

Sakata, Eri (A02)

Title	PhD
First name	Eri
Name	Sakata
Current position	Group Leader (current contract until 31.12.2025)
Current institution(s)/site(s), country	Institut für Auditorische Neurowissenschaften Universitätsmedizin Göttingen Göttingen, Germany
Identifiers/ORCID	0000-0002-8580-3683

Qualifications and Career

Stages	Periods and Details	
Degree programme	1998 - 2002	B.Sc. in Pharmaceutical Sciences Nagoya City University, Japan
	2002 - 2004	M.Sc. in Pharmaceutical Sciences, Nagoya City University, Japan
Doctorate	2007	Ph.D., supervisor: Prof. Koichi Kato, Pharma-ceutical Sciences, Nagoya City University, Japan
Stages of academic/ professional career	Since 2019	Group Leader, Institute for Auditory Neuroscience, University Medical Center Göttingen (UMG)
	2013 - 2019	Project Group Leader, Max Planck Institute of Biochemistry, Martinsried, Germany
	2011 - 2013	Postdoctoral fellow, Yale University, New Haven, USA (Prof. Mark Hochstrasser)
	2007 - 2011	Joint Postdoctoral Fellow, Max Planck Institute of Biochemistry, Martinsried, Germany (Prof. Wolfgang Baumeister) and Tokyo Metropolitan Institute of Medical Science, Tokyo, Japan (Prof. Keiji Tanaka)

Supplementary Career Information

Parental leave for two children: 2015-2016, 7 months and 2019-2020, 7 months

Engagement in the Research System

- 2020 - 2022 Project leader (A11), Collaborative Research Centre (CRC) 889, German Research Foundation (DFG)
- 2019 - 2025 Board member, Excellence Cluster EXC 2067/1 (DFG)
- 2019 - 2025 Group Leader, Excellence Cluster EXC 2067/1 (DFG)
- 2016 - 2020 Project leader (A01), Collaborative Research Centre CRC 1035 (DFG)

Scientific Results**Category A**

1. Shein M, Hitzenberger M[#], Cheng CT, Rout SR, Leidl K, Sato Y, Zacharias M[#], **Sakata E[#]**, Schütz AK[#] (2024) Unravelling ATP processing by the AAA+ protein p97 at the atomic level. *Nat Chem* 16:363-372. doi: [10.1038/s41557-024-01440-0](https://doi.org/10.1038/s41557-024-01440-0) (OA)
Contribution: Designed the research, supervised the experiments and drafted the manuscript.

Significance: We elucidated that multidisciplinary approach combining several structural studies (Cryo-EM, NMR and MD simulation) enabled us to understand chemical reaction in macromolecule, which was supported by CRC 899. This is the first cryo-EM structure in the natural post-nucleotide hydrolysis (ADP.Pi) state. Our structure demonstrated the allosteric regulation of the conformational dynamics.

2. Hung K, Klumpe S, Eisele MR, Elsasser S, Tian E, Sun S, Moroco J, Cheng T, Joshi T, Seibel T, Van Dalen D, Feng X, Lu Y, Ovaa H, Engen JO, Lee B[#], Rudack T[#], **Sakata E[#]**, Finley D[#] (2022) Allosteric control of Ubp6 and the proteasome via a bidirectional switch. *Nat Commun* 13(1):838. doi: [10.1038/s41467-022-28186-y](https://doi.org/10.1038/s41467-022-28186-y) (OA)

Contribution: Designed the research, supervised the experiments and drafted the manuscript.

Significance: We reported that Ubp6 shifts the structure of the 26S proteasome to an inhibitory state to trim poly-ubiquitin chain. This work was supported by CRC 889.

3. **Sakata E**, Eisele MR, Baumeister W (2021) Molecular and cellular dynamics of the 26S proteasome. *Biochim Biophys Acta Proteins Proteom* 1869(3):140583. doi: [10.1016/j.bbapap.2020.140583](https://doi.org/10.1016/j.bbapap.2020.140583) (OA)

Contribution: Wrote the review and created figures.

Significance: The review focuses on current understandings on the structural dynamics of the 26S proteasome. This work was supported by CRC 889.

4. Eisele MR, Reed RG, Rudack T, Schweitzer A, Beck F, Nagy I, Pfeifer G, Plitzko JM, Baumeister W, Tomko RJ Jr, **Sakata E** (2018) Expanded coverage of the 26S proteasome conformational landscape reveals mechanisms of peptidase gating. *Cell Rep* 24:1301-1315. doi: [10.1016/j.celrep.2018.07.004](https://doi.org/10.1016/j.celrep.2018.07.004) (OA)

Significance: This paper demonstrated the structural regulation of the 26S proteasome upon ATP hydrolysis events on the AAA+ ATPases.

5. Wehmer M, Rudack T, Beck F, Aufderheide A, Pfeifer G, Plitzko JM, Förster F, Schulten K, Baumeister W[#], **Sakata E[#]** (2017) Structural insights into the functional cycle of the ATPase module of the 26S proteasome. *Proc Natl Acad Sci U S A* 114(6):1305-1310. doi: [10.1073/pnas.1621129114](https://doi.org/10.1073/pnas.1621129114) (OA)

Significance: The paper provided the first overview of the structural dynamics of the 26S proteasome.

6. Wehmer M, **Sakata E** (2016) Recent advances in the structural biology of the 26S proteasome. *Int J Biochem Cell Biol* 79:437-442. doi: [10.1016/j.biocel.2016.08.008](https://doi.org/10.1016/j.biocel.2016.08.008) (OA)

Significance: This review focuses on the structure of the 26S proteasome.

7. **Sakata E**, Bohn S, Miharache O, Kiss P, Beck F, Nickell S, Tanaka K, Saeki Y, Förster F, Baumeister W (2012) Localization of the proteasomal ubiquitin receptors Rpn10 and Rpn13 by electron cryomicroscopy. *Proc Natl Acad Sci U S A* 109:1479-1484. doi: [10.1073/pnas.1119394109](https://doi.org/10.1073/pnas.1119394109) (OA)

Significance: We provided the first evidence of the localization of the ubiquitin receptors by cryo-EM.

8. **Sakata E^{*}**, Stengel F^{*}, Fukunaga K, Zhou M, Saeki Y, Förster F, Tanaka K, Baumeister W, Robinson CV (2011) The catalytic activity of Ubp6 enhances maturation of the proteasomal regulatory particle. *Mol Cell* 42:637-649. doi: [10.1016/j.molcel.2011.04.021](https://doi.org/10.1016/j.molcel.2011.04.021) (OA)

Significance: We addressed the function of Ubp6 in the process of the proteasome assembly combining biochemistry and Mass spectrometry.

9. **Sakata E^{*}**, Satoh T^{*}, Yamamoto S, Yamaguchi Y, Yagi-Utsumi M, Kurimoto E, Tanaka K, Wakatsuki S, Kato K (2010) Crystal structure of Ubch5b~ubiquitin intermediate: Insight into the formation of the self-assembled E2~Ub conjugates. *Structure* 18:138-147. doi: [10.1016/j.str.2009.11.007](https://doi.org/10.1016/j.str.2009.11.007) (OA)

Significance: We reported the structural basis for the self-assembly of the E2 ubiquitin conjugating enzyme by crystallography.

10. **Sakata E**, Yamaguchi Y, Kurimoto E, Kikuchi J, Yokoyama S, Yamada S, Kawahara H, Yokosawa H, Hattori N, Mizuno Y, Tanaka K, Kato K (2003) Parkin binds the Rpn10 subunit of 26S proteasomes through its ubiquitin-like domain. *EMBO Rep* 4:301-306. doi: [10.1038/sj.embor.embor764](https://doi.org/10.1038/sj.embor.embor764) **(OA)**

Significance: We reported the structure of the UBL domain of protein parkin which is related to the pathogenesis of autosomal recessive juvenile parkinsonism (AR-JP). This paper was cited by more than 300 scientific articles.

*Equal contribution, #Shared correspondence.

(OA): Publicly available (e.g. open access, open archive, preprint, free access, etc.).

Academic Distinctions

2013 - 2017	Marie Curie Career Integration Grant
2011 - 2012	Postdoctoral Research Fellowship (Uehara Memorial Foundation)
2009	Poster Award (Tokyo Metropolitan Institute of Medical Sciences, Japan)
2007 - 2010	Postdoctoral Research Fellowship (Japan Society for the Promotion of Science)
2003 - 2007	PhD Research Fellowship (Japan Society for the Promotion of Science)
2003	Poster Award (15 th Naito conference on molecular biological approaches for intractable diseases, Japan)