Curriculum vitae

PERSONAL INFORMATION

Family name, First name:	Standfuss, Jörg
Date of birth:	01.10.1974
Nationality:	German
Family Status:	Married, two children
Web site:	www.psi.ch/en/lbr/people/jorg-standfuss
Publications:	https://bit.ly/3kLtC4j

EDUCATION

2005	PhD in Biochemistry (supervision: Prof. Dr. Werner Kühlbrandt) Structural Biology, Max Planck Institute of Biophysics, Germany Faculty of Biochemistry, Chemistry and Pharmacy, Goethe University Frankfurt, Germany
2000	Diploma in Biology Johannes Gutenberg University Mainz Max Planck Institute of Biophysics, Germany

CURRENT POSITION

Since 2019	Deputy Head and Group Leader Laboratory of Biomolecular Research, Paul Scherrer Institute, Switzerland

PREVIOUS POSITIONS

Since 2014	Scientific Group Leader (tenured) Laboratory of Biomolecular Research, Paul Scherrer Institute, Switzerland
2010 – 2014	Principal Investigator and Scientist Laboratory of Biomolecular Research, Paul Scherrer Institute, Switzerland
2006 – 2010	Marie Curie and EMBO Long-Term Fellow Laboratory of Molecular Biology, Medical Research Council, United Kingdom

FELLOWSHIPS AND AWARDS

2009	EMBO Long-Term Fellowship
2007	Marie-Curie Intra-European Fellowship
2005	Departmental Award for the Structure Determination of LHC-II

SUPERVISION OF GRADUATE STUDENTS AND POSTDOCTORAL FELLOWS

2010 – 2021	Supervision of 7 Postdocs, 7 PhDs and 1 Master Student Laboratory of Biomolecular Research, Paul Scherrer Institute, Switzerland Department of Biology, ETH Zürich, Switzerland (PhD students until 2019) Department of Biochemistry, University of Zürich, Switzerland (PhD students since 2019)

TEACHING ACTIVITIES

From 2022	Lecture and practical workshop “Experimental Structural Biology” University of Zürich and Paul Scherrer Institute, Switzerland
From 2021	Lecture “Protein Structure Determination” University of Zürich, Switzerland
Since 2019	Lecture “Molecular Cell Biology, Module Cell Cycle”

	University of Zürich, Switzerland
Since 2014	Mentoring of Postdoctoral Researchers into academic positions (two professorships in the US and the Netherlands and one Ambizione Fellow at the ETH Zürich)
Since 2011	Training and mentoring of PhD students as Principal Investigator in the Life Science Graduate School Zürich

ORGANISATION OF SCIENTIFIC MEETINGS

2020	Organization Committee "NCCR MUST Meeting 2020", Switzerland (postponed)
2019	Organization Committee "Drug Discovery@SwissFEL", Switzerland
2012	Organization Committee "15th Internat. Conference on Retinal Proteins", Switzerland
Since 2010	Regular Session chair and Speaker at International Conferences including ICRP, Gordon Research Conferences, the European Crystallographic Meeting and EMBO Workshops

INSTITUTIONAL RESPONSIBILITIES

Since 2020	Contributing to the science case of the new Porthos beamline for SwissFEL
Since 2019	Deputy Head of the Laboratory of Biomolecular Research
Since 2018	Member of the steering committee for the Cristallina endstation at SwissFEL
2016	Co-founder InterAx Biotech AG
Since 2016	User Support for Serial Crystallography at SLS and SwissFEL
Since 2014	Coordination of SwissFEL applications in the Biology and Chemistry Division

REVIEWING ACTIVITIES

From 2022	Member of the review panel for the SPB/SFX instrument at the European XFEL
Since 2017	Member of the PSI research committee
Since 2010	Regular peer review of scientific articles including NSMB, PNAS, Science and Nature
Since 2010	Peer review for national and international research funding organizations

MEMBERSHIPS OF SCIENTIFIC SOCIETIES

Since 2020	Member of the Swiss Society of Photon Sciences
Since 2018	Principal Investigator in the National Center of Competence in Research for the Development of Methods in Ultrafast Science and Technology
Since 2012	Principal Investigator in the Life Science Zürich Graduate School
Since 2011	Member of the German Association of University Professors and Lecturers
2006 – 2009	Research Associate to Darwin College, University of Cambridge

CURRENT EXTERNAL COLLABORATIONS

Andrea Cavalli, Italian Institute of Technology, Molecular Dynamic Simulations
Joachim Heberle, Free University of Berlin, Time-resolved spectroscopy on crystals
Igor Schapiro, The Hebrew University of Jerusalem, Quantum mechanics, molecular mechanics simulations
Joseph Wachtveitl, University of Frankfurt, Ultrafast spectroscopy on synthetic photoswitches
Amadeu Llebaria, MCS Barcelona, Synthesis and characterization of photoswitches
Richard Neutze, University of Gothenburg, Time-resolved serial crystallography on rhodopsins
Manuel Maestre Reyna, Academia Sinica, Time-resolved serial crystallography on photolyases
Sebastian Westenhoff, University of Gothenburg, Time-resolved serial crystallography on phytochromes
Michael, Hennig, LeadXpro, Time-resolved serial crystallography on G protein-coupled receptors
Przemek Nogly, ETH Zürich, Time-resolved serial crystallography
So Iwata, University of Kyoto, Time-resolved serial crystallography at SACLA
BioXFEL consortium, Development of time-resolved serial crystallography

TEN-YEAR TRACK RECORD

Key Bibliographic Data 2011 - 2021
Number of publications: 52 Number of citations: 3480 H-Index: 26
Full publication list: https://bit.ly/3kLtC4j

Ten-year research summary
The central paradigm of structural biology is the notion that the function of a protein is determined by its structure. Yet in many ways this is an oversimplification since proteins are not static entities but typically require correctly timed structural rearrangements to perform their function. Time-resolved structural biology aims at providing molecular insights into such changes to better understand biological activity.
In the last few years my group has been pushing the boundaries of what is possible by time-resolved serial crystallography using synchrotrons and X-ray free electron laser sources[1]. Together with the EU training network Nanomem, we demonstrated the use of high-viscosity sample injectors to determine room temperature structures at the European Synchrotron Radiation Facility[2]. At the Swiss Light Source (SLS), we implemented routine serial crystallographic techniques including phasing and ligand soaking on soluble and membrane proteins[3]. Next, we pioneered the use of high-viscosity injectors for time-resolved measurements in order to increase sample efficiency at the Linac Coherent Light Source[4]. These developments allowed us to reconstruct the pumping cycle of the light-driven proton-pump bacteriorhodopsin using 40 structural snapshots obtained by time-resolved crystallography at the synchrotron and X-ray lasers. The work combines the light-induced isomerization of retinal within the first picosecond[5], the following proton release steps within microseconds[6] and the uptake reaction in the early milliseconds[7] into the most complete overview of a membrane pump in action.
Next, we established time-resolved crystallography at the Swiss X-ray Free Electron laser (SwissFEL) to resolve how cations[8] and anions (Mous *et al.*, Science in revision) are transported by light activated cellular transporters. The methods we developed using microbial rhodopsins, are directly transferable to the study of the light-sensitive G protein-coupled receptor (GPCR) rhodopsin. In collaboration with the group of Prof. Schertler, we collected data temporal range from 1 ps to 8 ms to study the molecular basis of our visual sense (unpublished). GPCRs form a major family of human transmembrane signalling proteins that is the target of many drugs. Numerous GPCR mutations are known to cause human disease often linked to increased constitutive activity of the receptor. Our crystal structures of E113Q[9] and M257Y[10] visual rhodopsin provided the first molecular insights into how single GPCR point mutations can lead to increased constitutive activity. The structural, biochemical and spectroscopic analysis of G90D[11] and T94I[12] rhodopsin demonstrated how interference with a critical activation switch in the retinal binding site causes either retinitis pigmentosa or the milder non-progressive form congenital stationary night blindness. In collaboration with Hoffmann-La Roche, we have used the structural information to selected pharmacological chaperones as promising lead compounds against the progressing blindness in patients with rhodopsin-mediated retinitis pigmentosa[13]. Later we employed the same technology to identify new compounds to silence the human C-C chemokine receptor 7[14] involved in the metastasis of many cancers.
In our latest series of experiments at SwissFEL, we demonstrated the use of photochemical affinity switches to capture ultrafast ligand dynamics of proteins not naturally activated by light. On the examples of tubulin and the adenosine A2a G protein-coupled receptor we have explored the use of such photopharmacological compounds to dramatically increase the number of proteins that can be studied by time-resolved methods (in preparation). A series of temporal snapshots of pharmaceutical relevant targets will shed light onto the molecular principles of ligand recognition as one of the most fundamental regulatory systems in biology. Clearly time-resolved serial crystallography has opened a new domain in structural biology as it allows to collect high-resolution structural data at physiological temperatures and time-resolution down to the ultrafast regime. Now is the time to expand our repertoire of time-resolved structural biology techniques to include time-resolved cryo-electron microscopy to study larger conformational changes not possible in crystals and towards the study of new fundamentally relevant biological targets such as cancer related kinases.

Ten-year publication highlights
First, Last and/or corresponding authorship *

1* Standfuss, J. Membrane protein dynamics studied by X-ray lasers - or why only time will tell. *Curr Opin Struct Biol* **57**, 63-71, doi:10.1016/j.sbi.2019.02.001 (2019).
2* Nogly, P. *et al.* Lipidic cubic phase serial millisecond crystallography using synchrotron radiation. *IUCrJ* **2**, 168-176, doi:10.1107/S2052252514026487 (2015).
3* Weinert, T. *et al.* Serial millisecond crystallography for routine room-temperature structure determination at synchrotrons. *Nat Commun* **8**, 542, doi:10.1038/s41467-017-00630-4 (2017).
4* Nogly, P. *et al.* Lipidic cubic phase injector is a viable crystal delivery system for time-resolved serial crystallography. *Nat Commun* **7**, 12314, doi:10.1038/ncomms12314 (2016).
5* Nogly, P. *et al.* Retinal isomerization in bacteriorhodopsin captured by a femtosecond x-ray laser. *Science* **361**, doi:10.1126/science.aat0094 (2018).
6 Nango, E. *et al.* A three-dimensional movie of structural changes in bacteriorhodopsin. *Science* **354**, 1552-1557, doi:10.1126/science.aah3497 (2016).
7* Weinert, T. *et al.* Proton uptake mechanism in bacteriorhodopsin captured by serial synchrotron crystallography. *Science* **365**, 61-65, doi:10.1126/science.aaw8634 (2019).
8* Skopintsev, P. *et al.* Femtosecond-to-millisecond structural changes in a light-driven sodium pump. *Nature*, doi:10.1038/s41586-020-2307-8 (2020).
9* Standfuss, J. *et al.* The structural basis of agonist-induced activation in constitutively active rhodopsin. *Nature* **471**, 656-660, doi:10.1038/nature09795 (2011).
10* Deupi, X. *et al.* Stabilized G protein binding site in the structure of constitutively active metarhodopsin-II. *Proc Natl Acad Sci U S A* **109**, 119-124, doi:10.1073/pnas.1114089108 (2012).
11* Singhal, A. *et al.* Insights into congenital stationary night blindness based on the structure of G90D rhodopsin. *EMBO Rep* **14**, 520-526, doi:10.1038/embor.2013.44 (2013).
12* Singhal, A. *et al.* Structural role of the T94I rhodopsin mutation in congenital stationary night blindness. *EMBO Rep* **17**, 1431-1440, doi:10.15252/embr.201642671 (2016).
13* Mattle, D. *et al.* Ligand channel in pharmacologically stabilized rhodopsin. *Proc Natl Acad Sci U S A* **115**, 3640-3645, doi:10.1073/pnas.1718084115 (2018).
14* Jaeger, K. *et al.* Structural Basis for Allosteric Ligand Recognition in the Human CC Chemokine Receptor 7. *Cell* **178**, 1222-1230 e1210, doi:10.1016/j.cell.2019.07.028 (2019).

Ten-year selected presentations
2021 EMBO workshop: Recent Advances in Structural Biology of Membrane Proteins (EMBL, Hamburg)
2020 Manfred-Eigen Winterseminar (Klosters, Switzerland)
2020 Invited Research Seminar (Academia Sinica, Taiwan)
2019 International Conference on Photobiology (Barcelona, Spain)
2019 International Conference on Ultrafast Structural Dynamics (Daejeon, Korea)
2018 17th International Conference on Retinal Proteins (Ontario, Canada)
2018 5th Ringberg Workshop on Structural Biology with FELs (Ringberg, Germany)
2017 24th International Union of Crystallography Meeting (Hyderabad, India)
2017 IGER International Symposium on Physics of Life (Nagoya, Japan)
2016 30th European Crystallography Meeting (Basel, Switzerland)
2016 3rd Annual BioXFEL conference (San Juan, Puerto Rico)
2015 LCLS Users Meeting (Stanford University, USA)
2015 Invited Research Seminar (Physics Department, Arizona State University, USA)
2014 16th International Conference on Retinal Proteins (Nagahama, Japan)
2014 Gordon Research Conference "Ligand recognition and Molecular Gating" (Ventura, USA)
2013 5th Annual PEGS Europe (Lisbon, Portugal)
2013 Invited Research Seminar (Department of Chemistry, Yale University, USA)
2012 15th International Conference on Retinal Proteins (Ascona, Switzerland)
2011 25 years of Biostructure Research at Roche (Basel, Switzerland)
2011 Keystone Symposium "Transmembrane Signaling by GPCRs and Channels" (Taos, USA)