_L1 : assignment of the imino and adenine H2 resonances. *Nuc. Acids Res.* **12**, 4035–4047.
45. Reilly, E.B., Reilly, R.M., Breyer, R.M., Sauer, R.T. & Eisen, H.N. (1984) Amino acid and nucleotide sequences of variable regions of mouse immunoglobulin light chains of the $\lambda 3$ subtype. *J. Immunol.* **133**, 471–475.
44. Weiss, M., Patel, D.J., Sauer, R.T. & Karplus, M. (1984) Two dimensional $^1\text{H NMR}$ study of the λ operator site O_L1 : a sequential assignment strategy and its application. *Proc. Nat. Acad. Sci. USA* **81**, 130–134.
43. Youderian, P., Vershon, A., Bouvier, S., Sauer, R.T. & Susskind, M.M. (1983) Changing the DNA-binding specificity of a repressor. *Cell* **35**, 777–783.
42. Weiss, M.A., Karplus, M., Patel, D.J. & Sauer, R.T. (1983) Solution NMR studies of intact lambda repressor. *J. Biomol. Struct. Dynam.* **1**, 151–157.
41. Poteete, A.R., Sauer, R.T. & Hendrix, R.W. (1983) Domain structure and quaternary organization of the bacteriophage P22 erf Protein. *J. Mol. Biol.* **171**, 401–418.
40. Sauer, R.T., Nelson, H.C.M., Hehir, K., Hecht, M.H., Gimble, F.S., DeAnda, J. & Poteete, A.R. (1983) The λ and P22 phage repressors. *J. Biomol. Structure and Dynamics* **1**, 1011–1022.
39. DeAnda, J., Poteete, A.R. & Sauer, R.T. (1983) P22 c2 repressor: domain structure and function. *J. Biol. Chem.* **258**, 10536–10542.
38. Sauer, R.T., Krovatin, W., DeAnda, J., Youderian, P. & Susskind, M. (1983) Primary structure of the *immI* immunity region of bacteriophage P22. *J. Mol. Biol.* **168**, 699–713.
37. Gussin, G., Johnson, A.D., Pabo, C.O. & Sauer, R.T. (1983) Repressor and Cro protein: structure, function, and role in lysogenization. in *Lambda II* (R.W. Hendrix, R.A. Weisberg, J.W. Roberts, and F.W. Stahl, eds.), Cold Spring Harbor Press, pps. 93–121.
36. Hecht, M.H., Nelson, H.C.M. & Sauer, R.T. (1983) Mutations in λ repressor's amino-terminal domain: implications for protein stability and DNA binding. *Proc. Nat. Acad. Sci. USA* **80**, 2676–2680.

35. Berget, P.B., Poteete, A.R. & Sauer, R.T. (1983) Control of P22 tail protein synthesis by transcription termination. *J. Mol. Biol.* **164**, 561–572.
34. Nelson, H.C.M., Hecht, M.H. & Sauer, R.T. (1983) Mutations defining the operator binding sites of bacteriophage λ repressor. *Cold Spring Harbor Symposium* **47**, 441–449.
33. Sauer, R.T. & Pabo, C. (1983) Protein-DNA recognition: the λ repressor-operator complex. *ASM News* **49**, 131–135.
32. Koshland, D., Sauer, R.T. & Botstein, D. (1982) Diverse effects of mutations in the signal sequence on the secretion of β -lactamase in *Salmonella typhimurium*. *Cell* **30**, 903–914.
31. Keng, T., Webster, T.A., Sauer, R.T. & Schimmel, P. (1982) Gene for *E. coli* glycyl-tRNA synthetase has tandem subunit coding regions in the same reading frame. *J. Biol. Chem.* **257**, 12503–12508.
30. Sauer, R.T., Krovatin, W., Poteete, A.R. & Berget, P. (1982) Phage P22 tail protein: gene and amino acid sequence. *Biochemistry* **21**, 5811–5815.
29. Pabo, C.O., Krovatin, W., Jeffrey, A. & Sauer, R.T. (1982) The N-terminal arms of λ repressor wrap around the operator. *Nature* **298**, 441–443.
28. Sauer, R.T., Yocum, R.R., Doolittle, R.F., Lewis, M. & Pabo, C.O. (1982) Homology among DNA-binding proteins suggests use of a conserved super-secondary structure. *Nature* **298**, 447–451.
27. Sauer, R.T., Ross, M.J. & Ptashne, M. (1982) Cleavage of the λ and P22 repressors by RecA protein. *J. Biol. Chem.* **257**, 4458–4462.
26. Johnson, A.D., Poteete, A.R., Lauer, G., Sauer, R.T., Ackers, G. & Ptashne, M. (1981) λ Repressor and Cro: components of an efficient molecular switch. *Nature* **294**, 217–223.
25. Sauer, R.T., Allen, D.W. & Niall, H.D. (1981) Amino acid sequence of p15 from avian myeloblastosis complex. *Biochemistry* **20**, 3784–3791.
24. Sauer, R.T., Pan, J., Hopper, P., Hehir, K., Brown, J. & Poteete, A.R. (1981) Primary structure of the phage P22 repressor and its gene *c2*. *Biochemistry* **20**, 3591–3598.
23. Breyer, R.M., Sauer, R.T. & Eisen, H.N. (1981) The variable region of mouse λ 3 chains. in *Immunoglobulin Idiotypes* (C.A. Janeway, E.E. Sercarz, H. Wigzell and C.F. Fox, eds.) ICN-UCLA Symposia on Molecular and Cellular Biology, Academic Press, NY, pps. 105–110.
22. Putney, S.D., Sauer, R.T. & Schimmel, P.R. (1981) Purification and properties of alanine tRNA synthetase from *Escherichia coli*. *J. Biol. Chem.* **256**, 198–204.
21. Ptashne, M., Jeffrey, A., Johnson, A., Maurer, R., Meyer, B.J., Pabo, C.O., Roberts, T.M. & Sauer, R.T. (1980) Turning genes off and on with repressors in bacteriophage λ . *Cell* **19**, 1–11.

20. Johnson, A.D., Pabo, C.O. & Sauer, R.T. (1980) Bacteriophage λ repressor and Cro proteins: interaction with operator DNA. *Methods Enz.* **65**, 839–856.
19. Sauer, R.T., Pabo, C.O., Meyer, B.J., Ptashne, M. & Backman, K.C. (1979) The regulatory functions of the λ repressor reside in the amino terminal domain. *Nature* **279**, 396–400.
18. Pabo, C.O., Sauer, R.T., Sturtevant, J.M. & Ptashne, M. (1979) The λ Repressor Contains Two Domains. *Proc. Nat. Acad. Sci. USA* **76**, 1608–1612.
17. Sauer, R.T. (1979) Molecular characterization of the λ repressor and its gene *cI*. Ph.D. Dissertation, Harvard University, Cambridge, Massachusetts.
16. Sauer, R.T. (1978) DNA sequence of the bacteriophage λ *cI* gene. *Nature* **276**, 301–302.
15. Sauer, R.T. & Andereg, R. (1978) The primary structure of the λ repressor. *Biochemistry* **17**, 1092–1100.
14. Tregear, G.W., van Reitschoten, J., Sauer, R.T., Niall, H.D., Keutmann, H.T. & Potts, J.T. Jr. (1977) Synthesis, purification, and chemical characterization of the amino terminal 1–34 fragment of bovine parathyroid hormone synthesized by the solid phase procedure. *Biochemistry* **16**, 2817–2823.
13. Segre, G.B., Niall, H.D., Sauer, R.T. & Potts, J.T. Jr. (1977) Edman degradation of radioiodinated parathyroid hormone: application to sequence analysis and hormone metabolism *in vivo*. *Biochemistry* **16**, 2417–2427.
12. Ptashne, M., Backman, K.C., Humayun, M.Z., Jeffrey, A., Maurer, R., Meyer, B. & Sauer, R.T. (1976) Autoregulation and function of a repressor in bacteriophage λ . *Science* **194**, 156–161.
11. Humayun, M.Z., Meyer, B., Sauer, R., Backman, K. & Ptashne, M. (1976) Transcriptional and translational (?) control of the λ repressor gene (*cI*). in *Molecular Mechanisms in the Control of Gene Expression*, Academic Press, New York, NY, p. 76.
10. Niall, H.D., Jacobs, J.W., Sauer, R.T., Keutmann, H.T. & Potts, J.T. Jr. (1974) High sensitivity analysis of polypeptide hormones. in *Endocrinology 1973*, Heinemann Medical Books, London, p. 437.
9. Sauer, R.T., Niall, H.D., Hogan, M.L., Keutmann, H.T., O'Riordan, J.L.H. & Potts, J.T. Jr. (1974) The amino acid sequence of porcine parathyroid hormone. *Biochemistry* **13**, 1994–1999.
8. Niall, H.D., Sauer, R.T., Jacobs, J.W., Keutmann, H.T., Segre, G.B., O'Riordan, J.L.H., Aurbach, G.D. & Potts, J.T. Jr. (1974) The amino acid sequence of the amino-terminal 37 residues of human parathyroid hormone. *Proc. Nat. Acad. Sci. USA* **71**, 384–388.
7. Niall, H.D., Sauer, R.T., Keutmann, H.D., Lequin, R.M. & Potts, J.T. Jr. (1972) Automated Edman degradation of proteins. in *Progress in Peptide Research 2*, Gordon and Breach, New York, NY, p. 191.

6. Potts, J.T. Jr., Tregear, G.W., Keutmann, H.T., Niall, H.D., Sauer, R.T., Deftos, L.J., Dawson, B.F., Hogan, M.L. & Aurbach, G.D. (1971) Synthesis of a biologically active tetratriacontapeptide of parathyroid hormone. *Proc. Nat. Acad. Sci. USA* **68**, 63–67.
5. Niall, H.D., Sauer, R.T., Hogan, M.L., Rosenblum, I.Y. & Greenwood, F.C. (1971) Pituitary and placental lactogenic and growth hormones: evolution from a primordial peptide by gene duplication. *Proc. Nat. Acad. Sci. USA* **68**, 866–870.
4. Potts, J.T. Jr., Niall, H.D., Tregear, G.W., Keutmann, H.T., Sauer, R.T., Hogan, M.L., Dawson, B.F. & Aurbach, G.D. (1971) The chemistry of parathyroid hormone. in *Cellular Mechanisms for Calcium Transport and Homeostasis*, Academic Press, New York, NY, p. 394.
3. Niall, H.D., Keutmann, H.T., Sauer, R.T., Hogan, M.L., Dawson, B.F., Aurbach, G.D. & Potts, J.T. Jr. (1970) The amino acid sequence of bovine parathyroid hormone. *Hoppe Seylers Z. Physiol. Chem.* **351**, 1586–1588.
2. Allen, D.W., Sarma, P.S., Niall, H.D. & Sauer, R.T. (1970) Isolation of a second group specific antigen from avian myeloblastosis virus. *Proc. Nat. Acad. Sci. USA* **64**, 837–842.
1. Niall, H.D., Sauer, R.T. & Allen, D.W. (1970) The N-terminal amino acid sequence of two avian leukosis group specific antigens. *Proc. Nat. Acad. Sci. USA* **67**, 1804–1809.