

## Supplementary Data: Database Reference List

The data for the label-database is extracted from the following 120 publications:

### Reference List

- [**Akyuz et al. 2013**] Akyuz, Nurunisa, Roger B. Altman, Scott C. Blanchard, and Olga Boudker (2013). “Transport dynamics in a glutamate transporter homologue”. In: *Nature* 502.7469, pp. 114–118.
- [**Akyuz et al. 2015**] Akyuz, Nurunisa, Elka R Georgieva, Zhou Zhou, Sebastian Stolzenberg, Michel A Cuendet, George Khelashvili, Roger B Altman, Daniel S Terry, Jack H Freed, Harel Weinstein, Olga Boudker, and Scott C Blanchard (2015). “Transport domain unlocking sets the uptake rate of an aspartate transporter”. In: *Nature* 518.7537, pp. 68–73.
- [**Andreou and Klostermeier 2014**] Andreou, Alexandra Zoi and Dagmar Klostermeier (2014). “EIF4B and eIF4G jointly stimulate eIF4A ATPase and unwinding activities by modulation of the eIF4A conformational cycle”. In: *Journal of Molecular Biology* 426.1, pp. 51–61.
- [**Bavishi et al. 2018**] Bavishi, Krutika, Darui Li, Stine Eiersholt, Emma N. Hooley, Troels C. Petersen, Birger Lindberg Møller, Nikos S. Hatzakis, and Tomas Laursen (2018). “Direct observation of multiple conformational states in Cytochrome P450 oxidoreductase and their modulation by membrane environment and ionic strength”. In: *Scientific Reports* 8.1, pp. 1–9.
- [**Boer et al. 2019a**] Boer, Marijn de, Giorgos Gouridis, Yusran Abdillah Muthahari, and Thorben Cordes (2019a). “Single-Molecule Observation of Ligand Binding and Conformational Changes in FeuA”. In: *Biophysical Journal* 117.9, pp. 1642–1654.
- [**Boer et al. 2019b**] Boer, Marijn de, Giorgos Gouridis, Ruslan Vietrov, Stephanie L Begg, Gea K Schuurman-Wolters, Florence Husada, Nikolaos Eleftheriadis, Bert Poolman, Christopher A McDevitt, and Thorben Cordes (2019b). “Conformational and dynamic plasticity in substrate-binding proteins underlies selective transport in ABC importers”. In: *eLife* 8. Ed. by Richard Aldrich, Baron Chanda, Baron Chanda, and Marcel P Goldschen-Ohm, e44652.
- [**Bohr and Hatzakis 2018**] Bohr, Freja and Nikos Hatzakis (2018). “Structural dynamics of Cpf1 by FRET”. In: *UCPH NanoScience - a student research journal* 2.201804 11pp.
- [**Cao et al. 2018**] Cao, Can, Qiuxiang Tan, Chanjuan Xu, Lingli He, Linlin Yang, Ye Zhou, Yiwei Zhou, Anna Qiao, Minmin Lu, Cuiying Yi, Gye Won Han, Xianping Wang, Xuemei Li, Huaiyu Yang, Zihe Rao, Hualiang Jiang, Yongfang Zhao, Jianfeng Liu, Raymond C. Stevens, Qiang Zhao, Xuejun C. Zhang, and Beili Wu (2018). “Structural basis for signal recognition and transduction by platelet-activating-factor receptor”. In: *Nature Structural and Molecular Biology* 25.6, pp. 488–495.

- [**Carrillo et al. 2019**] Carrillo, Elisa, Sana A Shaikh, Vladimir Berka, Ryan J Durham, Douglas B Litwin, Garam Lee, David M MacLean, Linda M Nowak, and Vasanthi Jayaraman (2019). “Mechanism of modulation of AMPA receptors by TARP- $\gamma 8$ ”. In: *Journal of General Physiology* 152.1.
- [**Cerminara et al. 2020**] Cerminara, Michele, Antonie Schöne, Ilona Ritter, Matteo Gabba, and Jörg Fitter (2020). “Mapping Multiple Distances in a Multidomain Protein for the Identification of Folding Intermediates”. In: *Biophysical Journal* 118.3, pp. 688–697.
- [**Chen et al. 2017**] Chen, Yang, Lei Zhang, Laura Graf, Bing Yu, Yue Liu, Georg Kochs, Yongfang Zhao, and Song Gao (2017). “Conformational dynamics of dynamin-like MxA revealed by single-molecule FRET”. In: *Nature Communications* 8.1, p. 15744.
- [**Cheng et al. 2020**] Cheng, Ricky C, Ayush Krishnamoorti, Vladimir Berka, Ryan J Durham, Vasanthi Jayaraman, and Merritt Maduke (2020). “Single-molecule FRET monitors CLC transporter conformation and subunit independence”. In: *bioRxiv*, p. 2020.09.07.28683
- [**Ciftci et al. 2020**] Ciftci, Didar, Gerard H M Huysmans, Xiaoyu Wang, Changhao He, Daniel Terry, Zhou Zhou, Gabriel Fitzgerald, Scott C Blanchard, and Olga Boudker (2020). “Single-molecule transport kinetics of a glutamate transporter homolog shows static disorder”. In: *Science Advances* 6.22, eaaz1949.
- [**Comstock et al. 2015**] Comstock, Matthew J., Kevin D. Whitley, Haifeng Jia, Joshua Sokoloski, Timothy M. Lohman, Taekjip Ha, and Yann R. Chemla (2015). “Direct observation of structure-function relationship in a nucleic acid -processing enzyme”. In: *Science* 348.6232, pp. 352–354.
- [**Cooper et al. 2015**] Cooper, David R., Drew M. Dolino, Henriette Jaurich, Bo Shuang, Swarna Ramaswamy, Caitlin E. Nurik, Jixin Chen, Vasanthi Jayaraman, and Christy F. Landes (2015). “Conformational Transitions in the Glycine-Bound GluN1 NMDA Receptor LBD via Single-Molecule FRET”. In: *Biophysical Journal* 109.1, pp. 66–75.
- [**Craggs et al. 2019**] Craggs, Timothy D, Marko Sustarsic, Anne Plochowitz, Majid Mosayebi, Hendrik Kaju, Andrew Cuthbert, Johannes Hohlbein, Laura Domicieva, Philip C Biggin, Jonathan P K Doye, and Achillefs N Kapanidis (2019). “Substrate conformational dynamics facilitate structure-specific recognition of gapped DNA by DNA polymerase”. eng. In: *Nucleic acids research* 47.20, pp. 10788–10800.
- [**Dai et al. 2016**] Dai, Yawei, Markus Seeger, Jingwei Weng, Song Song, Wenning Wang, and Yan-Wen Tan (2016). “Lipid Regulated Intramolecular Conformational Dynamics of SNARE-Protein Ykt6”. In: *Scientific Reports* 6.1, p. 30282.
- [**Dimura et al. 2016**] Dimura, Mykola, Thomas O Peulen, Christian A Hanke, Aiswaria Prakash, Holger Gohlke, and Claus A M Seidel (2016). “Quantitative FRET studies and integrative modeling unravel the structure and dynamics of biomolecular systems”. In: *Current Opinion in Structural Biology* 40, pp. 163–185.
- [**Dolino et al. 2016**] Dolino, Drew M., Soheila Rezaei Adariani, Sana A. Shaikh, Vasanthi Jayaraman, and Hugo Sanabria (2016). “Conformational selection and submillisecond

- dynamics of the ligand-binding domain of the N-methyl-D-aspartate receptor”. In: *Journal of Biological Chemistry* 291.31, pp. 16175–16185.
- [**Dolino et al. 2017**] Dolino, Drew M, Sudeshna Chatterjee, David M MacLean, Charlotte Flatebo, Logan D C Bishop, Sana A Shaikh, Christy F Landes, and Vasanthi Jayaraman (2017). “The structure–energy landscape of NMDA receptor gating”. In: *Nature Chemical Biology* 13.12, pp. 1232–1238.
- [**Dollinger 2018**] Dollinger, Peter (2018). “Lipase-specific foldase-aided folding of Lipase A from *Pseudomonas aeruginosa*”. PhD thesis. HHU Düsseldorf.
- [**Durham et al. 2020**] Durham, Ryan J, Nabina Paudyal, Elisa Carrillo, Nidhi Kaur Bhatia, David M Maclean, Vladimir Berka, Drew M Dolino, Alemayehu A Gorfe, and Vasanthi Jayaraman (2020). “Conformational spread and dynamics in allostery of NMDA receptors”. In: *Proceedings of the National Academy of Sciences* 117.7, 3839 LP –3847.
- [**Dyla et al. 2017**] Dyla, Mateusz, Daniel S. Terry, Magnus Kjaergaard, Thomas L.M. Sørensen, Jacob Lauwring Andersen, Jens Peter Andersen, Charlotte Rohde Knudsen, Roger B. Altman, Poul Nissen, and Scott C. Blanchard (2017). “Dynamics of P-type ATPase transport revealed by single-molecule FRET”. In: *Nature* 551.7680, pp. 346–351.
- [**Erkens et al. 2013**] Erkens, Guus B, Inga Hänelt, Joris M H Goudsmits, Dirk Jan Slotboom, and Antoine M van Oijen (2013). “Unsynchronised subunit motion in single trimeric sodium-coupled aspartate transporters”. In: *Nature* 502.7469, pp. 119–123.
- [**Feng et al. 2016**] Feng, Yitao, Lu Zhang, Shaowen Wu, Zhijun Liu, Xin Gao, Xu Zhang, Maili Liu, Jianwei Liu, Xuhui Huang, and Wenning Wang (2016). “Conformational Dynamics of apo-GlnBP Revealed by Experimental and Computational Analysis”. In: *Angewandte Chemie - International Edition* 55.45, pp. 13990–13994.
- [**Fijen et al. 2020**] Fijen, Carel, Mariam M. Mahmoud, Meike Kronenberg, Rebecca Kaup, Mattia Fontana, Jamie B. Towle-Weicksel, Joann B. Sweasy, and Johannes Hohlbein (2020). “Using single-molecule FRET to probe the nucleotide-dependent conformational landscape of polymerase  $\beta$ -DNA complexes”. In: *The Journal of biological chemistry* 295.27, pp. 9012–9020.
- [**Fitzgerald et al. 2019**] Fitzgerald, Gabriel A, Daniel S Terry, Audrey L Warren, Matthias Quick, Jonathan A Javitch, and Scott C Blanchard (2019). “Quantifying secondary transport at single-molecule resolution”. In: *Nature* 575.7783, pp. 528–534.
- [**Flynn et al. 2010**] Flynn, E. Megan, Jeffrey A. Hanson, Tom Alber, and Haw Yang (2010). “Dynamic active-site protection by the M. tuberculosis protein tyrosine phosphatase PtpB lid domain”. In: *Journal of the American Chemical Society* 132.13, pp. 4772–4780.
- [**Gabba et al. 2014**] Gabba, Matteo, Simón Poblete, Tobias Rosenkranz, Alexandros Katranidis, Daryan Kempe, Tina Züchner, Roland G. Winkler, Gerhard Gompfer, and Jörg Fitter (2014). “Conformational state distributions and catalytically relevant

- dynamics of a hinge-bending enzyme studied by single-molecule fret and a coarse-grained simulation”. In: *Biophysical Journal* 107.8, pp. 1913–1923.
- [**Gadkari et al. 2018**] Gadkari, Varun V, Sophie R Harvey, Austin T Raper, Wen-Ting Chu, Jin Wang, Vicki H Wysocki, and Zucui Suo (2018). “Investigation of sliding DNA clamp dynamics by single-molecule fluorescence, mass spectrometry and structure-based modeling”. eng. In: *Nucleic acids research* 46.6, pp. 3103–3118.
- [**Gahl et al. 2014**] Gahl, Robert F, Yi He, Shiqin Yu, and Nico Tjandra (2014). “Conformational rearrangements in the pro-apoptotic protein, Bax, as it inserts into mitochondria: a cellular death switch”. eng. In: *The Journal of biological chemistry* 289.47, pp. 32871–32882.
- [**Gahl, Tekle, and Tjandra 2014**] Gahl, Robert F., Ephrem Tekle, and Nico Tjandra (2014). “Single color FRET based measurements of conformational changes of proteins resulting from translocation inside cells”. In: *Methods* 66.2, pp. 180–187.
- [**Glaenzer et al. 2017**] Glaenzer, Janin, Martin F. Peter, Gavin H. Thomas, and Gregor Hagelueken (2017). “PELDOR Spectroscopy Reveals Two Defined States of a Sialic Acid TRAP Transporter SBP in Solution”. In: *Biophysical Journal* 112.1, pp. 109–120.
- [**Goudsmits, Slotboom, and Oijen 2017**] Goudsmits, Joris M H, Dirk Jan Slotboom, and Antoine M van Oijen (2017). “Single-molecule visualization of conformational changes and substrate transport in the vitamin B12 ABC importer BtuCD-F”. In: *Nature Communications* 8.1, p. 1652.
- [**Gouridis et al. 2019**] Gouridis, Giorgos, Bianca Hetzert, Kristin Kiosze-Becker, Marijn de Boer, Holger Heinemann, Elina Nürenberg-Goloub, Thorben Cordes, and Robert Tampé (2019). “ABCE1 Controls Ribosome Recycling by an Asymmetric Dynamic Conformational Equilibrium”. In: *Cell Reports* 28.3, 723–734.e6.
- [**Gouridis et al. 2015**] Gouridis, Giorgos, Gea K Schuurman-Wolters, Evelyn Ploetz, Florence Husada, Ruslan Vietrov, Marijn de Boer, Thorben Cordes, and Bert Poolman (2015). “Conformational dynamics in substrate-binding domains influences transport in the ABC importer GlnPQ”. In: *Nat Struct Mol Biol* 22.1, pp. 57–64.
- [**Gregorio et al. 2017**] Gregorio, G. Glenn, Matthieu Masurel, Daniel Hilger, Daniel S. Terry, Manuel Juette, Hong Zhao, Zhou Zhou, Jose Manuel Perez-Aguilar, Maria Hauge, Signe Mathiasen, Jonathan A. Javitch, Harel Weinstein, Brian K. Kobilka, and Scott C. Blanchard (2017). “Single-molecule analysis of ligand efficacy in  $\beta$ 2AR-G-protein activation”. In: *Nature* 547.7661, pp. 68–73.
- [**Grohmann et al. 2010**] Grohmann, Dina, Daniel Klose, Johann P. Klare, Christopher W.M. Kay, Heinz Jürgen Steinhoff, and Finn Werner (2010). “RNA-binding to archaeal RNA polymerase subunits F/E: A DEER and FRET study”. In: *Journal of the American Chemical Society* 132.17, pp. 5954–5955.
- [**Han et al. 2017**] Han, Lei, Yongping Zhu, Min Liu, Ye Zhou, Guangyuan Lu, Lan Lan, Xianping Wang, Yongfang Zhao, and Xuejun C. Zhang (2017). “Molecular mechanism

- of substrate recognition and transport by the AtSWEET13 sugar transporter”. In: *Proceedings of the National Academy of Sciences of the United States of America* 114.38, pp. 10089–10094.
- [**Hanson et al. 2007**] Hanson, Jeffrey A., Karl Duderstadt, Lucas P. Watkins, Sucharita Bhattacharyya, Jason Brokaw, Jhih Wei Chu, and Haw Yang (2007). “Illuminating the mechanistic roles of enzyme conformational dynamics”. In: *Proceedings of the National Academy of Sciences of the United States of America* 104.46, pp. 18055–18060.
- [**He et al. 2015**] He, Yufan, Mohammad Mahfuzul Haque, Dennis J Stuehr, and H Peter Lu (2015). “Single-molecule spectroscopy reveals how calmodulin activates NO synthase by controlling its conformational fluctuation dynamics”. In: *Proceedings of the National Academy of Sciences* 112.38, 11835 LP –11840.
- [**He, Lu, and Lu 2013**] He, Yufan, Maolin Lu, and H. Peter Lu (2013). “Single-molecule photon stamping FRET spectroscopy study of enzymatic conformational dynamics”. In: *Physical Chemistry Chemical Physics* 15.3, pp. 770–775.
- [**Heiss et al. 2019**] Heiss, Gregor, Evelyn Ploetz, Lena Voith von Voithenberg, Ramya Viswanathan, Samson Glaser, Peter Schluesche, Sushi Madhira, Michael Meisterernst, David T. Auble, and Don C. Lamb (2019). “Conformational changes and catalytic inefficiency associated with Mot1-mediated TBP-DNA dissociation”. In: *Nucleic acids research* 47.6, pp. 2793–2806.
- [**Hellenkamp et al. 2017**] Hellenkamp, B, P Wortmann, F Kandzia, M Zacharias, and T Hugel (2017). “Multi-domain structure and correlated dynamics determined by self-consistent FRET networks”. In: *Nature methods* 14.2, pp. 174–180.
- [**Hellenkamp et al. 2018**] Hellenkamp, Björn, Johann Thurn, Martina Stadlmeier, and Thorsten Hugel (2018). “Kinetics of Transient Protein Complexes Determined via Diffusion-Independent Microfluidic Mixing and Fluorescence Stoichiometry”. In: *Journal of Physical Chemistry B* 122.49, pp. 11554–11560.
- [**Höfig et al. 2018**] Höfig, Henning, Michele Cerminara, Ilona Ritter, Antonie Schöne, Martina Pohl, Victoria Steffen, Julia Walter, Ignacio Vergara Dal Pont, Alexandros Katranidis, and Jörg Fitter (2018). “Single-molecule studies on a FRET biosensor: Lessons from a comparison of fluorescent protein equipped versus dye-labeled species”. In: *Molecules* 23.12.
- [**Hohlbein et al. 2013**] Hohlbein, Johannes, Louise Aigrain, Timothy D Craggs, Oya Bermek, Olga Potapova, Pouya Shoolizadeh, Nigel D F Grindley, Catherine M Joyce, and Achillefs N Kapanidis (2013). “Conformational landscapes of DNA polymerase I and mutator derivatives establish fidelity checkpoints for nucleotide insertion”. In: *Nature Communications* 4.1, p. 2131.
- [**Husada et al. 2018**] Husada, Florence, Kiran Bountra, Konstantinos Tassis, Marijn de Boer, Maria Romano, Sylvie Rebuffat, Konstantinos Beis, and Thorben Cordes (2018). “Conformational dynamics of the ABC transporter McjD seen by single-molecule FRET”. In: *The EMBO Journal* 37.21, e100056.

- [Jazi et al. 2017] Jazi, Atieh Aminian, Evelyn Ploetz, Muhamad Arizki, Balasubramaniam Dhandayuthapani, Izabela Waclawska, Reinhard Krämer, Christine Ziegler, and Thorben Cordes (2017). “Caging and Photoactivation in Single-Molecule Förster Resonance Energy Transfer Experiments”. In: *Biochemistry* 56.14, pp. 2031–2041.
- [Joseph et al. 2011] Joseph, Benesh, Gunnar Jeschke, Birke A Goetz, Kaspar P Locher, and Enrica Bordignon (2011). “Transmembrane gate movements in the type II ATP-binding cassette (ABC) importer BtuCD-F during nucleotide cycle.” In: *The Journal of biological chemistry* 286.47, pp. 41008–17.
- [Kahra et al. 2011] Kahra, Dana, Michael Kovermann, Christian Löw, Verena Hirschfeld, Caroline Haupt, Jochen Balbach, and Christian Gerhard Hübner (2011). “Conformational Plasticity and Dynamics in the Generic Protein Folding Catalyst SlyD Unraveled by Single-Molecule FRET”. In: *Journal of Molecular Biology* 411.4, pp. 781–790.
- [Kempe et al. 2017] Kempe, Daryan, Michele Cerminara, Simón Poblete, Antonie Schöne, Matteo Gabba, and Jörg Fitter (2017). “Single-Molecule FRET Measurements in Additive-Enriched Aqueous Solutions”. In: *Analytical Chemistry* 89.1, pp. 694–702.
- [Kim et al. 2013a] Kim, Eunkyung, Sanghwa Lee, Aram Jeon, Jung Min Choi, Hee Seung Lee, Sungchul Hohng, and Hak Sung Kim (2013a). “A single-molecule dissection of ligand binding to a protein with intrinsic dynamics”. In: *Nature Chemical Biology* 9.5, pp. 313–318.
- [Kim et al. 2013b] Kim, Jiho, Moon-Hyeong Seo, Sangsik Lee, Kyukwang Cho, Aerin Yang, Kyunghwa Woo, Hak-Sung Kim, and Hee-Sung Park (2013b). “Simple and efficient strategy for site-specific dual labeling of proteins for single-molecule fluorescence resonance energy transfer analysis.” eng. In: *Analytical chemistry* 85.3, pp. 1468–1474.
- [Koh et al. 2018] Koh, Hye Ran, Rahul Roy, Maria Sorokina, Guo Qing Tang, Divya Nandakumar, Smita S. Patel, and Taekjip Ha (2018). “Correlating Transcription Initiation and Conformational Changes by a Single-Subunit RNA Polymerase with Near Base-Pair Resolution”. In: *Molecular Cell* 70.4, 695–706.e5.
- [König et al. 2015] König, Iwo, Arash Zarrine-Afsar, Mikayel Aznauryan, Andrea Soranno, Bengt Wunderlich, Fabian Dingfelder, Jakob C Stüber, Andreas Plückthun, Daniel Nettels, and Benjamin Schuler (2015). “Single-molecule spectroscopy of protein conformational dynamics in live eukaryotic cells”. In: *Nature Methods* 12.8, pp. 773–779.
- [Kriegsmann et al. 2009] Kriegsmann, J., M. Brehs, J. P. Klare, M. Engelhard, and J. Fitter (2009). “Sensory rhodopsin II/transducer complex formation in detergent and in lipid bilayers studied with FRET”. In: *Biochimica et Biophysica Acta - Biomembranes* 1788.2, pp. 522–531.
- [Lamboy et al. 2013] Lamboy, Jorge A, Hajin Kim, Holly Dembinski, Taekjip Ha, and Elizabeth A Komives (2013). “Single-Molecule FRET Reveals the Native-State Dynamics of the  $\text{I}\kappa\text{B}\alpha$  Ankyrin Repeat Domain”. In: *Journal of Molecular Biology* 425.14, pp. 2578–2590.

- [Lee et al. 2016] Lee, Taehyung C, Minjin Kang, Chan Hyuk Kim, Peter G Schultz, Eli Chapman, and Ashok A Deniz (2016). “Dual Unnatural Amino Acid Incorporation and Click-Chemistry Labeling to Enable Single-Molecule FRET Studies of p97 Folding”. eng. In: *Chembiochem : a European journal of chemical biology* 17.11, pp. 981–984.
- [Lehmann et al. 2020] Lehmann, Kathrin, Suren Felekyan, Ralf Kühnemuth, Mykola Dimura, Katalin Tóth, Claus A M Seidel, and Jörg Langowski (2020). “Dynamics of the nucleosomal histone H3 N-terminal tail revealed by high precision single-molecule FRET”. In: *Nucleic Acids Research* 48.3, pp. 1551–1571.
- [Litwin et al. 2019] Litwin, Douglas B, Elisa Carrillo, Sana A Shaikh, Vladimir Berka, and Vasanthi Jayaraman (2019). “The structural arrangement at intersubunit interfaces in homomeric kainate receptors”. In: *Scientific Reports* 9.1, p. 6969.
- [Litwin et al. 2020] Litwin, Douglas B, Nabina Paudyal, Elisa Carrillo, Vladimir Berka, and Vasanthi Jayaraman (2020). “The structural arrangement and dynamics of the heteromeric GluK2/GluK5 kainate receptor as determined by smFRET”. In: *Biochimica et Biophysica Acta (BBA) - Biomembranes* 1862.1, p. 183001.
- [Liu et al. 2018] Liu, Yanqing, Yue Liu, Lingli He, Yongfang Zhao, and Xuejun C. Zhang (2018). “Single-molecule fluorescence studies on the conformational change of the ABC transporter MsbA”. In: *Biophysics Reports* 4.3, pp. 153–165.
- [Lou et al. 2017] Lou, Fei, Jie Yang, Si Wu, and Sarah Perrett (2017). “A co-expression strategy to achieve labeling of individual subunits within a dimeric protein for single molecule analysis”. In: *Chemical Communications* 53.57, pp. 7986–7989.
- [Lu 2011] Lu, H. Peter (2011). “Revealing time bunching effect in single-molecule enzyme conformational dynamics”. In: *Physical Chemistry Chemical Physics* 13.15, pp. 6734–6749.
- [Majumdar et al. 2007] Majumdar, Devdoot S., Irina Smirnova, Vladimir Kasho, Eyal Nir, Xiangxu Kong, Shimon Weiss, and H. Ronald Kaback (2007). “Single-molecule FRET reveals sugar-induced conformational dynamics in LacY”. In: *Proceedings of the National Academy of Sciences of the United States of America* 104.31, pp. 12640–12645.
- [Mapa et al. 2010] Mapa, Koyeli, Martin Sikor, Volodymyr Kudryavtsev, Karin Waegemann, Stanislav Kalinin, Claus A M Seidel, Walter Neupert, Don C Lamb, and Dejana Mokranjac (2010). “The Conformational Dynamics of the Mitochondrial Hsp70 Chaperone”. In: *Molecular Cell* 38.1, pp. 89–100.
- [McCann et al. 2011] McCann, James J., Liqiang Zheng, Salvatore Chiantia, and Mark E. Bowen (2011). “Domain Orientation in the N-Terminal PDZ Tandem from PSD-95 Is Maintained in the Full-Length Protein”. In: *Structure* 19.6, pp. 810–820.
- [McCann et al. 2012] McCann, James J, Liqiang Zheng, Daniel Rohrbeck, Suren Felekyan, Ralf Kühnemuth, R Bryan Sutton, Claus A M Seidel, and Mark E Bowen (2012). “Supertertiary structure of the synaptic MAGuK scaffold proteins is con-

- served”. In: *Proceedings of the National Academy of Sciences* 109.39, 15775 LP – 15780.
- [**Medina et al. 2020**] Medina, Exequiel, Pablo Villalobos, George L. Hamilton, Elizabeth A. Komives, Hugo Sanabria, César A. Ramírez-Sarmiento, and Jorge Babul (2020). “Intrinsically disordered regions of the DNA-binding domain of human FoxP1 facilitate domain swapping”. In: *Journal of Molecular Biology*.
- [**Morrison et al. 2012**] Morrison, Emma A., Gregory T. Dekoster, Supratik Dutta, Reza Vafabakhsh, Michael W. Clarkson, Arjun Bahl, Dorothee Kern, Taekjip Ha, and Katherine A. Henzler-Wildman (2012). “Antiparallel EmrE exports drugs by exchanging between asymmetric structures”. In: *Nature* 481.7379, pp. 45–52.
- [**Myong et al. 2005**] Myong, Sua, Ivan Rasnik, Chirlmin Joo, Timothy M. Lohman, and Taekjip Ha (2005). “Repetitive shuttling of a motor protein on DNA”. In: *Nature* 437.7063, pp. 1321–1325.
- [**Orte et al. 2008**] Orte, Angel, Timothy D Craggs, Samuel S White, Sophie E Jackson, and David Klenerman (2008). “Evidence of an Intermediate and Parallel Pathways in Protein Unfolding from Single-Molecule Fluorescence”. In: *Journal of the American Chemical Society* 130.25, pp. 7898–7907.
- [**Peter et al. 2021**] Peter, Martin F, Christian Gebhardt, Janin Glaenger, Niels Schneberger, Marijn de Boer, Gavin H Thomas, Thorben Cordes, and Gregor Hagelueken (2021). “Triggering Closure of a Sialic Acid TRAP Transporter Substrate Binding Protein through Binding of Natural or Artificial Substrates”. In: *Journal of Molecular Biology* 433.3, p. 166756.
- [**Peter et al. 2020**] Peter, Martin F, Christian Gebhardt, Rebecca Mächtel, Janin Glaenger, Gavin H Thomas, Thorben Cordes, and Gregor Hagelueken (2020). “Cross-validation of distance measurements in proteins by PELDOR/DEER and single-molecule FRET”. In: *bioRxiv*, p. 2020.11.23.394080.
- [**Peulen, Opanasyuk, and Seidel 2017**] Peulen, Thomas-Otavio, Oleg Opanasyuk, and Claus A M Seidel (2017). “Combining Graphical and Analytical Methods with Molecular Simulations To Analyze Time-Resolved FRET Measurements of Labeled Macromolecules Accurately”. In: *The Journal of Physical Chemistry B* 121.35, pp. 8211–8241.
- [**Pliotas et al. 2012**] Pliotas, Christos, Richard Ward, Emma Branigan, Akiko Rasmussen, Gregor Hagelueken, Hexian Huang, Susan S Black, Ian R Booth, Olav Schiekmann, and James H Naismith (2012). “Conformational state of the MscS mechanosensitive channel in solution revealed by pulsed electron-electron double resonance (PELDOR) spectroscopy”. eng. In: *Proceedings of the National Academy of Sciences of the United States of America* 109.40, E2675–E2682.
- [**Quast et al. 2019**] Quast, Robert B, Fataneh Fatemi, Michel Kranendonk, Emmanuel Margeat, and Gilles Truan (2019). “Accurate Determination of Human CPR Confor-



- mational Equilibrium by smFRET Using Dual Orthogonal Noncanonical Amino Acid Labeling”. In: *ChemBioChem* 20.5, pp. 659–666.
- [**Ratzke, Hellenkamp, and Hugel 2014**] Ratzke, C., B. Hellenkamp, and T. Hugel (2014). “Four-colour FRET reveals directionality in the Hsp90 multicomponent machinery”. In: *Nature Communications* 5.May.
- [**Riederer et al. 2018**] Riederer, Erika A, Paul J Focke, Elka R Georgieva, Nurunisa Akyuz, Kimberly Matulef, Peter P Borbat, Jack H Freed, Scott C Blanchard, Olga Boudker, and Francis I Valiyaveetil (2018). “A facile approach for the in vitro assembly of multimeric membrane transport proteins”. In: *eLife* 7. Ed. by Kenton Jon Swartz, e36478.
- [**Rosam et al. 2018**] Rosam, Mathias, Daniela Krader, Christina Nickels, Janine Hochmair, Katrin C Back, Ganesh Agam, Anders Barth, Cathleen Zeymer, Jelle Hendrix, Markus Schneider, Iris Antes, Jochen Reinstein, Don C Lamb, and Johannes Buchner (2018). “Bap (Sll1) regulates the molecular chaperone BiP by coupling release of nucleotide and substrate”. In: *Nature Structural & Molecular Biology* 25.1, pp. 90–100.
- [**Rosenkranz et al. 2011**] Rosenkranz, Tobias, Ramona Schlesinger, Matteo Gabba, and Jörg Fitter (2011). “Native and unfolded states of phosphoglycerate kinase studied by single-molecule FRET”. In: *ChemPhysChem* 12.3, pp. 704–710.
- [**Roth et al. 2020**] Roth, Aurélie, Chloé Martens, Thomas van Oene, Anders Barth, Simon Wanninger, Don C Lamb, Jelle Hendrix, and Cédric Govaerts (2020). “Substrate binding modulates the conformational kinetics of the secondary multidrug transporter LmrP”. In: *bioRxiv*, p. 2020.04.09.034439.
- [**Sadler, Kapanidis, and Tucker 2016**] Sadler, Emma E., Achillefs N. Kapanidis, and Stephen J. Tucker (2016). “Solution-Based Single-Molecule FRET Studies of K<sup>+</sup> Channel Gating in a Lipid Bilayer”. In: *Biophysical Journal* 110.12, pp. 2663–2670.
- [**Sadoine 2018**] Sadoine, Mayuri (2018). “Selective dual-labeling of cell-free synthesized proteins for single-molecule FRET studies . A case study of human calmodulin .” PhD thesis. RWTH Aachen.
- [**Sadoine et al. 2017**] Sadoine, Mayuri, Michele Cerminara, Noémie Kempf, Michael Gerrits, Jörg Fitter, and Alexandros Katranidis (2017). “Selective Double-Labeling of Cell-Free Synthesized Proteins for More Accurate smFRET Studies”. In: *Analytical Chemistry* 89.21, pp. 11278–11285.
- [**Sanabria et al. 2020**] Sanabria, Hugo, Dmitro Rodnin, Katherina Hemmen, Thomas-Otavio Peulen, Suren Felekyan, Mark R Fleissner, Mykola Dimura, Felix Koberling, Ralf Kühnemuth, Wayne Hubbell, Holger Gohlke, and Claus A M Seidel (2020). “Resolving dynamics and function of transient states in single enzyme molecules”. In: *Nature Communications* 11.1, p. 1231.
- [**Sánchez-Rico et al. 2017**] Sánchez-Rico, Carolina, Lena Voith von Voithenberg, Lisa Warner, Don C Lamb, and Michael Sattler (2017). “Effects of Fluorophore Attachment

- on Protein Conformation and Dynamics Studied by spFRET and NMR Spectroscopy”. In: *Chemistry – A European Journal* 23.57, pp. 14267–14277.
- [**Schmid, Götz, and Hugel 2018**] Schmid, Sonja, Markus Götz, and Thorsten Hugel (2018). “Effects of Inhibitors on Hsp90’s Conformational Dynamics, Cochaperone and Client Interactions”. In: *ChemPhysChem* 19.14, pp. 1716–1721.
- [**Seo et al. 2014**] Seo, Moon-Hyeong, Jeongbin Park, Eunkyung Kim, Sungchul Hohng, and Hak-Sung Kim (2014). “Protein conformational dynamics dictate the binding affinity for a ligand”. In: *Nature Communications* 5, p. 3724.
- [**Shank et al. 2010**] Shank, Elizabeth A., Ciro Cecconi, Jesse W. Dill, Susan Marqusee, and Carlos Bustamante (2010). “The folding cooperativity of a protein is controlled by its chain topology”. In: *Nature* 465.7298, pp. 637–640.
- [**Sharma et al. 2008**] Sharma, Shruti, Kausik Chakraborty, Barbara K Müller, Nagore Astola, Yun-Chi Tang, Don C Lamb, Manajit Hayer-Hartl, and F Ulrich Hartl (2008). “Monitoring Protein Conformation along the Pathway of Chaperonin-Assisted Folding”. In: *Cell* 133.1, pp. 142–153.
- [**Sheppard et al. 2016**] Sheppard, Carol, Fabian Blombach, Adam Belsom, Sarah Schulz, Tina Daviter, Katherine Smollett, Emilie Mahieu, Susanne Erdmann, Philip Tinnefeld, Roger Garrett, Dina Grohmann, Juri Rappsilber, and Finn Werner (2016). “Repression of RNA polymerase by the archaeo-viral regulator ORF145/RIP”. In: *Nature Communications* 7.May, pp. 1–13.
- [**Shi et al. 2020**] Shi, Pan, Yanan Zhang, Pei Lv, Wei Fang, Shenglong Ling, Xiaoqi Guo, Dong Li, Sanling Liu, Demeng Sun, Longhua Zhang, Dongsheng Liu, Ji Shen Zheng, and Changlin Tian (2020). “A genetically encoded small-size fluorescent pair reveals allosteric conformational changes of G proteins upon its interaction with GPCRs by fluorescence lifetime based FRET”. In: *Chemical Communications* 56.51, pp. 6941–6944.
- [**Sikkema and Poolman 2020**] Sikkema, Henkrik and Bert Poolman (2020). *In Silico Method for Selecting Residue Pairs for Single-Molecule Microscopy and Spectroscopy*.
- [**Smirnova et al. 2007**] Smirnova, Irina, Vladimir Kasho, Jun-Yong Choe, Christian Altenbach, Wayne L Hubbell, and H Ronald Kaback (2007). “Sugar binding induces an outward facing conformation of LacY.” eng. In: *Proceedings of the National Academy of Sciences of the United States of America* 104.42, pp. 16504–16509.
- [**Socher and Imperiali 2008**] Socher, Elke and Barbara Imperiali (2008). “FRET-CAPTURE: A sensitive method for the detection of dynamic protein interactions”. In: *Chembiochem*. 23.1, pp. 1–7.
- [**Stelljes et al. 2018**] Stelljes, Jampa Tsedön, Daniela Weidlich, Airat Gubaev, and Dagmar Klostermeier (2018). “Gyrase containing a single C-terminal domain catalyzes negative supercoiling of DNA by decreasing the linking number in steps of two”. In: *Nucleic Acids Research* 46.13, pp. 6773–6784.

- [**Tassis et al. 2020**] Tassis, Konstantinos, Ruslan Vietrov, Matthijs De Koning, Marijn De Boer, and Giorgos Gouridis (2020). “Single-molecule studies of conformational states and dynamics in the ABC importer OpuA”. In: *bioRxiv*.
- [**Terry et al. 2018**] Terry, Daniel S, Rachel A Kolster, Matthias Quick, Michael V LeVine, George Khelashvili, Zhou Zhou, Harel Weinstein, Jonathan A Javitch, and Scott C Blanchard (2018). “A partially-open inward-facing intermediate conformation of LeuT is associated with Na<sup>+</sup> release and substrate transport”. In: *Nature Communications* 9.1, p. 230.
- [**Theissen et al. 2008**] Theissen, Bettina, Anne R Karow, Jürgen Köhler, Airat Gubaev, and Dagmar Klostermeier (2008). “Cooperative binding of ATP and RNA induces a closed conformation in a DEAD box RNA helicase”. eng. In: *Proceedings of the National Academy of Sciences of the United States of America* 105.2, pp. 548–553.
- [**Tsytlonok et al. 2019**] Tsytlonok, Maksym, Hugo Sanabria, Yuefeng Wang, Suren Felekyan, Katherina Hemmen, Aaron H Phillips, Mi-Kyung Yun, M Brett Waddell, Cheon-Gil Park, Sivaraja Vaithiyalingam, Luigi Iconaru, Stephen W White, Peter Tompa, Claus A M Seidel, and Richard Kriwacki (2019). “Dynamic anticipation by Cdk2/Cyclin A-bound p27 mediates signal integration in cell cycle regulation”. In: *Nature Communications* 10.1, p. 1676.
- [**Uphoff et al. 2010**] Uphoff, Stephan, Seamus J. Holden, Ludovic Le Reste, Javier Periz, Sebastian Van De Linde, Mike Heilemann, and Achillefs N. Kapanidis (2010). “Monitoring multiple distances within a single molecule using switchable FRET”. In: *Nature Methods* 7.10, pp. 831–836.
- [**Vera et al. 2019**] Vera, Andrés Manuel, Albert Galera-Prat, Michał Wojciechowski, Bartosz Różycki, Douglas Vinson Laurents, Mariano Carrión-Vázquez, Marek Cieplak, and Philip Tinnefeld (2019). “smFRET Detects Dual Binding Modes Modulated by Proline Isomerization in a Mega-Dalton Multi-Enzyme Complex”. In: *bioRxiv*, p. 2019.12.19.882373.
- [**Verbrugge, Lansky, and Peterman 2009**] Verbrugge, Sander, Zdenek Lansky, and Erwin J G Peterman (2009). “Kinesin’s step dissected with single-motor FRET”. eng. In: *Proceedings of the National Academy of Sciences of the United States of America* 106.42, pp. 17741–17746.
- [**Vishwakarma et al. 2018**] Vishwakarma, Rishi Kishore, Anne Marinette Cao, Zakhia Morichaud, Ayyappasamy Sudalaiyadum Perumal, Emmanuel Margeat, and Konstantin Brodolin (2018). “Single-molecule analysis reveals the mechanism of transcription activation in *M. tuberculosis*”. In: *Science Advances* 4.5, pp. 1–8.
- [**Voith von Voithenberg et al. 2016**] Voith von Voithenberg, Lena, Carolina Sánchez-Rico, Hyun-Seo Kang, Tobias Madl, Katia Zanier, Anders Barth, Lisa R Warner, Michael Sattler, and Don C Lamb (2016). “Recognition of the 3’ splice site RNA by the U2AF heterodimer involves a dynamic population shift”. In: *Proceedings of the National Academy of Sciences* 113.46, E7169 LP –E7175.

- [Vöpel et al. 2014] Vöpel, Tobias, Carola S Hengstenberg, Thomas-Otavio Peulen, Yathrib Ajaj, Claus A M Seidel, Christian Herrmann, and Johann P Klare (2014). “Triphosphate Induced Dimerization of Human Guanylate Binding Protein 1 Involves Association of the C-Terminal Helices: A Joint Double Electron–Electron Resonance and FRET Study”. In: *Biochemistry* 53.28, pp. 4590–4600.
- [Wang et al. 2016] Wang, Shizhen, Reza Vafabakhsh, William F. Borschel, Taekjip Ha, and Colin G. Nichols (2016). “Structural dynamics of potassium-channel gating revealed by single-molecule FRET”. In: *Nature Structural and Molecular Biology* 23.1, pp. 31–36.
- [Wang et al. 2014] Wang, Yong, Yanxin Liu, Hannah A DeBerg, Takeshi Nomura, Melinda Tonks Hoffman, Paul R Rohde, Klaus Schulten, Boris Martinac, and Paul R Selvin (2014). “Single molecule FRET reveals pore size and opening mechanism of a mechano-sensitive ion channel”. In: *eLife* 3. Ed. by Benoit Roux, e01834.
- [Wu, Liu, and Wang 2018] Wu, Shaowen, Jianwei Liu, and Wenning Wang (2018). “Dissecting the Conformational Dynamics-Modulated Enzyme Catalysis with Single-Molecule FRET”. In: *Journal of Physical Chemistry B* 122.23, pp. 6179–6187.
- [Wu et al. 2018] Wu, Shaowen, Dongdong Wang, Jingwei Weng, Jianwei Liu, and Wenning Wang (2018). “A revisit of the conformational dynamics of SNARE protein rYkt6”. In: *Biochemical and Biophysical Research Communications* 503.4, pp. 2841–2847.
- [Yanez Orozco et al. 2018] Yanez Orozco, Inna S., Frank A. Mindlin, Junyan Ma, Bo Wang, Brie Levesque, Matheu Spencer, Soheila Rezaei Adariani, George Hamilton, Feng Ding, Mark E. Bowen, and Hugo Sanabria (2018). “Identifying weak interdomain interactions that stabilize the supertertiary structure of the N-terminal tandem PDZ domains of PSD-95”. In: *Nature Communications* 9.1.
- [Yang et al. 2018a] Yang, Mengyi, Sijia Peng, Ruirui Sun, Jingdi Lin, Nan Wang, and Chunlai Chen (2018a). “The Conformational Dynamics of Cas9 Governing DNA Cleavage Are Revealed by Single-Molecule FRET”. In: *Cell Reports* 22.2, pp. 372–382.
- [Yang et al. 2018b] Yang, Min, Nurit Livnat Levanon, Burçin Acar, Burcu Aykac Fas, Gal Masrati, Jessica Rose, Nir Ben-Tal, Turkan Haliloglu, Yongfang Zhao, and Oded Lewinson (2018b). “Single-molecule probing of the conformational homogeneity of the ABC transporter BtuCD”. In: *Nature Chemical Biology* 14.7, pp. 715–722.
- [Ye et al. 2018] Ye, Weixiang, Markus Götz, Sirin Celiksoy, Laura Tüting, Christoph Ratzke, Janak Prasad, Julia Ricken, Seraphine V. Wegner, Rubén Ahijado-Guzmán, Thorsten Hugel, and Carsten Sönnichsen (2018). “Conformational Dynamics of a Single Protein Monitored for 24 h at Video Rate”. In: *Nano Letters* 18.10, pp. 6633–6637.
- [Yoo et al. 2020] Yoo, Janghyun, Jae-Yeol Kim, John M Louis, Irina V Gopich, and Hoi Sung Chung (2020). “Fast three-color single-molecule FRET using statistical inference”. In: *Nature Communications* 11.1, p. 3336.

- [Zander et al. 2014] Zander, Adrian, Phil Holzmeister, Daniel Klose, Philip Tinnefeld, and Dina Grohmann (2014). “Single-molecule FRET supports the two-state model of argonaute action”. In: *RNA Biology* 11.1, pp. 45–56.
- [Zhu et al. 2019] Zhu, Yongping, Lingli He, Yue Liu, Yongfang Zhao, and Xuejun C. Zhang (2019). “smFRET Probing Reveals Substrate-Dependent Conformational Dynamics of E. coli Multidrug MdfA”. In: *Biophysical Journal* 116.12, pp. 2296–2303.
- [Zhu et al. 2017] Zhu, Yongping, Lei Zhang, Xuejun C Zhang, and Yongfang Zhao (2017). “Structural dynamics of Gi $\alpha$  protein revealed by single molecule FRET”. In: *Biochemical and Biophysical Research Communications* 491.3, pp. 603–608.