

**CURRICULUM VITAE****NAME**

Dr. rer. nat. Numan Oezguen

**CURRENT POSITION AND ADDRESS**

Postdoctoral Fellow  
 Department of Biochemistry and Molecular Biology  
 Sealy Center for Structural Biology and Molecular Biophysics  
 Computational Biology  
 University of Texas Medical Branch  
 301 University Boulevard  
 Galveston, TX 77555-0857

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**EDUCATION AND TRAINING**

1987 - 1994 Physics, Dipl., RWTH, Aachen, Germany  
 1994 - 1995 Studies in Economics, RWTH, Aachen, Germany  
 1995 - 1999 Dr. rer. nat., RWTH, Aachen, Germany  
 1/2004-4/2004 Advanced Management Certificate Program, UH Clear Lake, TX

**TEACHING/RESEARCH EXPERIENCE**

1993 - 1994 Teaching Assistant, RWTH, Aachen, Germany  
 1995 - 2000 Research Scientist, RWTH, Aachen, Germany  
 2000 - present Postdoctoral Fellow, University of Texas Medical Branch, Galveston, TX  
 2003 - present Teaching Assistant and Mentor to students, UTMB, Galveston, TX

**AWARDS**

1998 - 1999 Scholarship of the Garg-Stiftung  
 2001 2nd Prize, Postdoctoral Fellow Category at the 6th Annual Structural Biology Symposium, May 18-20, Galveston, TX  
 2004 1st Prize, Postdoctoral Category at the 9th Annual Structural Biology Symposium, April 30-May 1, Galveston, TX

**LANGUAGES**

German, English, Turkish (fluent)

**COMPUTER EXPERIENCE**

Operating systems LINUX/UNIX, WINDOWS (Administrator of a LINUX-cluster and individual Servers and Desktops)  
 Programming language PERL, C/C++, FORTRAN, PASCAL  
 Software packages AMBER, AutoDock, MolMol, NOAH, DIAMOD, FANTOM, InsightII (Discover), MS-Office

**MEMBERSHIPS**

1989 - 2006 Member of the German Physical Society, Bad Honnef  
 1996 - 2007 Member of the German-Turkish Friendship Association EuroTurk Aachen e. V., Board Member 1999 - 2000  
 2002 - present Member of the Biophysical Society, Bethesda, MD

## PUBLICATIONS

19. \***Oezguen**, N., \*Kumar, S., Hindupur, A., Braun, W., Muralidhara, B.K., Halpert, J. Conserved motifs in CYP2 family. *J Biol Chem.* 2008 May 21. [Epub ahead of print].
18. Leonard, V.H.J., Sinn, P.L., Hodge, G., Miest, T., Devaux, P., **Oezguen**, N., Braun, W. McCray Jr., P.B., McChesney, M.B., and Cattaneo, R., Selectively epithelial cell receptor-blind measles virus is virulent but shedding-restricted. *J. Clin. Invest.* 118(7):2448-2458, 2008.
17. \*Mantha, AK., \***Oezguen**, N., Tadahide, I., Braun, W., and Mitra, S., Cys 99 Residue, a Critical Modulator of DNA Binding in Human AP-endonuclease1 (hAPE1), *J. Mol. Biol.* 379: 28-37, 2008.
16. Navaratnarajah, C.K., Vongpunsawad, S., **Oezguen**, N. Stehle, T., Braun, W., Hashiguchi, T., Maenaka, K., Yanagi, Y., Cattaneo, R., Dynamic interaction of the measles virus Hemagglutinin with its receptor SLAM. *J. Biol. Chem.* 283(17), 11763-11771, 2008.
15. Negi, S., Schein, C.H., **Oezguen**, N., Power, T.D. and Braun, W. InterProSurf: a web server for predicting interacting sites on protein surfaces. *Bioinformatics.* 23(24):3397-9, 2007. (cited: 1)
14. **Oezguen**, N., Schein, C.H., Power, T. D., Izumi, T., Braun, W. A "Moving metal" mechanism for substrate cleavage by human Endonuclease APE-1. *Proteins.* 68(1):313-323, 2007. (cited: 2)
13. Schein, C.H., **Oezguen**, N, Volk, D.E., Paul, A. A novel, structure-based mechanism for uridylylation of the genome-linked peptide (VPg) of picornaviruses. *Proteins.* 63(4):719-26, 2006 (cited: 1)
12. Schein, C.H., **Oezguen**, N., Volk, D.E., Garimella, R., Paul, A., Braun, W. NMR structure of the peptide linked to the genome (VPg) of poliovirus. *Peptides* 27(7):1676-84, 2006 (cited: 2)
11. von Messling, V., **Oezguen**, N., Zheng, Q., Vongpunsawas, S., Braun, W. and Cattaneo, R. Nearby clusters of hemagglutinin residues sustain SLAM-dependent canine distemper virus entry in peripheral blood mononuclear cells. *J. Virol.*, 79(9):5857-5862, 2005 (cited: 7).
10. Schein, C.H., Zhou, B., **Oezguen**, N., Mathura, V.S. and Braun, W. Molego based definition of the architecture and specificity of metal binding sites. *Proteins.* 58(1):200-210, 2005 (cited: 8).
9. \*Ivanciuc, O., \***Oezguen**, N., \*Venkatarajan, M.S., Schein, C.H., Xu, Y. and Braun, W. Using property based sequence motifs and 3D modeling to determine structure and functional regions of proteins. *Curr. Med. Chem.* 11:583-593, 2004 (cited: 11).

8. Izumi, T., Schein, C.H., **Oezguen**, N., Feng, Y. and Braun, W. Effects of backbone contacts 3' to the abasic site on the cleavage and the product binding by human apurinic/apyrimidinic endonuclease (APE1). *Biochemistry* 43(3):684-689, 2004 (cited: 6).
7. Vongpunsawad, S., **Oezguen**, N., Braun, W. and Cattaneo R. Selectively receptor-blind measles viruses: identification of residues necessary for SLAM- or CD46-induced fusion and their localization on a new hemagglutinin structural model. *J. Virol.* 78(1):302-313, 2004 (cited: 44).
6. Schein, C.H., **Ozgun**, N., Izumi, T. and Braun, W. Total sequence decomposition and genomic cross-networking distinguishes functional modules in apurinic/apyrimidinic endonucleases. *BMC Bioinformatics*, 3(1):37, 2002 (cited: 9).
5. Murtazina, D., Puchkaev, A.V., Schein, C.H., **Oezguen**, N., Braun, W., Nanavati, A. and Pikuleva, I.A. Membrane-protein interactions contribute to efficient 27-hydroxylation of cholesterol by mitochondrial cytochrome P450 27A1. *J. Biol. Chem.* 277(40):37582-37589, 2002 (cited: 25).
4. **Oezguen**, N., Adamian, L., Xu, Y., Rajarathnam, K. and Braun, W. Automated assignment and 3D structure calculations using combinations of 2D homonuclear and 3D heteronuclear NOESY spectra. *J. Biomol. NMR* 22(3):249-263, 2002 (cited: 12).
3. **Oezguen**, N., Nick, B., Jung, B., Wortmann, F.-J. and Hocker, H. Modeling of  $\Theta$ -conditions for bisphenol-A polycarbonate single chains. *Macromol. Symp.* 127:151-159, 1998 (cited: 1).
2. **Oezguen**, N., Nick, B., Jung, B., Wortmann, F.-J. and Höcker, H. Molecular dynamic simulations with bisphenol-A polycarbonate under  $\Theta$ -conditions. *Jahresbericht DWI* (1998)
1. **Ozgun**, N. Molekulardynamische simulationen an polycarbonaten unter  $\Theta$ -Bedingungen. D 82 (Diss. RWTH, Aachen), Verlag Mainz, Aachen, Germany, ISBN 3-89653-703-2 (1998).

#### Accepted

- **Oezguen**, N., Zhou, B., Negi, S., Ivanciuc, O., Braun, W. Homology modeling of allergenic proteins and analysis of surface epitope residues, *Molecular Immunology*, 2008.

## **INVITED TALKS**

Oezguen, N., Sequence decomposition of metal sites and MD simulations suggest a novel "moving ion" mechanism for the DNA repair endonuclease APE1. 60th Southwest Regional Meeting of the American Chemical Society, Fort Worth, TX, September 29-October 2, 2004.

Oezguen, N., Dynamics of the Mg<sup>2+</sup> metal ion and the metal binding sites in APE1. 47th Annual Meeting of the Biophysical Society, San Antonio, TX (March 1-5, 2003), Biophysical Journal 84 (2): 13a-14a Part 2 Suppl. S Feb 2003.

## POSTER PRESENTATIONS

52. Mantha, A., Bhakat, K.K., Oezguen, N., Izumi, T., Braun, W. and Mitra, S. Exploring Potential Link Between Seven Cys Residues of HAPE1'S Repair and Redox Functions: a Multi Functional DNA Repair Enzyme. 13th Annual Sealy Center for Structural Biology and Molecular Biophysics Symposium, University of Texas Medical Branch, Galveston, TX (May 16-17).
51. Oezguen, N., Mantha, A.K., Bhakat, K.K., Izumi, T., Mitra, S. and Braun, W. Influence of a Distant Ser Residue on the Active Site Over 16 Angstroms: Unusual Affect of C99S APE1 on Endonuclease Activity Or Repair Function. 13th Annual Sealy Center for Structural Biology and Molecular Biophysics Symposium, University of Texas Medical Branch, Galveston, TX (May 16-17, 2008).
50. Anderson, K., Navaratnarajah, C., Cattaneo, R., Braun, W. and Oezguen, N. MD Simulations of Measles Virus Hemagglutinin Y228A and N274A Mutants. 13th Annual Sealy Center for Structural Biology and Molecular Biophysics Symposium, University of Texas Medical Branch, Galveston, TX (May 16-17, 2008).
49. Oezguen, N., Zhou, B., Negi, S., Ivanciuc, O., Braun, W. Comprehensive modeling of allergenic proteins and structural analysis of linear IgE epitopes. Computational & Theoretical Biology Symposium, Rice University, Houston, TX (December 7-9, 2007).
48. Oezguen, N., Zhou, B., Surendra, SN., Ivanciuc, O., and Braun, W. Homology Modeling Of Allergenic Proteins And Surface Analysis Of Known Epitopes. Sealy Center for Structural Biology and Molecular Biophysics 12th Annual Structural Biology Symposium, University of Texas Medical Branch, Galveston, TX (May 18-19, 2007).
47. Oezguen, N., Espinoza, R.C.D., Cattaneo, R and Braun, W. 3D Model of the Complex of Measles Virus Haemagglutinin and its Human Receptor SLAM. Sealy Center for Structural Biology and Molecular Biophysics 11th Annual Structural Biology Symposium, University of Texas Medical Branch, Galveston, TX (May 19-20, 2006).
46. Espinoza, R.C.D.,Oezguen, N., Cattaneo, R and Braun, W. Determination Of The Potential Receptor Binding Site Of The Measles Virus Haemagglutinin. The Academy of Medicine, Engineering and Science of Texas conference on Bugs, Drugs & Vaccines, Galveston, TX (April5-6, 2006).
45. Oezguen, N., Negi, S., Cattaneo, R.B., Braun, W. Comparison of the Surface Properties of the Domain of Human SLAM (CD150) Recognized by Measles Virus with that of its Mouse Homologue, and Implications for Cell Entry. 2006 McLaughlin Colloquium on Infection and Immunity, University of Texas Medical Branch, Galveston, TX (January 19).
44. Edwards, A., Ivanciuc, O., Oezguen, N. and Schein, C.H. Correlation Between Allergy to Insect Proteins and Asthma: Relating Cross Reactivity to the Sequence and Structure of Allergens. High School Summer Research Program Poster Session, University of Texas Medical Branch, Galveston, TX (July 29).
43. Oezguen, N., Zhou, B., Avery, M.H., Negi, S.S., Ivanciuc, O.I., Garcia, T.I., Schein, C.H., Labesse, G. and Braun, W. Large scale homology modeling of allergenic proteins.

- Sealy Center for Structural Biology 10th Annual Structural Biology Symposium,  
University of Texas Medical Branch, Galveston, TX (May 20-21, 2005).
42. Oezguen, N., Hindupur, A. and Braun, W. Sequence analysis of P450 families CYP1, CYP2 and CYP3. Sealy Center for Structural Biology 10th Annual Structural Biology Symposium, University of Texas Medical Branch, Galveston, TX (May 20-21, 2005).
  41. Avery, M.H., Oezguen, N., Schein, C.H., Zhou, B. and Braun, W. Prediction of 3D structures of proteins by template combination: application to the walnut allergen Jug r 2. Sealy Center for Structural Biology 10th Annual Structural Biology Symposium, University of Texas Medical Branch, Galveston, TX (May 20-21, 2005).
  40. Schein, C.H., Oezguen, N., Volk, D.E., Garimella, R., Paul, A.V. and Braun, W. NMR structure of poliovirus VPg in a stabilizing solvent. The 46th Experimental Nuclear Magnetic Resonance Conference (ENC), Rhode Island Convention Center, Providence, RI (April 10-15, 2005).
  39. Oezguen, N., Negi, S.S., Tuzun, E., Christadoss, P. And Braun, W. Structural analysis of the alpha 9-subunit of the neuronal acetylcholine receptor. Sealy Center for Molecular Science and Sealy Center for Cancer Cell Biology: 13th Annual Science Forum, University of Texas Medical Branch, Galveston, TX (April 8, 2005).
  38. Oezguen, N., Power, T.D., Schein, C.H., Zhou, B., Mathura, V., Izumi, T. and Braun, W. Sequence decomposition of metal sites and MD simulations suggest a novel "moving ion" mechanism for the DNA repair endonuclease APE1. Keck/HAMBP Annual Research Conference, NASA Hilton, Clear Lake, TX (October 8, 2004).
  37. Oezguen, N., Schein, C.H., Power, T.D., Izumi, T. and Braun W. Moving ion mechanism in APE1. Sealy Center for Molecular Science-Science Forum 2004, Galveston, TX (May 6-7, 2004).
  36. Power, T.D., Oezguen, N. and Braun, W. Analysis of the catalytic mechanism of human APE1 by QM/MM ONIOM calculations. Sealy Center for Molecular Science-Science Forum 2004, Galveston, TX (May 6-7, 2004).
  35. Power, T.D., Oezguen, N. and Braun, W. Analysis of the catalytic mechanism of human APE1 by QM/MM ONIOM calculations. 9th Annual Sealy Center for Structural Biology Symposium, Galveston, TX (April 31-May 1, 2004).
  34. Oezguen, N., Schein, C.H., Power, D.Y., Izumi, T. and Braun, W. Moving ion mechanism in APE1. 9th Annual Sealy Center for Structural Biology (SCSB) Symposium, Galveston, TX (April 30-May 2, 2004).
  33. Oezguen, N., Schein, C.H., Power, D.Y., Izumi, T. and Braun, W. Moving ion mechanism in APE1. 9th Annual Sealy Center for Structural Biology (SCSB) Symposium, Galveston, TX (April 30-May 2, 2004).
  32. Oezguen, N., Schein, C.H., Venkatarajan, M.S., Izumi, T. and Braun, W. Dynamics of the Mg<sup>2+</sup> metal ion in APE1. 8th Annual Sealy Center for Structural Biology (SCSB) Symposium, Galveston, TX (May 2-4, 2003).

31. Mathura, V.S., Schein, C. H., Oezguen, N. and Braun, W. PCPMer: physical-chemical property based protein sequence motif analyzer. 8th Annual Sealy Center for Structural Biology Symposium, Galveston, TX (May 2-4, 2003).
30. Fernandez, W.A., Oezguen, N., Schein, C.H., Braun, W. and Peterson, J.W. Structural basis for the interaction of PGE2-imidazole inhibitor with anthrax edema factor and mammalian adenylyl cyclases. The 2003 Annual Meeting of the Gulf Coast Tropical Medicine Association (GCTMA), Galveston, TX (April 24-26, 2003).
29. Vongpunsawad S., Oezguen N., Braun W., Cattaneo R. Selectively receptor-blind measles viruses. *Molecular Therapy* 7 (5): S28-S29 71 Part 2, May (2003)
28. Xu, Y., Oezguen, N. and Braun, W. A GUI based NOAH/DIAMOD programs for automated NOESY spectra assignment and protein structure determination. 8th Annual Structural Biology Symposium, Galveston, TX (May 2-4, 2003).
27. Oezguen, N., Schein, C.H., Mathura, V., Izumi, T. and Braun, W. Dynamics of the Mg<sup>2+</sup> metal ion in APE1. 8th Annual Structural Biology Symposium, Galveston, TX (May 2-4, 2003).
26. Mathura, V.S., Schein, C. H., Oezguen, N. and Braun, W. PCPMer: physical-chemical property based protein sequence motif analyzer. 8th Annual Sealy Center for Structural Biology Symposium, Galveston, TX (May 2-4, 2003).
25. Xu, Y., Oezguen, N. and Braun, W. Protein NMR structure determination using a new GUI design of NOAH/DIAMOD program suite. 44th Experimental Nuclear Magnetic Resonance Conference (ENC), Savannah, GA (March 30 - April 4, 2003).
24. Xu, Y., Oezguen, N. and Braun, W. GUI based NOAH/DIAMOD programs for automated NOESY spectra assignment and protein structure determination. 47th Annual Meeting of the Biophysical Society, San Antonio, TX (March 1-5, 2003).
23. Mathura, V.S., Schein, C.H., Oezguen, C.H. and Braun, W. PCPMer: a new program to use physical chemical property motifs to identify homologous proteins in sequence databases. 47th Annual Biophysical Society Meeting, San Antonio, TX (March 1-5, 2003).
22. Mathura, V., Schein, C.H., Oezguen, N., Ivanciuc, O., Xu, Y. and Braun, W. Automated generation of property based motifs to search for functional neighbors and to improve sequence alignments. 5th Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, Asilomar, CA (December 1-5, 2002).
21. Mathura, V., Ivanciuc, O., Oezguen, N., Schein, C.H., Xu, Y. and Braun, W. Evaluating sequence alignment of fold-recognition tools by quantitative scoring of physical-chemical property based motifs. 5th Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, Asilomar, CA (December 1-5, 2002).
20. Oezguen, N., Schein, C.H., Izumi, T. and Braun, W. Dynamics of the metal binding sites in APE1. Keck/GCC 2002 Bioinformatics Symposium, Rice University, Houston, TX (October 14-15, 2002).

19. Mathura, V., Schein, C.H., Oezguen, N. and Braun, W. Defining physical-chemical properties based motifs specific for members of the APE family of DNA repair proteins. 7th Annual Structural Biology Symposium, Galveston, TX (May 17-19, 2002).
18. Oezguen, N., Schein, C.H., Izumi, T. and Braun, W. APE1: mobility of metal ion and recognition sites at the protein/DNA interface of wild type and mutant apurinic/apyrimidinic endonucleases. 7th Annual Structural Biology Symposium, Galveston, TX (May 17-19, 2002).
17. Mathura, V., Schein, C.H., Oezguen, N. and Braun, W. Sequence and structural analysis of APE1 protein family using physical-chemical properties based motifs. 6th Annual International Conference on Research in Computational Molecular Biology (RECOMB), Washington, DC (April 18-21, 2002).
16. Ozgun, N., Garimella, R., Schein, C.H., Xu, Y. and Braun, W. Automatic NOESY assignment and structure determination of the protein structures using NOAH/DIAMOD. 43rd Experimental Nuclear Magnetic Resonance Conference (ENC), Asilomar, CA (April 14-19, 2002).
15. Schein, C.H., Ozgun, N., Izumi, T., Venkatarajan, M.S. and Braun, W. Structural and functional motifs of apurinic/apyrimidinic endonuclease. 2002 Keystone Symposia, Frontiers of Structural Biology, Session J2, Breckenridge, CO (January 5-11, 2002).
14. Ozgun, N., Schein, C. H., Venkatarajan, M., Izumi, T. and Braun, W. Mobility of metal ion and recognition sites at the protein/DNA interface of wild type and mutant apurinic/apyrimidinic endonucleases. The Cell Biology Forum, Galveston, TX (October 2, 2001).
13. Ozgun, N., Schein, C. H., Venkatarajan, M., Izumi, T. and Braun, W. Identifying motifs by MASIA and metal ion position by MD-simulations. Annual KECK Research Conference, Galveston, TX (September 21, 2001).
12. Schein, C. H., Ozgun, N., Izumi, T. and Braun, W. Defining moieties with MASIA: a modular approach to nuclease function. Annual KECK Research Conference, Galveston, TX (September 21, 2001).
11. Ozgun, N., Schein, C. H., Venkatarajan, M., Izumi, T. and Braun, W. Defining the mode of DNA repair by apurinic/apyrimidinic endonuclease using MASIA sequence decomposition, MD-simulations, and structure-driven protein design. 222nd American Chemical Society National Meeting, Chicago, IL (August 26-30, 2001).
10. Oezguen, N., Kosynkina, L., Xu, Y., Rajarathnam, K. and Braun, W. Minimal NMR spectral data needed for automated fold determination by NOAH/DIAMOD. 5th Annual Life Sciences Symposium, Galveston, TX (May 25, 2001).
9. Ozgun, N., Schein, C. H., Venkatarajan, M., Izumi, T. and Braun, W. Defining the mode of action of APE1 using MASIA motif searching, MD-simulations and site directed mutagenesis. *Biochemistry* 40 (29): 167 Jul 24 (2001)

8. Ozgun, N., Xu, Y., Rajarathnam, K. and Braun, W. Automated structure determination from 3D heteronuclear edited NMR spectra using NOAH/DIAMOD. 6th Annual Structural Biology Symposium, Galveston, TX (May 18-20, 2001).
7. Schein, C. H., Ozgun, N., Venkatarajan, M., Izumi, T. and Braun, W. Defining the mode of action of APE1 using MASIA motif searching, MD-simulations and site directed mutagenesis. 6th Annual Structural Biology Symposium, Galveston, TX (May 18-20, 2001).
6. Schein, C. H., Oezguen, N. and Braun, W. Relating structure and function of endonucleases that repair abasic sites in DNA. Science Forum, Galveston, TX (March 28, 2001).
5. Oezguen, N., Kosynkina, L., Xu, Y., Rajarathnam, K. and Braun, W. Minimal NMR spectral data needed for automated fold determination by NOAH/DIAMOD. 42nd Experimental Nuclear Magnetic Resonance Conference (ENC), Orlando, FL (March 11-16, 2001).
4. Ozgun, N., Nick, B., Jung, B., Wortmann, F. -J. and Hocker, H. Bestimmung der Glasübergangstemperatur für polycarbonate aus molekulardynamik simulationen und einzelketten. Aachener Textiltagung, (1999).
3. Ozgun, N., Nick, B., Jung, B., Wortmann, F. J. and Hocker, H. Determination of the glass transition temperature for bisphenol-a-polycarbonate from MD-simulations in theta-state. Am. Chem. Soc. Abs. 215:210-PMSE, Part 2 (1998).
2. Ozgun, N., Nick, B., Jung, B., Wortmann, F. -J. and Hocker, H. Modeling of  $\Theta$ -conditions for bisphenole-a-polycarbonate single chains. Rolduc Symposium, (1997).
1. Ozgun, N., Koltun, R., Melzow, A. and Guntherodt, G. Tunnelspektroskopie am  $\text{Bi}_2\text{Sr}_2\text{Ca}(\text{Cu}_{1-x}\text{Fe}_x)_2\text{O}_{8+y}$  System. Frühjahrstagung der DPG in Munster, (1994).