QIANG GUO

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Date of birth: 07.10.1986

1) EDUCATION

2009.09-2014.07， Ph.D., School of Life Sciences, Tsinghua University；
2005.09-2009.07， B.S., School of Life Sciences, Lanzhou University.

2) PROFESSIONAL APPOINTMENT

2020.08-Present, Assistant Professor, School of Life Sciences, Peking University, Beijing, China；
2020.08-Present, Investigator, Peking-Tsinghua Center for Life Sciences, Peking University, Beijing, China；
2014.09-2020.07, Postdoc Research fellow, Max Planck Institute of Biochemistry, Martinsried, Germany.

3) HONORS AND AWARDS

2024, The Beijing Natural Science Fund for Distinguished Young Scholars;
2021, Bayer Investigator;
2020, Yi-Fang Scholar；
2015, EMBO Long Term Fellowship；
2015, Humboldt Fellowship.

4) SERVICES AND PROFESSIONAL ACTIVITIES

Committee Member of Cryo-Electron Microscopy Subsociety, Biophysical Society of China；
Committee Member of Cytogenetics Subsociety, Genetics Society of China;
Co-chair/Organizer of The Westlake Cryo-ET Conference, 2024;
Session Chair of The 8th National Symposium of Cryo-Electron Microscopy, 2023;
Co-chair of The 3rd PKU-Thermo Fisher in situ Structure Biology Symposium, 2023;
Session Chair of Chinese Biophysics Congress, 2021;
Co-chair of The 2nd PKU-Thermo Fisher in situ Structure Biology Symposium, 2021.

5) RESEARCH INTERESTS

We are an *in situ* Structural Biology lab, we study **Cellular Architecture**—how subcellular compartments build up a functional cell, and **Macromolecule Sociology**—what's the relationship between macromolecules and organelles.
Based on the state-of-the-art imaging techniques, our research focus:

- To capture molecular snapshots of fundamental cellular processes in their physiological context.
- To better understand the structural mechanisms of human diseases, especially aging-related degenerative diseases.
- To optimize a practical workflow for high-resolution in situ structural biology.

6) FULL LIST OF PUBLICATIONS

* co-first authors, # corresponding author

Lu, M. *, Qian, Y., Ma, L., Guo, Q. #, and Gao, N. # (2024). Molecular mechanism of the flotillin complex in membrane microdomain organization. ***bioRxiv***.

Wu, L. *, Wang, J. *, Wang, Y. *, Yang, J., Yao, Y., Huang, D., Hu, Y., Xu, X., Wang, R., Du, W., Shi, Y., Li, Q., Liu, Lu., Zhu, Y., Wang, X., Guo, Q. #, Xu, L. #, Li, P. #, and Chen, X. # (2024). CLCC1 Governs Bilayer Equilibration at the Endoplasmic Reticulum to Maintain Cellular and Systemic Lipid Homeostasis. ***bioRxiv***.

Singh, D.*, Soni, N.*, Hutchings, J.*, Echeverria, I., Shaikh, F., Duquette, M., Suslov, S., Li, Z., van Eeuwen, T., Molloy, K., Shi, Y., Wang, J., Guo, Q., Chait, B.T., Fernandez-Martinez, J., Rout, M.P.#, Sali, A.#, Villa, E.#, 2024. The molecular architecture of the nuclear basket. **Cell**.

Wang, C.*, Jiang, W.*, Leitz, J.*, Yang, K., Esquivies, L., Wang, X., Shen, X., Held, R., Adams, D.J., Basta, T., Hampton, L., Jian, R., Jiang, L., Stowell, M.H.B., Baumeister, W., Guo, Q.#, Brunger, A.T.#, (2024). Structure and topography of the synaptic V-ATPase–synaptophysin complex. ***Nature*** 631, 899-904.

Liu, J.*, Li, Z.*, Li, M.*, Du, W., Baumeister, W., Yang, J.#, and Guo, Q.# (2023). Vimentin regulates nuclear segmentation in neutrophils. ***Proceedings of the National Academy of Sciences*** 120, e2307389120.

Guo, Q.#, Baumeister, W., and Gao, N.# (2023). Atomic structures of ribosomes at work captured by in situ cryo-electron tomography. ***Science Bulletin*** 68, 2671-2673.

Wu, Y.*, Qin, C.*, Du, W.*, Guo, Z., Chen, L., and Guo, Q.# (2023). A practical multicellular sample preparation pipeline broadens the application of in situ cryo-electron tomography. ***Journal of Structural Biology*** 215, 107971.

Li, Z., Du, W., Yang, J., Lai, D.-H., Lun, Z.-R., Guo, Q.# (2023). Cryo-Electron Tomography of Toxoplasma gondii Indicates That the Conoid Fiber May Be Derived from Microtubules. ***Advanced Science*** 10, 2206595.

Saha, I., Yuste-Checa, P., Da Silva Padilha, M., Guo, Q., Körner, R., Holthusen, H., Trinkaus, V.A., Dudanova, I., Fernández-Busnadiego, R., Baumeister, W., Sanders, D.W., Gautam, S., Diamond, M.I., Hartl, F.U.#, Hipp, M.S.#, (2023). The AAA+ chaperone VCP disaggregates Tau fibrils and generates aggregate seeds in a cellular system. ***Nature Communications*** 14, 560.

Li, W.*, Lu, J.*, Xiao, K.*, Zhou, M.*, Li, Y., Zhang, X., Li, Z., Gu, L., Xu, X., Guo, Q.#, Xu, T.#, Ji, W.#, (2023). Integrated multimodality microscope for accurate and efficient target-guided cryo-lamellae preparation. ***Nature Methods*** 20, 268-275.

Jiang, W., Wagner, J., Du, W., Plitzko, J., Baumeister, W., Beck, F.#, and Guo, Q.# (2022). A transformation clustering algorithm and its application in polyribosomes structural profiling. **Nucleic Acids Research** 50, 9001-9011.

Riemenschneider, H.*, Guo, Q.*, Bader, J., Frottin, F., Farny, D., Kleinberger, G., Haass, C., Mann, M., Hartl, F.U., Baumeister, W. et al. (2022) Gel-like inclusions of C-terminal fragments of TDP-43 sequester stalled proteasomes in neurons. ***EMBO Reports***, 23, e53890

Peters, J.J., Leitz, J., Guo, Q., Beck, F., Baumeister, W. and Brunger, A.T. (2022) A feature-guided, focused 3D signal permutation method for subtomogram averaging. ***Journal of Structural Biology***, 214, 107851

Huang, B.*, Guo, Q.*, Niedermeier, M.L., Cheng, J., Engler, T., Maurer, M., Pautsch, A., Baumeister, W., Stengel, F., Kochanek, S., et al. (2021). Pathological polyQ expansion does not alter the conformation of the Huntingtin-HAP40 complex. ***Structure*** 29, 804-809.e805.

Trinkaus, V.A., Riera-Tur, I., Martínez-Sánchez, A., Bäuerlein, F.J.B., Guo, Q., Arzberger, T., Baumeister, W., Dudanova, I., Hipp, M.S., Hartl, F.U., et al. (2021). In situ architecture of neuronal α-Synuclein inclusions. ***Nature Communication***. 12, 2110.

Seefelder, M., Alva, V., Huang, B., Engler, T., Baumeister, W., Guo, Q., Fernandez-Busnadiego, R., Lupas, A.N., and Kochanek, S. (2020). The evolution of the huntingtin-associated protein 40 (HAP40) in conjunction with huntingtin. ***BMC Evolutionary Biology*** 20, 162

Yasuda, S.*, Tsuchiya, H.*, Kaiho, A.*, Guo, Q., Ikeuchi, K., Endo, A., Arai, N., Ohtake, F., Murata, S., Inada, T., et al. (2020). Stress- and ubiquitylation-dependent phase separation of the proteasome. ***Nature*** 578, 296–300.

Guo, Q.*, Bin, H.*, Cheng, J., Seefelder, M., Engler, T., Pfeifer, G., Oeckl, P., Otto, M., Moser, F., Maurer, M., Pautsch, A., Baumeister, W.#, Fernandez-Busnadiego, R.#, Kochanek, S.# (2018). The cryo-electron microscopy structure of huntingtin. ***Nature*** 555, 117–120.

Guo, Q., Lehmer, C., Martinez-Sanchez, A., Rudack, T., Beck, F., Hartmann, H., Hipp, M.S., Hartl, F.U., Edbauer, D.#, Baumeister, W.#, Fernandez-Busnadiego, R#. (2018) In Situ Structure of Neuronal C9orf72 Poly-GA Aggregates Reveals Proteasome Recruitment. ***Cell*** 172, 696-705.e612.

Zhao, Y., Zeng, X., Guo, Q., and Xu, M. (2018). An integration of fast alignment and maximum-likelihood methods for electron subtomogram averaging and classification. ***Bioinformatics*** 34, i227-i236.

Li, Z., Guo, Q., Zheng, L., Ji, Y., Xie, Y.T., Lai, D.H., Lun, Z.R., Suo, X., and Gao, N. (2017). Cryo-EM structures of the 80S ribosomes from human parasites Trichomonas vaginalis and Toxoplasma gondii. ***Cell Research*** 27, 1275-1288.

Mi, N., Chen, Y., Wang, S., Chen, M., Zhao, M., Yang, G., Ma, M., Su, Q., Luo, S., Shi, J., Xu, J., Guo, Q., et al. (2015). CapZ regulates autophagosomal membrane shaping by promoting actin assembly inside the isolation membrane. ***Nature Cell Biology*** 17, 1112-1123.

Feng, B., Mandava, CS., Guo, Q., Wang, J., Cao, W., et al. (2014) Structural and Functional Insights into the Mode of Action of a Universally Conserved Obg GTPase. ***PLoS Biology*** 12(5): e1001866.

Yang, Z.*, Guo, Q.*, Goto, S., Chen, Y., Li, N., Muto, A., Himeno, H., Deng, H., Lei, J.#, and Gao, N.# (2014). Characterization of the in vivo 30S ribosomal assembly intermediates reveals essential role of S5 and location of unprocessed ends of the 17S rRNA. ***Protein Cell*** 5, 394-407.

Li, N., Chen, Y., Guo, Q., Zhang, Y., Yuan, Y., Ma, C., Deng, H., Lei, J.#, and Gao, N.# (2013). Cryo-EM structures of the late-stage assembly intermediates of the bacterial 50S ribosomal subunit. ***Nucleic Acids Research*** 41, 7073-7083.

Guo, Q.*, Goto, S.*, Chen, Y.*, Feng, B., Xu, Y., Muto, A., Himeno, H., Deng, H., Lei, J., and Gao, N. (2013). Dissecting the in vivo assembly of the 30S ribosomal subunit reveals the role of RimM and general features of the assembly process. ***Nucleic Acids Research*** 41, 2609-2620.

Huang, W.*, Choi, W.*, Hu, W., Mi, N., Guo, Q., Ma, M., Liu, M., Tian, Y., Lu, P., Wang, F.L., et al. (2012). Crystal structure and biochemical analyses reveal Beclin 1 as a novel membrane binding protein. ***Cell Research*** 22, 473-489.

Guo, Q.*, Yuan, Y.*, Xu, Y., Feng, B., Liu, L., Chen, K., Sun, M., Yang, Z., Lei, J.#, and Gao, N.# (2011). Structural basis for the function of a small GTPase RsgA on the 30S ribosomal subunit maturation revealed by cryoelectron microscopy. ***Proceedings of the National Academy of Sciences*** 08, 13100-13105.