

CURRICULUM VITAE

February 2018

NAME: Pawel A. Penczek

PRESENT TITLE: Professor

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BIRTH DATE: February 4, 1955, Warsaw, Poland

CITIZENSHIP: U.S.

GRADUATE EDUCATION:

1979 Master of Science Degree in Medical Physics
1988 Ph.D. degree from Department of Physics, Warsaw University

ACADEMIC APPOINTMENTS:

1980 - 1989 Research Assistant, Medical Physics Laboratory
Institute of Experimental Physics, Warsaw University, Warsaw,
Poland

1989 - 2000 Research Scientist
Wadsworth Center for Laboratories and Research
Empire State Plaza, Albany, NY

1996 - 2000 Adjunct Associate Professor
Department of Computer Science
University at Albany, Albany, NY

1996 - 2000 Adjunct Associate Professor
School of Public Health, Department of Biomedical Sciences
University at Albany, Albany, NY

2000 – 2007 Associate Professor
Department of Biochemistry and Molecular Biology
The University of Texas Houston Medical School, Houston, TX

2007 - present Professor
Department of Biochemistry and Molecular Biology
The University of Texas Houston Medical School, Houston, TX

2005 - 2017 Director, UTH Structural Biology Imaging Center

2017 - present co-Director, UTH Structural Biology Imaging Center

PROFESSIONAL ORGANIZATIONS:

**SERVICE ON NATIONAL GRANT REVIEW PANELS, STUDY SECTIONS,
COMMITTEES:**

2002 Ad hoc reviewer for NIH BCB Study Section.
2002 - 2015 Reviewer for NIH Special Study Sections.
2002 - 2013 Reviewer for the US-Israel Binational Science Foundation (BSF).
2005 Reviewer for the NSF.
2004 - 2007 Permanent member of the Microscopic Imaging NIH Study Section.
2006 Reviewer for the Baylor Center for AIDS Research
2008 Reviewer for the American Heart Association
2008 Ad hoc reviewer for the NIH, Intercellular Interactions Study Section
2008 Reviewer for the NIH Instrumentation Study Section
2008-2011 Ad hoc reviewer for the NIH, Program Project Study Section
2008 Ad hoc reviewer for the NIH, Microscopic Imaging Study Section
2009 Reviewer for the American Heart Association
2009 Ad Hoc reviewer for the NIH, Advanced Instrumentation Study Section
2009 Ad Hoc reviewer of Challenge grants for the NIH
2010 Ad Hoc reviewer for the NIH
2010 Ad Hoc reviewer for the NIH, MSFC-S Study Section
2011 Ad Hoc reviewer of Eureka grants for the NIH
2011 Ad Hoc Reviewer for the NIH, EBIT Study Section
2012 Ad Hoc reviewer for the NIH, Advanced Instrumentation Study Section
2012-2013 Ad Hoc reviewer for the NIH, Fellowship Awards
2013 Reviewer for the NIH, Fellowship Awards Study Section
2014 Reviewer for the NIH: BCMB-S, Fellowship Awards Study Section, P01
2015 Reviewer for the NIH MIRA Study Section
2015 Reviewer for the NIH P41 Study Section
2016 Reviewer for the NIH P01 Study Section
2016 Reviewer for the NIH Special Emphasis Study Sections
2016 Ad hoc reviewer for the NIH BBMX Study Section
2016 Ad hoc reviewer for the NIH BCMB Study Section

2017 Ad hoc reviewer for the NIH MSFD Study Section

SERVICES ON COMMITTEES:

Curriculum Committee for term 09/01/98 - 03/31/00
School of Public Health, Department of Biomedical Sciences
University at Albany, Albany, NY.

Advisory Committee for a graduate student 2000-2005.
The University of Texas - School of Information Sciences.

Advisory Committees for graduate students 2000-2009.
GSBS, The University of Texas - Houston Medical School.

Faculty Appointments, Promotions and Tenure Committee (FAPTC) 2018.
The University of Texas - Houston Medical School.

SPONSORSHIP OF POSTDOCTORAL FELLOWS:

2000-2002	Laurent Joyeux
2001-2006	Srinivas Mullapudi
2002-2003	Kumaradhas Poomani
2002-2007	Zhong Huang
2003-2004	Ayse Tastan
2003-2006	Philip Baldwin
2003-2006	Lee Pullan
2004-2006	Grant Goodyear
2006-2009	Wei Zhang
2007-2010	Julien Bert
2010-2011	Julio Kovacs
2010-2012	Guozhi Tao
2006-2012	Zhengfan Yang
2009-2013	Jia Fang
2011-2012	Anna Romanowska-Pawliczek
2012-2013	Piotr Pawliczek
2014-2015	Ming Li
2014-2014	Tunay Durmaz
2015-present	Zhong Huang

CURRENT TEACHING RESPONSIBILITIES:

2006 - 2015 Computational methods in structural biology. Linear algebra and principal component analysis, 4h. The Baylor College of Medicine.

CURRENT GRANT SUPPORT:

Studies of the structural rearrangements associated with the dynamic spliceosome. Funding agency: NIH/GM 115598. Multi-PI, budget \$322,263, 08/01/2015 - 05/31/2019.

High resolution in single particle reconstruction. Funding agency: NIH/GM 60635. PI, 50% effort, NCO, 10/01/2017 - 09/30/2018.

PAST GRANT SUPPORT:

Transcontinental Electron Microscopy Initiative for Membrane Protein Structure. Funding agency: NIH/GM U54 R01 094598. PI, 20% effort, budget \$107,939, 09/30/2010 - 07/31/2015.

Direct Detector for a 300kV Cryoelectron Microscope. Funding agency: NIH/OD. PI: N. Waxham. Co-PI, High-end Instrumentation Grant, budget: \$596,000, 04/01/2013 - 03/31/2014.

Structure and function of CaM-kinase II. Funding agency: NIH/NS. Co-PI, 8% effort, PI: N. Waxham, budget \$234,000, 09/01/2009 - 08/31/2013.

Global optimization of refinement parameters. Funding agency: NIH/GM. Co-PI, R. Glaeser (PI, Program Project), 06/01/2003 - 05/31/2010.

3-D electron microscopy of the ATPase hrs-2. Funding agency: NIH/NS. PI, 04/01/2002-03/31/2007.

Posttranslational protein transport through the ER membrane: structure of the protein-conducting channel from yeast by cryo-electron microscopy. Funding agency: The Welch Foundation. Budget \$150,000, 06/01/2001-05/31/2004.

High Resolution Cryo-Electron Microscope. Funding agency: NIH. PI: J. Stoops. Co-PI, NCR Shared Instrument Grant, budget \$500,000, 04/01/2002-03/31/2003.

Phospholipids and Mitochondrial Function. Funding agency: NIH/GM. Co-Investigator, 10% effort, PI: W. Dowhan, budget \$234,000, 01/01/2008 - 12/31/2011.

PUBLICATIONS:

A. Abstracts

1. Leszczynski, K., Penczek, P. and Franaszczuk, P.: The reconstruction algorithm for NMR tomography. The VIIIth Int. Symposium on Nuclear Medicine, *Karlove Vary*, 1986.
2. Penczek, P., Srivastava, S. and Frank, J.: The structure of the 70S *E. Coli* ribosome in ice. Proc. XIIth Int. Congress for Electron Microscopy. San Francisco Press, San Francisco, 506-507, 1990.

3. Boisset, N., Grassucci, R., Penczek, P., Delain, E., Pochon, F., Frank, J., Lamy, J. N.: Location of thiol esters in the transformed α -macroglobulin molecule determined by monomaleimido nanogold labeling and three-dimensional cryoelectron microscopy. *Electron Microscopy 92*, Eds.: A. Rios, J. M. Arias, L. Megias-Megias, A. Lopez-Galindo, Vol. I, 405-406, University of Granada, Granada, 1992.
4. Boisset, N., Penczek, P., Pochon, F., Frank, J., Lamy, J. N.: Human α_2 -macroglobulin transformed by methylamine: three-dimensional reconstruction from randomly oriented particles observed in vitreous ice. Communication at the 33rd Annual Meeting of Soc. Fr. Microscop. Elect., Lyon, 1993. Abstract in *Biol. Cell*, 2a, 1993.
5. Marko, M., Leith, A., Penczek, P., Barnard, D., McEwen, B., Frank, J., Mannella, C.: Internal compartmentation of the rat liver mitochondrion. *Biophysical J.* **64** (abstracts), A78, 1993.
6. Lambert, O., Boisset, N., Penczek, P. and Lamy, J. N.: Three-dimensional reconstruction of *Octopus vulgaris* hemocynin from randomly oriented particles observed in vitreous ice. Communication at the 33rd Annual Meeting of Soc. Fr. Microscop. Elect., Lyon, 1993. Abstract in *Biol. Cell*, 2a 1993.
7. Boisset, N., Taveau, J. C., Penczek, P., Radermacher, M., Frank, J., Lamy, J. N.: Three-dimensional reconstruction of a hemocynin-Fab immunocomplex from randomly oriented particles. Communication at the 33rd Annual Meeting of Soc. Fr. Microscop. Elect., Lyon, 1993. Abstract in *Biol. Cell*, 2a, 1993.
8. Ramani, L. K., Penczek, P. and Frank, J.: Automatic particle picking from electron micrographs. Proc. 52nd Annual Meeting EMSA, New Orleans, 122, 1994.
9. Marko, M., Penczek, P., Feuerbach, R. and Frank, J. Use of a two-axis tilt series for electron tomography. Proc. 13th International Congress EM, Paris, 1:505-506, 1994.
10. Boisset, N., Taveau, J.-C., Penczek, P., Lamy, J., Frank, J. and Lamy, J. Three-dimensional reconstruction in vitreous ice of *Androctonus australis* hemocynin labeled with a monoclonal Fab fragment. Proc. 13th International Congress EM, Paris, 1:527-528, 1994.
11. Frank, J. Penczek, P., Grassucci, R., Srivastava, S. Modeling of the ribosome-tRNA(A)-5rRNA(P) complex based on a new cryo-EM reconstruction. Int. Ribosome Conference, 1995.
12. Penczek, P. A., Zhu, J. and Frank, J.: A simultaneous minimization method for determining orientations for $N > 3$ particle projections. ASBMB Symposium on Computational Biology: Methods in Biomolecular Imaging, Chateau Whistler Resort, British Columbia, Canada, 1996.

13. Penczek, P., Ban, N., Freeborn, B., Grassucci, R.A., Sweet, R., Moore, P.B., Steitz, T.A. and Frank, J.: Complementarity of EM and X-ray crystallographic information in the studies of ribosome function. Workshop on Structure Research of the Ribosome and its Functional Complexes. GKSS, Hamburg, Germany, 1998.
14. Penczek, P., Ban, N., Freeborn, B., Grassucci, R.A., Sweet, R., Moore, P.B., Steitz, T.A. and Frank, J.: *Haloarcula marismortui* 50S subunit - complementarity of EM and X-ray crystallographic information. International Symposium on Electron Crystallography, Granlibakken Conference Center, Lake Tahoe, USA, 1998.
15. Penczek, P.: SSNR-based resolution measure for tomography. Academy Colloquium Electron Tomography, Amsterdam, The Netherlands, 2001.
16. Gomez-Lorenzo, M.G., Spahn, Ch.M.T., Linde, L., Penczek, P., Ballesta, J.P.G., and Frank, J.: Structural studies of the *Saccharomyces cerevisiae* ribosomal stalk. The 15th International Congress on Electron Microscopy, Durban, South Africa, 2002.
17. Joyeux, L., Penczek, P.: Estimation of the Contrast Transfer Function parameters. Biophysical Society Discussions: Frontiers in Structural Cell Biology, Asilomar, CA, 2002.
18. Penczek, P.: Consistency of 3D reconstructions in single particle analysis. Biophysical Society Discussions: Frontiers in Structural Cell Biology, Asilomar, CA, 2002.
19. Penczek, P., Huang, Z.: Application of template matching technique to particle detection in electron micrographs. Multidisciplinary Workshop on Automatic Particle Selection for Cryo-Electron Microscopy. The Scripps Research Institute, La Jolla, CA, April 24-25, 2003.
20. Variance/covariance in macromolecules reconstructed from a set of their line projections. 48th Annual Meeting of the Biophysical Society, Baltimore, MD, February 14-18, 2004.
21. Penczek, P.A., Renka, R., Schomberg, H.: Gridding-based three-dimensional image reconstruction from projections with arbitrary directions. IEEE International Symposium on Biomedical Imaging, Arlington, VA, 15-18 April, 2004.
22. Baldwin, P., Penczek, P.A.: Estimating alignment errors in sets of images. IEEE International Symposium on Biomedical Imaging, Arlington, VA, 15-18 April, 2004.
23. Penczek, P.A., Asturias, F. J.: *Ab initio* cryo-EM structure determination as a validation problem. IEEE International Conference on Image Processing, Paris, 27-30 October, 2014.

24. T. V. Budkevich; E. Behrmann; J. Loerke; K. Yamamoto; A. Schmidt; P. A. Penczek; M. R. Vos; J. Bürger; T. Mielke; P. Scheerer; C. M. T. Spahn. Structural landscape of actively translating human ribosomes. 40th FEBS Congress, Berlin, Germany, 4-9 July, 2015.
25. J. von der Ecken, M. Müller, W. Lehman, D. Manstein, P.A. Penczek, Stefan Raunser. Structure of the F-Actin-Tropomyosin Complex Revealed by Electron Cryomicroscopy. Biophysical Society Meeting. Los Angeles, CA, 27 February – 2 March, 2016.

B. Refereed Original Articles in Journals

1. Grochulski, W. and Penczek, P.: The use of fast digital filters for the processing of scintigraphic pictures (in Polish). *Post. Fiz. Med.* **17**:1-14, 1982.
2. Bylina, A., Gluzinski, L., Lesniak, K., Radwanski, B. and Penczek, P.: Numerical representation of the structural pattern as a way of predict HPLC retention. *Chromatographia* **17**:132-138, 1983.
3. Leszczynski, K., Penczek, P. and Grochulski, W.: Sugeno's fuzzy measure and fuzzy clustering. *Fuzzy Sets and Systems* **15**:147-158, 1985.
4. Grochulski, W., Mitraszewski, P. and Penczek, P.: Application of combined median-averaging filters to scintigraphic image processing. *Nuklearmedizin* **24**:164-168, 1985.
5. Grochulski, W., Penczek, P. and Posielski, J.: Segmentation of the epileptic EEG by means of finite state automaton. *Int. J. Bio-Medical Computing* **18**:35-44, 1986.
6. Grochulski, W. and Penczek, P.: Syntactic analysis of the epileptic electroencephalogram. *Int. J. Bio-Medical Computing* **19**:219-234, 1986.
7. Penczek, P., Grochulski, W. and Kowalczyk, M.: Computer-aided analysis of the epileptic EEG. *Acta Physiol. Pol.* **37**:262-274, 1986.
8. Penczek, P., Grochulski, W., Grzyb, J. and Kowalczyk, M.: The use of a multichannel Kalman Filter algorithm in structural analysis of the epileptic EEG. *Int. J. Bio-Medical Computing* **20**:135-151, 1987.
9. Rump, S., Kowalczyk, M. and Penczek, P.: Application of computerized analysis of bioelectrical activity of the brain to the study of effect of anticonvulsant drugs. *Activ. Nerv. Sup. (Praha)* **29**:200-202, 1987.
10. Leszczynski, K., Franaszczuk, P. and Penczek, P.: Alternative reconstruction algorithm for NMR imaging. *Med. & Biol. Eng. & Comput.* **26**:186-192 1988.
11. Rump, S., Kowalczyk, M. and Penczek, P.: Syntactic analysis of the experimental epileptic EEG. *Pol. J. Pharmacol. Pharm.* **40**:585-592, 1988.
12. Penczek, P. and Grochulski, W.: Analysis of the multi-channel epileptiform EEG using the Markov chains formalism. *Meth. Inform. Med.* **28**:160-167, 1989.

13. Frank, J., Penczek, P., Grassucci, R. and Srivastava, S.: Three-dimensional reconstruction of the 70S *Escherichia Coli* ribosome in ice: the distribution of ribosomal RNA. *J. Cell Biol.* **115**:597-605, 1991.
14. Penczek, P., Radermacher, R. and Frank, J.: Three-dimensional reconstruction of single particles embedded in ice. *Ultramicroscopy* **40**:33-53, 1992.
15. Frank, J., Penczek, P. and Liu, W.: Alignment, classification, and 3-D reconstruction of single particles embedded in ice. *Scanning Microscopy Supplement* **6**:11-22, 1992.
16. Boisset, N., Grassucci, R., Penczek, P., Delain, E., Pochon, F., Frank, J. and Lamy, J.N.: Three-dimensional reconstruction of a complex of human α_2 -macroglobulin with monomaleimido nanogold (Au_{1.4 nm}) embedded in ice. *J. Struct. Biol.* **109**:39-45, 1992.
17. Boisset, N., Penczek, P., Pochon, F., Frank, J. and Lamy, J.N.: Three-dimensional architecture of human α_2 -macroglobulin transformed with methylamine. *J. Mol. Biol.* **232**:522-529, 1993.
18. Lambert, O., Boisset, N., Penczek, P., Lamy, J., Taveau, J.C., Frank, J., and Lamy, J.N.: Quaternary structure of *Octopus vulgaris* hemocynin. Three-dimensional reconstruction and intramolecular location of functional units *O_ve* and *O_vb*. *J. Mol. Biol.* **238**:75-87, 1994.
19. Manella, C., Marko, M., Penczek, P., Barnard, D. and Frank, J.: The internal compartmentation of rat-liver mitochondria: a tomographic study using the high-voltage transmission electron microscope. *J. Microsc. Res. Tech.* **27**:278-283, 1994.
20. Penczek, P., Grassucci, R. A. and Frank, J.: The ribosome at improved resolution: new techniques for merging and orientation refinement in 3D cryo electron microscopy of biological particles. *Ultramicroscopy* **53**:251-270, 1994.
21. Boisset, N., Penczek, P., Prochon, F., Frank, J. and Lamy, J.: Three-dimensional reconstruction of human α_2 -macroglobulin and refinement of the localization of thiol ester bonds with monomaleimido nanogold. *Annals of the New York Academy of Sciences* **737**:229-244, 1994.
22. Frank, J. and Penczek, P.: On the correction of the contrast transfer function in biological electron microscopy. *Optik* **98**:125-129, 1995.
23. Liu, Y., Penczek, P., McEwen, B. and Frank, J.: A marker-free alignment method for electron tomography. *Ultramicroscopy* **58**:393-402, 1995.
24. Lata, R.K., Penczek, P. and Frank, J.: Automatic particle picking from electron micrographs. *Ultramicroscopy* **58**:381-391, 1995.
25. Frank, J., Zhu, J., Penczek, P., Li, Y., Srivastava, S., Verschoor, A., Radermacher, M., Grassucci, R., Ramani Lata, K. and Agrawal, R.K.: A model of protein synthesis based on cryoelectron microscopy of the *E. coli* ribosome. *Nature* **376**:441-444, 1995.

26. Boisset, N., Penczek, P., Taveau, J.C., Lamy, J. Frank, J. and Lamy, J.: Three-dimensional reconstruction of *Androctonus australis* hemocynin labeled with a monoclonal Fab fragments. *J. Struct. Biol.* **115**:16-29, 1995.
27. Penczek, P., Marko, M., Buttle, K. and Frank, J.: Double-tilt electron tomography. *Ultramicroscopy* **60**:393-410, 1995.
28. Frank, J., Verschoor, A., Li, Y., Zhu, J., Lata, R.K., Radermacher, M., Penczek, P., Grassucci, R., Agrawal, R.K. and Srivastava, S.: A model of the translational apparatus based on three-dimensional reconstruction of the *Escherichia coli* ribosome. *Biochem. Cell Biol.* **73**:757-765, 1995.
29. Agrawal, R.K., Penczek, P., Grassucci, R.A., Li, Y., Leith, A., Nierhaus, K.H. and Frank, J.: Direct visualisation of A-, P-, and E-site tRNAs in *Escherichia coli* ribosome. *Science* **271**:1000-1002, 1996.
30. Frank, J., Radermacher, M., Penczek, P., Zhu, J., Li, Y., Ladjadj, M. and Leith, A.: SPIDER and WEB: processing and visualization of images in 3D electron microscopy and related fields. *J. Struct. Biol.* **116**:190-199, 1996.
31. Lata, K.R., Agrawal, R., Penczek, P., Grassucci, R., Zhu, J. and Frank, J.: Three-dimensional reconstruction of the *Escherichia coli* 30S ribosomal subunit in ice. *J. Mol. Bio.* **262**:43-52, 1996.
32. Penczek, P., Zhu, J. and Frank, J.: A common-lines based method for determining orientations for $N > 3$ particle projections simultaneously. *Ultramicroscopy* **63**:205-218, 1996.
33. Kolodziej, S.J., Penczek, P.A., Schroeter, J.P. and Stoops, J.K.: Structure-function relationships of the *Saccharomyces cerevisiae* fatty acid synthase. *J. Biol. Chem.* **45**:28422-28429, 1996.
34. Wadzack, J., Burkhardt, N., Jünemann, R., Diedrich, G., Nierhaus, K.H., Frank, J., Penczek, P., Meerwinck, W., Schmitt, M., Willumeit, R. and Stuhmann, H.B.: Direct localization of the tRNAs within the elongating ribosome by means of neutron scattering (proton-spin contrast-variation). *J. Mol. Biol.* **266**:343-356, 1997.
35. Zhu, J., Penczek, P.A., Schröder, R. and Frank, J.: Three-dimensional reconstruction with contrast transfer function correction from energy-filtered cryoelectron micrographs: procedure and application to the 70S *Escherichia coli* ribosome. *J. Struct. Biol.* **118**:197-219, 1997.
36. Kolodziej, S.J., Penczek, P.A. and Stoops, J.K.: Utility of butvar support film and methylamine tungstate stain in three-dimensional electron microscopy: agreement between stain and frozen-hydrated reconstructions. *J. Struct. Biol.* **120**:158-167, 1997.
37. Beckmann, R., Bubeck, D., Grassucci, R., Penczek, P., Verschoor, A., Blobel, G. and Frank, J.: Alignment of conduits for the nascent polypeptide chain in the ribosome-sec61 complex. *Science* **278**:2123-2126, 1997.

38. Penczek, P.A., Zhu, J., Schröder, R. and Frank, J.: Three-dimensional reconstruction with contrast transfer function compensation from defocus series. *Scanning Microscopy Supplement* **11**:1-10, 1997/2000.
39. Agrawal, R.K., Penczek, P., Grassucci, R.A. and Frank, J.: Visualization of elongation factor G on the *Escherichia coli* 70S ribosome: The mechanism of translocation. *Proc. Natl. Acad. Sci. USA* **95**:6134-6138, 1998.
40. Sharma, R.M., Penczek, P., Grassucci, R., Xin, H., Fleischer, S. and Wagenknecht, T.: Cryoelectron microscopy and image analysis of the cardiac ryanodine receptor. *J. Biol. Chem.* **273**:18429-18434, 1998.
41. Malhotra, A., Penczek, P., Agrawal, R.K., Gabashvili, I. S., Grassucci, R.A., Jünemann, R., Burkhardt, N., Nierhaus, K.H. and Frank, J.: *Escherichia coli* 70S ribosome at 15 Å resolution by cryo-electron microscopy: localization of fMet-tRNA^{Met} and fitting of L1 protein. *J. Mol. Biol.* **280**:103-116, 1998.
42. Ban, N., Freeborn, B., Nissen, P., Penczek, P., Grassucci, R.A., Sweet, R., Frank, J., Moore, P. B. and Steitz, T.A.: A 9 Å resolution X-ray crystallographic map of the large ribosomal subunit. *Cell* **93**:1105-1115, 1998.
43. Boisset, N. Penczek, P. A., Taveau, J., You, V., deHaas, F. and Lamy, J.: Overabundant single particle electron microscopy views induce a three-dimensional reconstruction artifact. *Ultramicroscopy* **74**:201-207, 1998.
44. Agrawal, R.K., Penczek, P., Grassucci, R.A., Burkhardt, N., Nierhaus, K.H. and Frank, J. Effect of buffer conditions on the position of tRNAs on the 70S ribosome as visualized by cryoelectron microscopy. *J. Biol. Chem.* **274**:8723-8729, 1999.
45. Agrawal, R.K., Heagle, A.B., Penczek, P., Grassucci, R.A. and Frank, J.: EF-G-dependent GTP hydrolysis induces translocation accompanied by large conformational changes in the 70S ribosome. *Nature Struct. Biol.* **6**:643-647, 1999.
46. Penczek, P., Ban, N., Grassucci, R.A., Agrawal, R.K. and Frank, J.: *Haloarcula marismortui* 50S subunit - complementarity of EM and X-ray crystallographic information. *J. Struct. Biol.* **128**:44-50, 1999.
47. Spahn, Ch.M.T., Grassucci, R.A., Penczek, P. and Frank, J.: Direct three-dimensional localization and positive identification of RNA helices within the ribosome by means of genetic tagging and cryo-electron microscopy. *Structure Fold Des* **7**:1567-1573, 1999.
48. Gabashvili, I.S., Agrawal, R.A., Spahn, Ch.M.T., Grassucci, R.A., Svergun, D.I., Frank, J., and Penczek, P.: Solution structure of the *E.coli* 70S ribosome at 11.5Å resolution. *Cell* **100**:537-549, 2000.
49. Frank, J., Penczek, P., Agrawal, R.K., Grassucci, R.A. and Heagle, A.B.: Three-dimensional cryoelectron microscopy of ribosomes. *Methods Enzymol.* **317**:276-91, 2000.

50. Gomez-Lorenzo, M.G., Spahn, Ch.M.T., Agrawal, R.K., Grassucci, R.A., Penczek, P., Chakraborty, K., Ballesta, J.P., Lavandera, J.L., Garcia-Bustos, J.F. and Frank, J.: Three-dimensional cryo-electron microscopy localization of EF2 in the *Saccharomyces cerevisiae* 80S ribosome at 17.5 Å resolution. *EMBO J.* **19**:2710-2718, 2000.
51. Agrawal, R.K., Spahn, Ch.M.T., Penczek, P., Grassucci, R.A., Nierhaus, K.N. and Frank, J.: Visualization of tRNA movements on the *Escherichia coli* 70S ribosome during the elongation cycle. *J. Cell Biol.* **150**:447-459, 2000.
52. Spahn, Ch.M.T., Penczek, P.A., Leith, A. and Frank, J.: A method for differentiating proteins from nucleic acids in intermediate-resolution density maps: cryo-electron microscopy defines the quaternary structure of the *Escherichia coli* 70S ribosome. *Structure* **8**:937-948, 2000.
53. Spahn, Ch.M.T., Kieft, J.S., Grassucci, R.A., Penczek, P.A., Zhou, K., Doudna, J.A. and Frank, J.: Hepatitis C virus IRES RNA induced changes in the conformation of the 40S subunit. *Science* **291**:1959-1962, 2001.
54. Spahn, Ch.M.T., Blaha, G., Agrawal, R.K., Penczek, P.A., Grassucci, R.A., Trieber, C.A., Connell, S.R., Taylor, D.E., Nierhaus, K.H. and Frank, J.: Localization of the ribosomal protection protein Tet(O) on the ribosome and the mechanism of tetracycline resistance. *Molecular Cell* **7**:1037-1045, 2001.
55. Mouche, F., Boisset, N. and Penczek, P.A.: *Lumbricus terrestris* hemoglobin - the architecture of linker chains and structural variation of the central toroid. *J. Struct. Biol.* **133**:176-192, 2001.
56. Beckmann, R., Spahn, C. M. T., Eswar, N., Helmers, J., Penczek, P.A., Sali, A., Frank, J. and Blobel, G.: Architecture of the protein-conducting channel associated with the translating 80S ribosome. *Cell* **107**:361-372, 2001.
57. Beckmann, R., Spahn, C. M. T., Eswar, N., Penczek, P.A., Sali, A., Blobel, G. and Frank, J.: Structure of the 80S ribosome from *Saccharomyces cerevisiae* - tRNA-ribosome and subunit-subunit interactions. *Cell* **107**:373-386, 2001.
58. Joyeux, L. and Penczek, P.A.: Efficiency of 2D alignment methods. *Ultramicroscopy* **92**:33-46, 2002.
59. Penczek, P.A.: Three-dimensional Spectral Signal-to-Noise Ratio for a class of reconstruction algorithms. *J. Struct. Biol.* **138**:34-46, 2002.
60. Huang, Z., Baldwin, P.R., Mullapudi, S.R. and Penczek, P.A.: Automated determination of parameters describing power spectra of micrograph images in electron microscopy. *J. Struct. Biol.* **144**:79-94, 2003.
61. Carragher, B. and Penczek, P.A.: Analytical methods and software tools for macromolecular microscopy. *J. Struct. Biol.* **144**:1-3, 2003.
62. Huang, Z. and Penczek, P.A.: Application of template matching technique to particle detection in electron micrographs. *J. Struct. Biol.* **145**:29-40, 2004.

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105. Moriya, T., Saur, M., Stabrin, M., Merino, F., Voicu, H., Huang, Z., Penczek, P.A., Raunser, S., Gatsogiannis, Ch.: High-resolution Single Particle Analysis from Electron Cryo-microscopy Images using SPHIRE. *J. Vis. Exp.*, **123**:e55448, 2017.
106. Brignole, E. J., Tsai, K. L., Chittuluru, J., Li, H., Aye, Y., Penczek, P. A., Stubbe, J., Drennan, C. L., Asturias, F.: 3.3-A resolution cryo-EM structure of human ribonucleotide reductase with substrate and allosteric regulators bound. *Elife*, **7**: e31502, 2018.

C. Chapters

1. Frank, J., Penczek, P., Grassucci, R.A., Heagle, A., Spahn, Ch.M.T. and Agrawal, R.K.: Cryo-electron microscopy of the translational apparatus: experimental evidence for the paths of mRNA, tRNA, and the polypeptide chain. In: Garret, R.A., Douthwaite, S.R., Liljas, A., Matheson, A.T., Moore, P.B. and Noller H.F. (Eds.), *The Ribosome: Structure, Antibiotics, and Cellular Interactions*. ASM Press, Washington, D.C., 45-51, 2000.

2. VanLoock M.S., Malhotra, A., Case, D.A., Agrawal, R.K., Penczek, P., Easterwood, T.R., Frank, J. and Harvey, S.C.: Functional interpretation of the cryo-electron microscopy map of the 30S ribosomal subunit from *Escherichia coli*. In: Garret, R.A., Douthwaite, S.R., Liljas, A., Matheson, A.T., Moore, P.B. and Noller H.F. (Eds.), *The Ribosome: Structure, Antibiotics, and Cellular Interactions*. ASM Press, Washington, D.C., 165-171, 2000.
3. Penczek, P.A., Frank, J.: Resolution in Electron Tomography, *in* J. Frank (Ed.), *Electron Tomography: Methods for Three-Dimensional Visualization of Structures in the Cell*, 2 edn., Springer, Berlin, 307-330, 2006.
4. Vainshtein, B.K., Penczek, P.A.: Three-dimensional reconstruction, *in* U. Shmueli (Ed.), *International Tables for Crystallography 3 edn.*, vol. B *Reciprocal Space*, 2008.
5. Penczek, P.A.: Single Particle Reconstruction, *in* U. Shmueli (Ed.), *International Tables for Crystallography 3 edn.*, vol. B *Reciprocal Space*, 2008.

D. Other Professional Communications

1. Lecturer, Workshop on Advanced Image Processing Methods in Electron Microscopy. Pittsburgh Supercomputer Center, June 1990.
2. Lecturer, Detectors in physics, medicine and environmental protection. TEMPUS workshop. Warsaw, Poland, April 1995.
3. Lecturer, Workshop on Single Particle Reconstruction from Electron Microscope Images. Pittsburgh Supercomputer Center, July 1999.
4. Lecturer, Workshop on Single Particle Reconstruction, Visualization and Animation. National Center for Macromolecular Imaging, Houston, TX, December 2002.
5. Lecturer, Workshop on Single Particle Reconstruction, Visualization and Animation. National Center for Macromolecular Imaging, Houston, TX, March 2005.
6. Lecturer, A Practical Course in Molecular Microscopy. Center for Integrative Molecular Biosciences (CIMBio), The Scripps Research Institute (TSRI), La Jolla, CA, November 2005.
7. Lecturer, Workshop on Single Particle Reconstruction and Visualization. National Center for Macromolecular Imaging, Houston, TX, March 2007.
8. Lecturer, Workshop on Advanced Topics in EM Structure Determination. Center for Integrative Molecular Biosciences (CIMBio), The Scripps Research Institute (TSRI), La Jolla, CA, November 2007.
9. Lecturer, Workshop on Single Particle Reconstruction, Map Interpretation and Visualization. National Center for Macromolecular Imaging, Houston, TX, December 2008.

10. Lecturer, Workshop on Advanced Topics in EM Structure Determination: Challenging Molecules. Center for Integrative Molecular Biosciences (CIMBio), The Scripps Research Institute (TSRI), La Jolla, CA, November 8–13, 2009.
11. Lecturer, Workshop on Single Particle Reconstruction. The University of Cape Town, Cape Town, South Africa, December 14-18, 2009.
12. Lecturer, Computational Methods in Structural Biology. Silesian University of Technology, Gliwice, Poland, May 4-7, 2010.
13. Lecturer, Workshop on Single Particle Reconstruction, Validation and Analysis. National Center for Macromolecular Imaging, Houston, TX, March 2011.
14. Lecturer, TEMIMPS Electron Crystallography Workshop, University of Washington School of Medicine, Seattle, WA, August 2011.
15. Chair of the Software Development session. Gordon Research Conference, Les Diablerets, Switzerland, May 27 – June 1, 2012.
16. Lecturer, EMBO course on Cryo-Electron Microscopy and 3D Image Processing, Heidelberg, Germany, August 26 – September 2, 2012.
17. Lecturer, EMBL course on Single Particle Image Processing with SPARX, Grenoble, France, March 30 – April 02, 2014.
18. Lecturer, Workshop on Single Particle Reconstruction, Structural Variability and Modeling. National Center for Macromolecular Imaging, Houston, TX, October 30 - November 2, 2015.
19. Introduction to single particle cryo-EM analysis with SPARX. Vollum Institute, Portland, OR, USA, December 1-3, 2015.
20. Chair of High Resolution Single Particle Analysis session. Cryo-EM 3D Image Analysis Symposium. Granlibakken, CA, USA, March 30 – April 1, 2016.
21. Organizer and Lecturer, First International SPHIRE Workshop. MPI, Dortmund, May 8-10, 2017.
22. Organizer and Lecturer, Second International SPHIRE Workshop. MPI, Bonn, September 11-12, 2017.
22. Organizer and Lecturer, Third International SPHIRE Workshop. Rice University, Houston, TX, November 6-8, 2017.

E. Invited Lectures

1. *E. coli* ribosome: alignment, classification, and merged reconstruction. Gordon Research Conference, New Hampton, NH, USA, 1991.
2. The 70S ribosome at 15Å resolution and functional states of the elongation cycle. Gordon Research Conference, Henniker, NH, USA, 1997.

3. Parallel processing - the future of single particle reconstruction with SPIDER Biomedical Image Analysis & Visualization Workshop. Pittsburgh Supercomputer Center, USA, 1998.
4. Complementarity of EM and X-ray crystallographic information in the studies of ribosome function. Workshop on Structure Research of the Ribosome and its Functional Complexes. GKSS, Hamburg, Germany, 1998.
5. *Haloarcula marismortui* 50S subunit - complementarity of EM and X-ray crystallographic information. International Symposium on Electron Crystallography, Granlibakken Conference Center, Lake Tahoe, USA, 1998.
6. Advances in high-resolution cryo-EM studies: the quaternary structure of the 70S *E. coli* ribosome revealed at 11.5Å resolution. Microscopy and Microanalysis 2000, Philadelphia, PA, 2000.
7. Single particle analysis of proteins and molecular assemblies. 7th Workshop on “Experimental strategies for Ribosomal Research“ Schloß Ringberg, Germany, 16th – 20th April 2001.
9. Variance in three-dimensional reconstructions from projections. Proc. IEEE Symposium on Biomedical Imaging, Washington DC, July 7-10, 2002, p.749-752.
9. Algebraic methods for 3-D reconstructions from projections in electron microscopy. SIAM Conference on Applied Linear Algebra, Williamsburg, VA, July 15-19, 2003.
10. Analysis of conformational heterogeneity of macromolecules in cryo-electron microscopy. 21st Annual Houston Conference on Biomedical Engineering Research, Houston, TX, February 12-13, 2004.
11. Single particle analysis of symmetrical macromolecular assemblies. Charité-Universitäts-medizin Berlin, Germany, June 2004.
12. Philtering improves alignment in cryo-EM. Gordon Research Conference, New London, NH, USA, 2005.
13. Cryo-electron microscopy: prospect and challenges. Midwest Microscopy and Microanalysis Society Meeting, Evanston, IL, USA, March 24, 2006.
14. Determination of Resolution in Electron Tomography. Microscopy and Microanalysis, Chicago, IL, July 30, 2006.
15. Conformational Analysis of Macromolecules Analyzed by Cryo-Electron Microscopy. Proceedings Microscopy and Microanalysis, Chicago, IL, July 30, 2006, Cambridge University Press, 12(Supp 2), CD386.
16. Conformational Modes in Macromolecules Analyzed by Cryo-Electron Microscopy. 62nd Southwest Regional Meeting of The American Chemical Society, Houston, TX, October 20, 2006.

17. Molecules in Motion – towards 4D cryo-EM. Image Analysis Challenges in Molecular Microscopy, UCLA Institute for Pure and Applied Mathematics, Los Angeles, CA, January 28, 2008.
18. Molecules in Motion – towards 4D cryo-EM. Gordon Research Conference. II Ciocco, Italy, 2008.
19. Analysis of conformational variability of macromolecules in cryo-electron microscopy. Keynote address at the 47th Conference of the Microscopy Society of Southern Africa. Durban, South Africa, 2009.
20. Stability and reproducibility as standards for objective 2D alignment and clustering. Gordon Research Conference. Colby-Sawyer College, New London, NH, USA, 2011.
21. Visualization of macromolecular variability by cryo-EM. 6th International Conference on Structural Analysis of Supramolecular Assemblies by Hybrid Methods. Granlibakken, CA, USA, March 14-18, 2012.
22. Visualization of conformational states of the ribosome by cryo-electron microscopy. 28th Southern Biomedical Engineering Conference. Houston, TX, USA, May 5, 2012.
23. Resampling-based Assessment of Variability in 3D Reconstructions of Biological Molecules. SIAM Conference on Imaging Science. Philadelphia, PA, USA, May 20-22, 2012.
24. Geometrical Consistency in Processing of Helical Filaments. Workshop on Advanced Topics in EM Structure Determination: Optimization and Validation. La Jolla, CA, USA, November 11–16, 2012.
25. *Ab initio* cryo-EM structure determination as a validation problem. NRAMM Workshop on Advanced Topics in EM Structure Determination. La Jolla, CA, USA, November 10–14, 2014.
26. Identification of reproducible 3D structures in heterogeneous cryo-EM data sets. Cryo-EM 3D Image Analysis Symposium. Granlibakken, CA, USA, March 30 – April 1, 2016.
27. Cryo-EM structure determination as a validation problem. Max-Planck Institute workshop. Ringberg, Germany, October 10, 2016.
28. SPHIRE – a new single particle cryo-EM computational environment. Third Coast Workshop on Biological Cryo-EM. The University of Chicago. March 3, 2017.
29. Analysis of structural heterogeneity in SPHIRE. 6th International caesar conference OVERCOMING BARRIERS – Atomic Resolution and Beyond: Advances in Molecular Electron Microscopy. Max Planck Society, Bonn, Germany. September 12 -15, 2017.