Stanford

Axel Brunger

Professor of Molecular and Cellular Physiology, of Neurology, of Photon Science and, by courtesy, of Structural Biology

Molecular & Cellular Physiology

Bio

BIO

Axel Brunger received his Physics Diploma at the University of Hamburg in 1980, and his Ph.D. degree from the Technical University of Munich in 1982 working with Klaus Schulten. He held a NATO postdoctoral fellowship and subsequently became a research associate with Martin Karplus at the Department of Chemistry, Harvard University. In 1987 he joined the faculty in the Department of Molecular Biophysics and Biochemistry at Yale University. In 2000, he moved to Stanford University where he is Professor and Chair of the Department of Molecular and Cellular Physiology. He also holds an appointment as Investigator in the Howard Hughes Medical Institute. In 1995 he was awarded the Röntgen Prize for Biosciences from the University of Würzburg. In 2003, he received the Gregori Aminoff Award of the Royal Swedish Academy. In 2005 he was elected member of the National Academy of Sciences. In 2011 he received the DeLano Award of the American Society for Biochemistry and Molecular Biology, in 2014 he received the Bernard Katz Award of the Biophysical Society, and the Carl Hermann Medal of the German Crystallographic Society, and in 2016 he received the Trueblood Award of the American Crystallographic Association. In 2021 he was elected member of the American Academy of Arts & Sciences.

Early in his career, Brunger began developing tools for interpreting x-ray crystallography diffraction data. Scientists use x-ray crystallography to determine molecular structures by crystallizing the molecules and then bombarding them with x-rays. From the data produced by the diffracted x-rays, scientists can calculate a three-dimensional model of the molecule. Brunger’s powerful computational methodology revolutionized structural calculation, accelerating its automation and making protein crystallography accessible to non-experts.

Brunger also developed a major computational tool called the “free R value,” to rate a molecular model’s quality and how likely it is to be correct. The free R value has since become a standard criterion for judging agreement between a crystallographic model and its experimental x-ray diffraction data.

Since the mid-1990s, Brunger has applied his expertise in structural biology to study the molecular mechanisms of synaptic proteins that enable nerve cell communication.

In 1998, Brunger and his team showed that the corkscrew-shaped SNARE proteins assemble into quartets of one syntaxin-1, one synaptobrevin, and two SNAP-25 helices. The proteins all lie in parallel, with their heads pointing in the same direction, to promote membrane fusion.

Since moving to Stanford University in 2000, Brunger and his collaborators have developed a reconstituted system that enables them to study synaptic fusion at greater level of detail than possible in neurons. The team studied the molecular mechanism of neuronal SNAREs, complexin, and synaptotagmin, as well as other factors involved in priming and pre-synaptic plasticity.

In 2015, Brunger's team used electron cryo-microscopy to determine the structure of the supercomplex of SNAREs, the ATPase NSF, and the adapter protein #-SNAP. This subnanometer-resolution structure, along with functional studies, revealed first glimpses of the molecular mechanism of NSF-mediated SNARE complex disassembly, which allows SNARE to be recycled for the next round of synaptic vesicle fusion.

In 2017, the team determined atomic-resolution structures of the complex of the calcium sensor synaptotagmin-1, the regulator complexin, and the SNARE complex, revealing two essential interfaces that are essential for fast synchronous release of neurotransmitters. . These structures suggest an unlocking mechanism that is triggered by Ca2+binding to the synaptotagmin molecules, leading to SNARE complex zippering, and membrane fusion.

ACADEMIC APPOINTMENTS

- Professor, Molecular & Cellular Physiology
- Professor, Photon Science Directorate
- Professor, Neurology & Neurological Sciences
- Professor (By courtesy), Structural Biology
- Member, Bio-X
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- Chair, Department of Molecular and Cellular Physioogy, (2013-2017)

HONORS AND AWARDS

- Elected Member, American Academy of Arts & Sciences (2021)
- Trueblood Award, American Crystallographic Association (2016)
- Carl Hermann Medal, German Crystallographic Society (DGK) (2014)
- Katz Award, Exocytosis & Endocytosis Group, Biophysical Society (2014)
- DeLano Award, American Society for Biochemistry and Molecular Biology (2011)
- Elected Member, National Academy of Sciences (2005)
- Gregori Aminoff Prize, The Royal Swedish Academy of Sciences (2003)
- Röntgen Prize in Biosciences, University of Würzburg, Germany (1995)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Investigator, Howard Hughes Medical Institute (1987 - present)

PROFESSIONAL EDUCATION

- Diplom, University of Hamburg , Physics (1980)
- Ph.D., Technical Univ. of Munich , Biophysics (1982)

LINKS

- My Lab Site: http://atbweb.stanford.edu

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Nerve cells communicate by releasing the contents of neurotransmitter-bearing synaptic vesicles into the space between adjoining cells. This process depends on a handful of proteins that promote vesicle and nerve cell membrane fusion. The Brunger lab team uses structural and biophysical tools to capture this machinery at different stages of vesicle fusion. These structures (Figure 1) then provide the framework for further investigations, using microscopy and live neurons, into the functional and dynamic aspects of the system.

SNARE proteins, found in both nerve cell and vesicle membranes, set the stage for fusion by zipping together into a parallel, four-helix bundle that juxtaposes the two membranes. Brunger and his collaborators determined the first x-ray crystal structure of the neuronal SNARE complex, as well as the structures of other key components of the synaptic release machinery. Recently, the Brunger's team visualized the SNARE complex bound to the Ca2+-sensor synaptotagmin-1 and to the regulator complexin, revealing two interfaces that are essential for fast synchronous release of neurotransmitters. The structure of this three-part complex suggests that it is in a primed and locked state. Action-potential-driven Ca2+ ions bind to the synaptotagmin proteins, unlock the complex, and trigger membrane fusion on a sub-millisecond timescale.

After fusion has occurred, SNARE complexes are recycled by the ATPase NSF, which breaks down the SNARE complex into its individual components. The Brunger team visualized this molecular machine at near-atomic level and obtained the first glimpses of how this SNARE-recycling machine works. The SNARE complex resembles a rope with a left-handed twist, and NSF uses adapter proteins called SNAPs to grasp the "rope" in multiple places. The SNAPs wrap around the SNARE complex with a right-handed twist, suggesting that the disassembly occurs via a simple unwinding motion that frees the zipped SNARE proteins.

The Brunger team is also using structural and functional studies to explore other machinery relevant to neurotransmitter release, such as factors involved in priming and pre-synaptic plasticity. Their research may one day provide new possibilities for targeting therapeutics to control neurotransmitter release.

Teaching

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Nick Bax, Stephan Eismann, Lynnette Jackson, Anna Khalaj, Weijiang Zhou

Postdoctoral Faculty Sponsor

Sergio Couoh

Doctoral Dissertation Advisor (AC)

Nisha Gopal, Yousuf Khan, John Peters

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biophysics (Phd Program)
- Molecular and Cellular Physiology (Phd Program)
- Neurosciences (Phd Program)
- Structural Biology (Phd Program)

Publications

PUBLICATIONS

- **Sec17/Sec18 can support membrane fusion without help from completion of SNARE zippering.** *eLife*
  Song, H., Torng, T. L., Orr, A. S., Brunger, A. T., Wickner, W. T.
  2021; 10

- **Deorphanizing FAM19A proteins as pan-neurexin ligands with an unusual biosynthetic binding mechanism.** *The Journal of cell biology*
  Khalaj, A. J., Sterky, F. H., Sclip, A., Schwenk, J., Brunger, A. T., Fakler, B., Sudhof, T. C.
  2020; 219 (9)

- **Role of Aberrant Spontaneous Neurotransmission in SNAP25-Associated Encephalopathies.** *Neuron*
  Alten, B. n., Zhou, Q. n., Shin, O. H., Esquivies, L. n., Lin, P. Y., White, K. I., Sun, R. n., Chung, W. K., Monteggia, L. M., Brunger, A. T., Kavalali, E. T.
  2020

- **NSF-MEDIATED DISASSEMBLY OF ON- AND OFF PATHWAY SNARE COMPLEXES AND INHIBITION BY COMPLEXIN**
  Choi, U., Zhao, M., White, I., Brunger, A.
  WILEY.2019: 19–20

- **Synaptic vesicle fusion: today and beyond.** *Nature structural & molecular biology*
  Brose, N., Brunger, A., Cafiso, D., Chapman, E. R., Diao, J., Hughson, F. M., Jackson, M. B., Jahn, R., Lindau, M., Ma, C., Rizo, J., Shin, Y., Sollner, et al
  2019; 26 (8): 663–68

- **The pre-synaptic fusion machinery.** *Current opinion in structural biology*
  Brunger, A. T., Choi, U. B., Lai, Y., Leitz, J., White, K. I., Zhou, Q.
  2019; 54: 179–88

- **Nsf-Mediated Disassembly of On-and Off Pathway Snare Complexes and Inhibition by Complexin**
  Choi, U. B., Zhao, M., White, K., Brunger, A.
  CELL PRESS.2019: 528A

- **The pre-synaptic fusion machinery** *CURRENT OPINION IN STRUCTURAL BIOLOGY*
  Brunger, A. T., Choi, U. B., Lai, Y., Leitz, J., White, K., Zhou, Q.
  2019; 54: 179–88

- **Resolving indexing ambiguities in X-ray free-electron laser diffraction patterns** *ACTA CRYSTALLOGRAPHICA SECTION D-STRUCTURAL BIOLOGY*
  Uervirojnangkoorn, M., Lyubimov, A. Y., Zhou, Q., Weis, W. I., Brunger, A. T.
  2019; 75: 234–41

- **Resolving indexing ambiguities in X-ray free-electron laser diffraction patterns.** *Acta crystallographica. Section D, Structural biology*
  Uervirojnangkoorn, M., Lyubimov, A. Y., Zhou, Q., Weis, W. I., Brunger, A. T.
  2019; 75 (Pt 2): 234–41

- **Processing simultaneously collected MAD data from two closely spaced (90 eV) wavelengths measured at an X-ray free-electron laser**
  Mendez, D., Weis, W., Brunger, A., Wakatsuki, S., Sauter, N.
  INT UNION CRYSTALLOGRAPHY.2019: A244

- **Structures of neurexophilin-neurexin complexes reveal a regulatory mechanism of alternative splicing.** *The EMBO journal*
  Wilson, S. C., White, K. I., Zhou, Q. n., Pfuetzner, R. A., Choi, U. B., Südhof, T. C., Brunger, A. T.
  2019: e101603

- **Structural principles of SNARE complex recognition by the AAA+ protein NSF.** *eLife*
  White, K. I., Zhao, M., Choi, U. B., Pfuetzner, R. A., Brunger, A. T.
  2018; 7

- **NSF-mediated disassembly of on and off-pathway SNARE complexes and inhibition by complexin.** *eLife*
  Choi, U. B., Zhao, M., White, K. I., Pfuetzner, R. A., Esquivies, L., Zhou, Q., Brunger, A. T.
  2018; 7

- **Ca2+-Triggered Synaptic Vesicle Fusion Initiated by Release of Inhibition.** *Trends in cell biology*
  Brunger, A. T., Leitz, J. n., Zhou, Q. n., Choi, U. B., Lai, Y. n.
  2018
- **Molecular Mechanisms of Fast Neurotransmitter Release** *ANNUAL REVIEW OF BIOPHYSICS, VOL 47*
  Brunger, A. T., Choi, U. B., Lai, Y., Leitz, J., Zhou, Q., Dill, K. A.
  2018; 47: 469–97
- **The Conformational Flexibility of the Acyltransferase from the Disorazole Polyketide Synthase Is Revealed by an X-ray Free-Electron Laser Using a Room-Temperature Sample Delivery Method for Serial Crystallography** *BIOCHEMISTRY*
  Mathews, I. I., Allison, K., Robbins, T., Lyubimov, A. Y., Uervirojnangkoorn, M., Brunger, A. T., Khosla, C., DeMirci, H., McPhillips, S. E., Hollenbeck, M., Soltis, M., Cohen, A. E.
  2017; 56 (36): 4751–56
- **Morphologies of synaptic protein membrane fusion interfaces** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Gipson, P., Fukuda, Y., Danev, R., Lai, Y., Chen, D., Baumeister, W., Brunger, A. T.
  2017; 114 (34): 9110–15
- **Molecular Mechanisms of Synaptic Vesicle Priming by Munc13 and Munc18** *NEURON*
  Lai, Y., Choi, U. B., Leitz, J., Rhee, H., Lee, C., Altas, B., Zhao, M., Pfuetzner, R. A., Wang, A. L., Brose, N., Rhee, J., Brunger, A. T.
  2017; 95 (3): 591-+
- **Conformational change of syntaxin linker region induced by Munc13s initiates SNARE complex formation in synaptic exocytosis** *EMBO JOURNAL*
  Wang, S., Choi, U. B., Gong, J., Yang, X., Li, Y., Wang, A. L., Yang, X., Brunger, A. T., Ma, C.
  2017; 36 (6): 816-829
- **The primed SNARE-complexin-synaptotagmin complex for neuronal exocytosis.** *Nature*
  Zhou, Q. n., Zhou, P. n., Wang, A. L., Wu, D. n., Zhao, M. n., Südhof, T. C., Brunger, A. T.
  2017; 548 (7668): 420–25
- **Structure of photosystem II and substrate binding at room temperature** *NATURE*
  Young, I. D., Ibrahim, M., Chatterjee, R., Gul, S., Fuller, F. D., Koroidov, S., Brewster, A. S., Tran, R., Alonso-Mori, R., Kroll, T., Michels-Clark, T., Laksmono, H., Sierra, et al
  2016; 540 (7633): 453-?
- **C-terminal domain of mammalian complexin-1 localizes to highly curved membranes.** *Proceedings of the National Academy of Sciences of the United States of America*
  Gong, J., Lai, Y., Li, X., Wang, M., Leitz, J., Hu, Y., Zhang, Y., Choi, U. B., Cipriano, D., Pfuetzner, R. A., Südhof, T. C., Yang, X., Brunger, et al
  2016
- **Advances in X-ray free electron laser (XFEL) diffraction data processing applied to the crystal structure of the synaptotagmin-1 / SNARE complex.** *eLife*
  Lyubimov, A. Y., Uervirojnangkoorn, M., Zeldin, O. B., Zhou, Q., Zhao, M., Brewster, A. S., Michels-Clark, T., Holton, J. M., Sauter, N. K., Weis, W. I., Brunger, A. T.
  2016; 5
- **De novo phasing with X-ray laser reveals mosquito larvicide BinAB structure.** *Nature*
  Colletier, J., Sawaya, M. R., Gingery, M., Rodriguez, J. A., Cascio, D., Brewster, A. S., Michels-Clark, T., Hice, R. H., Coquelle, N., Boutet, S., Williams, G. J., Messerschmidt, M., Deponte, et al
  2016; 539 (7627): 43-47
- **Expression of C1ql3 in Discrete Neuronal Populations Controls Efferent Synapse Numbers and Diverse Behaviors.** *Neuron*
  Martinelli, D. C., Chew, K. S., Rohlmann, A., Lum, M. Y., Ressl, S., Hattar, S., Brunger, A. T., Missler, M., Südhof, T. C.
  2016; 91 (5): 1034-1051
- **Phosphorylation of residues inside the SNARE complex suppresses secretory vesicle fusion.** *EMBO journal*
  Malmersjö, S., Di Palma, S., Diao, J., Lai, Y., Pfuetzner, R. A., Wang, A. L., McMahon, M. A., Hayer, A., Porteus, M., Bodenmiller, B., Brunger, A. T., Meyer, T.
  2016; 35 (16): 1810-1821
- **N-terminal domain of complexin independently activates calcium-triggered fusion.** *Proceedings of the National Academy of Sciences of the United States of America*

Lai, Y., Choi, U. B., Zhang, Y., Zhao, M., Pfuetzner, R. A., Wang, A. L., Diao, J., Brunger, A. T.
2016; 113 (32): E4698-707

- **Complexin induces a conformational change at the membrane-proximal C-terminal end of the SNARE complex** *ELIFE*
  Choi, U. B., Zhao, M., Zhang, Y., Lai, Y., Brunger, A. T.
  2016; 5

- **IOTA: integration optimization, triage and analysis tool for the processing of XFEL diffraction images** *JOURNAL OF APPLIED CRYSTALLOGRAPHY*
  Lyubimov, A. Y., Uervirojnangkoorn, M., Zeldin, O. B., Brewster, A. S., Murray, T. D., Sauter, N. K., Berger, J. M., Weis, W. I., Brunger, A. T.
  2016; 49: 1057-1064

- **Recent Advances in Deciphering the Structure and Molecular Mechanism of the AAA plus ATPase N-Ethylmaleimide-Sensitive Factor (NSF)** *JOURNAL OF MOLECULAR BIOLOGY*
  Zhao, M., Brunger, A. T.
  2016; 428 (9): 1912-1926

- **Simultaneous single-molecule epigenetic imaging of DNA methylation and hydroxymethylation** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Song, C., Diao, J., Brunger, A. T., Quake, S. R.
  2016; 113 (16): 4338-4343

- **Atomic resolution experimental phase information reveals extensive disorder and bound 2-methyl-2,4-pentanediol in Ca2+-calmodulin** *ACTA CRYSTALLOGRAPHICA SECTION D-STRUCTURAL BIOLOGY*
  Lin, J., van den Bedem, H., Brunger, A. T., Wilson, M. A.
  2016; 72: 83-92

- **High-density grids for efficient data collection from multiple crystals.** *Acta crystallographica. Section D, Structural biology*
  Baxter, E. L., Aguila, L., Alonso-Mori, R., Barnes, C. O., Bonagura, C. A., Brehmer, W., Brunger, A. T., Calero, G., Caradoc-Davies, T. T., Chatterjee, R., DeGrado, W. F., Fraser, J. S., Ibrahim, et al
  2016; 72: 2-11

- **A high-transparency, micro-patternable chip for X-ray diffraction analysis of microcrystals under native growth conditions** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Murray, T. D., Lyubimov, A. Y., Ogata, C. M., Huy Vo, H., Uervirojnangkoorn, M., Brunger, A. T., Berger, J. M.
  2015; 71: 1987-1997

- **Architecture of the synaptotagmin-SNARE machinery for neuronal exocytosis.** *Nature*
  Zhou, Q., Lai, Y., Bacaj, T., Zhao, M., Lyubimov, A. Y., Uervirojnangkoorn, M., Zeldin, O. B., Brewster, A. S., Sauter, N. K., Cohen, A. E., Soltis, S. M., Alonso-Mori, R., Chollet, et al
  2015; 525 (7567): 62-67

- **ATG14 promotes membrane tethering and fusion of autophagosomes to endolysosomes.** *Nature*
  Diao, J., Liu, R., Rong, Y., Zhao, M., Zhang, J., Lai, Y., Zhou, Q., Wilz, L. M., Li, J., Vivona, S., Pfuetzner, R. A., Brunger, A. T., Zhong, et al
  2015; 520 (7548): 563-566

- **ATG14 promotes membrane tethering and fusion of autophagosomes to endolysosomes** *NATURE*
  Diao, J., Liu, R., Rong, Y., Zhao, M., Zhang, J., Lai, Y., Zhou, Q., Wilz, L. M., Li, J., Vivona, S., Pfuetzner, R. A., Brunger, A. T., Zhong, et al
  2015; 520 (7548): 563-?

- **Munc18a Does Not Alter Fusion Rates Mediated by Neuronal SNAREs, Synaptotagmin, and Complexin.** *journal of biological chemistry*
  Zhang, Y., Diao, J., Colbert, K. N., Lai, Y., Pfuetzner, R. A., Padolina, M. S., Vivona, S., Ressl, S., Cipriano, D. J., Choi, U. B., Shah, N., Weis, W. I., Brunger, et al
  2015; 290 (16): 10518-10534

- **Structures of C1q-like Proteins Reveal Unique Features among the C1q/TNF Superfamily** *STRUCTURE*
  Ressl, S., Vu, B. K., Vivona, S., Martinelli, D. C., Suedhof, T. C., Brunger, A. T.
  2015; 23 (4): 688-699

- **Capture and X-ray diffraction studies of protein microcrystals in a microfluidic trap array.** *Acta crystallographica. Section D, Biological crystallography*
  Lyubimov, A. Y., Murray, T. D., Koehl, A., Araci, I. E., Uervirojnangkoorn, M., Zeldin, O. B., Cohen, A. E., Soltis, S. M., Baxter, E. L., Brewster, A. S., Sauter, N. K., Brunger, A. T., Berger, et al

2015; 71: 928-940

- **Capture and X-ray diffraction studies of protein microcrystals in a microfluidic trap array** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Lyubimov, A. Y., Murray, T. D., Koehl, A., Araci, I. E., Uervirojnangkoorn, M., Zeldin, O. B., Cohen, A. E., Soltis, S. M., Baxter, E. L., Brewster, A. S., Sauter, N. K., Brunger, A. T., Berger, et al
  2015; 71: 928-940

- **Enabling X-ray Free Electron Laser Crystallography for Challenging Biological Systems from a Limited Number of Crystals** *ELIFE*
  Uervirojnangkoorn, M., Zeldin, O. B., Lyubimov, A. Y., Hattne, J., Brewster, A. S., Sauter, N. K., Brunger, A. T., Weis, W. I.
  2015; 4

- **Mechanistic insights into the recycling machine of the SNARE complex.** *Nature*
  Zhao, M., Wu, S., Zhou, Q., Vivona, S., Cipriano, D. J., Cheng, Y., Brunger, A. T.
  2015; 518 (7537): 61-67

- **Mechanistic insights into the recycling machine of the SNARE complex** *NATURE*
  Zhao, M., Wu, S., Zhou, Q., Vivona, S., Cipriano, D. J., Cheng, Y., Brunger, A. T.
  2015; 518 (7537): 61-?

- **Data Exploration Toolkit for serial diffraction experiments.** *Acta crystallographica. Section D, Biological crystallography*
  Zeldin, O. B., Brewster, A. S., Hattne, J., Uervirojnangkoorn, M., Lyubimov, A. Y., Zhou, Q., Zhao, M., Weis, W. I., Sauter, N. K., Brunger, A. T.
  2015; 71: 352-356

- **Data Exploration Toolkit for serial diffraction experiments** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Zeldin, O. B., Brewster, A. S., Hattne, J., Uervirojnangkoorn, M., Lyubimov, A. Y., Zhou, Q., Zhao, M., Weis, W. I., Sauter, N. K., Brunger, A. T.
  2015; 71: 352-356

- **Enabling X-ray free electron laser crystallography for challenging biological systems from a limited number of crystals.** *eLife*
  Uervirojnangkoorn, M., Zeldin, O. B., Lyubimov, A. Y., Hattne, J., Brewster, A. S., Sauter, N. K., Brunger, A. T., Weis, W. I.
  2015; 4

- **Mapping the conformational landscape of a dynamic enzyme by multitemperature and XFEL crystallography.** *eLife*
  Keedy, D. A., Kenner, L. R., Warkentin, M., Woldeyes, R. A., Hopkins, J. B., Thompson, M. C., Brewster, A. S., Van Benschoten, A. H., Baxter, E. L., Uervirojnangkoorn, M., McPhillips, S. E., Song, J., Alonso-Mori, et al
  2015; 4

- **Towards reconstitution of membrane fusion mediated by SNAREs and other synaptic proteins** *CRITICAL REVIEWS IN BIOCHEMISTRY AND MOLECULAR BIOLOGY*
  Brunger, A. T., Cipriano, D. J., Diao, J.
  2015; 50 (3): 231-241

- **Goniometer-based femtosecond crystallography with X-ray free electron lasers** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Cohen, A. E., Soltis, S. M., Gonzalez, A., Aguila, L., Alonso-Mori, R., Barnes, C. O., Baxter, E. L., Brehmer, W., Brewster, A. S., Brunger, A. T., Calero, G., Chang, J. F., Chollet, et al
  2014; 111 (48): 17122-17127

- **Direct visualization of trans-synaptic neurexin-neuroligin interactions during synapse formation.** *journal of neuroscience*
  Tsetsenis, T., Boucard, A. A., Araç, D., Brunger, A. T., Südhof, T. C.
  2014; 34 (45): 15083-15096

- **Deformable elastic network refinement for low-resolution macromolecular crystallography** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Schroeder, G. F., Levitt, M., Brunger, A. T.
  2014; 70: 2241-2255

- **Deformable elastic network refinement for low-resolution macromolecular crystallography.** *Acta crystallographica. Section D, Biological crystallography*
  Schröder, G. F., Levitt, M., Brunger, A. T.
  2014; 70: 2241-2255

- **Complexin inhibits spontaneous release and synchronizes Ca2+-triggered synaptic vesicle fusion by distinct mechanisms.** *eLife*
  Lai, Y., Diao, J., Cipriano, D. J., Zhang, Y., Pfuetzner, R. A., Padolina, M. S., Brunger, A. T.
  2014; 3
- **Complexin inhibits spontaneous release and synchronizes Ca2+-triggered synaptic vesicle fusion by distinct mechanisms.** *eLife*
  Lai, Y., Diao, J., Cipriano, D. J., Zhang, Y., Pfuetzner, R. A., Padolina, M. S., Brunger, A. T.
  2014; 3
- **Model morphing and sequence assignment after molecular replacement** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Terwilliger, T. C., Read, R. J., Adams, P. D., Brunger, A. T., Afonine, P. V., Hung, L.
  2013; 69: 2244-2250
- **Complexin-1 Enhances the On-Rate of Vesicle Docking via Simultaneous SNARE and Membrane Interactions.** *Journal of the American Chemical Society*
  Diao, J., Cipriano, D. J., Zhao, M., Zhang, Y., Shah, S., Padolina, M. S., Pfuetzner, R. A., Brunger, A. T.
  2013; 135 (41): 15274-15277
- **Disassembly of all SNARE complexes by N-ethylmaleimide-sensitive factor (NSF) is initiated by a conserved 1:1 interaction between a-soluble NSF attachment protein (SNAP) and SNARE complex.** *journal of biological chemistry*
  Vivona, S., Cipriano, D. J., O'Leary, S., Li, Y. H., Fenn, T. D., Brunger, A. T.
  2013; 288 (34): 24984-24991
- **Processive ATP-driven substrate disassembly by the N-ethylmaleimide-sensitive factor (NSF) molecular machine.** *journal of biological chemistry*
  Cipriano, D. J., Jung, J., Vivona, S., Fenn, T. D., Brunger, A. T., Bryant, Z.
  2013; 288 (32): 23436-23445
- **Ultrahigh-resolution imaging reveals formation of neuronal SNARE/Munc18 complexes in situ.** *Proceedings of the National Academy of Sciences of the United States of America*
  Pertsinidis, A., Mukherjee, K., Sharma, M., Pang, Z. P., Park, S. R., Zhang, Y., Brunger, A. T., Südhof, T. C., Chu, S.
  2013; 110 (30): E2812-20
- **Ultrahigh-resolution imaging reveals formation of neuronal SNARE/Munc18 complexes in situ** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Pertsinidis, A., Mukherjee, K., Sharma, M., Pang, Z. P., Park, S. R., Zhang, Y., Brunger, A. T., Suedhof, T. C., Chu, S.
  2013; 110 (30): E2812-E2820
- **Studying protein-reconstituted proteoliposome fusion with content indicators in vitro** *BIOESSAYS*
  Diao, J., Zhao, M., Zhang, Y., Kyoung, M., Brunger, A. T.
  2013; 35 (7): 658-665
- **Properties of native brain a-synuclein.** *Nature*
  Burré, J., Vivona, S., Diao, J., Sharma, M., Brunger, A. T., Südhof, T. C.
  2013; 498 (7453): E4-6
- **Properties of native brain alpha-synuclein** *NATURE*
  Burre, J., Vivona, S., Diao, J., Sharma, M., Brunger, A. T., Suedhof, T. C.
  2013; 498 (7453): E4-E6
- **Native alpha-synuclein induces clustering of synaptic-vesicle mimics via binding to phospholipids and synaptobrevin-2/VAMP2** *ELIFE*
  Diao, J., Burre, J., Vivona, S., Cipriano, D. J., Sharma, M., Kyoung, M., Suedhof, T. C., Brunger, A. T.
  2013; 2
- **Studying calcium-triggered vesicle fusion in a single vesicle-vesicle content and lipid-mixing system.** *Nature protocols*
  Kyoung, M., Zhang, Y., Diao, J., Chu, S., Brunger, A. T.
  2013; 8 (1): 1-16
- **Gently does it for submicron crystals.** *eLife*
  Zeldin, O. B., Brunger, A. T.
  2013; 2: e01662
- **Advances, Interactions, and Future Developments in the CNS, Phenix, and Rosetta Structural Biology Software Systems** *ANNUAL REVIEW OF BIOPHYSICS, VOL 42*

Adams, P. D., Baker, D., Brunger, A. T., Das, R., DiMaio, F., Read, R. J., Richardson, D. C., Richardson, J. S., Terwilliger, T. C.
2013; 42: 265-287

- **Studying calcium-triggered vesicle fusion in a single vesicle-vesicle content and lipid-mixing system** *NATURE PROTOCOLS*
  Kyoung, M., Zhang, Y., Diao, J., Chu, S., Brunger, A. T.
  2013; 8 (1): 1-16
- **Native a-synuclein induces clustering of synaptic-vesicle mimics via binding to phospholipids and synaptobrevin-2/VAMP2.** *eLife*
  Diao, J., Burré, J., Vivona, S., Cipriano, D. J., Sharma, M., Kyoung, M., Südhof, T. C., Brunger, A. T.
  2013; 2
- **Synaptic proteins promote calcium-triggered fast transition from point contact to full fusion** *ELIFE*
  Diao, J., Grob, P., Cipriano, D. J., Kyoung, M., Zhang, Y., Shah, S., Amie Nguyen, A., Padolina, M., Srivastava, A., Vrljic, M., Shah, A., Nogales, E., Chu, et al
  2012; 1
- **Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Terwilliger, T. C., Read, R. J., Adams, P. D., Brunger, A. T., Afonine, P. V., Grosse-Kunstleve, R. W., Hung, L.
  2012; 68: 861-870
- **Improving the accuracy of macromolecular structure refinement at 7 Å resolution.** *Structure*
  Brunger, A. T., Adams, P. D., Fromme, P., Fromme, R., Levitt, M., Schröder, G. F.
  2012; 20 (6): 957-966
- **Improving the Accuracy of Macromolecular Structure Refinement at 7 angstrom Resolution** *STRUCTURE*
  Brunger, A. T., Adams, P. D., Fromme, P., Fromme, R., Levitt, M., Schroeder, G. F.
  2012; 20 (6): 957-966
- **Application of DEN refinement and automated model building to a difficult case of molecular-replacement phasing: the structure of a putative succinyl-diaminopimelate desuccinylase from Corynebacterium glutamicum** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Brunger, A. T., Das, D., Deacon, A. M., Grant, J., Terwilliger, T. C., Read, R. J., Adams, P. D., Levitt, M., Schroeder, G. F.
  2012; 68: 391-403
- **A novel evolutionarily conserved domain of cell-adhesion GPCRs mediates autoproteolysis** *EMBO JOURNAL*
  Arac, D., Boucard, A. A., Bolliger, M. F., Nguyen, J., Soltis, S. M., Suedhof, T. C., Brunger, A. T.
  2012; 31 (6): 1364-1378
- **A grid-enabled web service for low-resolution crystal structure refinement** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  O'Donovan, D. J., Stokes-Rees, I., Nam, Y., Blacklow, S. C., Schroeder, G. F., Brunger, A. T., Sliz, P.
  2012; 68: 261-267
- **Beltless Translocation Domain of Botulinum Neurotoxin A Embodies a Minimum Ion-conductive Channel** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Fischer, A., Sambashivan, S., Brunger, A. T., Montal, M.
  2012; 287 (3): 1657-1661
- **Synaptic proteins promote calcium-triggered fast transition from point contact to full fusion.** *eLife*
  Diao, J., Grob, P., Cipriano, D. J., Kyoung, M., Zhang, Y., Shah, S., Nguyen, A., Padolina, M., Srivastava, A., Vrljic, M., Shah, A., Nogales, E., Chu, et al
  2012; 1
- **Post-Translational Modifications and Lipid Binding Profile of Insect Cell-Expressed Full-Length Mammalian Synaptotagmin 1** *BIOCHEMISTRY*
  Vrljic, M., Strop, P., Hill, R. C., Hansen, K. C., Chu, S., Brunger, A. T.
  2011; 50 (46): 9998-10012
- **A New Generation of Crystallographic Validation Tools for the Protein Data Bank** *STRUCTURE*
  Read, R. J., Adams, P. D., Arendall, W. B., Brunger, A. T., Emsley, P., Joosten, R. P., Kleywegt, G. J., Krissinel, E. B., Luetteke, T., Otwinowski, Z., Perrakis, A., Richardson, J. S., Sheffler, et al
  2011; 19 (10): 1395-1412
- **In vitro system capable of differentiating fast Ca2+-triggered content mixing from lipid exchange for mechanistic studies of neurotransmitter release** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Kyoung, M., Srivastava, A., Zhang, Y., Diao, J., Vrljic, M., Grob, P., Nogales, E., Chu, S., Brunger, A. T.

2011; 108 (29): E304-E313

- **Reintroducing Electrostatics into Macromolecular Crystallographic Refinement: Application to Neutron Crystallography and DNA Hydration** *STRUCTURE*
  Fenn, T. D., Schnieders, M. J., Mustyakimov, M., Wu, C., Langan, P., Pande, V. S., Brunger, A. T.
  2011; 19 (4): 523-533

- **Towards Structural Biology with Single Molecules** *Experimental Biology Meeting 2011*
  Brunger, A., Strop, P., Vrljic, M., Chu, S., Weninger, K.
  FEDERATION AMER SOC EXP BIOL.2011

- **Three-dimensional molecular modeling with single molecule FRET** *JOURNAL OF STRUCTURAL BIOLOGY*
  Brunger, A. T., Strop, P., Vrljic, M., Chu, S., Weninger, K. R.
  2011; 173 (3): 497-505

- **A smooth and differentiable bulk-solvent model for macromolecular diffraction** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Fenn, T. D., Schnieders, M. J., Brunger, A. T.
  2010; 66: 1024-1031

- **Iterative Structure-Based Peptide-Like Inhibitor Design against the Botulinum Neurotoxin Serotype A** *PLOS ONE*
  Zuniga, J. E., Hammill, J. T., Drory, O., Nuss, J. E., Burnett, J. C., Gussio, R., Wipf, P., Bavari, S., Brunger, A. T.
  2010; 5 (6)

- **Polarizable Atomic Multipole X-Ray Refinement: Hydration Geometry and Application to Macromolecules** *BIOPHYSICAL JOURNAL*
  Fenn, T. D., Schnieders, M. J., Brunger, A. T., Pande, V. S.
  2010; 98 (12): 2984-2992

- **The Longin SNARE VAMP7/TI-VAMP Adopts a Closed Conformation** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Vivona, S., Liu, C. W., Strop, P., Rossi, V., Filippini, F., Brunger, A. T.
  2010; 285 (23): 17965-17973

- **Neurexins Physically and Functionally Interact with GABA(A) Receptors** *NEURON*
  Zhang, C., Atasoy, D., Arac, D., Yang, X., Fucillo, M. V., Robison, A. J., Ko, J., Brunger, A. T., Sudhof, T. C.
  2010; 66 (3): 403-416

- **Super-resolution biomolecular crystallography with low-resolution data** *NATURE*
  Schroeder, G. F., Levitt, M., Brunger, A. T.
  2010; 464 (7292): 1218-U146

- **Single-molecule FRET-derived model of the synaptotagmin 1-SNARE fusion complex** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*
  Choi, U. B., Strop, P., Vrljic, M., Chu, S., Brunger, A. T., Weninger, K. R.
  2010; 17 (3): 318-U84

- **Molecular mechanism of the synaptotagmin-SNARE interaction in Ca2+-triggered vesicle fusion** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*
  Vrljic, M., Strop, P., Ernst, J. A., Sutton, R. B., Chu, S., Brunger, A. T.
  2010; 17 (3): 325-U92

- **Warren L. DeLano 21 June 1972-3 November 2009 OBITUARY** *NATURE STRUCTURAL & MOLECULAR BIOLOGY*
  Brunger, A. T., Wells, J. A.
  2009; 16 (12): 1202-1203

- **Neuroligin-1 performs neurexin-dependent and neurexin-independent functions in synapse validation** *EMBO JOURNAL*
  Ko, J., Zhang, C., Arac, D., Boucard, A. A., Brunger, A. T., Suedhof, T. C.
  2009; 28 (20): 3244-3255

- **Receptor and substrate interactions of clostridial neurotoxins** *6th International Conference on Basic and Therapeutic Aspects of Botulinum and Tetanus Toxins*
  Brunger, A. T., Rummel, A.
  PERGAMON-ELSEVIER SCIENCE LTD.2009: 550–60

- **Polarizable atomic multipole X-ray refinement: application to peptide crystals** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Schnieders, M. J., Fenn, T. D., Pande, V. S., Brunger, A. T.
  2009; 65: 952-965
- **Mechanistic insights into active site-associated polyubiquitination by the ubiquitin-conjugating enzyme Ube2g2** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Li, W., Tu, D., Li, L., Wollert, T., Ghirlando, R., Brunger, A. T., Ye, Y.
  2009; 106 (10): 3722-3727
- **SINGLE MOLECULE STUDIES OF THE SYNAPTIC VESICLE FUSION MACHINERY** *40th Annual Meeting of the American-Society-for-Neurochemistry*
  Brunger, A. T., Weninger, K., Vrljic, M., Choi, U. B., Bowen, M. A., Chu, S.
  WILEY-BLACKWELL.2009: 55–55
- **X-ray structure determination at low resolution** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Brunger, A. T., DeLaBarre, B., Davies, J. M., Weis, W. I.
  2009; 65: 128-133
- **Single-Molecule Studies of the Neuronal SNARE Fusion Machinery** *ANNUAL REVIEW OF BIOCHEMISTRY*
  Brunger, A. T., Weninger, K., Bowen, M., Chu, S.
  2009; 78: 903-928
- **A Potent Peptidomimetic Inhibitor of Botulinum Neurotoxin Serotype A Has a Very Different Conformation than SNAP-25 Substrate** *STRUCTURE*
  Zuniga, J. E., Schmidt, J. J., Fenn, T., Burnett, J. C., Arac, D., Gussio, R., Stafford, R. G., Badie, S. S., Bavari, S., Brunger, A. T.
  2008; 16 (10): 1588-1597
- **Highly specific interactions between botulinum neurotoxins and synaptic vesicle proteins** *CELLULAR AND MOLECULAR LIFE SCIENCES*
  Brunger, A. T., Jin, R., Breidenbach, M. A.
  2008; 65 (15): 2296-2306
- **Botulinum neurotoxin interactions with substrate** *6th International Conference on Basic and Therapeutic Aspects of Botulinum and Tetanus Toxins*
  Brunger, A.
  PERGAMON-ELSEVIER SCIENCE LTD.2008: 2–2
- **Improved structures of full-length p97, an AAA ATPase: Implications for mechanisms of nucleotide-dependent conformational change** *STRUCTURE*
  Davies, J. M., Brunger, A. T., Weis, W. I.
  2008; 16 (5): 715-726
- **Accessory proteins stabilize the acceptor complex for synaptobrevin, the 1 : 1 syntaxin/SNAP-25 complex** *STRUCTURE*
  Weninger, K., Bowen, M. E., Choi, U. B., Chu, S., Brunger, A. T.
  2008; 16 (2): 308-320
- **Rab and arl GTPase family members cooperate in the localization of the golgin GCC185** *CELL*
  Burguete, A. S., Fenn, T. D., Brunger, A. T., Pfeffer, S. R.
  2008; 132 (2): 286-298
- **The structure of the yeast plasma membrane SNARE complex reveals destabilizing water-filled cavities** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Strop, P., Kaiser, S. E., Vrljic, M., Brunger, A. T.
  2008; 283 (2): 1113-1119
- **Structures of neuroligin-1 and the Neuroligin-l/Neurexin-1 beta complex reveal specificprotein-protein and protein-Ca2+ interactions** *NEURON*
  Arac, D., Boucard, A. A., Ozkan, E., Strop, P., Newell, E., Sudhof, T. C., Brunger, A. T.
  2007; 56 (6): 992-1003
- **Transglutaminase 2 undergoes a large conformational change upon activation** *PLOS BIOLOGY*
  Pinkas, D. M., Strop, P., Brunger, A. T., Khosla, C.
  2007; 5 (12): 2788-2796
- **Combining efficient conformational sampling with a deformable elastic network model facilitates structure refinement at low resolution** *STRUCTURE*

Schroeder, G. F., Brunger, A. T., Levitt, M.
2007; 15 (12): 1630-1641

- **Structure and function of the yeast U-box-containing ubiquitin ligase Ufd2p** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Tu, D., Li, W., Ye, Y., Brunger, A. T.
  2007; 104 (40): 15599-15606

- **Structural and biochemical studies of botulinum neurotoxin serotype C1 light chain protease: Implications for dual substrate specificity** *BIOCHEMISTRY*
  Jin, R., Sikorra, S., Stegmann, C. M., Pich, A., Binz, T., Brunger, A. T.
  2007; 46 (37): 10685-10693

- **Botulinum neurotoxin heavy chain belt as an intramolecular chaperone for the light chain** *PLOS PATHOGENS*
  Brunger, A. T., Breidenbach, M. A., Jin, R., Fischer, A., Santos, J. S., Montal, M.
  2007; 3 (9): 1191-1194

- **Crystal structure of a hyperactive Escherichia coli glycerol kinase mutant Gly230 -> Asp obtained using microfluidic crystallization devices** *BIOCHEMISTRY*
  Anderson, M. J., DeLaBarre, B., Raghunathan, A., Palsson, B. O., Brunger, A. T., Quake, S. R.
  2007; 46 (19): 5722-5731

- **A ubiquitin ligase transfers preformed polyubiquitin chains from a conjugating enzyme to a substrate** *NATURE*
  Li, W., Tu, D., Brunger, A. T., Ye, Y.
  2007; 446 (7133): 333-337

- **Inhibition of metalloprotease botulinum serotype A from a pseudo-peptide binding mode to a small molecule that is active in primary neurons** *JOURNAL OF BIOLOGICAL CHEMISTRY*
  Burnett, J. C., Ruthel, G., Stegmann, C. M., Panchal, R. G., Nguyen, T. L., Hermone, A. R., Stafford, R. G., Lane, D. J., Kenny, T. A., McGrath, C. F., Wipf, P., Stahl, A. M., Schmidt, et al
  2007; 282 (7): 5004-5014

- **Ab initio molecular-replacement phasing for symmetric helical membrane proteins** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Strop, P., Brzustowicz, M. R., Brunger, A. T.
  2007; 63: 188-196

- **Single molecule studies of SNARE-dependent fusion** *51st Annual Meeting of the Biophysical-Society*
  Brunger, A., Chu, S., Bowen, M., Weninger, K., Vrljic, M.
  CELL PRESS.2007: 375A–375A

- **Version 1.2 of the Crystallography and NMR system** *NATURE PROTOCOLS*
  Brunger, A. T.
  2007; 2 (11): 2728-2733

- **Botulinum neurotoxin B recognizes its protein receptor with high affinity and specificity** *NATURE*
  Jin, R., Rummel, A., Binz, T., Brunger, A. T.
  2006; 444 (7122): 1092-1095

- **Structural and functional comparisons of nucleotide pyrophosphatase/phosphodiesterase and alkaline phosphatase: Implications for mechanism and evolution** *BIOCHEMISTRY*
  Zalatan, J. G., Fenn, T. D., Brunger, A. T., Herschlag, D.
  2006; 45 (32): 9788-9803

- **Ensemble molecular dynamics yields submillisecond kinetics and intermediates of membrane fusion** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Kasson, P. M., Kelley, N. W., Singhal, N., Vrljic, M., Brunger, A. T., Pande, V. S.
  2006; 103 (32): 11916-11921

- **Considerations for the refinement of low-resolution crystal structures** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  DeLaBarre, B., Brunger, A. T.
  2006; 62: 923-932

- **Conformation of the synaptobrevin transmembrane domain** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Bowen, M., Brunger, A. T.
  2006; 103 (22): 8378-8383
- **Central pore residues mediate the p97/VCP activity required for ERAD** *MOLECULAR CELL*
  DeLaBarre, B., Christianson, J. C., Kopito, R. R., Brunger, A. T.
  2006; 22 (4): 451-462
- **Towards an understanding of the molecular mechanism of neurotransmitter release** *Experimental Biology 2006 Annual Meeting*
  Brunger, A. T.
  FEDERATION AMER SOC EXP BIOL.2006: A1309–A1309
- **The structure of nucleotide pyrophosphatase/phosphodiesterase and implications for enzyme evolution in the alkaline phosphatase superfamily** *Experimental Biology 2006 Annual Meeting*
  Zalatan, J., Fenn, T., Brunger, A., Herschlag, D.
  FEDERATION AMER SOC EXP BIOL.2006: A477–A477
- **Neuronal SNAREs do not trigger fusion between synthetic membranes but do promote PEG-mediated membrane fusion** *BIOPHYSICAL JOURNAL*
  Dennison, S. M., Bowen, M. E., Brunger, A. T., Lentz, B. R.
  2006; 90 (5): 1661-1675
- **Automated crystallographic ligand building using the medial axis transform of an electron-density isosurface** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Aishima, J., Russel, D. S., Guibas, L. J., Adams, P. D., Brunger, A. T.
  2005; 61: 1354-1363
- **A hybrid machine-learning approach for segmentation of protein localization data** *BIOINFORMATICS*
  Kasson, P. M., Huppa, J. B., DAVIS, M. M., Brunger, A. T.
  2005; 21 (19): 3778-3786
- **SNARE complex between reconstituted vesicles does not trigger but does promote PEG-triggered fusion** *230th National Meeting of the American-Chemical-Society*
  Lentz, B., Dennison, M., Bowen, M. E., Brunger, A. T.
  AMER CHEMICAL SOC.2005: U1075–U1075
- **Single-molecule studies of synaptotagmin and complexin binding to the SNARE complex** *BIOPHYSICAL JOURNAL*
  Bowen, M. E., Weninger, K., Ernst, J., Chu, S., Brunger, A. T.
  2005; 89 (1): 690-702
- **X-ray scattering from unilamellar lipid vesicles** *JOURNAL OF APPLIED CRYSTALLOGRAPHY*
  Brzustowicz, M. R., Brunger, A. T.
  2005; 38: 126-131
- **Structure and function of SNARE and SNARE-interacting proteins** *QUARTERLY REVIEWS OF BIOPHYSICS*
  Brunger, A. T.
  2005; 38 (1): 1-47
- **Structure of a human A-type potassium channel accelerating factor DPPX, a member of the dipeptidyl aminopeptidase family** *49th Annual Meeting of the Biophysical-Society*
  Strop, P., Bankovich, A. J., Hansen, K. C., Garcia, K. C., Brunger, A. T.
  CELL PRESS.2005: 456A–456A
- **X-ray scattering from unilamellar lipid vesicles** *49th Annual Meeting of the Biophysical-Society*
  Brzustowicz, M. R., Brunger, A. T.
  CELL PRESS.2005: 17A–17A
- **Deformable modeling for improved calculation of molecular velocities from single-particle tracking** *IEEE Computational Systems Bioinformatics Conference*
  Kasson, P., Davis, M. M., Brunger, A. T.
  IEEE COMPUTER SOC.2005: 208–211

- **Observation of single liposome-bilayer fusion induced by SNARE proteins** *Meeting of the Division of Chemical Toxicology of the American-Chemical-Society held at the 228th National Meeting of the American-Chemical-Society*
  Weninger, K. R., Bowen, M. E., Brunger, A. T., Chu, S.
  AMER CHEMICAL SOC.2004: U207–U207
- **Effect of SNARE complex on PEG-mediated membrane fusion** *48th Annual Meeting of the Biophysical-Society*
  Dennison, S. M., Bowen, M., Brunger, A., Lentz, B. R.
  CELL PRESS.2004: 518A–518A
- **Quantitative analysis of membrane protein localization and signalling** *IEEE Computational Systems Bioinformatics Conference (CSB 2004)*
  Kasson, P. M., Huppa, J. B., DAVIS, M. M., Brunger, A. T.
  IEEE COMPUTER SOC.2004: 540–541
- **Structure of N-ethyl maleimide sensitive factor by electron cryo-microscopy at 11 angstrom resolution** *48th Annual Meeting of the Biophysical-Society*
  Furst, J., Sutton, R. B., Chen, J., Brunger, A. T., Grigorieff, N.
  CELL PRESS.2004: 78A–78A
- **Quantitative analysis of lymphocyte membrane protein redistribution from fluorescence microscopy** *International Conference on Image Processing (ICIP 2004)*
  Kasson, P. M., Huppa, J. B., DAVIS, M. M., Brunger, A. T.
  IEEE.2004: 2933–2936
- **Single molecule studies of SNARE effector binding** *48th Annual Meeting of the Biophysical-Society*
  Bowen, M. E., Chu, S., Weninger, K., Brunger, A. T.
  CELL PRESS.2004: 237A–238A
- **A structural analysis of full length VCP, a AAA protein.** *47th Annual Meeting of the Biophysical-Society*
  DeLaBarre, B., Rouiller, I., May, A. P., Weis, W. I., Wilson-Kubalek, E. M., Brunger, A. T.
  CELL PRESS.2003: 356A–356A
- **SNARE proteins alter poly(ethylene glycol) (PEG)-mediated fusion of model membranes** *47th Annual Meeting of the Biophysical-Society*
  Dennison, S. M., Bowen, M., Brunger, A., Lentz, B.
  CELL PRESS.2003: 195A–195A
- **Conformational changes of the multifunction VCP/p97 AAA ATPase during the ATPase cycle** *42nd Annual Meeting of the American-Society-for-Cell-Biology*
  Rouiller, I., DeLaBarre, B., May, A. P., Weiss, W. I., Brunger, A. T., Milligan, R. A., Wilson-Kubalek, E. M.
  AMER SOC CELL BIOLOGY.2002: 263A–263A
- **Macromolecular assemblages machines and networks - Editorial overview** *CURRENT OPINION IN STRUCTURAL BIOLOGY*
  Saibil, H. R., Brunger, A. T.
  2002; 12 (2): 215-216
- **Mutational analysis of synaptobrevin transmembrane domain oligomerization**
  Bowen, M. E., Engelman, D. M., Brunger, A. T.
  AMER SOC CELL BIOLOGY.2001: 473A–473A
- **The 1.0 angstrom crystal structure of Ca+2-bound calmodulin: An analysis of disorder and implications for functionally relevant plasticity**
  Wilson, M. A., Brunger, A. T.
  CELL PRESS.2001: 398A–398A
- **Biophysical methods - New approaches to study macromolecular structure and function - Editorial overview** *CURRENT OPINION IN STRUCTURAL BIOLOGY*
  Brunger, A. T., Laue, E. D.
  2000; 10 (5): 557-557
- **Algorithmic challenges in computational molecular biophysics** *JOURNAL OF COMPUTATIONAL PHYSICS*
  Schlick, T., Skeel, R. D., Brunger, A. T., Kale, L. V., Board, J. A., Hermans, J., Schulten, K.
  1999; 151 (1): 9-48
- **Phase improvement by multi-start simulated annealing refinement and structure-factor averaging** *JOURNAL OF APPLIED CRYSTALLOGRAPHY*

Rice, L. M., Shamoo, Y., Brunger, A. T.
1998; 31: 798-805

- **New applications of simulated annealing in crystallographic refinement** *NATO Advanced Study Institute on Direct Methods for Solving Macromolecular Structures*
  Brunger, A. T., Adams, P. D., Rice, L. M.
  SPRINGER.1998: 143–157

- **Site-directed dichroism as a method for obtaining rotational and orientational constraints for oriented polymers** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*
  Arkin, I. T., MacKenzie, K. R., Brunger, A. T.
  1997; 119 (38): 8973-8980

- **Crystallographic refinement by simulated annealing: Methods and applications** *MACROMOLECULAR CRYSTALLOGRAPHY, PT B*
  Brunger, A. T., Rice, L. M.
  1997; 277: 243-269

- **STRUCTURAL MODEL OF THE PHOSPHOLAMBAN ION-CHANNEL IN MEMBRANES** *1995 Miami Bio/Technology Winter Symposium - Advances in Gene Technology: Protein Engineering and Structural Biology*
  Arkin, I. T., Adams, P. D., LUDLAM, C. F., Aimoto, S., Rothschild, K. J., Brunger, A. T., Engelman, D. M., Smith, S. O.
  OXFORD UNIV PRESS.1995: 44–44