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Radiation Protection Manager

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Research areas

Our research focuses on elucidating the molecular details of signal transduction processes in membrane proteins and in metalloenzymes. In particular we are interested on structural investigations of various G-protein-coupled receptor (GPCRs), photoreceptors (e.g. vertebrate cone and rhodopsins, microbial rhodopsins, phytochromes, photolyases, melanopsins), GPCR-related signaling proteins (e.g. G-proteins, arrestins, phosphodiesterases, dishevelled) and several metalloenzymes (e.g. [NiFe]-hydrogenases and lipoxygenases). In my lab we apply a wide array of different techniques to study different protein systems, such as membrane and soluble protein production (e.g. different heterologous cell expression systems), molecular biology, biochemical, biophysical (e.g. multi-angle light scattering, differential scanning calorimetry, microscale thermophoresis) and crystallization (using robot-platforms, conventional, lipid cubic phase (LCP), micelle/bicelle). Our core skills are protein-production and -engineering, protein X-ray crystallography and combined crystallographic-spectroscopic approaches with a broad network of international collaborators and access to several high-end synchrotrons. In the last years, we established also conventional and pump-probe methods for our protein samples at free electron laser facility LCLS-SLAC in Stanford, USA. In parallel, we started a collaboration with our in-house partners on cryo-electron microscopy to investigate several membrane protein and protein-complex targets.

Research key words

Protein X-ray crystallography, membrane proteins, signal transduction, X-ray structure analysis, molecular structure, dynamics and function of proteins, molecular modelling, methodological development of a combined crystallographic and spectroscopic approach, free-electron laser techniques, photoreceptors and related signal transduction proteins, G-protein-coupled receptor, GPCR, rhodopsin, arrestin, G-protein, channelrhodopsin,

microbial opsins, melanopsin, phytochrome, photolyase, cryptochrome, [NiFe]-hydrogenase, metallo-proteins, Two-component regulatory systems, CpxRAP system, phosphodiesterase, PRG's

Funding for approved projects / grants / applications

01/ 2017 – 12/ 2020 - 2. Period - SFB 1078-B6 Full Project: "Proton-coupled conformational changes in photoreceptors" shared with Prof. Peter Hildebrandt (TU-Berlin) – Collaborative Research Center 1078 "Protonation Dynamics in Protein Function " supported by the German Research Foundation (DFG) - (Host: Freie Universität Berlin - <http://www.sfb1078.de/index.html>)

01/ 2015 – 12/ 2018 SFB 740-B6 Full Project: "Structural elucidation of the GPCR allosteric machine"– Collaborative Research Center 740 "From Molecules to Modules: Organisation and Dynamics of Functional Units in Cells" supported by the German Research Foundation (DFG) - (Host: Charité – University Medicine Berlin - <http://www.sfb740.de/en/>)

01/ 2017 – 01/ 2020 – Industry-Cooperation with Bayer AG

11/ 2012 – 12/ 2018 UniCat Full Project - Research area E3-1: "Structural investigations of oxygen-tolerant [NiFe] hydrogenases" – Cluster of Excellence "Unifying Concepts in Catalysis" supported by the German Research Foundation (DFG) - (Host: Technische Universität Berlin - <http://www.unicat.tu-berlin.de/>)

01/ 2013 – 12/ 2016 - 1. Period - SFB 1078-B6 Full Project: "Proton-coupled conformational changes in photoreceptors" shared with Prof. Peter Hildebrandt (TU-Berlin) – Collaborative Research Center 1078 "Protonation Dynamics in Protein Function " supported by the German Research Foundation (DFG) - (Host: Freie Universität Berlin - <http://www.sfb1078.de/index.html>)

01/ 2013 – 12/ 2020 European Synchrotron Radiation Facility (ESRF) synchrotron beamtime application – shared with Dr. N. Krauss (KIT, Karlsruhe / Prof. A. Zouni (Humboldt Universität Berlin) / Dr. P. Scheerer (Charité – Universitätsmedizin Berlin) - Period: 01/2015-12/2018 (continuation from 2007) - Research topics: G-protein-coupled receptors, rhodopsin, phytochromes, photolyases, photosystems, [NiFe]-hydrogenase etc.

01/ 2006 – 12/ 2022 Helmholtz-Zentrum Berlin (HZB)-BESSY II (periods 2006 - 2017) - Synchrotron – beamtime application-grants: Topic: G-protein-coupled receptors, rhodopsin, phytochromes, photolyases, [NiFe]-hydrogenase and others.

2015 – 2018 - SLAC-LCLS – Free electron Laser - Linac Coherent Light Source beamtime application-grants: Topic: Rhodopsin, Phytochrome, [NiFe]-hydrogenase

Memberships

Deutsche Gesellschaft für Biophysik (DGfB), Deutschen Gesellschaft für Kristallographie (DGK), Humboldt-Universitäts-Gesellschaft, Berlin Institute of Health (BIH) Young Science, Einstein Centre for Catalysis EC²

Refereeing Activities

e.g. Nature, Nature Chemical Biology, Nature Communications, Faseb J., J. Biol. Inorg. Chem, etc.

Protein structure database related entries (<http://www.rcsb.org/>)

(6GYH; 6G1Y; 6G1Z; 6G20; 6ELW; 5MDL; 5MDK; 5MDJ; 5T4X; 5U5Q; 5MND; 5TRX; 5KCM; 5LFA; 5LC8; 5IR4; 5IR5; 5I5L; 5HSQ; 5L49; 5L48; 5L4D; 5L4A; 5L4B; 5L4C; 5D51; 5FLX; 3JCJ; 3JCN; 5AJ0; 4U63; 4V6T; 4PXF; 4TTT; 4IUB; 4IUC; 4IUD; 4J2Q; 4DJA; 3RGW; 3ITF; 3PXO; 3PQR; 3DQB; 3CAP; 3J18; 3J19; 3RJS; 2OR9; 2ORB; 2I9E; 2OBI; 1ZEA)

Summary of all publications

Source “[Google Scholar](#)” – h-index = 27 (*i10-index* 42; (since 2013): *h-index* = 24, *i10-index* = 38)

69 publications (> 4770 citations) in scientific journals - period 08-2018 – 01-2004

(and 5 submitted manuscripts)

(* These first authors contributed equally to this work)

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2018

- (69) Qureshi BM, Schmidt A, Behrmann E, Bürger J, Mielke T, Spahn CMT, Heck M, **Scheerer P[§]**. Mechanistic insights into the role of prenyl-binding protein PrBP/ δ in membrane dissociation of phosphodiesterase 6. *Nature Communications* 2018, 9(1):90. PMID: 29311697
- (68) Clément K, Biebermann H, Farooqi IS, Van der Ploeg L, Wolters B, Poitou C, Puder L, Fiedorek F, Gottesdiener K, Kleinau G, Heyder N, **Scheerer P**, Blume-Peytavi U, Jahnke I, Sharma S, Mokrosinski J, Wiegand S, Müller A, Weiß K, Mai K, Spranger J, Grüters A, Blankenstein O, Krude H, Kühnen P. MC4R agonism promotes durable weight loss in patients with leptin receptor deficiency. *Nature Medicine*. 2018, 24(5):551-555. PMID: 29736023
- (67) Kalms J, Schmidt A, Frielingsdorf S, Utesch T, Gotthard G, von Stetten D, van der Linden P, Royant A, Mroginski MA, Carpentier P, Lenz O, **Scheerer P[§]**. Tracking the route of molecular oxygen in O₂-tolerant membrane-bound [NiFe] hydrogenase. *Proc Natl Acad Sci U S A* 2018, 115(10):E2229-E2237. PMID: 29463722
- (66) Khajavi N, Finan B, Kluth O, Müller TD, Mergler S, Schulz A, Kleinau G, **Scheerer P**, Schürmann A, Gudermann T, Tschöp MH, Krude H, DiMarchi RD, Biebermann H. An incretin-based tri-agonist promotes superior insulin secretion from murine pancreatic islets via PLC activation. *Cellular Signalling*. 2018, 51:13-22. PMID: 30055232
- (65) Saleh N, Kleinau G, Heyder N, Clark T, Hildebrand PW[§], **Scheerer P[§]**. Binding, Thermodynamics, and Selectivity of a Non-peptide Antagonist to the Melanocortin-4 Receptor. *Frontiers in Pharmacology*. 2018, 9:560. PMID: 29910730
- (64) Borchert A, Kalms J, Roth SR, Rademacher M, Schmidt A, Holzhutter HG, Kuhn H[§], **Scheerer P[§]**. Crystal structure and functional characterization of selenocysteine-containing glutathione peroxidase 4 suggests an alternative mechanism of peroxide reduction. *Biochim Biophys Acta. (BBA) - Molecular and Cell Biology of Lipids* 2018, 1863(9):1095-1107. PMID: 29883798
- (63) Bräunig J, Dinter J, Höfig CS, Paisdzior S, Szczepek M, **Scheerer P**, Rosowski M, Mittag J, Kleinau G, Biebermann H. The Trace Amine-Associated Receptor 1 Agonist 3-Iodothyronamine Induces Biased Signaling at the Serotonin 1b Receptor. *Frontiers in Pharmacology*. 2018, 9:222. PMID: 29593543
- (62) Elgeti M, Kazmin R, Rose AS, Szczepek M, Hildebrand PW, Bartl FJ, **Scheerer P**, Hofmann KP. *J Biol Chem*. 2018, 293(12):4403-4410. PMID: 29363577

2017

- (61) **Scheerer P[§]**, Sommer ME[§]. Structural mechanism of arrestin activation. *Current Opinion in Structural Biology*. 2017, 45:160-169. PMID: 28600951
- (60) Oberthuer D, Knoška J, Wiedorn MO, Beyerlein KR, Bushnell DA, Kovaleva EG, Heymann M, Gumprecht L, Kirian RA, Barty A, Mariani V, Tolstikova A, Adriano L, Awel S, Barthelmess M, Dörner K, Xavier PL, Yefanov O, James DR, Nelson G, Wang D, Calvey G, Chen Y, Schmidt A, Szczepek M, Frielingsdorf S, Lenz O, Snell E, Robinson PJ, Šarler B, Belšak G, Maček M, Wilde F, Aquila A, Boutet S, Liang M, Hunter MS, **Scheerer P**, Lipscomb JD, Weierstall U, Kornberg RD, Spence JC, Pollack L,

Chapman HN, Bajt S. Double-flow focused liquid injector for efficient serial femtosecond crystallography. *Scientific Reports*. 2017, 7:44628. PMID: 28300169

- (59) Kleinau G, Worth CL, Kreuchwig A, Biebermann H, Marcinkowski P, **Scheerer P**, Krause G. Structural-Functional Features of the Thyrotropin Receptor: A Class A G-Protein-Coupled Receptor at Work. *Frontiers in Endocrinology*. 2017, 8:86. PMID: 28484426
- (58) Lamparter T[§], Krauß N[§], **Scheerer P[§]**. Phytochromes from *Agrobacterium fabrum*. *Photochem Photobiol*. 2017, 93(3):642-655. PMID: 28500698
- (57) Velázquez Escobar F, Buhrke D, Michael N, Sauthof L, Wilkening S, Tavraz NN, Salewski J, Frankenberg-Dinkel N, Mroginski MA, **Scheerer P**, Friedrich T, Siebert F, Hildebrandt P. Common Structural Elements in the Chromophore Binding Pocket of the Pfr State of Bathy Phytochromes. *Photochem Photobiol*. 2017, 93(3):724-732. PMID: 28500706
- (56) Kacprzak S, Njimona I, Renz A, Feng J, Reijerse E, Lubitz W, Krauss N, **Scheerer P**, Nagano S, Lamparter T, Weber S. Intersubunit distances in full-length, dimeric, bacterial phytochrome Agp1, as measured by pulsed electron-electron double resonance (PELDOR) between different spin label positions, remain unchanged upon photoconversion. *J Biol Chem*. 2017, 292(18):7598-7606. PMID: 28289094
- (55) Kalms J, Banthiya S, Galemou Yoga E, Hamberg M, Holzhutter HG, Kuhn H[§], **Scheerer P[§]**. The crystal structure of *Pseudomonas aeruginosa* lipoyxygenase Ala420Gly mutant explains the improved oxygen affinity and the altered reaction specificity. *Biochim Biophys Acta. (BBA) - Molecular and Cell Biology of Lipids* 2017, 1862(5):463-473. PMID: 28093240
- (54) Ma H, Zhang F, Ignatz E, Suehnel M, Xue P, **Scheerer P**, Essen LO, Krauß N, Lamparter T. Divalent Cations Increase DNA Repair Activities of Bacterial (6-4) Photolyases. *Photochem Photobiol*. 2017, 93(1):323-330. PMID: 27992646
- (53) Zhang F, Ma H, Bowatte K, Kwiatkowski D, Mittmann E, Qasem H, Krauß N, Zeng X, Ren Z, **Scheerer P[§]**, Yang X[§], Lamparter T[§]. Crystal Structures of Bacterial (6-4) Photolyase Mutants with Impaired DNA Repair Activity. *Photochem Photobiol*. 2017, 93(1):304-314. PMID: 27992645

2016

- (52) Müller A, Berkmann JC, **Scheerer P**, Biebermann H, Kleinau G. Insights into Basal Signaling Regulation, Oligomerization, and Structural Organization of the Human G-Protein Coupled Receptor 83. *PLoS One*. 2016, 11(12):e0168260. PMID: 27936173
- (51) Banthiya S, Kalms J, Yoga E, Ivanov I, Tauber R, Carpena X, Hamberg M, Kuhn H[§], **Scheerer P[§]**. Structural and functional basis of phospholipid oxygenase activity of bacterial lipoyxygenase from *Pseudomonas aeruginosa*. *Biochim Biophys Acta. (BBA) - Molecular and Cell Biology of Lipids* 2016, 1861(11):1681-1692. PMID: 27500637
- (50) Nagano S*, **Scheerer P***, Zubow K, Michael N, Inomata K, Lamparter T, Krauß N. The Crystal Structures of the N-Terminal Photosensory Core Module of *Agrobacterium* Phytochrome Agp1 as Parallel and Anti-parallel Dimers. *J Biol Chem*. 2016, 291(39):20674-91. PMID: 27466363
- (49) Kalms J, Schmidt A, Frielingsdorf S, van der Linden P, von Stetten D, Lenz O, Carpentier P, **Scheerer P[§]**. Krypton Derivatization of an O₂-Tolerant Membrane-Bound [NiFe] Hydrogenase Reveals a Hydrophobic Tunnel Network for Gas Transport. *Angew Chem Int Ed Engl*. 2016, 55(18):5586-5590. PMID: 26913499
- (48) Kalms J, Schmidt A, Frielingsdorf S, van der Linden P, von Stetten D, Lenz O, Carpentier P, **Scheerer P[§]**. Ein Netzwerk aus hydrophoben Tunneln zum Transport gasförmiger Reaktanten in einer O₂-

toleranten, membrangebundenen [NiFe]- Hydrogenase, aufgedeckt durch Derivatisierung mit Krypton. *Angewandte Chemie* 2016, 128(18):5676–5680. (not „peer-reviewed“)

- (47) Sprink T, Ramrath DJ, Yamamoto H, Yamamoto K, Loerke J, Ismer J, Hildebrand PW, **Scheerer P**, Bürger J, Mielke T, Spahn CM. Structures of ribosome-bound initiation factor 2 reveal the mechanism of subunit association. *Science Advances*. 2016, 2(3):e1501502. PMID: 26973877

2015

- (46) Yamamoto H, Collier M, Loerke J, Ismer J, Schmidt A, Hilal T, Sprink T, Yamamoto K, Mielke T, Bürger J, Shaikh TR, Dabrowski M, Hildebrand PW, **Scheerer P**, Spahn CM. Molecular architecture of the ribosome-bound Hepatitis C Virus internal ribosomal entry site RNA. *EMBO Journal*. 2015, 34(24):3042-3058. PMID: 26604301
- (45) Sommer ME, Elgeti M, Hildebrand PW, Szczepek M, Hofmann KP, **Scheerer P**. Structure-based biophysical analysis of the interaction of rhodopsin with G protein and arrestin. *Methods Enzymol*. 2015, 556:563-608. PMID: 25857800
- (44) Behrmann E, Loerke J, Budkevich TV, Yamamoto K, Schmidt A, Penczek PA, Vos MR, Bürger J, Mielke T, **Scheerer P**, Spahn CM. Structural snapshots of actively translating human ribosomes. *Cell* 2015, 161(4):845-857. PMID: 25957688
- (43) Velazquez Escobar F, Piwowarski P, Salewski J, Michael N, Fernandez Lopez M, Rupp A, **Scheerer P**, Bartl F, Frankenberg-Dinkel N, Siebert F, Mroginski MA, Hildebrandt P. A protonation-coupled feedback mechanism controls the signaling process in bathy phytochromes. *Nature Chemistry* 2015, 7(5):423-430. PMID: 2590182
- (42) Kazmin R, Rose A, Szczepek M, Elgeti M, Ritter E[§], Piechnick R, Hofmann KP, **Scheerer P**[§], Hildebrand PW, Bartl FJ[§]. The activation pathway of human rhodopsin in comparison to bovine rhodopsin. *J Biol Chem*. 2015, 290(33):20117-20127. PMID: 26105054
- (41) Rose AS, Zachariae U, Grubmüller H, Hofmann KP, **Scheerer P**, Hildebrand PW. Role of Structural Dynamics at the Receptor G Protein Interface for Signal Transduction. *PLoS One*. 2015, 10(11):e0143399. PMID: 26606751
- (40) Graf D, Wesslowski J, Ma H, **Scheerer P**, Krauß N, Oberpichler I, Zhang F, Lamparter T. Key Amino Acids in the Bacterial (6-4) Photolyase PhrB from *Agrobacterium fabrum*. *PLoS One*. 2015, 10(10):e0140955. PMID: 26489006
- (39) Siebert E, Rippers Y, Frielingsdorf S, Fritsch J, Schmidt A, Kalms J, Katz S, Lenz O, **Scheerer P**, Paasche L, Pelmenschikov V, Kuhlmann U, Mroginski MA, Zebger I, Hildebrandt P. Resonance Raman Spectroscopic Analysis of the [NiFe] Active Site and the Proximal [4Fe-3S] Cluster of an O₂-Tolerant Membrane-Bound Hydrogenase in the Crystalline State. *J Phys Chem B*. 2015, 119(43):13785-13796. PMID: 26201814
- (38) **Scheerer P**[§], Zhang F, Kalms J, von Stetten D, Krauß N, Oberpichler I, Lamparter T[§]. The class III cyclobutane pyrimidine dimer photolyase structure reveals a new antenna chromophore binding site and alternative photoreduction pathways. *J Biol Chem*. 2015, 290(18):11504-14. PMID: 25784552

2014


- (37) Szczepek M, Beyrière F, Hofmann KP, Elgeti M, Kazmin R, Rose A, Bartl FJ, von Stetten D, Heck M, Sommer ME, Hildebrand PW, **Scheerer P**[§]. Crystal structure of a common GPCR binding interface for G protein and arrestin. *Nature Communications* 2014, 5:4801. PMID: 25205354



F1000Prime article factor FFa=3

- (36) Rose AS, Elgeti M, Zachariae U, Grubmüller H, Hofmann KP, **Scheerer P**, Hildebrand PW. Position of Transmembrane Helix 6 Determines Receptor G Protein Coupling Specificity. *J Am Chem Soc.* 2014, 136(32):11244-11247. PMID: 25046433
- (35) Frielingsdorf S, Fritsch J, Schmidt A, Hammer M, Löwenstein J, Siebert E, Pelmeshnikov V, Jaenicke T, Kalms J, Rippers Y, Lenz O, Zebger I, Teutloff T, Kaupp M, Bittl R, Hildebrandt P, Friedrich B, Lenz O, **Scheerer P**[§]. Reversible [4Fe-3S] cluster morphing in an O₂-tolerant [NiFe] hydrogenase. *Nature Chemical Biology* 2014, 10(5):378-85. PMID: 24705592
- (34) Lamparter T, Zhang F, Graf D, Wesslowski J, Oberpichler I, Schünemann V, Krauß N, **Scheerer P**. A prokaryotic (6-4) photolyase with a DMRL chromophore and an iron sulfur cluster. *Encyclopedia of Inorganic and Bioinorganic Chemistry* 2014; 1-13. (book article)

2013

- (33) Kim YJ, Hofmann KP, Ernst OP, **Scheerer P**[§], Choe HW[§], Sommer ME[§]. Crystal structure of pre-activated arrestin p44. *Nature* 2013, 497 (7447):142-6. PMID: 23604253
-  F1000Prime article factor FFa=3
- (32) Zhang F*, **Scheerer P***, Oberpichler I, Lamparter T, Krauß N. Crystal structure of a prokaryotic (6-4) photolyase with an Fe-S cluster and a 6,7-dimethyl-8-ribityllumazine antenna chromophore. *Proc Natl Acad Sci U S A* 2013, 110 (18):7217-22. PMID: 23589886
- (31) Salewski J, Velazquez Escobar F, Kaminski S, von Stetten D, Keidel A, Rippers Y, Michael N, **Scheerer P**, Piwowarski P, Bartl F, Frankenberg-Dinkel N, Ringsdorf S, Gaertner W, Lamparter T, Mroginski MA, Hildebrandt P. The structure of the biliverdin cofactor in the Pfr state of bathy and prototypical phytochromes. *J Biol Chem.* 2013, 288(23):16800-14. PMID: 23603902
- (30) Qureshi BM, Hofmann NE, Arroyo-Olarte RD, Nickl B, Hoehne W, Jungblut PR, Lucius R, **Scheerer P**[§], Gupta N[§]. Dynein light chain 8a of *Toxoplasma gondii*, a unique conoid-localized β -strand-swapped homodimer, is required for an efficient parasite growth. *FASEB J.* 2013, 27(3):1034-47. PMID: 23233536
- (29) Horn T, Ivanov I, Di Venere A, Kakularam KR, Reddanna P, Conrad ML, Richter C, **Scheerer P**, Kuhn H. Molecular basis for the catalytic inactivity of a naturally occurring near-null variant of human ALOX15. *Biochim Biophys Acta. (BBA) - Molecular and Cell Biology of Lipids* 2013, 1831(12):1702-1713. PMID: 23958500

2012

- (28) Ramrath D, Yamamoto H, Rother K, Wittek D, Pech M, Mielke T, Loerke J, **Scheerer P**, Ivanov P, Teraoka Y, Shpanchenko O, Nierhaus K, Spahn CM. The complex of tmRNA•SmpB and EF-G on translocating ribosomes. *Nature* 2012, 485(7399):526-9. PMID: 22622583



F1000Prime article factor FFa=2


- (27) Piechnick R, Ritter E, Hildebrand PW, Ernst OP, **Scheerer P**, Hofmann KP, Heck M. The effect of channel mutations on the uptake and release of the retinal ligand in opsin. *Proc Natl Acad Sci U S A* 2012, 109(14):5247-52. PMID: 2243161

2011

- (26) Fritsch J*, **Scheerer P***,[§] Frielingsdorf S, Kroschinsky S, Friedrich B, Lenz O[§], Spahn CM[§]. The crystal structure of an oxygen-tolerant hydrogenase uncovers a novel iron-sulphur centre. *Nature* 2011, 479(7372):249-52. PMID: 22002606



F1000Prime article factor FFa=8

- (25) Ivanov I, Di Venere A, Horn T, **Scheerer P**, Nicolai E, Stehling S, Richter C, Skrzypczak-Jankun E, Mei G, Maccarrone M, Kühn H. Tight association of N-terminal and catalytic subunits of rabbit 12/15-lipoxygenase is important for protein stability and catalytic activity. *Biochim Biophys Acta. (BBA) - Molecular and Cell Biology of Lipids* 2011, 1811(12):1001-10. PMID: 21875687
- (24) Elgeti M, Kazmin R, Heck M, Morizumi T, Ritter E, **Scheerer P**, Ernst OP, Siebert F, Hofmann KP, Bartl FJ. Conserved Tyr223^{5,58} plays different roles in the activation and G-protein interaction of rhodopsin. *J Am Chem Soc.* 2011, 133(18):7159-65. PMID: 21506561
- (23) Choe HW, Kim YJ, Park JH, Morizumi T, Pai EF, Krauß N, Hofmann KP, **Scheerer P**, Ernst OP. Crystal structure of Metarhodopsin II. *Nature* 2011, 471(7340):651-5. PMID: 2138998
-  F1000Prime article factor FFa=1
- (22) Zhou X, Keller R, Volkmer R, Krauß N, **Scheerer P**^s, Hunke S^s. Structural basis for two-component system inhibition and pilus sensing by the auxiliary CpxP protein. *J Biol Chem.* 2011, 286(11):9805-14. PMID: 21239493



2010

- (21) **Scheerer P**, Michael N, Park JH, Nagano S, Choe H-W, Inomata K, Borucki B, Krauß N, Lamparter T. Light induced conformational changes of the chromophore and the protein in phytochromes: bacterial phytochromes as model systems. *ChemPhysChem* 2010, 11 (6): 1090-1105. PMID: 20373318
- (20) Winter G, Dökel S, Jones AK, **Scheerer P**, Krauß N, Höhne W, Friedrich B. Crystallization and preliminary X-ray crystallographic analysis of the [NiFe] hydrogenase maturation factor HypF1 from *Ralstonia eutropha* H16. *Acta Crystallogr Sect F Struct Biol Cryst Commun.* 2010, 66 (Pt 4):452-455. PMID: 20383020
- (19) Piwowarski P, Ritter E, Hofmann KP, Hildebrandt P, von Stetten D, **Scheerer P**, Michael N, Lamparter T, Bartl F. Light Induced Activation of Bacterial Phytochrome Agp1 Monitored by Static and Time Resolved FTIR Spectroscopy, *ChemPhysChem* 2010, 19 (1):35-48. PMID: 19849721
- (18) Knobloch D, Schmidt A, **Scheerer P**, Krauss N, Wessner H, Scholz C, Küttner G, von Rintelen T, Wessel A, Höhne W. A coleopteran triosephosphate isomerase: X-ray structure and phylogenetic impact of insect sequences. *Insect Mol Biol.* 2010, 19 (1):35-48. PMID: 19849721

2009

- (17) Hofmann KP, **Scheerer P**, Hildebrand PW, Choe HW, Park JH, Heck M, Ernst OP. A G protein-coupled receptor at work: the rhodopsin model. *Trends Biochem Sci.* 2009, 34 (11):540-552. PMID: 19836958
- (16) **Scheerer P**^{*}, Heck M^{*}, Goede A, Park JH, Choe HW, Ernst OP, Hofmann KP, Hildebrand PW. Structural and kinetic modeling of an activating helix switch in the rhodopsin-transducin interface. *Proc Natl Acad Sci U S A* 2009, 106 (26):10660-10665. PMID: 19541654
- (15) Mroginski MA, von Stetten D, Escobar FV, Strauss HM, Kaminski S, **Scheerer P**, Günther M, Murgida DH, Schmieder P, Bongards C, Gärtner W, Mailliet J, Hughes J, Essen LO, Hildebrandt P. Chromophore structure of cyanobacterial phytochrome Cph1 in the Pr state: reconciling structural and spectroscopic data by QM/MM calculations. *Biophys J.* 2009, 96 (10):4153-4163. PMID: 19450486
- (14) Hildebrand PW^{*}, **Scheerer P**^{*}, Park JH, Choe HW, Piechnick R, Ernst OP, Hofmann KP, Heck M. A ligand channel through the G protein coupled receptor opsin. *PLoS One* 2009; 4 (2): e4382. PMID: 19194506

2008

- (13) **Scheerer P***, Park JH*, Hildebrand PW, Kim YJ, Krauss N, Choe HW, Hofmann KP, Ernst OP. Crystal structure of opsin in its G-protein-interacting conformation. *Nature* 2008, 455 (7212):497-502. PMID: 18818650
-  F1000Prime article factor FFa=6
- (12) Park JH*, **Scheerer P***, Hofmann KP, Choe HW, Ernst OP. Crystal structure of the ligand-free G-protein-coupled receptor opsin. *Nature* 2008, 454 (7201):183-187. PMID: 18563085
-  F1000 article factor FFa=9
- (11) von Stetten D, Günther M, **Scheerer P**, Murgida DH, Mroginski MA, Krauss N, Lamparter T, Zhang J, Anstrom DM, Vierstra RD, Forest KT, Hildebrandt P. Chromophore heterogeneity and photoconversion in phytochrome crystals and solution studied by resonance Raman spectroscopy. *Angew Chem Int Ed Engl.* 2008; 47 (25):4753-4755. PMID: 1848457
- (10) von Stetten D, Günther M, **Scheerer P**, Murgida DH, Mroginski MA, Krauß, N, Lamparter T, Zhang J, Anstrom DM, Vierstra RD, Forest KT, Hildebrandt P. Resonanz-Raman-spektroskopische Untersuchung der Chromophorheterogenität und Photokonversion von Phytochromkristallen und –lösungen. *Angewandte Chemie* 2008; 120, 4831-4833. (not „peer-reviewed“)
- (9) Krauss N, Wessner H, Welfle K, Welfle H, Scholz C, Seifert M, Zubow K, Aÿ J, Hahn M, **Scheerer P**, Skerra A, Höhne W. The structure of the anti-c-myc antibody 9E10 Fab fragment/epitope peptide complex reveals a novel binding mode dominated by the heavy chain hypervariable loops. *Proteins* 2008, 73 (3):552-565. PMID: 18473392

2007

- (8) **Scheerer P**, Kramer A, Otte L, Seifert M, Wessner H, Scholz C, Krauss N, Schneider-Mergener J, Höhne W. Structure of an anti-cholera toxin antibody Fab in complex with an epitope-derived D-peptide: a case of polyspecific recognition. *J Mol Recognit.* 2007, 20 (4):263-274. PMID: 17712773
- (7) **Scheerer P**, Borchert A, Krauss N, Wessner H, Gerth C, Höhne W, Kuhn H. Structural basis for catalytic activity and enzyme polymerization of phospholipid hydroperoxide glutathione peroxidase-4 (GPx4). *Biochemistry* 2007, 46 (31):9041-9049. PMID: 17630701
- (6) von Stetten D, Seibeck S, Michael N, **Scheerer P**, Mroginski MA, Murgida DH, Krauss N, Heyn MP, Hildebrandt P, Borucki B, Lamparter T. Highly conserved residues Asp-197 and His-250 in Agp1 phytochrome control the proton affinity of the chromophore and Pfr formation. *J Biol Chem.* 2007, 282 (3):2116-2123. PMID: 17121858

2006

- (5) Park JH, Pulvermüller A, **Scheerer P**, Rausch S, Giessl A, Höhne W, Wolfrum U, Hofmann KP, Ernst OP, Choe HW, Krauss N. Insights into functional aspects of centrins from the structure of N-terminally extended mouse centrin 1. *Vision Res.* 2006, 46 (27):4568-4574. PMID: 17027898
- (4) Inomata K, Noack S, Hammam MA, Khawn H, Kinoshita H, Murata Y, Michael N, **Scheerer P**, Krauss N, Lamparter T. Assembly of synthetic locked chromophores with agrobacterium phytochromes Agp1 and Agp2. *J Biol Chem.* 2006, 281 (38):28162-28173. PMID: 16803878
- (3) **Scheerer P***, Michael N*, Park JH*, Noack S, Förster C, Hammam MA, Inomata K, Choe HW, Lamparter T, Krauss N. Crystallization and preliminary X-ray crystallographic analysis of the N-

terminal photosensory module of phytochrome Agp1, a biliverdin-binding photoreceptor from *Agrobacterium tumefaciens*. *J Struct Biol*. 2006, 153 (1):97-102. PMID: 16377207

2005

- (2) Park JH, Krauss N, Pulvermüller A, **Scheerer P**, Höhne W, Giessl A, Wolfrum U, Hofmann KP, Ernst OP, Choe HW. Crystallization and preliminary X-ray studies of mouse centrin1. *Acta Crystallogr Sect F Struct Biol Cryst Commun*. 2005, 61 (Pt 5):510-513. PMID: 16511082

2004

- (1) Hilpert K, Wessner H, Scholz C, **Scheerer P**, Volkmer-Engert R, Krauß N. Crystallization and preliminary x-ray analysis of complexes of porcine pancreatic elastase with two natural inhibitors. *Protein Pept Lett*. 2004, 11 (4):393-399. PMID: 15327373

Submitted manuscripts

(5) Schmidt M, Sauthof L, Szczepek M, Lopez M, Velázquez F, Qureshi B, Michael N, Buhrke D, Stevens T, Kwiatkowski D, von Stetten D, Mroginski MA, Krauß N, Lamparter T, Hildebrandt P, **Scheerer P**[§]. Structural snapshot of a bacterial phytochrome in its functional intermediate state. **2018**, under review.

(4) Fudim R, Szczepek M, Vierock J, Vogt A, Schmidt A, Kleinau G, Fischer P, Bartl F, **Scheerer P**[§], Hegemann P[§]. Design of a light-gated proton channel based on a high-resolution structure of *Coccomyxa rhodopsin*. **2018**, submitted.

(3) Dembny P, Newman A, Singh M, Hinz M, Szczepek M, Krüger C, Adalbert R, al-Dzaye O, Trimbuch T, Wallach T, Kleinau G, Derkow K, Schipke C, Scheiderei C, Golenbock D, Peters O, Coleman M, **Scheerer P**, Tarabykin V, Ruprecht K, Izsvak Z, Mayer J, Lehnardt S. Human endogenous retrovirus HERV-K(HML-2) RNA causes neurodegeneration through Toll-like receptors. **2018**, submitted.

(2) Klein W, Rutz C, Eckhard J, Provinciael B, Specker E, Neuenschwander M, Kleinau G, **Scheerer P**, von Kries JP, Nazare M, Vermeire K, Schüle R. Use of a sequential high throughput screening assay to identify novel inhibitors of the eucaryotic Sec61 translocon pathway. **2018**, under review.

(1) Biebermann H, Kleinau G, Schnabel D, Bockenbauer D, Wilson LC, Tully I, Kiff S, **Scheerer P**, Reyes M, Paisdzior S, Gregory JW, Allgrove J, Krude H, Mannstadt M, Gardella TJ, Dattani M, Jüppner H, Grüters A. A new multi-system disorder caused by a novel *Gas* mutation **2018**, under review.

Awards and press releases

- 2016** **Spotlight on Science** at European Synchrotron Radiation Facility (ESRF), Grenoble, France –
“High-pressure cryocooling of protein crystals reveals gas transport channels in a hydrogen-converting enzyme”
- 2015** **ESRF HIGHLIGHT 2014 in structural biology** at European Synchrotron Radiation Facility ESRF, Grenoble,
France – Article: “Crystal structure of a common GPCR binding interface for G protein and arrestin”
- 2014** **Hohe Platzierungen für Dr. Patrick Scheerer im Zitations-Ranking des Laborjournals zum Thema
"Proteinforschung": Publikationsanalyse des Laborjournals (Stichtag 19.05.2014) zum Thema
"Proteinforschung" im Zeitraum von 2008-2012 für den gesamten deutschsprachigen Raum
Platz 7 und 9** unter den „meistzitierten Artikeln“
und **Platz 28** mit insgesamt 1510 Zitationen bei 17 gezählten Publikationen unter den „meistzitierten Köpfen“
- 2014** **ESRF HIGHLIGHT 2013 in structural biology** at European Synchrotron Radiation Facility ESRF, Grenoble,
France – “Crystal structure of pre-activated arrestin p44” – Article: “How arrestin is activated for GPCR binding”
- 2013** **Webpresentation am Helmholtz-Zentrum Berlin (HZB)** - Das Zentrum im Überblick - Gesundheitsforschung –
„Wie Proteine das Sehen steuern“
- 2013** **Interview** in der Druckschrift des Helmholtz Zentrums Berlin, Lichtblick: "Wie Proteine das Sehen steuern"
- 2012** **Spotlight on Science** at European Synchrotron Radiation Facility (ESRF), Grenoble, France – “How an oxygen-
tolerant hydrogenase protects itself from oxygen”
- 2012** **Interview – Special** – Laborpraxis – “Dem Sauerstoff trotzen – Hydrogenasen als Wasserstoffproduzenten”
- 2011** **Current research highlight in structural biology** at European Synchrotron Radiation Facility ESRF, Grenoble,
France – “The crystal structure of an oxygen-tolerant hydrogenase uncovers a novel iron-sulphur centre”
- 2011** **Interview** – Biotechnologie.de – “Sehrezceptor in Aktion geblitzt“
- 2011** **Structure of the Month** at Bessy II -Helmholtz Zentrum Berlin – “Crystal structure of Metarhodopsin II”
- 2009** **First poster award** – Helmholtz Zentrum Berlin User Meeting at Bessy II, Germany
- 2008** **Interview** – Biotechnologie.de – “Strukturbiologischer Schnappschuss vom Sehen”
- 2008** **Poster award** – Jahrestagung der DGfB (Deutsche Gesellschaft für Biophysik) in Berlin, Germany
- 2008** **Interview** –Sichtbar (Ausgabe 03) – Magazin der Helmholtz-Zentrum Berlin für Materialien und Energie GmbH
“Rhodopsin – Sehen wie man sieht - Aktive Proteinkristalle”
- 2005** **Shared second poster award** – GBM-Tagung (Gesellschaft für Biochemie und Molekularbiologie) in Berlin,
Germany
- 2003** **First poster award** – 2.Studententag der Diplomanden und Doktoranden der Lebenswissenschaften in Berlin,
Germany
- 2003** **First poster award** – 11.Jahrestagung der DGK (Deutsche Gesellschaft für Kristallographie) in Berlin, Germany